

# R Reference Card

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## Help and basics

Most R functions have online documentation.

**help(topic)** documentation on *topic*

**?topic** id.

**help.search("topic")** search the help system

**apropos("topic")** the names of all objects in the search list matching the regular expression "topic"

**help.start()** start the HTML version of help

**str(a)** display the internal \*str\*ucture of an R object

**summary(a)** gives a "summary" of *a*, usually a statistical summary but it is *generic* meaning it has different operations for different classes of *a*

**ls()** show objects in the search path; specify *pat*="pat" to search on a pattern

**ls.str()** str() for each variable in the search path

**dir()** show files in the current directory

**methods(a)** shows S3 methods of *a*

**methods(class=class(a))** lists all the methods to handle objects of class *a*

**options(...)** set or examine many global options; common ones: width, digits, error

**library(x)** load add-on packages; **library(help=x)** lists datasets and functions in package *x*.

**attach(x)** database *x* to the R search path; *x* can be a list, data frame, or R data file created with **save**. Use **search()** to show the search path.

**detach(x)** *x* from the R search path; *x* can be a name or character string of an object previously attached or a package.

## Input and output

**load()** load the datasets written with **save**

**data(x)** loads specified data sets

**read.table(file)** reads a file in table format and creates a data frame from it; the default separator *sep*=" " is any whitespace; use *header*=TRUE to read the first line as a header of column names; use *as.is*=TRUE to prevent character vectors from being converted to factors; use *comment.char*=" " to prevent "#" from being interpreted as a comment; use *skip*=*n* to skip *n* lines before reading data; see the help for options on row naming, NA treatment, and others

**read.csv("filename",header=TRUE)** id. but with defaults set for reading comma-delimited files

**read.delim("filename",header=TRUE)** id. but with defaults set for reading tab-delimited files

**read.fwf(file,widths,header=FALSE,sep=" ",as.is=FALSE)** read a table of fixed width formatted data into a 'data.frame'; *widths* is an integer vector, giving the widths of the fixed-width fields

**save(file,...)** saves the specified objects (...) in the XDR platform-independent binary format

**save.image(file)** saves all objects

**cat(..., file="", sep=" ")** prints the arguments after coercing to character; *sep* is the character separator between arguments

**print(a, ...)** prints its arguments; *generic*, meaning it can have different methods for different objects

**format(x,...)** format an R object for pretty printing

**write.table(x,file="",row.names=TRUE,col.names=TRUE, sep=" ")** prints *x* after converting to a data frame; if *quote* is TRUE, character or factor columns are surrounded by quotes (""); *sep* is the field separator; *eol* is the end-of-line separator; *na* is the string for missing values; use *col.names*=NA to add a blank column header to get the column headers aligned correctly for spreadsheet input

**sink(file)** output to file, until **sink()**

Most of the I/O functions have a file argument. This can often be a character string naming a file or a connection. *file*="" means the standard input or output. Connections can include files, pipes, zipped files, and R variables.

On windows, the file connection can also be used with *description* = "clipboard". To read a table copied from Excel, use

```
x <- read.delim("clipboard")
```

To write a table to the clipboard for Excel, use

```
write.table(x,"clipboard",sep="\t",col.names=NA)
```

For database interaction, see packages RODBC, DBI, RMySQL, RPgSQL, and ROracle. See packages XML, hdf5, netCDF for reading other file formats.

## Data creation

**c(...)** generic function to combine arguments with the default forming a vector; with *recursive*=TRUE descends through lists combining all elements into one vector

**from:to** generates a sequence; ":" has operator priority; 1:4 + 1 is "2,3,4,5"

**seq(from,to)** generates a sequence by= specifies increment; length= specifies desired length

**seq(along=x)** generates 1, 2, ..., length(x); useful for for loops

**rep(x,times)** replicate *x* times; use *each*= to repeat "each" element of *x* each times; **rep(c(1,2,3),2)** is 1 2 3 1 2 3; **rep(c(1,2,3),each=2)** is 1 1 2 2 3 3

**data.frame(...)** create a data frame of the named or unnamed arguments; **data.frame(v=1:4,ch=c("a","B","c","d"),n=10)**; shorter vectors are recycled to the length of the longest

**list(...)** create a list of the named or unnamed arguments; **list(a=c(1,2),b="hi",c=3i)**;

**array(x,dim=)** array with data *x*; specify dimensions like **dim=c(3,4,2)**; elements of *x* recycle if *x* is not long enough

**matrix(x,nrow=,ncol=)** matrix; elements of *x* recycle

**factor(x,levels=)** encodes a vector *x* as a factor

**gl(n,k,length=n\*k,labels=1:n)** generate levels (factors) by specifying the pattern of their levels; *k* is the number of levels, and *n* is the number of replications

**expand.grid()** a data frame from all combinations of the supplied vectors or factors

**rbind(...)** combine arguments by rows for matrices, data frames, and others

**cbind(...)** id. by columns

## Slicing and extracting data

Indexing lists

**x[n]** list with elements *n*

**x[[n]]** *n*<sup>th</sup> element of the list

**x[["name"]]** element of the list named "name"

**x\$name** id.

Indexing vectors

**x[n]** *n*<sup>th</sup> element

**x[-n]** all *but* the *n*<sup>th</sup> element

**x[1:n]** first *n* elements

**x[-(1:n)]** elements from *n*+1 to the end

**x[c(1,4,2)]** specific elements

**x["name"]** element named "name"

**x[x > 3]** all elements greater than 3

**x[x > 3 & x < 5]** all elements between 3 and 5

**x[x %in% c("a","and","the")]** elements in the given set

Indexing matrices

**x[i,j]** element at row *i*, column *j*

**x[i,]** row *i*

**x[,j]** column *j*

**x[,c(1,3)]** columns 1 and 3

**x["name",]** row named "name"

Indexing data frames (matrix indexing plus the following)

**x[["name"]]** column named "name"

**x\$name** id.

## Variable conversion

**as.array(x), as.data.frame(x), as.numeric(x), as.logical(x), as.complex(x), as.character(x), ...** convert type; for a complete list, use **methods(as)**

## Variable information

**is.na(x), is.null(x), is.array(x), is.data.frame(x), is.numeric(x), is.complex(x), is.character(x), ...** test for type; for a complete list, use **methods(is)**

**length(x)** number of elements in *x*

**dim(x)** Retrieve or set the dimension of an object; **dim(x) <- c(3,2)**

**dimnames(x)** Retrieve or set the dimension names of an object

**nrow(x)** number of rows; **NROW(x)** is the same but treats a vector as a one-row matrix

**ncol(x)** and **NCOL(x)** id. for columns

**class(x)** get or set the class of *x*; **class(x) <- "myclass"**

**unclass(x)** remove the class attribute of *x*

**attr(x,which)** get or set the attribute *which* of *x*

**attributes(obj)** get or set the list of attributes of *obj*

## Data selection and manipulation

**which.max(x)** returns the index of the greatest element of *x*

**which.min(x)** returns the index of the smallest element of *x*

**rev(x)** reverses the elements of *x*

**sort(x)** sorts the elements of *x* in increasing order; to sort in decreasing order: **rev(sort(x))**

**cut(x,breaks)** divides *x* into intervals (factors); *breaks* is the number of cut intervals or a vector of cut points

**match(x, y)** returns a vector of the same length than *x* with the elements of *x* which are in *y* (NA otherwise)

**which(x == a)** returns a vector of the indices of *x* if the comparison operation is true (TRUE), in this example the values of *i* for which *x*[*i*] == *a* (the argument of this function must be a variable of mode logical)

**choose(n, k)** computes the combinations of *k* events among *n* repetitions =  $n! / [(n - k)!k!]$

**na.omit(x)** suppresses the observations with missing data (NA) (suppresses the corresponding line if *x* is a matrix or a data frame)

**na.fail(x)** returns an error message if *x* contains at least one NA

**unique(x)** if *x* is a vector or a data frame, returns a similar object but with the duplicate elements suppressed

**table(x)** returns a table with the numbers of the differents values of *x* (typically for integers or factors)

**subset(x, ...)** returns a selection of *x* with respect to criteria (...), typically comparisons: *x*\$V1 < 10); if *x* is a data frame, the option *select* gives the variables to be kept or dropped using a minus sign

**sample(x, size)** resample randomly and without replacement *size* elements in the vector *x*, the option *replace* = TRUE allows to resample with replacement

**prop.table(x,margin=)** table entries as fraction of marginal table

Math

**sin,cos,tan,asin,acos,atan,atan2,log,log10,exp**

**max(x)** maximum of the elements of *x*

**min(x)** minimum of the elements of *x*

**range(x)** id. then *c*(*min(x)*, *max(x)*)

**sum(x)** sum of the elements of *x*

**diff(x)** lagged and iterated differences of vector *x*

**prod(x)** product of the elements of *x*

**mean(x)** mean of the elements of *x*

**median(x)** median of the elements of *x*

**quantile(x,probs=)** sample quantiles corresponding to the given probabilities (defaults to 0,25,5,75,1)

**weighted.mean(x, w)** mean of *x* with weights *w*

**rank(x)** ranks of the elements of *x*

**var(x)** or *cov(x)* variance of the elements of *x* (calculated on *n* – 1); if *x* is a matrix or a data frame, the variance-covariance matrix is calculated

**sd(x)** standard deviation of *x*

**cor(x)** correlation matrix of *x* if it is a matrix or a data frame (1 if *x* is a vector)

**var(x, y)** or *cov(x, y)* covariance between *x* and *y*, or between the columns of *x* and those of *y* if they are matrices or data frames

**cor(x, y)** linear correlation between *x* and *y*, or correlation matrix if they are matrices or data frames

**round(x, n)** rounds the elements of *x* to *n* decimals

**log(x, base)** computes the logarithm of *x* with base *base*

**scale(x)** if *x* is a matrix, centers and scales the data; to center only use the option *scale*=FALSE, to scale only *center*=FALSE (by default *center*=TRUE, *scale*=TRUE)

**pmin(x,y,...)** a vector which *i*th element is the minimum of *x*[*i*], *y*[*i*],...

**pmax(x,y,...)** id. for the maximum

**cumsum(x)** a vector which *i*th element is the sum from *x*[1] to *x*[*i*]

**cumprod(x)** id. for the product

**cummin(x)** id. for the minimum

**cummax(x)** id. for the maximum

**union(x,y),intersect(x,y),setdiff(x,y),setequal(x,y),is.element(e1,set)** “set” functions

**Re(x)** real part of a complex number

**Im(x)** imaginary part

**Mod(x)** modulus; *abs(x)* is the same

**Arg(x)** angle in radians of the complex number

**Conj(x)** complex conjugate

**convolve(x,y)** compute the several kinds of convolutions of two sequences

**fft(x)** Fast Fourier Transform of an array

**mvfft(x)** FFT of each column of a matrix

**filter(x,filter)** applies linear filtering to a univariate time series or to each series separately of a multivariate time series

Many math functions have a logical parameter *na.rm*=FALSE to specify missing data (NA) removal.

Matrices

**t(x)** transpose

**diag(x)** diagonal

**%%** matrix multiplication

**solve(a,b)** solves a  $%% x = b$  for *x*

**solve(a)** matrix inverse of *a*

**rowsum(x)** sum of rows for a matrix-like object; **rowSums(x)** is a faster version

**colsum(x), colSums(x)** id. for columns

**rowMeans(x)** fast version of row means

**colMeans(x)** id. for columns

Advanced data processing

**apply(X,INDEX,FUN=)** a vector or array or list of values obtained by applying a function *FUN* to margins (*INDEX*) of *X*

**lapply(X,FUN)** apply *FUN* to each element of the list *X*

**tapply(X,INDEX,FUN=)** apply *FUN* to each cell of a ragged array given by *X* with indexes *INDEX*

**by(data,INDEX,FUN)** apply *FUN* to data frame *data* subsetted by *INDEX*

**ave(x,...,FUN=mean)** subsets of *x* are averaged (or other function specified by *FUN*), where each subset consist of those observations with the same factor levels

**merge(a,b)** merge two data frames by common columns or row names

**xtabs(a b,data=x)** a contingency table from cross-classifying factors

**aggregate(x,by,FUN)** splits the data frame *x* into subsets, computes summary statistics for each, and returns the result in a convenient form; *by* is a list of grouping elements, each as long as the variables in *x*

**stack(x, ...)** transform data available as separate columns in a data frame or list into a single column

**unstack(x, ...)** inverse of *stack()*

**reshape(x, ...)** 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; use (*direction*=”wide”) or (*direction*=”long”)

Strings

**paste(...)** concatenate vectors after converting to character; *sep*= is the string to separate terms (a single space is the default); *collapse*= is an optional string to separate “collapsed” results

**substr(x,start,stop)** substrings in a character vector; can also assign, as *substr(x, start, stop) <- value*

**strsplit(x,split)** split *x* according to the substring *split*

**grep(pattern,x)** searches for matches to *pattern* within *x*; see *?regex*

**gsub(pattern,replacement,x)** replacement of matches determined by regular expression matching *sub()* is the same but only replaces the first occurrence.

**tolower(x)** convert to lowercase

**toupper(x)** convert to uppercase

**match(x,table)** a vector of the positions of first matches for the elements of *x* among *table*

**x %in% table** id. but returns a logical vector

**pmatch(x,table)** partial matches for the elements of *x* among *table*

**nchar(x)** number of characters

Dates and times

The class *Date* has dates without times. *POSIXct* has dates and times, including time zones. Comparisons (e.g. >), *seq()*, and *difftime()* are useful. *Date* also allows + and –. *?DateTimeClasses* gives more information. See also package *chron*.

**as.Date(s)** and **as.POSIXct(s)** convert to the respective class; *format(dt)* converts to a string representation. The default string format is “2001-02-21”. These accept a second argument to specify a format for conversion. Some common formats are:

- %a, %A Abbreviated and full weekday name.
- %b, %B Abbreviated and full month name.
- %d Day of the month (01–31).
- %H Hours (00–23).
- %I Hours (01–12).
- %j Day of year (001–366).
- %m Month (01–12).
- %M Minute (00–59).
- %p AM/PM indicator.
- %S Second as decimal number (00–61).
- %U Week (00–53); the first Sunday as day 1 of week 1.
- %w Weekday (0–6, Sunday is 0).
- %W Week (00–53); the first Monday as day 1 of week 1.
- %y Year without century (00–99). Don’t use.
- %Y Year with century.
- %z (output only.) Offset from Greenwich; –0800 is 8 hours west of.
- %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. See *?strftime*.

Graphics devices

**x11()**, **windows()** open a graphics window

**postscript(file)** starts the graphics device driver for producing PostScript graphics; use `horizontal = FALSE`, `onefile = FALSE`, `paper = "special"` for EPS files; `family=` specifies the font (AvantGarde, Bookman, Courier, Helvetica, Helvetica-Narrow, NewCenturySchoolbook, Palatino, Times, or ComputerModern); `width=` and `height=` specifies the size of the region in inches (for `paper="special"`, these specify the paper size).

**ps.options()** set and view (if called without arguments) default values for the arguments to `postscript`

**pdf, png, jpeg, bitmap, xfig, pictex;** see ?Devices

**dev.off()** shuts down the specified (default is the current) graphics device; see also `dev.cur`, `dev.set`

Plotting

**plot(x)** plot of the values of x (on the y-axis) ordered on the x-axis

**plot(x, y)** bivariate plot of x (on the x-axis) and y (on the y-axis)

**hist(x)** histogram of the frequencies of x

**barplot(x)** histogram of the values of x; use `horiz=FALSE` for horizontal bars

**dotchart(x)** if x is a data frame, plots a Cleveland dot plot (stacked plots line-by-line and column-by-column)

**pie(x)** circular pie-chart

**boxplot(x)** “box-and-whiskers” plot

**sunflowerplot(x, y)** id. than `plot()` but the points with similar coordinates are drawn as flowers which petal number represents the number of points

**stripplot(x)** plot of the values of x on a line (an alternative to `boxplot()` for small sample sizes)

**coplot(x~y | z)** bivariate plot of x and y for each value or interval of values of z

**interaction.plot(f1, f2, y)** if f1 and f2 are factors, plots the means of y (on the y-axis) with respect to the values of f1 (on the x-axis) and of f2 (different curves); the option `fun` allows to choose the summary statistic of y (by default `fun=mean`)

**matplot(x,y)** bivariate plot of the first column of x vs. the first one of y, the second one of x vs. the second one of y, etc.

**fourfoldplot(x)** visualizes, with quarters of circles, the association between two dichotomous variables for different populations (x must be an array with `dim=c(2, 2, k)`, or a matrix with `dim=c(2, 2)` if `k=1`)

**assocplot(x)** Cohen–Friendly graph showing the deviations from independence of rows and columns in a two dimensional contingency table

**mosaicplot(x)** ‘mosaic’ graph of the residuals from a log-linear regression of a contingency table

**pairs(x)** if x is a matrix or a data frame, draws all possible bivariate plots between the columns of x

**plot.ts(x)** if x is an object of class “ts”, plot of x with respect to time, x may be multivariate but the series must have the same frequency and dates

**ts.plot(x)** id. but if x is multivariate the series may have different dates and must have the same frequency

**qqnorm(x)** quantiles of x with respect to the values expected under a normal law

**qqplot(x, y)** quantiles of y with respect to the quantiles of x

**contour(x, y, z)** contour plot (data are interpolated to draw the curves), x and y must be vectors and z must be a matrix so that `dim(z)=c(length(x), length(y))` (x and y may be omitted)

**filled.contour(x, y, z)** id. but the areas between the contours are coloured, and a legend of the colours is drawn as well

**image(x, y, z)** id. but with colours (actual data are plotted)

**persp(x, y, z)** id. but in perspective (actual data are plotted)

**stars(x)** if x is a matrix or a data frame, draws a graph with segments or a star where each row of x is represented by a star and the columns are the lengths of the segments

**symbols(x, y, ...)** draws, at the coordinates given by x and y, symbols (circles, squares, rectangles, stars, thermometres or “boxplots”) which sizes, colours ... are specified by supplementary arguments

**termplot(mod.obj)** plot of the (partial) effects of a regression model (mod.obj)

The following parameters are common to many plotting functions:

**add=FALSE** if TRUE superposes the plot on the previous one (if it exists)

**axes=TRUE** if FALSE does not draw the axes and the box

**type="p"** specifies the type of plot, "p": points, "l": lines, "b": points connected by lines, "o": id. but the lines are over the points, "h": vertical lines, "s": steps, the data are represented by the top of the vertical lines, "S": id. but the data are represented by the bottom of the vertical lines

**xlim=, ylim=** specifies the lower and upper limits of the axes, for example with `xlim=c(1, 10)` or `xlim=range(x)`

**xlab=, ylab=** annotates the axes, must be variables of mode character

**main=** main title, must be a variable of mode character

**sub=** sub-title (written in a smaller font)

Low-level plotting commands

**points(x, y)** adds points (the option `type=` can be used)

**lines(x, y)** id. but with lines

**text(x, y, labels, ...)** adds text given by labels at coordinates (x,y); a typical use is: `plot(x, y, type="n"); text(x, y, names)`

**mtext(text, side=3, line=0, ...)** adds text given by text in the margin specified by side (see `axis()` below); line specifies the line from the plotting area

**segments(x0, y0, x1, y1)** draws lines from points (x0,y0) to points (x1,y1)

**arrows(x0, y0, x1, y1, angle= 30, code=2)** id. with arrows at points (x0,y0) if code=2, at points (x1,y1) if code=1, or both if code=3; angle controls the angle from the shaft of the arrow to the edge of the arrow head

**abline(a,b)** draws a line of slope b and intercept a

**abline(h=y)** draws a horizontal line at ordinate y

**abline(v=x)** draws a vertical line at abscissa x

**abline(lm.obj)** draws the regression line given by lm.obj

**rect(x1, y1, x2, y2)** draws a rectangle which left, right, bottom, and top limits are x1, x2, y1, and y2, respectively

**polygon(x, y)** draws a polygon linking the points with coordinates given by x and y

**legend(x, y, legend)** adds the legend at the point (x,y) with the symbols given by legend

**title()** adds a title and optionally a sub-title

**axis(side)** adds an axis at the bottom (side=1), on the left (2), at the top (3), or on the right (4); `at=vect` (optional) gives the abscissa (or ordinates) where tick-marks are drawn

**box()** draw a box around the current plot

**rug(x)** draws the data x on the x-axis as small vertical lines

**locator(n, type="n", ...)** returns the coordinates (x,y) after the user has clicked n times on the plot with the mouse; also draws symbols (type="p") or lines (type="l") with respect to optional graphic parameters (...); by default nothing is drawn (type="n")

Graphical parameters

These can be set globally with **par(...)**; many can be passed as parameters to plotting commands.

**adj** controls text justification (0 left-justified, 0.5 centred, 1 right-justified)

**bg** specifies the colour of the background (ex. : `bg="red"`, `bg="blue"`, ... the list of the 657 available colours is displayed with `colors()`)

**bty** controls the type of box drawn around the plot, allowed values are: "o", "l", "7", "c", "u" ou "]" (the box looks like the corresponding character); if `bty="n"` the box is not drawn

**cex** a value controlling the size of texts and symbols with respect to the default; the following parameters have the same control for numbers on the axes, `cex.axis`, the axis labels, `cex.lab`, the title, `cex.main`, and the sub-title, `cex.sub`

**col** controls the color of symbols and lines; use color names: "red", "blue" see `colors()` or as "#RRGGBB"; see `rgb()`, `hsv()`, `gray()`, and `rainbow()`; as for cex there are: `col.axis`, `col.lab`, `col.main`, `col.sub`

**font** an integer which controls the style of text (1: normal, 2: italics, 3: bold, 4: bold italics); as for cex there are: `font.axis`, `font.lab`, `font.main`, `font.sub`

**las** an integer which controls the orientation of the axis labels (0: parallel to the axes, 1: horizontal, 2: perpendicular to the axes, 3: vertical)

**lty** controls the type of lines, can be an integer or string (1: "solid", 2: "dashed", 3: "dotted", 4: "dotdash", 5: "longdash", 6: "twodash", or a string of up to eight characters (between "0" and "9") which specifies alternatively the length, in points or pixels, of the drawn elements and the blanks, for example `lty="44"` will have the same effect than `lty=2`

**lwd** a numeric which controls the width of lines, default 1

**mar** a vector of 4 numeric values which control the space between the axes and the border of the graph of the form `c(bottom, left, top, right)`, the default values are `c(5.1, 4.1, 4.1, 2.1)`

**mfc**col a vector of the form `c(nr,nc)` which partitions the graphic window as a matrix of nr lines and nc columns, the plots are then drawn in columns

**mfrow** id. but the plots are drawn by row

**pch** controls the type of symbol, either an integer between 1 and 25, or any single character within ""

1 ○ 2 △ 3 + 4 × 5 ◇ 6 ▽ 7 ☒ 8 ✱ 9 ⊕ 10 ⊕ 11 ☒ 12 ⊕ 13 ☒ 14 ☒ 15 ■  
16 ● 17 ▲ 18 ◆ 19 ● 20 ● 21 ○ 22 □ 23 ◇ 24 △ 25 ▽ \* · . X X a a ? ?

**ps** an integer which controls the size in points of texts and symbols

**pty** a character which specifies the type of the plotting region, "s": square, "m": maximal

**tck** a value which specifies the length of tick-marks on the axes as a fraction of the smallest of the width or height of the plot; if `tck=1` a grid is drawn

**tc1** a value which specifies the length of tick-marks on the axes as a fraction of the height of a line of text (by default `tc1=-0.5`)

**xaxis**, **yaxis** style of axis interval calculation; default "r" for an extra space; "i" for no extra space

**xaxt** if `xaxt="n"` the x-axis is set but not drawn (useful in conjunction with `axis(side=1, ...)`)

**yaxt** if `yaxt="n"` the y-axis is set but not drawn (useful in conjunction with `axis(side=2, ...)`)

## Lattice (Trellis) graphics

**xyplot(y~x)** bivariate plots (with many functionalities)

**barchart(y~x)** histogram of the values of `y` with respect to those of `x`

**dotplot(y~x)** Cleveland dot plot (stacked plots line-by-line and column-by-column)

**densityplot(~x)** density functions plot

**histogram(~x)** histogram of the frequencies of `x`

**bwplot(y~x)** “box-and-whiskers” plot

**qqmath(~x)** quantiles of `x` with respect to the values expected under a theoretical distribution

**stripplot(y~x)** single dimension plot, `x` must be numeric, `y` may be a factor

**qq(y~x)** quantiles to compare two distributions, `x` must be numeric, `y` may be numeric, character, or factor but must have two ‘levels’

**splom(~x)** matrix of bivariate plots

**parallel(~x)** parallel coordinates plot

**levelplot(z~x\*y|g1\*g2)** coloured plot of the values of `z` at the coordinates given by `x` and `y` (`x`, `y` and `z` are all of the same length)

**wireframe(z~x\*y|g1\*g2)** 3d surface plot

**cloud(z~x\*y|g1\*g2)** 3d scatter plot

In the normal Lattice formula, `y ~ x|g1*g2` has combinations of optional conditioning variables `g1` and `g2` plotted on separate panels. Lattice functions take many of the same arguments as base graphics plus also `data=` the data frame for the formula variables and `subset=` for subsetting. Use `panel=` to define a custom panel function (see `apropos("panel")` and `?llines`). Lattice functions return an object of class `trellis` and have to be `print`-ed to produce the graph. Use `print(xyplot(...))` inside functions where automatic printing doesn’t work. Use `lattice.theme` and `lset` to change Lattice defaults.

## Optimization and model fitting

**optim(par, fn, method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN"))** general-purpose optimization; `par` is initial values, `fn` is function to optimize (normally minimize)

**nlm(f, p)** minimize function `f` using a Newton-type algorithm with starting values `p`

**lm(formula)** fit linear models; `formula` is typically of the form `response termA + termB + ...`; use `I(x*y) + I(x^2)` for terms made of nonlinear components

**glm(formula, family=)** fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution; `family` is a description of the error distribution and link function to be used in the model; see `?family`

**nls(formula)** nonlinear least-squares estimates of the nonlinear model parameters

**approx(x, y=)** linearly interpolate given data points; `x` can be an `xy` plotting structure

**spline(x, y=)** cubic spline interpolation

**loess(formula)** fit a polynomial surface using local fitting

Many of the formula-based modeling functions have several common arguments: `data=` the data frame for the formula variables, `subset=` a subset of variables used in the fit, `na.action=` action for missing values: `"na.fail"`, `"na.omit"`, or a function. The following generics often apply to model fitting functions:

**predict(fit, ...)** predictions from `fit` based on input data

**df.residual(fit)** returns the number of residual degrees of freedom

**coef(fit)** returns the estimated coefficients (sometimes with their standard-errors)

**residuals(fit)** returns the residuals

**deviance(fit)** returns the deviance

**fitted(fit)** returns the fitted values

**logLik(fit)** computes the logarithm of the likelihood and the number of parameters

**AIC(fit)** computes the Akaike information criterion or AIC

## Statistics

**aov(formula)** analysis of variance model

**anova(fit, ...)** analysis of variance (or deviance) tables for one or more fitted model objects

**density(x)** kernel density estimates of `x`

**binom.test()**, **pairwise.t.test()**, **power.t.test()**, **prop.test()**, **t.test()**, ... use `help.search("test")`

## Distributions

**rnorm(n, mean=0, sd=1)** Gaussian (normal)

**rexp(n, rate=1)** exponential

**rgamma(n, shape, scale=1)** gamma

**rpois(n, lambda)** Poisson

**rweibull(n, shape, scale=1)** Weibull

**rcauchy(n, location=0, scale=1)** Cauchy

**rbeta(n, shape1, shape2)** beta

**rt(n, df)** ‘Student’ (*t*)

**rf(n, df1, df2)** Fisher–Snedecor (*F*) ( $\chi^2$ )

**rchisq(n, df)** Pearson

**rbinom(n, size, prob)** binomial

**rgeom(n, prob)** geometric

**rhyper(nn, m, n, k)** hypergeometric

**rlogis(n, location=0, scale=1)** logistic

**rlnorm(n, meanlog=0, sdlog=1)** lognormal

**rnbinom(n, size, prob)** negative binomial

**runif(n, min=0, max=1)** uniform

**rwilcox(nn, m, n), rsignrank(nn, n)** Wilcoxon’s statistics

All these functions can be used by replacing the letter `r` with `d`, `p` or `q` to get, respectively, the probability density (`dfunc(x, ...)`), the cumulative probability density (`pfunc(x, ...)`), and the value of quantile (`qfunc(p, ...)`), with  $0 < p < 1$ .

## Programming

**function( arglist ) expr** function definition

**return(value)**

**if(cond) expr**

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

**for(var in seq) expr**

**while(cond) expr**

**repeat expr**

**break**

**next**

Use braces `{}` around statements

**ifelse(test, yes, no)** a value with the same shape as `test` filled with elements from either `yes` or `no`

**do.call(funname, args)** executes a function call from the name of the function and a list of arguments to be passed to it