Package 'bmisc'

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Type Package

Title Miscellaneous functions

Version 0.2-12

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Description This package has different functions that I have accumulated with time. This is the Alpha version.

Depends car, lattice, zoo, robustbase, methods

License LGPL >= 3.0

R topics documented:

`att.strp` *Attibute stripper*

Description

Strips an object of its attributes

Usage

```
att.strp(x)
```

Arguments

`x`	the name of an object (`vector, matrix, data.frame, array or list`)

Details

This function strips an object of its attributes. In the case of a `vector`, all attributes are removed. For a `matrix` or an `array`, only `c('dim','dimnames')` are kept. When `att.strp` is used on a `data.frame`, all attributes of the variables are striped and only `c('names','row.names','na.action', 'class')` are kept for the `data.frame` object.

Value

returns an object of the same `class` as the original one.

Author(s)

Benoit Bruneau

Examples

```
#######################################
#   Creating different objects        #
#    with added attributes (label)    #
#######################################

### numerical vector ###
x <- 1:10
attr(x,"label") <- "test1"
attributes(x)

### data frame ###
z=data.frame(x,x)
attr(z,"labels") <- "test2"
attributes(z)
attributes(z[,1])
attributes(z[,2])

### array ###
y=array(x,c(2,2,2))
attr(y,"labels") <- "test3"
attributes(y)
```

```
attributes(y[,,1])
attributes(y[,,2])

### list containing the vector, ###
### data frame and array        ###
u=list(x,z,y)
attr(u,"labels") <- "test4"
attributes(u)
attributes(u[[1]])
attributes(u[[2]])
attributes(u[[3]])

#######################################
#        attribute stripping          #
#######################################
x2=att.strp(x)
z2=att.strp(z)
y2=att.strp(y)
u2=att.strp(u)

#######################################
#   verification of the attributes    #
#    for all stripped objects         #
#######################################

### numerical vector ###
attributes(x2)

### data frame ###
attributes(z2)
attributes(z2[,1])
attributes(z2[,2])

### array ###
attributes(y2)
attributes(y2[,,1])
attributes(y2[,,2])

### list containing the vector, ###
### data frame and array        ###
attributes(u2)
attributes(u2[[1]])       # vector in the list

attributes(u2[[2]])       # data frame in the list
attributes(u2[[2]][,1])   # data frame in the list
attributes(u2[[2]][,2])   # data frame in the list

attributes(u2[[3]]        # array in the list
attributes(u2[[3]][,,1])  # array in the list
attributes(u2[[3]][,,2])  # array in the list
```

`bmisc` *Miscellaneous functions*

Description

This package has different functions that I have accumulated with time. I am not the author of all of them even though I have modified most of them. This is the Alpha version.

Format

Package:	bmisc
Type:	Package
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Details

For pdf version of the help, write `vignette("bmisc")`.

Author(s)

Benoit Bruneau

Maintainer: Benoit Bruneau <benoit.bruneau1@gmail.com>

`ceiling.lg` *ceiling largest*

Description

Ceiling to largest digit

Usage

```
ceiling.lg(x)
```

Arguments

`x`	Numeric vector

Details

Gives the ceiling to largest digit (i.e., 54 -> 60).

Examples

```
ceiling.lg(250)
ceiling.lg(25000000)
```

clean *Clean a Data Frame*

Description

Cleans a `data.frame` from a starting point with a defined threshold

Usage

```
clean(data= x,  col.start =1,  min.val=NULL)
```

Arguments

`data`	then name of the `data.frame`
`col.start`	indicate the columns from which to start reading
`min.val`	`numeric`. Read details

Details

`min.val` is the minimum value accepted in a column. Colomns with this value or higher will be kept in the `data.frame`.

More will be added to this function.

Value

returns the data.frame with the clean columns

Author(s)

Benoit Bruneau

Examples

```
x=rnorm(50 , 20,  12)
y=runif(50 )
z=rpois(50,  3)
v=x*y/z
t=z*v
pp=data.frame(aa=x,  bb=y, cc=v,  dd=z,  ee=t)
summary(pp)

pp1 = clean(pp, min.val=0.06)
```

`corr.perm` *Pearson Correlation by Permutation*

Description

Tests the Pearson correlation estimate (r) by use of permutation

Usage

```
corr.perm(x,y,nperm=999)
```

Arguments

`x,y`	Two vectors of same length used for correlation analysis
`nperm`	Number of permutations (default = 999)

Value

`Correlation`	Pearson r
`t.stat`	Calculated test statistic (t)
`No.perm`	number of permutations
`P.perm`	pvalue estimated by permutations
`P.para`	parametric pvalue estimated
`inf`	inferior limit of the confidence interval
`sup`	superior limit of the confidence interval
`df`	degree of freedom

Examples

```
x <- rnorm(50,0,1)
y <- runif(50,0,1)*x
toto = corr.perm(x, y)
```

`cv` *Coefficient of Variation (CV)*

Usage

```
cv(x, na.rm=T)
```

Arguments

`x`	an R object (vector, matrix,...)
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds

Details

The coefficient of variation (CV) is the ratio of the standard deviation to the mean. The CV is defined for the absolute value of the mean to ensure it is always positive.

Examples

```
x=rnorm(50)
cv(x)
```

`day` *day*

Description

Day of year as decimal number (001-366).

Usage

```
day(x)
```

Arguments

```
x
```

Examples

```
# will soon be available
```

`Errbar` *error bars*

Description

Adds error bars on a plot

Usage

```
Errbar(x, y, xinf=NULL, xsup=NULL, yinf=NULL, ysup=NULL, yCI=NULL,
       xCI=NULL, cap=0.05,...)
```

Arguments

`x`	numeric vector
`y`	numeric vector
`xinf, xsup`	numeric vectors containing the upper (xsup) and/or lower (xinf) limits of the confidence interval for x-axis values.
`yinf, ysup`	numeric vectors containing the upper (ysup) and/or lower (yinf) limit of the confidence interval for y-axis values.
`xCI`	numeric vectors containing the confidence intervals for x-axis values.
`yCI`	numeric vectors containing the confidence intervals for y-axis values.
`...`	additional graphical arguments (par) such as `col, lty, lwd` and/or arguments for `arrows` .

Details

If `xCI` and/or `yCI` are defined, individually defined limits (ie. `xinf, xsup, yinf, ysup`) are not used.

See Also

arrows, par

Examples

```
x <- 1:10
y <- x + rnorm(10)

yci <- runif(10)
xci <- runif(10)

plot(x,y, ylim=c(min(y-yci),max(y+yci)))
Errbar( x, y, yCI=yci)

plot(x,y, xlim=c(min(x-xci),max(x+xci)))
Errbar( x, y, xCI=xci )

plot(x,y, ylim=c(min(y-yci),max(y+yci)), xlim=c(min(x-xci),max(x+xci)))
Errbar( x, y, yCI=yci, xCI=xci )

# Gives an Error message
```

```
#plot(x,y, ylim=c(min(y-yci),max(y+yci)))  ## adds the yCI and gives
#Errbar( x, y, ysup=1, yCI=yci)            ## an error message for the ysup
```

`fct` *Print bmisc functions*

Description

Print all functions of bmisc package

Usage

```
fct()
```

`format.hms` *Format seconds into hours*

Description

Transforms time format

Usage

```
format.hms(sec)
```

Arguments

`sec`	time expressed in seconds

Value

returns hrs:min:sec

Examples

```
format.hms(20000)
```

`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,...)
## Default S3 method:
gam.Check(b,
          main=c("Normal Q-Q Plot","Resids vs. Linear Pred.",
          "Histogram of Residuals","Response vs. Fitted Values"),

          xlab=c("Theorical Quantiles", "Linear Predictor",
          "Residuals","Fitted Values"),

          ylab= c("Sample Quantiles","Residuals","Frequency",
          "Response"),

          text=NULL, args.histplot=NULL, ...))
```

Arguments

`b`	a fitted gam object as produced by `gam()`.
`main`	a character vector containing the four titles to be used.
`xlab`	a character vector containing the four x labels to be used.
`ylab`	a character vector containing the four y labels to be used.
`text`	a character or `expression` vector specifying the text to be written.
`args.histplot`	`list` of additional arguments to pass to `histplot()`
`...`	additional text and graphical parameters (see `par`, `mtext`)

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.

This is a modified version of `gam.check` from `mgcv-package` so that main titles, x labels and y labels can be customized.

References

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

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.check(b, main=c("A","B","C","D"))
```

`get.partial.etas` *get partial etas*

Usage

```
get.partial.etas(model)
```

Arguments

```
model
```

Examples

```
# will soon be available
```

histplot *histplot*

Usage

```
histplot(dat, breaks="Sturges", barc="steelblue", borc="white",
         fit.norm=TRUE, lcol="brown", stat=NULL,
         stat.lab=c("Mean","Median"), box=TRUE, rug=TRUE,
         main,...)
```

Arguments

dat	one of: • a numeric vector, • an object of class "norm" resulting from a call to norm.test
breaks	one of: • a vector giving the breakpoints between histogram cells, • a single number giving the number of cells for the histogram, • a character string naming an algorithm to compute the number of cells (see 'Details'), • a function to compute the number of cells. In the last three cases the number is a suggestion only.
barc	a color to be used to fill the bars.
borc	a color to be used for the borders the bars.
fit.norm	a logical variable indicating whether to fit a normal density curve (TRUE) or not (FALSE).
lcol	color of the normal density curve
stat	the statistic to add on the graph. One of (c("all","mean","median")). Default is NULL.
stat.lab	a character vector with the labels for the estimated mean and/or median. Default is c("Mean","Median").
rug	a logical variable indicating whether to superpose a rug (TRUE) or not (FALSE).
main	the main title of the graph
...	additional arguments to be passed to plot (see par)

Details

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). Alternatively, a function can be supplied which will compute the intended number of breaks as a function of x.

See Also

hist

Examples

```
x=rnorm(50)
histplot(x)

norm.x=norm.test(x)
histplot(norm.x)
```

`inv.pred` *Inverse Predictions with SE*

Usage

```
xxx( data ,  ,  ,  )
```

Arguments

`data`

Author(s)

Benoit Bruneau

`is.even` *is even*

Description

Identifies if a value is even or not

Usage

```
is.even(x)
```

Arguments

`x`	numeric vector

Details

Will returns TRUE if `roundup`(x) is an even number.

Value

logical

See Also

`is.odd`

Examples

```
is.even(5)
is.even(6)
```

`is.odd` *is odd*

Description

Identifies if a value is odd or not

Usage

```
is.odd(x)
```

Arguments

`x`	numeric vector

Details

Will returns TRUE if `roundup`(x) is an odd number.

Value

logical

See Also

`is.even`

Examples

```
is.odd(5)
is.odd(6)
```

`last` *last*

Usage

```
last(x)
```

Arguments

```
x
```

Examples

```
# will soon be available
```

`lev` *Levene type tests*

Description

Tests heteroscedasticity after an Anova

Usage

```
lev(y, ...)
## S3 method for class 'formula'
lev(y, data=NULL,  ...)
## S3 method for class 'lm'
lev(y, ...)
## Default S3 method:
lev(y, group, data=NULL , trim.alpha = 0.1, type="abs",...)
```

Arguments

`y`	response variable for the `default` method, `lm` class object for the `lm` method or `formula` class object for the `formula` methode. If `y` is a linear-model object or a formula, the variables on the right-hand-side of the model must all be factors and must be completely crossed. See details.
`group`	for the default method, factor (concatenated factor when multiple factors). See details.
`data`	`data.frame` where the dependant variable and the factor(s) are
`trim.alpha`	Alpha level (percentiles) trimming the data on which the mean will be evaluated
`type`	Type of transformation made on the residuals. Either "abs" for absolute values or "sq" for sqared values
`...`	arguments to be passed down, e.g., `data` for the `formula` method or other options such as `type` and `trim.alpha`.

Details

When using the `lm` method, `data` doesn't need to be defined. When using the `formula` or `default` methods, `data` can be defined if the data used is in a `data.frame`.

When group is manually defined in the default method, use `paste(x,y,z)` or* `interaction(x,y,z)`form where`"x"`, `"y"` and `"z"` are the factors. There is no restrictions on the number of factors.

O'Brien's (1981) performs test for equality of variances within each group: based on transforming each observation in relation to its group variance and its deviation from its group mean; and performing an ANOVA on these transformed scores (for which the group mean is equal to the variance of the original observations). The procedure is recognised to be robust against violations of normality (unlike F-max).

Value

`Model`	The model
`Levene`	Results for Levene's test
`LeveneTrimMean`	Results for Levene's test on the trimmed mean
`Brown.Forsythe`	Results for Brown-Forsythe's test
`OBrien`	Results for O'Brien's test

See Also

`leveneTest` from `{car}`

Examples

```
z=data.frame( yy=c(rep("c",50),rep("d",50)),
              x=c(rnorm(50),rnorm(50,10)),
              s=rep(c(rep("a",25),rep("b",25)),2),
              qq=rep(c(rep("w",10),rep("t",10)),5))

mod=lm(x~yy*qq*s, data=z)
formula= x~yy*qq*s

lev(y=x, group= paste(yy,qq,s), data=z, type="abs")
lev(y=x, group= paste(yy,qq,s), data=z, type="sq")

lev(y=x, group= interaction(yy,qq,s), data=z)

lev(y=formula, data=z)
lev(mod)
```

`lib.code` *Retreives the code for* `lib()`.

Description

Will print in the R windows the code for `lib()` **(READ DETAILS)**.

Usage

```
lib.code()
lib(pack, install=TRUE, load=TRUE, quietly=TRUE,
    warn.conflicts=FALSE)
```

Arguments

`pack`	Character vector specifying which package(s) to load/install.

Details

USE `lib.code()` TO GET THE CODE FOR THE FUNCTION `lib()`.

`lib.code()` prints in R the code for `lib()`. Copy and paste the code for `lib()` in the file `"C:/Program Files/R/R-2.12.1/etc/Rprofile.site"` (Windows) or `"~/.Rprofile"` (Mac).

`lib()` will load packages named in a charcater vector. If install is `TRUE`, packages not yet installed will be installed.

Author(s)

Benoit Bruneau

Examples

```
lib.code()
```

`lsmean` *Least Squares Means*

Description

THIS FUNCTION IS FROM PACKAGE `pda` THAT IS STILL UNDER CONSTRUCTION ON R-Forge. IT HAS BEEN INCLUDED IN `bmisc` FOR PRACTICAL REASONS.

Caution: This routine is not fully tested for models with nested factors or mixed models. Please check results against another package (e.g. SAS proc mixed). It appears to correctly handle `lme` objects, but does not work well for `aov` objects that include `Error()` type nesting in the formula. Further, it does not properly handle polynomial terms–only the linear term is included. For now, create dummies like x2 = x*x manually and include x2 in your model.

Usage

```
lsmean(object, ...)
## Default S3 method:
lsmean(object, ..., factors, effects = FALSE, se.fit = TRUE,
   adjust.covar = TRUE)
## S3 method for class 'lm'
lsmean(object, data, factors, expr, contrast, effects = FALSE,
   se.fit = TRUE, adjust.covar = TRUE, pdiff = FALSE,
   reorder = FALSE, lsd, level = .05, rdf, coef, cov, ...)
## S3 method for class 'lme'
lsmean(object, data, factors, ..., rdf, coef, cov)
## S3 method for class 'lmer'
lsmean(object, data, factors, expr, ..., rdf, coef, cov)
## S3 method for class 'listof'
lsmean(object, data, factors, stratum, expr, contrast, ...)
```

Arguments

`object`	response vector (default) or model object (lm).
`...`	factors and covariates (must be same length as y).
`data`	data frame in which to interpret variables(found from object if missing).
`factors`	character vector containing names of x.factor and trace.factoras first two entries. Must be in `names(data)` and `labels(object)`.Default is all factor names.
`effects`	drop intercept if `TRUE` (only works properly with sum-to-zero contrasts).
`se.fit`	compute pointwise standard errors if T.
`adjust.covar`	adjust means to average covariate values if T; otherwise use covariate mean for each combination of factors.
`pdiff`	Include letters to signify significant differences.
`reorder`	Reorder means from largest to smallest.
`lsd`	Include average LSD if `TRUE` (also need `pdiff=TRUE`).
`level`	Significance level for `pdiff` calculations.

`rdf`	Residual degrees of freedom.
`coef`	Coefficients for fixed effects in object.
`cov`	Covariance matrix for fixed effects.
`expr`	Call expression (formula)
`contrast`	Type of contrasts (default is attribute `contrasts` of `object`)
`stratum`	Name of stratum for lsmean calculation as character string.

Value

Data frame containing unique factor levels of factors, predicted response (pred) and standard errors (se). WARNING: lsmean may not function properly if there are empty cells. Standard errors for mixed models using methods `lmer` and `listof` are not fully debugged.

Author(s)

Brian S. Yandell

See Also

predict.

Examples

```
## Not run:
lsmean(y,x1,x2)
# the following does the same thing
fit <- lm(y~x1+x2)
data <- data.frame(y,x1,x2)
lsmean(fit,data,factors=c("x1","x2")

## End(Not run)
```

`make.z` *make z*

Usage

```
make.z(x, index = NULL)
```

Arguments

`x`

`index`

Examples

```
# will soon be available
```

`mc.long` *Pairwise t tests in long format*

Description

Calculate pairwise T tests between group levels with corrections for multiple testing presented in long format

Usage

```
mc.long(y, ...)
## S3 method for class 'formula'
mc.long( y, data=NULL, ...)
## S3 method for class 'lm'
mc.long( y, ...)
## Default S3 method:
mc.long(y, group,data=NULL, p.adjust.method="holm",
        column=NULL, digits=NULL, silent=FALSE, ...)
```

Arguments

`y`	response variable for the default method, or `lm` or `formula` object. If `y` is a linear-model object or a formula, the variables on the right-hand-side of the model must all be factors and must be completely crossed.
`group`	for the default method, factor (concatenated factor when multiple factors). See details.
`data`	`data.frame` where the dependant variable and the factor(s) are
`p.adjust.method`	method for adjusting p values. Default is Holm's method. (see `P.adjust`)
`column`	new names for the factor(s); this is optional
`digits`	controls the number of digits for the presented results presented
`silent`	a logical variable indicating whether to indicate the general `warning (FALSE)` or not `(TRUE)`.
`...`	additional arguments to pass to `P.adjust`, `pairwise.t.test` and/or `t.test`.

Details

When making multiple t tests for all combinations, the `n` option of `P.adjust` can be used to identify the number of comparisons that are actually used. This is only to simplify the uses p values corrections on the full output matrix when only some of the comparisons are meaningfull or chosen for hypothesis testing.

When `group` is manually defined, use `paste(x,y,z)` or `interaction(x,y,z)`form; `"x"`, `"y"` and `"z"` are the factors. There is no restrictions on the number of factors.

Value

Object of class `"data.frame"` containing the results.

See Also

P.adjust, pairwise.t.test, pair.diff, DTK.test, TukeyHSD and glht

Examples

```
z=data.frame( yy=c(rep("c",50),rep("d",50)),
              x=c(rnorm(50),rnorm(50,10)),
              s=rep(c(rep("a",25),rep("b",25)),2),
              qq=rep(c(rep("w",10),rep("t",10)),5))

mod=lm(x~yy*qq*s, data=z)
formula= x~yy*qq*s

mc.long(y=x, group= paste(yy,qq,s), data=z)
mc.long(y=x, group= paste(yy,qq,s), data=z, p.adjust.method="sidak")
mc.long(y=x, group= paste(yy,qq,s), data=z, p.adjust.method="sidak", n=15)
mc.long(y=x, group= interaction(yy,qq,s), data=z)

mc.long(y=formula, data=z)

mc.long(mod)

res <- mc.long(mod)   #### results are put in "res" object.
```

`mse` *Mean square error*

Description

Estimates the mean square error (mse)

Usage

```
mse(model)
```

Arguments

`model`	an object containing the results of a model.

Details

The mean square error is also known as the unexplained variance or the variance of the residuals.

Examples

```
z=data.frame( yy=c(rep("c",50),rep("d",50)),
              x=c(rnorm(50),rnorm(50,10)),
              s=rep(c(rep("a",25),rep("b",25)),2),
              qq=rep(c(rep("w",10),rep("t",10)),5))

mod=lm(x~yy*qq*s, data=z)

mse(mod)
```

`n` *Sample size (n)*

Description

Gives n without NA's

Usage

```
n(x)
```

Arguments

`x`	Vector (numeric or character)

Examples

```
x= rep(c(rnorm(30,20,5),NA),3)
n(x)
```

`norm.test` *Normality tests*

Description

Lilliefors (Kolmogorov-Smirnov), Shapiro-Francia, Shapiro-Wilk, D'Agostino Skewness, Anscombe-Glynn Kurtosis and D'Agostino-Pearson normality tests.

Usage

```
## Default S3 method:
 norm.test(norm.test(x, title=NULL, sk=c("G1","b1","mc"), type))
```

Arguments

`x`	numeric vector or an object of class `"lm"` (i.e. lm, aov, glm, gam, ...).
`title`	the title at the top of the results. Default is "Normality Tests".
`sk`	type of skewness used in D'Agostino skewness test. Can be `"G1"`,`"b1"` or `"mc"`. Read details.
`type`	type of residuals which should be used. See details.

Details

This function can be used on objects having `"lm"` in their `class` description. For example, `class`(aov.model) gives `"aov" "lm"` and `class`(glm.model) gives `"glm" "lm"`. The `type` of residuals can be defined. It generally includes `c("working", "response", "deviance", "pearson", "partial")`.

D'Agostino-Pearson's test is more appropriate for analysing a vector with duplicate values in it. The more duplicate values in a vector, the more Shapiro-Wilk will be far from correctly testing the $H0$ hypothesis.

Given samples from a population, the equation for the sample skewness $g1$ is a biased estimator of the population skewness. The use of $G1$ or $b1$ is advisable. For large samples, the various skewness estimates yield similar results. For small normal distributed samples, $b1$ is less biased than $G1$. However, for small non-normal distributed samples, $G1$ is less biased than $b1$. These two skewness estimate can be sensitive to outliers in the data (contaminated data). Therefore, the medcouple `mc` is also an option in `type`. It has a good performance on uncontaminated data and is robust on contaminated data. For more information on medcouple, please read references and/or type `mc` (`robustbase::mc`).

Here, d'Agostino skewness test is based on `mc` with default settings:

$g1 = m3/m2^{(}3/2)$.
: where $m3$ is the sample third central moment, and $m2$ is the sample variance.
This is the typical definition used in many older textbooks.

$G1 = g1 * [k3/(k2^{(}3/2))] = g1 * [sqrtn(n-1)/(n-2)]$.
: where $k3$ is the unique symmetric unbiased estimator of the third cumulant and $k2$ is the symmetric unbiased estimator of the second cumulant.
Used in SAS and SPSS.

$b1 = m3/s^3 = g1((n-1)/n)^{(}3/2)$.
: Used in MINITAB and BMDP.

More will be added to this section especially for Anscombe-Glynn Kurtosis test.

Value

A list is returned with the following two components

`D`	Lilliefor results
`W'`	Shapiro-Francia results
`W`	Shapiro-Wilk results
`Zb1`	D'Agostino Skewness results
`Zb2`	Anscombe-Glynn Kurtosis results
`Chi^2`	D'Agostino Pearson results

Author(s)

Benoit Bruneau

References

D. N. Joanes and C. A. Gill (1998), Comparing measures of sample skewness and kurtosis. *The Statistician*, **47**, 183–189.

G. Brys, M. Hubert and A. Struyf (2003), A Comparison of Some NewMeasures of Skewness. in *Developments in Robust Statistics* **ICORS 2001**, eds. R. Dutter, P. Filzmoser, U. Gather, and P.J. Rousseeuw, Heidelberg: Springer-Verlag, 98–113

G. Brys, M. Hubert and A. Struyf (2004), A Robust Measure of Skewness; *JCGS* **13** (4), 996–1017.

See Also

`residuals`, `residuals.lm`, `residuals.glm`, and `residuals.gam`

Examples

```
x <- rnorm(300, 50, 10)
y  <- 5*(x +10*(rnorm(300,1,2)))

norm.test(x)            ## mc skewness
norm.test(x, type="G1") ## G1 skewness
norm.test(x, type="b1") ## b1 skewness

mod <- lm(y~x)
norm.test(mod)
```

`P.adjust` *Adjust P-values for Multiple Comparisons*

Description

Given a set of p-values, returns p-values adjusted using one of several methods. This is a modified version of `p.ajust` from `stats`. It now includes `"sidak"` correction.

Usage

```
P.adjust(p, method = P.adjust.methods, n = length(p))

P.adjust.methods
 c("holm", "hochberg", "hommel", "sidak", "bonferroni", "BH",
   "BY", "fdr", "none")
```

Arguments

`p`	vector of p-values (possibly with `NA`s).
`method`	correction method
`n`	number of pvalues considered for correction; only set this (to non-default) when you know what you are doing! See details

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"`), and Benjamini & Yekutieli (2001) (`"BY"`), respectively. A pass-through option (`"none"`) is also included. The `P.adjust.methods` vector containes the set of correction methods for the benefit of methods that need to have the method as an option and pass it on to `P.adjust`.

The first five 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"` 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.

When making multiple comparisons, `n` can be used to identify the number of comparisons that are actually used. Correction is then done on the full output matrix when only some of the comparisons are meaningfull or chosen for hypothesis testing. This can be done with the `"bonferroni"` and `"sidak"` correction. If other methods are used, exclude the unwanted `p.values` before applying correction. Unless you know what you are doing, **DO NOT** modify `n` if all comparisons are used. Most of the time `n` should be equal to `length(p)`.

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.t.test`, `mc.long`, `DTK.test`, `TukeyHSD` and `glht`

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))
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)
```

`pack.list` *List of installed packages*

Description

Create a text file containing the list of the packages currently installed in R.

Usage

```
pack.list(n.names=7)
```

Arguments

`n.names`	Number of package names to put per line of the output text file.

Author(s)

Benoit Bruneau

Examples

```
pack.list()
pack.list(5)
```

`pair.diff` *Mean differences matrix and their associated standard Errors*

Description

Creates two lower triangle matrix: The mean differences and their standard error.

Usage

```
pair.diff(y, ...)
## S3 method for class 'formula'
pair.diff(y, data=NULL ...)
## S3 method for class 'lm'
pair.diff( y, ...)
## Default S3 method:
pair.diff( y, group, data=NULL, ...)
```

Arguments

`y`	response variable for the default method, or `lm` or `formula` object. If `y` is a linear-model object or a formula, the variables on the right-hand-side of the model must all be factors and must be completely crossed.
`group`	for the default method, factor (concatenated factor when multiple factors). See details.
`data`	`data.frame` where the dependant variable and the factor(s) are.
`...`	additional arguments to pass to `mean` and/or `sd`.

Details

When group is manually defined, use `paste(x,y,z)` or `interaction(x,y,z)` form where `"x"`, `"y"` and `"z"` are the factors. There is no restrictions on the number of factors.

This function can be usefull with `pairwise.t.test` since the matrix created are of the same format.

Value

Object of class `"list"` containing two matrices:

`diff.m`	Mean differences half matrix
`diff.se`	Standard error associated with the mean differences half matrix

See Also

Is included in `mc.long` for the long format of the results.

Examples

```
z=data.frame( yy=c(rep("c",50),rep("d",50)),
              x=c(rnorm(50),rnorm(50,10)),
              s=rep(c(rep("a",25),rep("b",25)),2),
              qq=rep(c(rep("w",10),rep("t",10)),5))

mod=lm(x~yy*qq*s, data=z)
y= x~yy*qq*s

pair.diff(y=x, group= paste(yy,qq,s), data=z)
pair.diff(y=x, group= interaction(yy,qq,s), data=z)
pair.diff(y=y, data=z)
pair.diff(mod)
```

`performance` *performance*

Usage

```
performance(expr, samples = 1, gcFirst = TRUE)
```

Arguments

`expr`

`samples`

`gcFirst`

Examples

```
# will soon be available
```

`plot.mat` *Standard plot for maturity ogive*

Usage

```
xxx( data ,  ,  ,  )
```

Arguments

`data`

Author(s)

Benoit Bruneau

`plot.ypr` *Standard Yield per Recruit plot.*

Description

Yield per Recruit and Spawning Stock Biomass per Recruit are plotted with standard reference points.

Usage

```
 ## S3 method for class 'ypr'
plot.ypr(object, main, ylab.ypr, ylab.ssb, xlab, col.ypr, col.ssb, ref, legend)
```

Arguments

`object`	an object of class `"ypr"` resulting from a call to `ypr.l`
`main`	main title for the graph
`ylab.ypr`	a label for the YPR `y` axis
`ylab.ssb`	a label for the SSB/R `y` axis
`xlab`	a label for the YPR `x` axis.
`col.ypr`	the color of the the color of the YPR line.
`col.ssb`	the color of the the color of the SSB/R line.
`ref`	logical; if `TRUE`, standard reference points are added to the plot.
`legend`	logical; if `TRUE`, a legend is added in the `'topright'` corner of the plot.

Details

More to come.

See Also

`ypr.l`

Examples

```
ypr.mod = ypr.l(fsel.type=list("ramp",650,900), vonB=c(1564.512,0.1205765),
                l.start=72.53,last.age=25,LW=c(exp( -18.47894),3.043), F.max=2,
                F.incr.YPR=0.01, M=0.2, mat=list('full',900), f.MSP=0.4, riv.calc=F)

plot(ypr.mod)
```

`QQplot` *QQplot*

Usage

```
QQplot(dat, quant=TRUE,cex.q=2,norm=T, ...)
```

Arguments

`dat`	one of: • a numeric vector, • an object of class `"norm"` resulting from a call to `norm.test`
`quant`	logical; T for adding quantiles 75, 50 (median) and 25.
`cex.q`	numeric vector giving the amount by which plotting symbols should be magnified relative to the default
`norm`	logical; T adds a line to a normal quantile-quantile plot.
`...`	additional arguments to be passed (see `par`, `qqnorm`)

Examples

```
x=rnorm(50)
QQplot(x)

norm.x=norm.test(x)
QQplot(norm.x)
```

`r.colors` *Pie charts of all R character colors*

Description

Creates a pdf file with pie charts of all the 657 basic character colors of R

Usage

```
r.colors(file)
```

Arguments

`file`	the directory in which the pdf file will be created

Details

Define the directory in which the file should saved by writing `file="C:/temp"` for example. If file is not defined, it will be saved in `"C:/"` on windows and in `"home"` on Mac.

Value

None

Examples

```
r.colors()
```

`reject.z` *reject z*

Usage

```
reject.z(x, index = NULL, threshold = 2)
```

Arguments

```
x
index
threshold
```

Examples

```
# will soon be available
```

`replace.z` *replace z*

Usage

```
replace.z(x, index = NULL, threshold = 2)
```

Arguments

```
x
index
threshold
```

Examples

```
# will soon be available
```

`resid.ortho` *Orthogonal residuals*

Usage

```
xxx( data ,  ,  ,  )
```

Arguments

`data`

Author(s)

Benoit Bruneau

`rivard` *Rivard Weights Calculation*

Description

This function applies Rivard equations to mid-year weight at age data to adjust values to Jan-1 basis.

Usage

```
rivard(pds, pred=FALSE, K=2, plus.gr=FALSE)
```

Arguments

`data`

Details

More to come. Will be adding interpolation for spawning season.

Examples

```
x=rnorm(30,800,10)
rivard(data.frame("2000"=x,"2001"=x*1.2, "2002"=x*0.8,"2003"=x*0.5))
```

`rm.levels` *rm factor levels*

Usage

```
rm.levels(factor)
```

Arguments

```
factor
```

Examples

```
# will soon be available
```

`rollmin` *rollmin*

Usage

```
rollmin(x, k, na.pad = FALSE, align = c("center", "left", "right"),
        ...)
```

Arguments

x	
k	
na.pad	
align	
...	

Examples

```
# will soon be available
```

`roundup` *roundup*

Description

The ”conventional” rounding of 5 to the higher value

Usage

```
roundup(x, numdigits = 0)
```

Arguments

`x`	numeric vector.
`digits`	integer indicating the number of decimal places to be used.

Details

Rounds a 5 to the next value. Therefore roundup(2.5) is 3. This can be usefull when the rounded values are to be presented in a document (eg. table, graph,...).

When rounded values are used in other calculations, `round` should be used since it follows the IEC 60559 standard.

Value

numeric vector.

See Also

`round`

Examples

```
round(2.5)
roundup(2.5)
```

`runmax` *runmax*

Usage

```
runmax(x, window)
```

Arguments

```
x
window
```

Examples

```
# will soon be available
```

`runmean` *runmean*

Usage

```
runmean(x, window)
```

Arguments

```
x
window
```

Examples

```
# will soon be available
```

`runmin` *runmin*

Usage

```
runmin(x, window)
```

Arguments

```
x
window
```

Examples

```
# will soon be available
```

`s.an` *Simulations for YPR model*

Usage

```
xxx( data ,  ,  ,  )
```

Arguments

`data`

Author(s)

Benoit Bruneau

`se` *Standard Error*

Usage

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

Arguments

`x`	an R object (vector, matrix,...)
`na.rm`	a logical value indicating whether NA values should be stripped before the computation proceeds

Details

The standard error of the mean is usually estimated by the sample standard deviation divided by the square root of the sample size.

Examples

```
x=rnorm(50)
se(x)
```

`show.North` *North arrow for a map*

Description

Draws North arrow on a map

Usage

```
show.North(pos, arrow.col="black", arrow.fill="black", arrow.lwd=1,
           N.cex=1, N.family="HersheyGothicEnglish")
```

Arguments

`pos`	Position of the arrow. Default is `'topright'`. See details.
`arrow.col`	Arrow color.
`arrow.fill`	Color inside the head of the arrow. `NA` for no color.
`arrow.lwd`	Line width of the arrow.
`N.cex`	Character size for 'N'.
`N.family`	Font family of 'N'.

Details

The position of the north arrow is defined by `pos` and can either be numeric or character.

If `pos` is numeric, it is a vector of the form `c(x,y)` where `x` and `y` are fractions of the plotting region. If `x` and `y` are not in the range of `c(0,1)`, then the north arrow is drawn ouside the bounds of the plotting region and a warning message is given.

If `pos` is character, it is one of `c('topright','topleft','bottomright','bottomleft')`.

Examples

```
plot(1)
show.North()
show.North(c(0.8,0.9))
show.North(c(1.01,0.9))  ### gives a warning
```

`sort.vdf` *Sort Data Frames and Vectors*

Description

Single function enabling `data.frame` and `vector` sorting

Usage

```
sort.vdf(x, by, increasing=TRUE)
```

Arguments

`x`	`data.frame` or `vector`
`by`	A one-sided formula using + for ascending and - for descending. Sorting is left to right in the formula. This is for data.frame only.
`increasing`	logical. Should the sort be increasing `(TRUE)` or decreasing `(FALSE)`? This is for sorting vectors only.

Details

See example.

Author(s)

Kevin Wright and modified by Benoit Bruneau

Examples

```
x=rnorm(10)
y=runif(30)
z=data.frame(x,y)

sort.vdf(x)                 ### Sort a vector in increasing order
sort.vdf(z)                 ### Gives an error message
sort.vdf(z,by= ~ +x)        ### Sort (z) by a column (+x)
sort.vdf(z,by= ~ +x +y)     ### Sort (z) by two column (+x and then +y)
sort.vdf(z,by= ~ +x -y)     ### Sort (z) by two column (+x and then -y)
```

`summary.ypr` *Summarizing the results of YPR models.*

Description

`summary` method for class `"ypr"`.

Usage

```
## S3 method for class 'ypr'
summary(object)
```

Arguments

`object`	an object of class `"ypr"` resulting from a call to `ypr.l`.

Examples

```
ypr.mod = ypr.l(fsel.type=list("ramp",650,900), vonB=c(1564.512,0.1205765),
                l.start=72.53,last.age=25,LW=c(exp( -18.47894),3.043), F.max=2,
                F.incr.YPR=0.01, M=0.2, mat=list('full',900), f.MSP=0.4, riv.calc=F)

summary(ypr.mod)
```

`ttest.perm` *Student's t-tests by Permutation*

Description

Performs two sample t-tests or paired t-test by use of permutation

Usage

```
ttest.perm(vec1, vec2, nperm=999, alternative = "two.sided",
           var.equal = T, silent=FALSE, type="i", exact=FALSE)
```

Arguments

`vec1, vec2`	two numeric vectors used for Student's t-test analysis
`nperm`	number of permutations (default = 999)
`alternative`	one of the following: "two.sided", "less" or "greater".
`var.equal`	a logical variable indicating whether to treat the two variances as being equal (`TRUE`) or not (`FALSE`).
`silent`	a logical variable indicating whether calculation results are printed (`FALSE`) to the R console or not (`TRUE`).
`type`	one of the following: "i" for independant samples or "p" for paired samples.
`exact`	a logical variable indicating whether to perform the exact test (`TRUE`) or not (`FALSE`).

Details

The permutational t-test does not require normality of the distributions of each variable. It is also quite robust to heteroscedasticity.

Use `exact=TRUE` to perform two sample t-test on all the possible combination. This option can only be used when the sum of the sample sizes ($n_1 + n_2$) is smaller than 20. It is recommended to use this option when sample sizes are small. It is not implemented yet in the paired t-test.

`nperm` can not be higher than the maximum number of combination possible (n_{comb}).

$n_{comb} = N!/(n_1!n_2!)$

where `n_comb` is the number of possible combinations, $N!$ is `factorial`$(n_1 + n_2)$, $n_1!$ is `factorial(n(vec1))` and $n_2!$ is `factorial(n(vec2))`.

There is more to come in this section. plot(x)

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Value

`t.ref`	reference value of the t-statistic
`p.param`	parametric p-value
`p.perm`	permutational p-value
`nperm`	number of permutations
`perm.t`	list of the t statistics (only for independant sample ttest), starting with the reference value, followed by all values obtained under permutations.

Examples

```
x <- rnorm(50,0,1)
y <- runif(50,0,1)*x
toto = ttest.perm(x, y)  ##independant samples ttest
```

`unload` *Unload packages*

Description

Unloads one or multiple packages.

Usage

```
unload(pack)
```

Arguments

`pack`	Character vector specifying which packages to unload.

Author(s)

Benoit Bruneau

Examples

```
library(mgcv)
search()
unload(mgcv)
search()
```

`week.1` *week.1*

Description

Week of the year starting on the first of January (01-53)

Usage

```
week.1(x)
```

Arguments

`x`

Author(s)

Denis Chabot

Examples

```
# will soon be available
```

`week.num` *week.num*

Description

Week of the year as decimal number (00-53) using Sunday or Monday as the first day 1 of the week (and typically with the first Sunday of the year as day 1 of week 1).

Usage

```
week.num(x, day=c("sunday", "monday"))
```

Arguments

`x`	A vector of dates.
`day`	Either "sunday" or "monday". Default is "sunday".

Details

Argument `day` indicates if the week starts on `"sunday"` or `"monday"`.

Examples

```
dated <-as.Date(c("2006-05-18","2006-05-07","2006-04-23",
                  "2006-04-24","2006-05-07","2007-05-17",
                  "2007-05-06","2007-04-22","2007-04-29"))

week.num(dated, "monday")
week.num(dated)
```

`ypr.l` *Length Based Yield Per Recruit*

Description

Length based Yield Per Recruit model is define by fishery selectivity and life history parameters related to length.

Usage

```
ypr.l(fsel.type, last.age, age.step, vonB, l.start, LW, F.max, F.incr.YPR, mat,
        M, f.MSP, riv.calc=FALSE, F.f=0, M.f=0.5)
```

Arguments

`fsel.type`	a list containing the type of fishery selectivity and the values needed for the function related to the type. See 'Details'.
`last.age`	last age to be considered in the model
`age.step`	steps used to generate ages (`0:last.age`). Default is `1`.
`vonB`	a vector containing `c(Linf,K)` from von Bertalanffy grotwh curve.
`l.start`	length at the starting age
`LW`	a vector containing `c(alpha,beta)` from length-weight curve.
`F.max`	maximum value of instantaneous rate of fishing mortality (`F`). Default is `2`.
`F.incr.YPR`	increment for generating the `F` values to be used for YPR calculation. Default is `0.0001`.
`M`	instantaneous rate of natural mortality (`M`). Default is `0.2`.
`mat`	a list containing the type of maturity definition and the values needed for the function related to the type. See 'Details'.
`f.MSP`	reference point defined as the fraction of maximum spawning potential. Default is `0.4`.
`riv.calc`	a logical value indicating whether to use Rivard weights calculation (`TRUE`) or not. Default is `FALSE`.
`F.f`	fraction of instantaneous rate of fishing mortality (`F`) before spawning.
`M.f`	fraction of instantaneous rate of natural mortality (`M`) before spawning.

Details

More to come.

Author(s)

Benoit Bruneau

Examples

```
ypr.l(fsel.type=list("ramp",650,900), vonB=c(1564.512,0.1205765),
      l.start=72.53,last.age=25,LW=c(exp( -18.47894),3.043), F.max=2,
      F.incr.YPR=0.01, M=0.2, mat=list('full',900), f.MSP=0.4, riv.calc=F)
```

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