AniMove
general R Reference Card

www.animove.org

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Getting help

`help(topic)` documentation on `topic`
`?topic` short alternative to `help`
`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
`methods(a)` e.g. methods(summary) gives all summary commands

Information about your data

`str(a)` display the internal structure 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
`dir()` show files in the current directory

Input and output

`source("script.R")` includes and executes script.R in this place
`read.table(f)` 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(f,header=TRUE)` id. but with defaults set for reading comma-delimited files
`print(a, ...)` prints its arguments; generic, meaning it can have different methods for different objects
`write.table(x, file=f,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
`data(f)` loads specified data sets

For database interaction, see packages `RODBC`, `DBI`, `RMySQL`, `RPgSQL`, `ROracle`, for other file formats see `XML`, `hdf5`, `netCDF`

Data creation & removal

`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` returns `2 3 4 5`
`seq(from,to)` generates a sequence `by=` specifies increment; `length=` specifies desired length
`seq(along=x)` generates `1, 2, ..., length(along)`; 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
`expand.grid()` a data frame from all combinations of the supplied vectors or factors
`cbind(df1, df2)`, `rbind(df1,df2)` combine arguments by columns (rows) for data frames and the like
`rm(obj)` removes object
`rm(list = ls(all = TRUE))` removes all objects

Indexing your data

addressing vectors

`v[n]`	n^{th} element
`v[-n]`	all *but* the n^{th} element
`v[1:n]`	first `n` elements
`v[-(1:n)]`	elements from `n+1` to the end
`v[c(1,4,2)]`	specific elements
`v["name"]`	element named `"name"`
`v[x > 3]`	all elements greater than 3
`v[x > 3 & x < 5]`	all elements between 3 and 5
`v[x %in% c("a","and","the")]`	elements in the given set

addressing lists

`x[n]`	list with elements `n`
`x[[n]]`	n^{th} element of the list
`x[["name"]]`	element of the list named `"name"`
`x$name`	id.

addressing 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"`

adressing data frames

similar functions as in the matrix indexing plus:

`df[["name"]]`	column named `"name"`
`df$name`	column named `"name"`
`df[,"name"]`	column named `"name"`

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(v)`, `which.min(v)` returns the index of the maximum (minimum) element of `v`

`rev(v)` reverses the elements of `v`
`sort(v)` sorts the elements of `v` 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`)
`na.omit(x)` suppresses the observations with missing data (`NA`)
`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

Math

`sin,cos,tan,asin,acos,atan,atan2,log,log10,exp`
`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(v, base)` computes the logarithm of `x` with base `base` `log10(v)` `base` =10
`scale(x)` if `x` is a matrix, centers and reduces the data; to center only use the option `center=FALSE`, to reduce only `scale=FALSE` (by default `center=TRUE, scale=TRUE`)
`pmin(x,y,...)` a vector which ith element is the minimum of `x[i]`, `y[i]`, ...
`pmax(x,y,...)` id. for the maximum
`cumsum(v)` a vector which ith element is the sum from `x[1]` to `x[i]`
`cumprod(v)` $f_i = \Pi_{j=1..i} x_j = (x_1, x_1 \cdot x_2, \ldots)$
`cummin(v)` $f_i = \min(x_1 \ldots x_i)$
`cummax(v)` id. for the maximum
`union(x,y)`, `intersect(x,y)`, `setdiff(x,y)`, `setequal(x,y)`, `is.element(el,set)` "set" functions
`fft(v)` Fast Fourier Transform `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

Matrices

`t(x)` transpose
`diag(x)` diagonal
`%*%` matrix multiplication and scalar product
`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

The apply family functions are very powerful and fast, they do replace a 'for loop' but are difficult to grasp.
`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`
`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(df,by,FUN)` splits a data frame 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 the data frame
`stack(x, ...)` transform data available as separate columns in a data frame or list into a single column
`unstack(x, ...)` inverse of `stack()`
`cast(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")
`melt(x, ...)` melts an object into a form suitable for casting

Strings

`paste(s1,s2, sep=" ")` concatenate vectors after converting to character; `collapse=` is an optional string to separate "collapsed" results `paste0(s1,s2)` paste without seperator (since R 2.15)
`substr(s,start,stop)` substrings in a character vector; can also assign, as `substr(s, start, stop) <- value`
`strsplit(s,split)` split `s` according to the substring `split`
`grep(pattern,s)` search `pattern` in `s`; see `?regex`
`tolower(s), toupper(s)` convert to lowercase (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

Dates and Times

All animal tracks come with a time stamp. 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 "2012-02-21". 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). Avoid it.
`%Y` Year with century.
`%z` (read only) Offset from Greenwich; `-0800` is 8 hours west of.
`%Z` (read 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`.

Plotting

Several plotting options exist in R to plot your results and these are constantly changing. Below you will find standard R plotting commands and further down more sophisticated options using e.g. ggplot2 functionality. Furthermore does R offer spatial data plotting options which can be found on the AniMove spatial cheat sheet.

`plot(y)` plot of the values of `y` (on the y-axis) ordered on the x-axis
`plot(x, y)` bivariate plot of `x` agains `y`
`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` (vertical line: =v)
`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, vect)` adds an axis at the bottom (`side=1`), on the left (2), at the top (3), or on the right (4); `vect` (optional) gives the abcissa (or ordinates) where tick-marks are drawn

`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 factor controlling the default size of texts and symbols; you can scale 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)`

`mfcol` 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` size in points of texts and symbols as integer
`pty` a character which specifies the type of the plotting region, `"s"`: square, `"m"`: maximal

ggplot2

ggplot2 comes with its own syntax which is different from normal R syntax. It takes quite a while to learn it but produces very fancy graphics.
`qplot(x=vx, y=vy, data=df)` plots columns df$vx and df$vy

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
`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

Statistics, optimization and model fitting

`aov(formula)` analysis of variance model
`anova(fit,...)` analysis of variance (or deviance) tables for one or more fitted model objects
`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
`glm()` generalized linear model
`gam()` generalized additive model
`kmeans()` kmeans clustering
`tree()` builds a decision tree
`rpart()` builds a decision tree
`randomForest()` random forest machine learning
`maxent()` Maximum Entropy model
`svm()` Support Vector Machines in the e1071 package, but other packages provide SVM as well such as: kernlab, klaR, svmpath, shogun
`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
`predict(fit,...)` predictions from `fit` based on input data
`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

Distributions

`rnorm(n, mean=0, sd=1)` Gaussian (normal)
`rexp(n, rate=1)` exponential
`rgamma(n, shape, scale=1)` gamma
`rpois(n, lambda)` Poisson
`rt(n, df)` 'Student' (t)
`rchisq(n, df)` Pearson
`rbinom(n, size, prob)` binomial
`rlogis(n, location=0, scale=1)` logistic
`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`

Examples in this document use the variables `df` = data frame object, `v` = vector, `s` = string, `f` = filename as string

Credits

This R reference card is adapted to AniMove needs by Martin Wegmann, Benjamin Leutner and Mirjana Bevanda but based on the reference card by Jonas Stein, Tom Short and Emmanuel Paradis.