

# Package ‘bmisc’

March 13, 2012

**Type** Package

**Title** Miscellaneous functions

**Version** 0.2-13

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**URL** <http://r-forge.r-project.org/projects/bmisc/>

## Description

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

**Depends** car, lattice, zoo, robustbase, methods, tcltk

**License** LGPL >= 3.0

**Repository** R-Forge

**Repository/R-Forge/Project** bmisc

**Repository/R-Forge/Revision** 114

**LazyLoad** yes

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att.strp

*Attribute stripper***Description**

Strips an object of its attributes

**Usage**

```
att.strp(obj)
```

**Arguments**

obj                    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 `obj`.

**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. This is the Alpha version.

**Format**

Package:	bmisc
Type:	Package
Version:	0.2-13
Date:	2011-10-03
License:	LGPL >= 3.0
LazyLoad:	yes

**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**

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

**Details**

`min.val` is the minimum value accepted in a column. Columns 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**

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

**Value**

<code>Correlation</code>	Pearson r
<code>t.stat</code>	Calculated test statistic (t)
<code>No.perm</code>	number of permutations
<code>P.perm</code>	pvalue estimated by permutations
<code>P.param</code>	parametric pvalue estimated
<code>inf</code>	inferior limit of the confidence interval
<code>sup</code>	superior limit of the confidence interval
<code>df</code>	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**

<code>x</code>	an R object (vector, matrix,...)
<code>na.rm</code>	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, xint=NULL,
       xint=NULL, cap=0.05, ...)
```

**Arguments**

<code>x</code>	numeric vector
<code>y</code>	numeric vector
<code>xinf, xsup</code>	numeric vectors containing the upper ( <code>xsup</code> ) and/or lower ( <code>xinf</code> ) limits of the confidence interval for x-axis values.
<code>yinf, ysup</code>	numeric vectors containing the upper ( <code>ysup</code> ) and/or lower ( <code>yinf</code> ) limit of the confidence interval for y-axis values.
<code>xint</code>	numeric vectors containing the confidence intervals for x-axis values.
<code>yint</code>	numeric vectors containing the confidence intervals for y-axis values.
<code>...</code>	additional graphical arguments ( <a href="#">par</a> ) such as <code>col</code> , <code>lty</code> , <code>lwd</code> and/or arguments for <a href="#">arrows</a> .

**Details**

If `xint` and/or `yint` 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, yint=yci)

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

plot(x, y, ylim=c(min(y-yci), max(y+yci)), xlim=c(min(x-xci), max(x+xci)))
Errbar( x, y, yint=yci, xint=xci )
```

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

---

`fct`*Print bmisc functions*

---

**Description**

Print all functions of bmisc package

**Usage**

```
fct()
```

find.beta

*Logistic curve parameter estimates***Description**

Finds the parameters of a logistic curve for given inflection points.

**Usage**

```
find.beta(beta=0.5, minv, maxv, prop=0.01)
```

**Arguments**

beta	stating value of beta. Default is 0.5.
minv	the minimum value on the abscissa is the first inflection point.
maxv	the maximum value on the abscissa is the second inflection point.
prop	the proportion of the instantaneous slope at 50% probability that should be used to define the position of the inflection points of the curve. Default is 0.01.

**Details**

A logistic curve is defined by:

$$y = 1/(1 + e^{-(\alpha + \beta x)}) \iff 1/(1 + e^{-\beta(x - x_{50})})$$

Depending on the sign of  $\beta$ , the curve will be negative or positive.

**Value**

find.beta() returns a [data.frame](#) with the following columns:

beta	the estimated $\beta$ for the given inflection points.
alpha	the estimated $\alpha$ for the given inflection points.
x50	the value of $x$ when $y$ is 0.5 ( $x_{50}$ ).
angle.x50	the angle of the instantaneous slope at $x_{50}$ .
min	the value of the first inflection point.
max	the value of the second inflection point.
angle.infl	the angle of the instantaneous slope at the inflection points.

**Author(s)**

Benoit Bruneau

**See Also**

[deriv](#)

**Examples**

```
res1=find.beta(beta=0.1,minv=1000,maxv=1700, prop=0.01)
res2=find.beta(beta=0.1,minv=500,maxv=1700, prop=0.01)
par(mfrow=c(2,1))

xlim=c(0,res1$max+((res1$max-0)*0.2))

curve(1/(1+exp(-res1$beta*(x-res1$x50))), xlim=xlim, ylab="Probability",lwd=2)
abline(v=c(res1$max,res1$min,res1$x50), col=c("red","red","blue"))
lines(x=c(-500,res1$x50),y=c(0.5,0.5), lty=2, col=gray(0.4))
text(x=0,y=0.5,labels="x50", pos=3, col=gray(0.4))

curve(1/(1+exp(-res2$beta*(x-res2$x50))), xlim=xlim,ylab="Probability",lwd=2)
abline(v=c(res2$max,res2$min,res2$x50),, col=c("red","red","blue"))
lines(x=c(-500,res2$x50),y=c(0.5,0.5), lty=2, col=gray(0.4))
text(x=0,y=0.5,labels="x50", pos=3, col=gray(0.4))
```

---

<code>format.hms</code>	<i>Format seconds into hours</i>
-------------------------	----------------------------------

---

**Description**

Transforms time format

**Usage**

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

**Arguments**

<code>sec</code>	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("Theoretical Quantiles", "Linear Predictor",
                  "Residuals", "Fitted Values"),

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

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

**Arguments**

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

**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: <ul style="list-style-type: none"> <li>• a numeric vector</li> <li>• an object of class <code>c('norm', 'lm', 'aov', 'glm', 'gam')</code> resulting from a calls to <code>c(norm.test, lm, aov, glm, gam)</code></li> </ul>
breaks	one of: <ul style="list-style-type: none"> <li>• a vector giving the breakpoints between histogram cells,</li> <li>• a single number giving the number of cells for the histogram,</li> <li>• a character string naming an algorithm to compute the number of cells (see 'Details'),</li> <li>• a function to compute the number of cells.</li> </ul> <p>In the last three cases the number is a suggestion only.</p>
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 <code>c("all", "mean", "median")</code> . Default is NULL.
stat.lab	a character vector with the labels for the estimated mean and/or median. Default is <code>c("Mean", "Median")</code> .
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 <code>par</code> )

**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**

```
inv.pred( object, cf=1:2, y )
```

**Arguments**

<code>object</code>	an object of class <code>c('lm', 'glm')</code> resulting from a calls to <code>c(lm, glm)</code>
<code>cf</code>	the linear coefficients ( <code>'intercept'</code> , <code>'slope'</code> ) to be used.
<code>y</code>	the <code>y</code> value for which <code>x</code> will be estimated with it's standard error.

**Details**

More to come.

**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	<i>is odd</i>
--------	---------------

---

**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**

Testing for homoscedasticity after an ANOVA.

**Usage**

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

**Arguments**

y	response variable for the default method, lm class object for the lm method or formula class object for the formula method. 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).
data	<a href="#">data.frame</a> containing the dependant variable and the factor(s).
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 squared values

**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 factors.

**Value**

lev returns an object of class (S4) "lev".

An object of class "ypr" has the the following slots:

statistics	statistics for each test.
p.value	p-value for each test.
residuals	residuals for each test (r-scores for O'Briens test.

## References

- Brown, Morton B. and Alan B. Forsythe (1974). Robust Tests for Equality of Variances, J. Am. Statistical Assoc., 69, 364-367.
- Fligner, Michael A. and Timothy J. Killeen (1976). Distribution-free two sample tests for scale. J. Am. Statistical Assoc., 71: 210-213.
- Levene, Howard (1960). "Robust tests for equality of variances". In Ingram Olkin, Harold Hotelling, et alia. Stanford University Press. pp. 278-292.
- O'Brien, R.G. (1981). A simple test for variance effects in experimental designs. Psychological Bulletin, 89, 570-574.
- Conover, William J., Johnson, Mark E., and Myrle M. Johnson (1981). A comparative study of tests for homogeneity of variances, with applications to the outer continental shelf bidding data. Technometrics 23, 351-361.

## See Also

[fligner.test](#)

## 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	<i>Retreives the code for lib().</i>
----------	--------------------------------------

---

**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**

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

<code>coef</code>	Coefficients for fixed effects in object.
<code>cov</code>	Covariance matrix for fixed effects.
<code>expr</code>	Call expression (formula)
<code>contrast</code>	Type of contrasts (default is <code>attribute contrasts of object</code> )
<code>stratum</code>	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	<i>make z</i>
--------	---------------

---

**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, subset, ...)
## 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, subset, silent=FALSE, ...)
```

**Arguments**

y	response variable for the default method, or <code>lm</code> or <code>formula</code> 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	<code>data.frame</code> where the dependant variable and the factor(s) are
p.adjust.method	method for adjusting p values. Default is Holm's method. (see <code>P.adjust</code> )
column	new names for the factor(s); this is optional
digits	controls the number of digits for the presented results presented
subset	logical expression indicating elements to keep: missing values are taken as false.
silent	a logical variable indicating whether to indicate the general warning (FALSE) or not (TRUE).
...	additional arguments to pass to <code>p.adjust</code> , <code>pairwise.t.test</code> and/or <code>t.test</code> .

**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 meaningful 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	<i>Sample size</i>
---	--------------------

---

**Description**

Gives sample size (n) without NA's

**Usage**

```
n(x)
```

**Arguments**

x	Vector (numeric or character)
---	-------------------------------

**Examples**

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

```
length(x)    ### 93
```

```
n(x)         ### 90
```

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:
plot(norm.test(x, title=NULL, type=c("G1", "b1", "mc")))
```

## Arguments

x	one of: <ul style="list-style-type: none"> <li>a numeric vector</li> <li>an object of class <code>c('lm', 'aov', 'glm', 'gam')</code> resulting from a calls to <code>c(lm, aov, glm, gam)</code></li> </ul>
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 belonging to `c('lm', 'aov', 'glm', 'gam')` classes. 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 there are duplicate values, the more Shapiro-Wilk will be far from correctly testing the  $H_0$  hypothesis.

Given samples from a population, the equation for the sample skewness  $g_1$  is a biased estimator of the population skewness. The use of  $G_1$  or  $b_1$  is advisable. For large samples, the various skewness estimates yield similar results. For small normal distributed samples,  $b_1$  is less biased than  $G_1$ . However, for small non-normal distributed samples,  $G_1$  is less biased than  $b_1$ . 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 in `mc{robustbase}`.

- Typical definition used in many older textbooks:

$$g_1 = \frac{m_3}{m_2^{3/2}},$$

where  $m_3$  is the sample third central moment, and  $m_2$  is the sample variance.

- Definition used in SAS and SPSS:

$$G_1 = g_1 \frac{k_3}{k_2^{3/2}} = g_1 \frac{\sqrt{n(n-1)}}{n-2}$$

where  $k_3$  is the unique symmetric unbiased estimator of the third cumulant and  $k_2$  is the symmetric unbiased estimator of the second cumulant.

- Definition used in MINITAB and BMDP:

$$b_1 = \frac{m_3}{s^3} = g_1 \left( \frac{n-1}{n} \right)^{3/2}$$

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

### Value

An S4 object of class 'norm' containig the following components:

statistics	the statistics for each analysis
p.value	estimated p-values based on the statistics
data	original data (data.frame)
data.name	names of the object called
title	title for the result

### 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 New Measures 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.

### 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.adjust` 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 NAs).
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 contains 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 meaningful 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

Creates a character vector of currently installed packages and prints it to either a text file or directly into Rprofile file.

### Usage

```
pack.list(rprofile=FALSE)
```

### Arguments

<code>rprofile</code>	logical. Should vector of currently installed packages be added to the Rprofile (TRUE) or saved in a text file (FALSE)
-----------------------	--

### Details

**rprofile = FALSE**

A SAVE dialog box opens.

**rprofile = TRUE**

For Mac and Linux users, `.Rprofile` is either modified or created. On Windows systems, users are prompted for `Rprofile.site` location. This file is usually in "`C:/Program Files/R/R-x.xx.x/etc`". Once it's selected, the file is modified to include the list of packages currently installed in R.

### Author(s)

Benoit Bruneau

### See Also

[Startup](#) explains what happens when R starts.

### Examples

```
pack.list()
pack.list(rprofile=T)
```

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 <code>lm</code> or <a href="#">formula</a> 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	<code>data.frame</code> where the dependant variable and the factor(s) are.
...	additional arguments to pass to <a href="#">mean</a> and/or <a href="#">sd</a> .

**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	<i>performance</i>
-------------	--------------------

---

**Usage**

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

**Arguments**

```
expr  
samples  
gcFirst
```

**Examples**

```
# will soon be available
```

---

`plot.lev`*Plot Diagnostics for an lev Object*

---

**Description**

Four boxplots (selectable by `which`) are available.

**Usage**

```
plot(obj, which=1L:4L, ...)
```

**Arguments**

<code>obj</code>	an object of class 'lev' resulting from a calls to <a href="#">lev</a> .
<code>which</code>	if a subset of the plots is required, specify a subset of the numbers 1:4: <ul style="list-style-type: none"><li>• 1 : residuals of mean (Levene)</li><li>• 2 : residuals of trimmed mean (Robust Levene)</li><li>• 3 : residuals of median (Brown-Forsythe)</li><li>• 3 : r scores (O'Brien)</li></ul>
<code>...</code>	arguments to be passed to <a href="#">boxplot</a> .

**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)
res=lev(mod)

plot(res)
```

---

plot.logit

*Standard plot for maturity ogive*


---

### Usage

```
plot.logit(object, se.pred=TRUE, leg=TRUE, ref=TRUE, range.x=c("data", "full"),
           warn.val=TRUE, ylab="Probabilit ", xlab="Longueur C  la fourche (mm)",
           main=NULL, enc.utf8=FALSE)
```

### Arguments

object	an object of class 'glm' resulting from a call to <a href="#">glm</a> .
se.pred	logical; if TRUE, SE is plotted.
leg	logical; if TRUE, a legend containing logistic equation and estimated values for the variables is plotted.
ref	logical; if TRUE, reference lines for L90, L50 and L10 are plotted.
range.x	the range used to define xlim in the plot. Read 'details'.
warn.val	logical; if TRUE plots x01 and x99 when the fit is suspicious.
main	an overall title for the plot. If NULL ...
ylab	a title for the y axis.
xlab	a title for the x axis.
enc.utf8	logical; if TRUE, <a href="#">iconv</a> (x, "utf-8") is used on text in the graph. Read 'details'.

### Details

When using RConsole inside of Eclipse, encoding is wrong. The use of `enc.utf8=TRUE` is a temporary fix for correctly plotting characters with accents.

### Author(s)

Benoit Bruneau

---

QQplot*QQplot*

---

**Usage**

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

**Arguments**

dat	one of: <ul style="list-style-type: none"><li>• a numeric vector</li><li>• an object of class <code>c('norm', 'lm', 'aov', 'glm', 'gam')</code> resulting from a calls to <code>c(norm.test, lm, aov, glm, gam)</code></li></ul>
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 <a href="#">par</a> , <a href="#">qqnorm</a> )

**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()
```



---

<code>reject.z</code>	<i>reject z</i>
-----------------------	-----------------

---

**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	<i>Orthogonal residuals</i>
-------------	-----------------------------

---

**Usage**

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

**Arguments**

data

**Author(s)**

Benoit Bruneau

---

`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	<i>runmax</i>
--------	---------------

---

**Usage**

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

**Arguments**

```
x  
window
```

**Examples**

```
# will soon be available
```

---

runmean	<i>runmean</i>
---------	----------------

---

**Usage**

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

**Arguments**

```
x  
window
```

**Examples**

```
# will soon be available
```

---

runmin	<i>runmin</i>
--------	---------------

---

**Usage**

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

**Arguments**

```
x  
window
```

**Examples**

```
# will soon be available
```



---

se	<i>Standard Error</i>
----	-----------------------

---

**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 defined as:

$$SE = \frac{sd}{\sqrt{n}}$$

where *sd* is the standard deviation of the sample and *n* is the sample size.

**Examples**

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

---

show.North	<i>North arrow for a map</i>
------------	------------------------------

---

### 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 a numeric vector, 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  $[0, 1]$ , then the north arrow is drawn outside the bounds of the plotting region and a warning message is given.

If `pos` is a character vector, it should be a single keyword from:

- `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

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

---

ttest.perm	<i>Student's t-tests by Permutation</i>
------------	---

---

**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.

**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	<i>Unload packages</i>
--------	------------------------

---

**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**

<code>x</code>	A vector of dates.
<code>day</code>	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)
```



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