Package 'bmisc'

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Type Package

Title Miscellaneous functions

Version 0.2-12

Author Benoit Bruneau

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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
Version:	0.2-12
Date:	04-08-2011
License:	LGPL >= 3.0

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()
```

---

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:

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

Depending on the sign of β, the curve will be negative or positive.

Value

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

beta	the estimated β for the given inflection points.
alpha	the estimated α 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$beta*(x-res1$L50))), xlim=xlim, ylab="Probability")
abline(v=c(res1$max,res1$min,res1$L50), col=c("red","red","blue"))
lines(x=c(-500,res1$L50),y=c(0.5,0.5), lty=2, col=gray(0.4))
text(x=0,y=0.5,labels="L50", pos=3, col=gray(0.4))

curve(1/(1+exp(-res2$beta*(x-res2$L50))), xlim=xlim,ylab="Probability")
abline(v=c(res2$max,res2$min,res2$L50),, col=c("red","red","blue"))
lines(x=c(-500,res2$L50),y=c(0.5,0.5), lty=2, col=gray(0.4))
text(x=0,y=0.5,labels="L50", pos=3, col=gray(0.4))
```

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 c('norm','lm','aov','glm','gam') resulting from a calls to c(norm.test,lm,aov,glm,gam)

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

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

Arguments

object	an object of class c('lm','glm') resulting from a calls to c(lm,glm)
cf	the linear coefficients ('intercept','slope') to be used.
y	the y value for which x 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`   *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:
 plot(norm.test(x, title=NULL, type=c("G1","b1","mc")))
```

Arguments

x   one of:

                • a numeric vector
                • an object of class c('lm','aov','glm','gam') resulting from a calls
                  to c(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 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 $H0$ 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 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.

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 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 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.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="ProbabilitC)",xlab="Longueur C  la fourche (mm)")
```

Arguments

`object`	an object of class 'glm' resulting from a call to glm.
`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'.

Details

More to come.

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

```
## S4 method for signature 'ypr'
plot(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 `c('norm','lm','aov','glm','gam')` resulting from a calls to `c(`norm.test`,`lm`,`aov`,`glm`,`gam`)`
`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*

Description

Not ready yet. Use `for` loops for now.

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 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   *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 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

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 for an object of class `"ypr"`.

Usage

```
## S4 method for signature '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.

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(LW, vonB, l.start, last.age, age.step=1, Fsel.type,
      F.max=2,F.incr.YPR=0.0001, M.l,  M=0.2, f.MSP=0.4,
      F.f=0, M.f=0.5, riv.calc=FALSE)
```

Arguments

LW   one of:

                    • a vector containing $c(\alpha, \beta)$ from length-weight curve. See 'Details'.

                    • an object of class 'nls' in which α and β were estimated. See 'Details'.

vonB   one of:

                    • a vector containing c(Linf,K) from von Bertalanffy grotwh curve. See 'Details'.

                    • an object of class 'glm' in which eqnLinf and eqnK were estimated. See 'Details'.

l.start   length at the starting age

last.age   last age to be considered in the model

age.step   steps used to generate ages. Default is 1.

Fsel.type   one of:

                    • a list containing the type of fishery selectivity and the values needed for the function related to the type. See 'Details'.

                    • an object of class 'glm' in which α and β were estimated by a logistic regression. See 'Details'.

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.l   one of:

                    • a list containing the type of maturity at length definition and the values needed for the function related to the type. See 'Details'.

                    • an object of class 'glm' in which α and β were estimated by a logistic regression. See 'Details'.

M   instantaneous rate of natural mortality (M). Default is 0.2.

f.MSP   reference point defined as the fraction of maximum spawning potential. Default is 0.4.

F.f	fraction of instantaneous rate of fishing mortality (F) before spawning.
M.f	fraction of instantaneous rate of natural mortality (M) before spawning.
riv.calc	a logical value indicating whether to use Rivard weights calculation (TRUE) or not. Default is FALSE.

Details

Length-Weight relationship can be provided either by indicating $c(\alpha, \beta)$ values in a vector or by directly using an object of class 'nls' or 'lm'. If α and β are estimated by lm, log(x, base=exp(1)) transformation should be applied to the data prior to fitting the linear model. If an object resulting from nls is used, variables should be named **alpha** and **beta** using the following equation:

$$W = \alpha L^{\beta}$$

where W is weight, L is length, α is the elevation of the curve, and β is the steepness of the curve. Both α and β are coefficients estimated by the regression.

Von Bartalanffy growth equation parameters can be provided either by indicating c(Linf,K) values in a vector or by directly using an object of class 'nls'. If an object resulting from nls is used, variables should be named **Linf** and **K**. As for t_0, any name may be used since only L_∞ and K are used in this length-based YPR model. The equation used in the nls for estimating L_∞ and K should be the following one:

$$L_t = L_\infty \left(1 - e^{-K(t-t_0)} \right)$$

where L_t is length-at-age t, L_∞ is the asymptotic average maximum length, K is a growth rate coefficient determinant of how quick the maximum is attained, and t_0 is the hypothetical age at length zero.

As stated above, since this length-based YPR model uses relative age, $t - t_0$ becomes a relative age (a). The Von Bartalanffy growth equation used in this length-based YPR model is defined as:

$$L_a = L_\infty \left(1 - e^{-Ka} \right) + L_s e^{-Ka}$$

where L_a is length at a relative age a and L_s is length at relative age zero.

The **fishery selectivity** and **maturity at length** components of the model can be defined as one of c("full", "ramp", "logistic") equations. The proper way to specify which equation to use is by the construct of a list where the first element is the name of one of the three types of equation. The following elements of the list are specific to the type of equation:

- **full:** element [[2]] is the length at which full maturity is achieved.
- **ramp:** element [[2]] is the maximum length at which maturity is null and element [[3]] is the minimum length at which maturity is fully achieved.

- **logistic** elements [[2]] and [[3]] are respectively α and β components of a logistic curve.

Alternatively, an object of class 'glm' can directly be used for the **fishery selectivity** and **maturity at length** components. The Generalized Linear Model should have the option family set to either binomial or quasibinomial keeping link function to the default (*i.e.* "logit"). Estimated coefficients are use as follow:

$$y = \frac{1}{1 + e^{-(\alpha + \beta x)}}$$

Reference points used for result output are defined as:

- **F.zero:** F level when there is no fishing (F=0).
- **F.01:** F level where the slope of yield curve is 10% of the slope at F.zero.
- **F.xx:** F level where the MSP is at the level defined by f.MSP option. Default is 40% (0.4).
- **F.max:** F level where yield is maximum.

More to come.

Value

ypr.l returns an object of class(S4) "ypr". The functions summary and plot are used to respectively obtain a summary and a standard plot of the results.

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

parms	the list of parameters used in the model.
base	a data.frame containing the starting values:
	• relative age classes
	• length at age
	• weight at age
refs	a data.frame containing values predicted by the model for the four reference points. See details.
YPR	a data.frame containing the results for all partial Fs.

Note that to have access to each slot of an "ypr" object, one must use "@" instead of "$".

Author(s)

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See Also

plot.logit

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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