Package 'basr'

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Title Basic, but hopefully useful, functions

Description This package provides a bunch of basic functions for a variety of usage.

Author Mathieu Basille, contributions from Samuel Brown, Marc in the box, Clement Calenge, Michael Hallquist, Jean Lobry, Kevin Wright

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Suggests devtools

License GPL (>= 3)

URL http://ase-research.org/basille/basr

RoxygenNote 6.0.0

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basr   *Utility functions*

Description

basr package

Details

This package provides a bunch of basic, but hopefully useful, functions for a variety of usage. For a list of documented functions, use library(help = "basr")

Author(s)

Mathieu Basille <basille@ase-research.org>, contributions from Samuel Brown, Marc in the box, Jean Lobry, Kevin Wright

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capwords   *Capitalizing*

Description

Capitalizing - every first letter of a word is changed to upper case.

Usage

```
capwords(s, strict = FALSE)
```

Arguments

s	A character vector, or an object that can be coerced to character by as.character.
strict	Logical: other letters than the first are converted to lower case

Value

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

Author(s)

From the help page of [chartr](#)

Examples

```
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'
```

---

colNA   *Number of NAs by column*

Description

Returns the number of NAs for each column of a data frame.

Usage

```
colNA(x)
```

Arguments

x   A data frame.

Value

A numeric vector

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
set.seed(123)
(df <- data.frame(matrix(sample(c(NA, 1:10), 100, TRUE), ncol = 4)))
colNA(df)
```

---

confint   *Confidence Intervals for Model Parameters*

Description

Modified version of the [confint](#) function, which displays the coefficients in addition to the CIs, and allows for more control on display parameters. A plot argument and function allow to graph the coefficients and their CIs.

Usage

```
confint(object, parm, level = 0.95, order = FALSE, groups, plot = FALSE,
  ...)

## S3 method for class 'confint'
plot(x, mar = c(5, 7, 3, 1) + 0.1, col = NULL,
  main = attr(x, "model"), pch = 19, add.signif = FALSE, ...)
```

Arguments

order	Logical. If TRUE, the results are ordered by descending order on the coefficient value.
groups	A factor in the sense that as.factor(f) defines the groups, or a list of such factors in which case their interaction is used for the groups. See [split](#).
plot	Whether to plot the results.
...	Further arguments passed to points.
x	A data.frame of class confint.
mar	The number of lines of margin, can be useful if the coefficient names do not fit in the left margin. See [par](#) for more details.
col	The color of each coefficient + CI; gray by default. If "groups", the color of each (sorted) group; use a hcl palette by default.
main	The title of the plot.
pch	The symbol to be used for the points. See [par](#) for more details.
add.signif	Logical, whether to add an asterik for variables with CIs non-overlapping with zero.
...	Further arguments passed to points.

Value

A data frame providing the CI and coefficients.

Author(s)

Mathieu Basille <basille@ase-research.org>

See Also

[confint](#) for more details on other parameters.

Examples

```
## Example of linear model
fit <- lm(100/mpg ~ disp + hp + wt + am, data = mtcars)
## Standard 'confint' function
stats::confint(fit)
## Same results with modified function
confint(fit)
## Argument 'level'
stats::confint(fit, level = .9)
confint(fit, level = .9)
## Argument 'order'
confint(fit, order = TRUE)
## Argument 'groups'
confint(fit, groups = c(3, 1, 1, 1, 2))
## Argument 'level', "'order' and 'groups' simultaneously
confint(fit, level = .9, order = TRUE, groups = c(3, 1, 1, 1, 2))
## Argument 'parm'
stats::confint(fit, "am")
confint(fit, "am")
##'
## Plot of the results
plot(confint(fit, order = TRUE, groups = c(3, 1, 1, 1, 2)))
confint(fit, order = TRUE, groups = c(3, 1, 1, 1, 2), plot = TRUE)
confint(fit, order = TRUE, groups = c(3, 1, 1, 1, 2), plot = TRUE,
    col = c("blue", "red", "green"), pch = 18, cex = 2)
confint(fit, order = TRUE, groups = c(3, 1, 1, 1, 2), level = 0.9,
    plot = TRUE, add.signif = TRUE)
```

---

cv   *Coefficient of variation*

Description

This function computes the coefficient of variation (i.e. sd / mean) of the values in x. If ci is TRUE then confidence intervals are also computed.

Usage

```
cv(x, na.rm = FALSE, ci = FALSE, conf.level = 0.95,
  method = c("mckaymod", "mckay", "naive"))
```

Arguments

x	A numeric vector
na.rm	Logical. Should missing values be removed?
ci	Logical. Should confidence intervals be computed?
conf.level	Confidence level of the interval.
method	The method to compute the confidence intervale. Either the naive (naive), the McKay (mckay) or the modified McKay (mckaymod, default) approximation.

Value

If `ci`, returns a list with the coefficient of variation. in the first element and the confidence interval in the second.

Original URL

<http://tolstoy.newcastle.edu.au/R/e2/help/07/06/19043.html>

Author(s)

From Kevin Wright, modified by Mathieu Basille <basille@ase-research.org>

References

Vangel, M. G. (1996) Confidence intervals for a normal coefficient of variation. The American Statistician, 50: 21-26

Examples

```
xx <- 1:10
cv(xx)
sd(xx)/mean(xx)
cv(xx, ci = TRUE)
```

---

dynamitePlot   *Dynamite Plots*

Description

Creates dynamite plots.

Usage

```
dynamitePlot(height, error, names.arg = NULL, significance = NA,
  ylim = c(0, maxLim), sym = FALSE, head = 0.7, lwd = par("lwd"),
  cex.sig = 1.2, ...)
```

Arguments

height	A vector of values describing the heights of the rectangular bars which make up the plot.
error	A vector of values indicating the length of error bars.
names.arg	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 names attribute of height.
significance	A character vector giving the group significance for each value.
ylim	Limits for the y axis. By default, ylim uses c(0, maxLim), where maxLim is the maximum height + error multiplied by a factor of 1.1.
sym	Logical. Whether to draw lower error bars.
head	A numeric, which gives the approximate width of the head, relative to the bar width.
lwd	The line width of the error bars, a _positive_ number, defaulting to par("lwd") (usually 1).
cex.sig	The magnification to be used for significance groups relative to the current setting of cex (which defaults to 1).
...	Arguments to be passed to barplot.

Original URL

<http://the-praise-of-insects.blogspot.ca/2012/04/dynamite-plots-in-r.html>

Note

Ben Bolker wrote an extensive discussion of the advantages and disadvantages of dynamite plots here: <http://emdbolker.wikidot.com/blog:dynamite>

Author(s)

Samuel Brown, modified by Mathieu Basille <basille@ase-research.org>

Examples

```
values <- c(1, 2, 5, 4)
errors <- c(0.25, 0.5, 0.33, 0.12)
names <- paste("Trial", 1:4)
sig <- c("a", "a", "b", "b")
dynamitePlot(values, errors)
par(mar = c(3, 5, 1, 1) + .1)
dynamitePlot(values, errors, names.arg = names, significance = sig,
    ylab = "Values", sym = TRUE, cex.lab = 1.5, cex.axis = 1.2,
    cex.names = 1.2, cex.sig = 1.5, space = c(0, 0.2, 0.8, 0.2),
    lwd = 2, head = 0, col = c(grey(0.5), "white"), border = c(NA,
        "black"))
```

---

extrange   *Extended range*

Description

Returns the range extended by a given proportion.

Usage

```
extrange(x, percent = 0.1, na.rm = FALSE)
```

Arguments

x	A numeric vector.
percent	The proportion to be added to the range.
na.rm	Logical, indicating if NA's should be omitted.

Details

If the regular range returns a single value, the proportion is computed on this value itself (and not on the range).

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
extrange(0:10)
extrange(0:10, percent = .5)
extrange(-10:10)
extrange(rep(10, 3))
```

---

getcolors   *Choosing colors visually*

Description

Allows for the selection of n colors by using a simplified color swatch.

Usage

```
getcolors(n)
```

Arguments

n	The number of colors to choose

Details

getcolors allows selection with a mouse using the locator function. Following selection, a second plot opens showing how these colors look next to each other and on a background gradient of black to white. The function uses an RGB color model: Red increases on the y-axis, Green increases on the x-axis, and Blue is a repeated sequence of levels across the x-axis.

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 ... 255). The optional alpha values range from 0 (fully transparent) to 255 (opaque).

Original URL

http://menugget.blogspot.com/2013/01/choosing-colors-visually-with-getcolors.html

Author(s)

Marc in the box

Examples

```
## Not run:
set.seed(1)
n <- 100
x <- seq(n)
y1 <- cumsum(rnorm(n))
y2 <- cumsum(rnorm(n))
y3 <- cumsum(rnorm(n))
y4 <- cumsum(rnorm(n))
ylim <- range(c(y1, y2, y3, y4))

cols <- getcolors(4)

plot(x, y1, ylim = ylim, t = "l", col = cols[1], lwd = 3, ylab = "")
lines(x, y2, col = cols[2], lwd = 3)
lines(x, y3, col = cols[3], lwd = 3)
lines(x, y4, col = cols[4], lwd = 3)
legend("topleft", legend = paste("y", 1:4, sep = ""), col = cols,
    lwd = 3)
## End(Not run)
```

---

manual   *Generate package reference manual*

Description

Generate package reference manual. This function requires the devtools package.

Usage

```
manual(pkg = ".", path = NULL, preview = TRUE, overwrite = FALSE)
```

Arguments

pkg	package description, can be path or package name. See `as.package` for more information
path	path in which to produce package. If NULL, defaults to the root directory of the package.
preview	preview generated PDF file
overwrite	overwrite output file if it exists

Author(s)

Mathieu Basille <basille@ase-research.org>

---

memUse   *Memory usage of saved objects*

Description

Show memory usage of saved objects.

Usage

```
memUse(pos = 1, pattern)

## S3 method for class 'memUse'
print(x, sort = c("size", "alphabetical"),
  decreasing = ifelse(sort == "size", TRUE, FALSE), n = 10, bytes = FALSE,
  ...)
```

Arguments

pos	Which environment to use to list the saved objects (as a position in the search list). See `ls`.
pattern	An optional regular expression. See `ls`.
x	An object of class `memUse`.
sort	Whether to sort the object list by `size` or `alphabetical` order.
decreasing	Logical. Should the sort order be increasing or decreasing?
n	A single integer, giving the number of objects to display.
bytes	Logical. Whether to display the raw size in bytes.

Value

A data frame of classe `memUse` providing object names, class and memory usage; or `0` if no object is present in the specified environment.

Original URL

<http://stackoverflow.com/a/9839949>. See also the complete Stack Overflow thread: https://stackoverflow.com/questions/1358003/tricks-to-manage-the-available-memory-in-an-r-session

Author(s)

Michael Hallquist, modified by Mathieu Basille <basille@ase-research.org>

Examples

```
## Create some data
rand <- rnorm(100)
data(iris)
foo <- function(x) print(x)
##'
## Check memory usage (and raw numbers in bytes)
memUse()
memUse()$bytes
```

---

mv   *Rename an R object.*

Description

Rename an R object.

Usage

```
mv(from, to)
```

Arguments

from   The name of an R object, with or without quotes.

to   The new name, with or without quotes.

Author(s)

Jean Lobry

Examples

```
bla <- 2
ls()
mv(bla, bli)
bli
ls()
```

---

nsubset   *Subset according to frequency of a column*

Description

Subset an object based on the frequency of a column (factor or not).

Usage

```
nsubset(x, col, n, sign = c(">=", "<=", ">", "<", "=="), select,
  drop = FALSE)
```

Arguments

x	object to be subsetted (e.g. `data.frame`, `matrix`, `Spatial*DataFrame`, etc.).
col	name of the column which stores the grouping factor (without quotes).
n	the reference number for the frequency of the grouping factor (must be a numeric of length 1).
sign	any comparison sign (>= by default, <=, >, <, or ==).
select	expression, indicating columns to select (either name(s) without quote or numeric indicating the column number(s)).
drop	passed on to '[' indexing operator.

Value

A subset of the object (with the same class).

Author(s)

Mathieu Basille <basille@ufl.edu>

Examples

```
set.seed(1)
bla <- data.frame(value = rnorm(100), group = sample(letters[1:4],
    size = 100, replace = TRUE, prob = (1:4) * 10))
table(bla$group)
bli <- nsubset(bla, group, 25)
table(bli$group)
blo <- nsubset(bla, group, 25, sign = ">", select = 1, drop = TRUE)
head(blo)
length(blo)
```

---

q *Terminate an R Session*

Description

A modified version of quit or its alias [q](q). See quit for the function details.

Usage

```
q(save = "default", status = 0, runLast = TRUE)

quit(save = "default", status = 0, runLast = TRUE)
```

Details

If save = "yes", the list of attached packages is automatically saved in a file .Rpackages. See savepkglist for more details.

Author(s)

R Core Team, modified by Mathieu Basille <basille@ase-research.org>

---

reclass *Reclassify the values of a vector.*

Description

Reclassify given values of a vector by new values. Note that all values need not to be documented, only the ones that need to be modified.

Usage

```
reclass(x, from, to = NULL, factor = FALSE, ...)
```

Arguments

x	A character or numeric vector.
from	A vector describing the values to change from, or a matrix of reclassification with two columns (from, to).
to	A vector describing the values to change to, or nothing if from is a matrix.
factor	Logical, whether to return a factor (default is FALSE).
...	Additional arguments passed to factor.

Value

A vector with the same length as x.

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
(bla <- rep(1:5, 3))
reclass(bla, c(3, 4), c(7, 3))
reclass(bla, c(3, 4), c("a", "b"))

## Conversion as a factor
reclass(bla, c(3, 4), c("a", "b"), factor = TRUE)
(bli <- rep(letters[1:5], 3))
reclass(bli, c("b", "d"), c(1, 2))

## With a matrix of reclassification
(mat <- matrix(c("b", "d", 1, 2), ncol = 2))
reclass(bli, mat)

## Fast computation time on large vectors
blu <- rpois(1e6, 10)
system.time(reclass(blu, c(3, 4), c(7, 3)))
```

---

save.image *Save the current workspace*

Description

A modified version of save.image that allows to save the commands history and the list of attached packages. See save.image for the function details.

Usage

```
save.image(file = ".RData", version = NULL, ascii = FALSE,
  compress = !ascii, safe = TRUE, hist = TRUE, h.file = ".Rhistory",
  pkglist = TRUE, p.file = ".Rpackages")
```

Arguments

hist	Logical. Whether to save or not the commands history.
h.file	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.
pkglist	Logical. Whether to save or not the list of attached packages (default is TRUE).
p.file	The name of the file in which to save the list of attached packages, or from which to load it. The path is relative to the current working directory.

Author(s)

R Core Team, modified by Mathieu Basille <basille@ase-research.org>

See Also

savehistory to save the commands history, and savepkglist to save the list of attached packages.

---

savepkglist	*Load or save the list of attached packages*

Description

Display, save or load the list of attached packages.

Usage

```
savepkglist(file = ".Rpackages")

attpkglist()

loadpkglist(file = ".Rpackages")

.loadpkglist()
```

Arguments

file   The name of the file in which to save the list of attached packages, or from which to load it. The path is relative to the current working directory.

Details

attpkglist simply lists all attached packages (i.e. not base packages).

savepkglist saves the list of all attached packages in a file, with one package per line.

loadpkglist loads a list of packages from a file. The file should contain one package name per line, without quotes, and no empty line. If the packages are not installed, the function sends a warning.

.loadpkglist automatically loads the .Rpackages file at startup (see the Note below).

Note

To automatically load a .Rpackages list at startup, add this in your .Rprofile:

Load packages at the start of R if the package list exists

basr:::.loadpkglist()

Essentially, the function appends the list of packages at the end of the defaultPackages option (see options for this option; see also Startup for more details about the initialization at start of an R session).

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
## Not run: savepkglist(file = "list.Rpackages")
## Not run: attpkglist()
## Not run: loadpkglist()
```

---

se   *Standard errors*

Description

This function computes the standard error (i.e. sd / sqrt(n)) of the values in x. If na.rm is TRUE then missing values are removed before computation proceeds.

Usage

```
se(x, na.rm = FALSE)
```

Arguments

x	A numeric vector or an R object which is coercible to one by as.vector.
na.rm	Logical. Should missing values be removed?

Original URL

http://cran.r-project.org/doc/manuals/R-intro.html

Author(s)

From the Writing R Extensions manual, modified by Mathieu Basille <basille@ase-research.org>

See Also

[var](var) and [sd](sd) for the variance and standard deviation.

Examples

```
bla <- rnorm(1000, sd = 100)
sd(bla)
sqrt(var(bla)/length(bla))
se(bla)

is.na(bla) <- 200:300
sd(bla, na.rm = TRUE)
se(bla, na.rm = TRUE)
```

---

summaryIC   *Summary of AIC/BIC*

Description

Summarizes IC differences to identify plausible models (models with highest empirical support).

Usage

```
summaryIC(x, delta = 2)
```

Arguments

x   A data frame with one row per model, and one column giving an information-theoretic index (AIC or BIC), such as returned by [AIC](#) or [BIC](#) with several models.

delta   The difference threshold to identify models with similar support.

Value

The input data frame with additional columns delta giving IC differences with the best model, and best identifying the best model(s) (* for the absolute best model, + for models within the threshold).

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
## Prepare two models:
lm1 <- lm(Fertility ~ . , data = swiss)
lm2 <- update(lm1, . ~ . -Examination)

## Check AIC:
AIC(lm1, lm2)

## Summary of AIC and BIC:
summaryIC(AIC(lm1, lm2))
summaryIC(BIC(lm1, lm2))
```

---

table   *Modified table function to handle NAs*

Description

A slight modification of the [table](#) function, to include NA values in the table by default. See [table](#) for details of the function.

Usage

```
table(..., exclude = if (useNA == "no") c(NA, NaN), useNA = c("ifany", "no",
  "always"), dnn = list.names(...), deparse.level = 1)
```

Arguments

useNA   Whether to include NA values in the table. Default is now ifany.

Author(s)

R Core Team, modified by Mathieu Basille <basille@ase-research.org>

Examples

```
d <- factor(rep(c("A", "B", "C"), 10), levels = c("A", "B", "C",
    "D", "E"))
is.na(d) <- 3:4
d
table(d)
```

---

togray   *Convert continuous variable to grey levels*

Description

Convert a continuous variable to the corresponding levels of grey.

Usage

```
togray(x, min = 0.1, max = 0.9, alpha = NULL, inverse = FALSE,
  sqrt = FALSE)

togrey(x, min = 0.1, max = 0.9, alpha = NULL, inverse = FALSE,
  sqrt = FALSE)
```

Arguments

x	A numeric vector.
min	The minimum grey level.
max	The maximum grey level.
alpha	The opacity.
inverse	Logical. By default, bigger is darker. If inverse = TRUE, bigger is lighter.
sqrt	Logical. Applies a square root transformation to get more progressive grey levels.

Value

A vector of colors of the same length as x.

Author(s)

From Clement Calenge, modified by Mathieu Basille <basille@ase-research.org>

Examples

```
bla <- runif(10000)
plot(bla, col = togray(bla, 0, 1), pch = 20)
plot(bla, col = togray(bla, 0, 1, sqrt = TRUE), pch = 20)
plot(bla, col = togray(bla, 0, 1, alpha = 0.5), pch = 20)
```

---

writeFunction	*Function output*

Description

Prints a function to a file.

Usage

```
writeFunction(fun, file = NULL)
```

Arguments

fun	A function.
file	A character string naming a file. By default, write the function in <fun>.R in the working directory.

Author(s)

Mathieu Basille <basille@ase-research.org>

Examples

```
f1 <- function(x) {
    ## Comment
    print(x)
}
writeFunction(f1)
rm(f1)
source("f1.R")
file.remove("f1.R")
f1(3)
```

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