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management functions used by the Rcmdr package in the R Commander GUI for R.

License GPL (>= 2)

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NeedsCompilation no

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assignCluster	<i>Append a Cluster Membership Variable to a Dataframe</i>
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Description

Correctly creates a cluster membership variable that can be attached to a dataframe when only a subset of the observations in that dataframe were used to create the clustering solution. NAs are assigned to the observations of the original dataframe not used in creating the clustering solution.

Usage

```
assignCluster(clusterData, origData, clusterVec)
```

Arguments

clusterData	The data matrix used in the clustering solution. The data matrix may have only a subset of the observations contained in the original dataframe.
origData	The original dataframe from which the data used in the clustering solution were taken.
clusterVec	An integer variable containing the cluster membership assignments for the observations used in creating the clustering solution. This vector can be created using <code>cutree</code> for clustering solutions generated by <code>hclust</code> or the <code>cluster</code> component of a list object created by <code>kmeans</code> or <code>KMeans</code> .

Value

A factor (with integer labels) that indicate the cluster assignment for each observation, with an NA value given to observations not used in the clustering solution.

Author(s)

Dan Putler

See Also

[hclust](#), [cutree](#), [kmeans](#), [KMeans](#)

Examples

```
data(USArrests)
USArrkm3 <- KMeans(USArrests[USArrests$UrbanPop<66, ], centers=3)
assignCluster(USArrests[USArrests$UrbanPop<66, ], USArrests, USArrkm3$cluster)
```

Barplot

Bar Plots

Description

Create bar plots for one or two factors scaled by frequency or percentages. In the case of two factors, the bars can be divided (stacked) or plotted in parallel (side-by-side). This function is a front end to [barplot](#) in the **graphics** package.

Usage

```
Barplot(x, by, scale = c("frequency", "percent"), conditional=TRUE,
        style = c("divided", "parallel"),
        col=if (missing(by)) "gray" else rainbow_hcl(length(levels(by))),
        xlab = deparse(substitute(x)), legend.title = deparse(substitute(by)),
        ylab = scale, main=NULL, legend.pos = "above", ...)
```

Arguments

x	a factor.
by	optionally, a second factor.
scale	either "frequency" (the default) or "percent".
conditional	if TRUE then percentages are computed separately for each value of x (i.e., conditional percentages of by within levels of x); if FALSE then total percentages are graphed; ignored if scale="frequency".
style	for two-factor plots, either "divided" (the default) or "parallel".
col	if by is missing, the color for the bars, defaulting to "gray"; otherwise colors for the levels of the by factor in two-factor plots, defaulting to colors provided by rainbow_hcl in the colorspace package.

<code>xlab</code>	an optional character string providing a label for the horizontal axis.
<code>legend.title</code>	an optional character string providing a title for the legend.
<code>ylab</code>	an optional character string providing a label for the vertical axis.
<code>main</code>	an optional main title for the plot.
<code>legend.pos</code>	position of the legend, in a form acceptable to the legend function; the default, "above", puts the legend above the plot.
<code>...</code>	arguments to be passed to the barplot function.

Value

Returns NULL invisibly.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[barplot](#), [legend](#), [rainbow_hcl](#)

Examples

```
if (require(car)){
  data(Mroz)
  with(Mroz, {
    Barplot(wc)
    Barplot(wc, col="lightblue")
    Barplot(wc, by=hc)
    Barplot(wc, by=hc, scale="percent")
    Barplot(wc, by=hc, style="parallel",
            scale="percent", legend.pos="center")
  })
}
```

binnedCounts

Binned Frequency Distribution of Numeric Variables

Description

Bins a numeric variable, as for a histogram, and reports the counts in each bin. The computations are done by the [hist](#) function, but no histogram is drawn. If supplied a numeric matrix or data frame, the distribution of each column is printed.

Usage

```
binnedCounts(x, breaks="Sturges", name=deparse(substitute(x)))
```

Arguments

x	a numeric vector, matrix, or data frame.
breaks	specification of the breaks between bins, to be passed to the hist function.
name	name for the variable; only used for vector argument x.

Value

For a numeric vector, invisibly returns the vector of counts, named with the end-points of the corresponding bins. For a matrix or data frame, invisibly returns NULL

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[hist](#)

Examples

```
with(Prestige, binnedCounts(income))
binnedCounts(Prestige[, 1:4])
```

binVariable

Bin a Numeric Variable

Description

Create a factor dissecting the range of a numeric variable into bins of equal width, (roughly) equal frequency, or at "natural" cut points. The [cut](#) function is used to create the factor. `bin.var` is a synonym for `binVariable`, retained for backwards compatibility.

Usage

```
binVariable(x, bins = 4, method = c("intervals", "proportions", "natural"),
           labels = FALSE)
```

```
bin.var(...)
```

Arguments

x	numeric variable to be binned.
bins	number of bins.
method	one of "intervals" for equal-width bins; "proportions" for equal-count bins; "natural" for cut points between bins to be determined by a k-means clustering.

labels if FALSE, numeric labels will be used for the factor levels; if NULL, the cut points are used to define labels; otherwise a character vector of level names.
 ... arguments to be passed to binVariable.

Value

A factor.

Author(s)

Dan Putler, slightly modified by John Fox <jfox@mcmaster.ca> with the original author's permission.

See Also

[cut](#), [kmeans](#).

Examples

```
summary(binVariable(rnorm(100), method="prop", labels=letters[1:4]))
```

colPercents

Row, Column, and Total Percentage Tables

Description

Percentage a matrix or higher-dimensional array of frequency counts by rows, columns, or total frequency.

Usage

```
colPercents(tab, digits=1)
rowPercents(tab, digits=1)
totPercents(tab, digits=1)
```

Arguments

tab a matrix or higher-dimensional array of frequency counts.
 digits number of places to the right of the decimal place for percentages.

Value

Returns an array of the same size and shape as tab percentaged by rows or columns, plus rows or columns of totals and counts, or by the table total.

Author(s)

John Fox <jfox@mcmaster.ca>

Examples

```
if (require(car)){
  data(Mroz) # from car package
  cat("\n\n column percents:\n")
  print(colPercents(xtabs(~ lfp + wc, data=Mroz)))
  cat("\n\n row percents:\n")
  print(rowPercents(xtabs(~ hc + lfp, data=Mroz)))
  cat("\n\n total percents:\n")
  print(totPercents(xtabs(~ hc + wc, data=Mroz)))
  cat("\n\n three-way table, column percents:\n")
  print(colPercents(xtabs(~ lfp + wc + hc, data=Mroz)))
}
```

DeltaMethod

Confidence Intervals by the Delta Method

Description

DeltaMethod is a wrapper for the [deltaMethod](#) function in the **car** package. It computes the asymptotic standard error of an arbitrary, usually nonlinear, function of model coefficients, which are named b_0 (if there is an intercept in the model), b_1 , b_2 , etc., and based on the standard error, a confidence interval based on the normal distribution.

Usage

```
DeltaMethod(model, g, level = 0.95)
## S3 method for class 'DeltaMethod'
print(x, ...)
```

Arguments

model	a regression model; see the deltaMethod documentation.
g	the expression — that is, function of the coefficients — to evaluate, as a character string.
level	the confidence level, defaults to 0.95.
x	an object of class "DeltaMethod".
...	optional arguments to pass to print to show the results.

Value

DeltaMethod returns an objects of class "DeltaMethod", for which a print method is provided.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[deltaMethod](#) function in the **car** package

Examples

```
if (require(car)){
  DeltaMethod(lm(prestige ~ income + education, data=Duncan), "b1/b2")
}
```

discretePlot

Plot Distribution of Discrete Numeric Variable

Description

Plot the distribution of a discrete numeric variable, optionally classified by a factor.

Usage

```
discretePlot(x, by, scale = c("frequency", "percent"),
             xlab = deparse(substitute(x)), ylab = scale, main = "")
```

Arguments

x	a numeric variable.
by	optionally a factor by which to classify x.
scale	either "frequency" (the default) or "percent".
xlab	optional character string to label the horizontal axis.
ylab	optional character string to label the vertical axis.
main	optional main label for the plot (ignored if the by argument is specified).

Details

If the by argument is specified, then one plot is produced for each level of by; these are arranged vertically and all use the same scale for x.

Value

Returns NULL invisibly.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[Hist](#), [link{Dotplot}](#).

Examples

```
if (require(datasets)){
  data(mtcars)
  mtcars$cyl <- factor(mtcars$cyl)
  with(mtcars, {
    discretePlot(carb)
    discretePlot(carb, scale="percent")
    discretePlot(carb, by=cyl)
  })
}
```

Dotplot

Dot Plots

Description

Dot plot of numeric variable, either using raw values or binned, optionally classified by a factor. Dot plots are useful for visualizing the distribution of a numeric variable in a small data set.

Usage

```
Dotplot(x, by, bin = FALSE, breaks, xlim,
        xlab = deparse(substitute(x)))
```

Arguments

x	a numeric variable.
by	optionally a factor by which to classify x.
bin	if TRUE (the default is FALSE), the values of x are binned, as in a histogram, prior to plotting.
breaks	breaks for the bins, in a form acceptable to the hist function; the default is "Sturges".
xlim	optional 2-element numeric vector giving limits of the horizontal axis.
xlab	optional character string to label horizontal axis.

Details

If the by argument is specified, then one dot plot is produced for each level of by; these are arranged vertically and all use the same scale for x. An attempt is made to adjust the size of the dots to the space available without making them too big.

Value

Returns NULL invisibly.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[hist](#)

Examples

```
if (require(car)){
  data(Duncan)
  with(Duncan, {
    Dotplot(education)
    Dotplot(education, bin=TRUE)
    Dotplot(education, by=type)
    Dotplot(education, by=type, bin=TRUE)
  })
}
```

Gumbel

The Gumbel Distribution

Description

Density, distribution function, quantile function and random generation for the Gumbel distribution with specified location and scale parameters.

Usage

```
dgumbel(x, location = 0, scale = 1)
pgumbel(q, location=0, scale=1, lower.tail=TRUE)
qgumbel(p, location=0, scale=1, lower.tail=TRUE)
rgumbel(n, location=0, scale=1)
```

Arguments

x, q	vector of quantiles (values of the variable).
p	vector of probabilities.
n	number of observations. If $\text{length}(n) > 1$, the length is taken to be the number required.
location	location parameter (default 0); potentially a vector.
scale	scale parameter (default 1); potentially a vector.
lower.tail	logical; if TRUE (the default) probabilities and quantiles correspond to $P(X \leq x)$, if FALSE to $P(X > x)$.

Author(s)

John Fox <jfox@mcmaster.ca>

References

See https://en.wikipedia.org/wiki/Gumbel_distribution for details of the Gumbel distribution.

Examples

```
x <- 100 + 5*c(-Inf, -1, 0, 1, 2, 3, Inf, NA)
dgumbel(x, 100, 5)
pgumbel(x, 100, 5)

p <- c(0, .25, .5, .75, 1, NA)
qgumbel(p, 100, 5)

summary(rgumbel(1e5, 100, 5))
```

 Hist

Plot a Histogram

Description

This function is a wrapper for the [hist](#) function in the base package, permitting percentage scaling of the vertical axis in addition to frequency and density scaling.

Usage

```
Hist(x, groups, scale=c("frequency", "percent", "density"), xlab=deparse(substitute(x)),
     ylab=scale, main="", breaks = "Sturges", ...)
```

Arguments

x	a vector of values for which a histogram is to be plotted.
groups	a factor to create histograms by group with common horizontal and vertical scales.
scale	the scaling of the vertical axis: "frequency" (the default), "percent", or "density".
xlab	x-axis label, defaults to name of variable.
ylab	y-axis label, defaults to value of scale.
main	main title for graph, defaults to empty.
breaks	see the breaks argument for hist .
...	arguments to be passed to hist .

Value

This function is primarily called for its side effect — plotting a histogram or histograms — but it also invisibly returns an object of class `hist` or a list of `hist` objects.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

`hist`

Examples

```
data(Prestige, package="car")
Hist(Prestige$income, scale="percent")
with(Prestige, Hist(income, groups=type))
```

indexplot

Index Plots

Description

Index plots with point identification.

Usage

```
indexplot(x, labels = seq_along(x), id.method = "y", type = "h",
  id.n = 0, ylab, ...)
```

Arguments

<code>x</code>	a numeric variable, a matrix whose columns are numeric variables, or a numeric data frame; if <code>x</code> is a matrix or data frame, plots vertically aligned index plots for the columns.
<code>labels</code>	point labels; if <code>x</code> is a data frame, defaults to the row names of <code>x</code> , otherwise to the case index.
<code>id.method</code>	method for identifying points; see <code>showLabels</code> .
<code>type</code>	to be passed to <code>plot</code> .
<code>id.n</code>	number of points to identify; see <code>showLabels</code> .
<code>ylab</code>	label for vertical axis; if missing, will be constructed from <code>x</code> ; for a data frame, defaults to the column names.
<code>...</code>	to be passed to <code>plot</code> .

Value

Returns labelled indices of identified points or (invisibly) NULL if no points are identified or if there are multiple variables with some missing data.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[showLabels](#), [plot.default](#)

Examples

```
if (require("car")){
  with(Prestige, indexplot(income, id.n=2, labels=rownames(Prestige)))
  indexplot(Prestige[, c("income", "education", "prestige")], id.n=2)
}
```

KMeans

K-Means Clustering Using Multiple Random Seeds

Description

Finds a number of k-means clustering solutions using R's `kmeans` function, and selects as the final solution the one that has the minimum total within-cluster sum of squared distances.

Usage

```
KMeans(x, centers, iter.max=10, num.seeds=10)
```

Arguments

<code>x</code>	A numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a dataframe with all numeric columns).
<code>centers</code>	The number of clusters in the solution.
<code>iter.max</code>	The maximum number of iterations allowed.
<code>num.seeds</code>	The number of different starting random seeds to use. Each random seed results in a different k-means solution.

Value

A list with components:

cluster	A vector of integers indicating the cluster to which each point is allocated.
centers	A matrix of cluster centres (centroids).
withinss	The within-cluster sum of squares for each cluster.
tot.withinss	The within-cluster sum of squares summed across clusters.
betweenss	The between-cluster sum of squared distances.
size	The number of points in each cluster.

Author(s)

Dan Putler

See Also

[kmeans](#)

Examples

```
data(USArrests)
KMeans(USArrests, centers=3, iter.max=5, num.seeds=5)
```

lineplot

Plot a one or more lines.

Description

This function plots lines for one or more variables against another variable — typically time series against time.

Usage

```
lineplot(x, ..., legend)
```

Arguments

x	variable giving horizontal coordinates.
...	one or more variables giving vertical coordinates.
legend	plot legend? Default is TRUE if there is more than one variable to plot and FALSE if there is just one.

Value

Produces a plot; returns NULL invisibly.

Author(s)

John Fox <jfox@mcmaster.ca>

Examples

```
if (require("car")){
  data(Bfox)
  Bfox$time <- as.numeric(rownames(Bfox))
  with(Bfox, lineplot(time, menwage, womwage))
}
```

mergeRows

Function to Merge Rows of Two Data Frames.

Description

This function merges two data frames by combining their rows.

Usage

```
mergeRows(X, Y, common.only = FALSE, ...)
```

```
## S3 method for class 'data.frame'
mergeRows(X, Y, common.only = FALSE, ...)
```

Arguments

X	First data frame.
Y	Second data frame.
common.only	If TRUE, only variables (columns) common to the two data frame are included in the merged data set; the default is FALSE.
...	Not used.

Value

A data frame containing the rows from both input data frames.

Author(s)

John Fox

See Also

For column merges and more complex merges, see [merge](#).

Examples

```

if (require(car)){
  data(Duncan)
  D1 <- Duncan[1:20,]
  D2 <- Duncan[21:45,]
  D <- mergeRows(D1, D2)
  print(D)
  dim(D)
}

```

normalityTest

Normality Tests

Description

Perform one of several tests of normality, either for a variable or for a variable by groups. The `normalityTest` function uses the `shapiro.test` function or one of several functions in the **nortest** package. If tests are done by groups, then adjusted p-values, computed by the Holm method, are also reported (see `p.adjust`).

Usage

```

normalityTest(x, ...)

## S3 method for class 'formula'
normalityTest(formula, test, data, ...)

## Default S3 method:
normalityTest(x,
  test=c("shapiro.test", "ad.test", "cvm.test", "lillie.test",
        "pearson.test", "sf.test"),
  groups, vname, gname, ...)

```

Arguments

<code>x</code>	numeric vector or formula.
<code>formula</code>	one-sided formula of the form $\sim x$ or two-sided formula of the form $x \sim \text{groups}$, where x is a numeric variable and <code>groups</code> is a factor.
<code>data</code>	a data frame containing the data for the test.
<code>test</code>	quoted name of the function to perform the test.
<code>groups</code>	optional factor to divide the data into groups.
<code>vname</code>	optional name for the variable; if absent, taken from <code>x</code> .
<code>gname</code>	optional name for the grouping factor; if absent, taken from <code>groups</code> .
<code>...</code>	any arguments to be passed down; the only useful such arguments are for the <code>pearson.test</code> function in the nortest package.

Value

If testing by groups, the function invisibly returns NULL; otherwise it returns an object of class "hstest", which normally would be printed.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[shapiro.test](#), [ad.test](#), [cvm.test](#), [lillie.test](#), [pearson.test](#), [sf.test](#).

Examples

```
data(Prestige, package="car")
with(Prestige, normalityTest(income))
normalityTest(income ~ type, data=Prestige, test="ad.test")
normalityTest(~income, data=Prestige, test="pearson.test", n.classes=5)
```

numSummary

Summary Statistics for Numeric Variables

Description

numSummary creates neatly formatted tables of means, standard deviations, coefficients of variation, skewness, kurtosis, and quantiles of numeric variables.

Usage

```
numSummary(data,
  statistics=c("mean", "sd", "se(mean)", "IQR",
    "quantiles", "cv", "skewness", "kurtosis"),
  type=c("2", "1", "3"),
  quantiles=c(0, .25, .5, .75, 1), groups)

## S3 method for class 'numSummary'
print(x, ...)
```

Arguments

data	a numeric vector, matrix, or data frame.
statistics	any of "mean", "sd", "se(mean)", "quantiles", "cv" (coefficient of variation — sd/mean), "skewness", or "kurtosis", defaulting to c("mean", "sd", "quantiles", "IQR").
type	definition to use in computing skewness and kurtosis; see the skewness and kurtosis functions in the e1071 package. The default is "2".
quantiles	quantiles to report; default is c(0, 0.25, 0.5, 0.75, 1).

groups optional variable, typically a factor, to be used to partition the data.
 x object of class "numSummary" to print.
 ... arguments to pass down from the print method.

Value

numSummary returns an object of class "numSummary" containing the table of statistics to be reported along with information on missing data, if there are any.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[mean](#), [sd](#), [quantile](#), [skewness](#), [kurtosis](#).

Examples

```
if (require("car")){
  data(Prestige)
  Prestige[1, "income"] <- NA
  print(numSummary(Prestige[,c("income", "education")],
    statistics=c("mean", "sd", "quantiles", "cv", "skewness", "kurtosis")))
  print(numSummary(Prestige[,c("income", "education")], groups=Prestige$type))
  remove(Prestige)
}
```

partial.cor

Partial Correlations

Description

Computes a matrix of partial correlations between each pair of variables controlling for the others.

Usage

```
partial.cor(X, tests=FALSE, use=c("complete.obs", "pairwise.complete.obs"))
```

Arguments

X data matrix.
 tests show two-sided p-value and p-value adjusted for multiple testing by Holm's method for each partial correlation?
 use observations to use to compute partial correlations, default is "complete.obs".

Value

Returns the matrix of partial correlations, optionally with adjusted and unadjusted p-values.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[cor](#)

Examples

```
data(DavisThin, package="car")
partial.cor(DavisThin)
partial.cor(DavisThin, tests=TRUE)
```

plotBoot

Plot Bootstrap Distributions

Description

The function takes an object of class "boot" and creates an array of density estimates for the bootstrap distributions of the parameters.

Usage

```
plotBoot(object, confint=NULL, ...)
## S3 method for class 'boot'
plotBoot(object, confint=NULL, ...)
```

Arguments

object	an object of class "boot".
confint	an object of class "confint.boot" (or an ordinary 2-column matrix) containing confidence limits for the parameters in object; if NULL (the default), these are computed from the first argument, using the defaults for "boot" objects.
...	not used

Details

Creates an array of adaptive kernel density plots, using [densityPlot](#) in the **car** package, showing the bootstrap distribution, point estimate, and (optionally) confidence limits for each parameter.

Value

Invisibly returns the object produced by [densityPlot](#).

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[densityPlot](#)

Examples

```
## Not run:
plotBoot(Boot(lm(prestige ~ income + education + type, data=Duncan)))

## End(Not run)
```

plotDistr

Plot a probability density, mass, or distribution function.

Description

This function plots a probability density, mass, or distribution function, adapting the form of the plot as appropriate.

Usage

```
plotDistr(x, p, discrete=FALSE, cdf=FALSE,
          regions=NULL, col="gray",
          legend=TRUE, legend.pos="topright", ...)
```

Arguments

x	horizontal coordinates
p	vertical coordinates
discrete	is the random variable discrete?
cdf	is this a cumulative distribution (as opposed to mass) function?
regions, col	for continuous distributions only, if non-NULL, a list of regions to fill with color col; each element of the list is a pair of x values with the minimum and maximum horizontal coordinates of the corresponding region; col may be a single value or a vector.
legend	plot a legend of the regions (default TRUE).
legend.pos	position for the legend (see legend , default "topright").
...	arguments to be passed to plot.

Value

Produces a plot; returns NULL invisibly.

Author(s)

John Fox <jfox@mcmaster.ca>

Examples

```
x <- seq(-4, 4, length=100)
plotDistr(x, dnorm(x), xlab="Z", ylab="p(z)", main="Standard Normal Density")
plotDistr(x, dnorm(x), xlab="Z", ylab="p(z)", main="Standard Normal Density",
  region=list(c(1.96, Inf), c(-Inf, -1.96)), col=c("red", "blue"))
plotDistr(x, dnorm(x), xlab="Z", ylab="p(z)", main="Standard Normal Density",
  region=list(c(qnorm(0), qnorm(.025)), c(qnorm(.975), qnorm(1)))) # same

x <- 0:10
plotDistr(x, pbinom(x, 10, 0.5), xlab="successes",
  discrete=TRUE, cdf=TRUE,
  main="Binomial Distribution Function, p=0.5, n=10")
```

plotMeans

Plot Means for One or Two-Way Layout

Description

Plots cell means for a numeric variable in each category of a factor or in each combination of categories of two factors, optionally along with error bars based on cell standard errors or standard deviations.

Usage

```
plotMeans(response, factor1, factor2,
  error.bars = c("se", "sd", "conf.int", "none"),
  level=0.95, xlab=deparse(substitute(factor1)),
  ylab=paste("mean of", deparse(substitute(response))),
  legend.lab=deparse(substitute(factor2)),
  legend.pos=c("farright", "bottomright", "bottom", "bottomleft",
    "left", "topleft", "top", "topright", "right", "center"),
  main="Plot of Means",
  pch=1:n.levs.2, lty=1:n.levs.2, col=palette(), connect=TRUE, ...)
```

Arguments

response	Numeric variable for which means are to be computed.
factor1	Factor defining horizontal axis of the plot.
factor2	If present, factor defining profiles of means
error.bars	If "se", the default, error bars around means give plus or minus one standard error of the mean; if "sd", error bars give plus or minus one standard deviation; if "conf.int", error bars give a confidence interval around each mean; if "none", error bars are suppressed.

level	level of confidence for confidence intervals; default is .95
xlab	Label for horizontal axis.
ylab	Label for vertical axis.
legend.lab	Label for legend.
legend.pos	Position of legend; if "farright" (the default), extra space is left at the right of the plot.
main	Label for the graph.
pch	Plotting characters for profiles of means.
lty	Line types for profiles of means.
col	Colours for profiles of means
connect	connect profiles of means, default TRUE.
...	arguments to be passed to plot.

Value

The function invisibly returns NULL.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[interaction.plot](#)

Examples

```
if (require(car)){
  data(Moore)
  with(Moore, plotMeans(conformity, fcategory, partner.status, ylim=c(0, 25)))
}
```

rcorr.adjust

Compute Pearson or Spearman Correlations with p-Values

Description

This function uses the [rcorr](#) function in the **Hmisc** package to compute matrices of Pearson or Spearman correlations along with the pairwise p-values among the correlations. The p-values are corrected for multiple inference using Holm's method (see [p.adjust](#)). Observations are filtered for missing data, and only complete observations are used.

Usage

```
rcorr.adjust(x, type = c("pearson", "spearman"),
use=c("complete.obs", "pairwise.complete.obs"))

## S3 method for class 'rcorr.adjust'
print(x, ...)
```

Arguments

x	a numeric matrix or data frame, or an object of class "rcorr.adjust" to be printed.
type	"pearson" or "spearman", depending upon the type of correlations desired; the default is "pearson".
use	how to handle missing data: "complete.obs", the default, use only complete cases; "pairwise.complete.obs", use all cases with valid data for each pair.
...	not used.

Value

Returns an object of class "rcorr.adjust", which is normally just printed.

Author(s)

John Fox, adapting code from Robert A. Muenchen.

See Also

[rcorr](#), [p.adjust](#).

Examples

```
if (require(car)){
  data(Mroz)
  print(rcorr.adjust(Mroz[,c("k5", "k618", "age", "lwg", "inc")]))
  print(rcorr.adjust(Mroz[,c("k5", "k618", "age", "lwg", "inc")], type="spearman"))
}
```

readSAS

Read a SAS b7dat Data Set

Description

readSAS reads a SAS "b7dat" data set, stored in a file of type .sas7bdat, into an R data frame; it provides a front end to the [read_sas](#) function in the **haven** package.

Usage

```
readSAS(file, rownames=FALSE,
        stringsAsFactors=default.stringsAsFactors())
```

Arguments

`file` path to a SAS b7dat file.

`rownames` if TRUE (the default is FALSE), the first column in the data set contains row names (which must be unique—i.e., no duplicates).

`stringsAsFactors` if TRUE then columns containing character data are converted to factors; the default is taken from `default.stringsAsFactors()`.

Value

a data frame

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[read_sas](#)

readSPSS

Read an SPSS Data Set

Description

readSPSS reads an SPSS data set, stored in a file of type `.sav` or `.por`, into an R data frame; it provides a front end to the [read_spss](#) function in the **haven** package and the [read.spss](#) function in the **foreign** package.

Usage

```
readSPSS(file, rownames=FALSE, stringsAsFactors=default.stringsAsFactors(),
         tolower=TRUE, use.value.labels=TRUE, use.haven=!por)
```

Arguments

`file` path to an SPSS `.sav` or `.por` file.

`rownames` if TRUE (the default is FALSE), the first column in the data set contains row names, which should be unique.

`stringsAsFactors` if TRUE then columns containing character data are converted to factors and factors are created from SPSS value labels; the default is taken from `default.stringsAsFactors()`.

<code>tolower</code>	change variable names to lowercase, default TRUE.
<code>use.value.labels</code>	if TRUE, the default, variables with value labels in the SPSS data set will become either factors or character variables (depending on the <code>stringsAsFactors</code> argument) with the value labels as their levels or values. As for read.spss , this is only done if there are at least as many labels as values of the variable (and values without a matching label are returned as NA).
<code>use.haven</code>	use read_spss from the haven package to read the file, in preference to read.spss from the foreign package; the default is TRUE for a <code>.sav</code> file and FALSE for a <code>.por</code> file.

Value

a data frame

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[read_spss](#), [read.spss](#)

readStata	<i>Read a Stata Data Set</i>
-----------	------------------------------

Description

`readStata` reads a Stata data set, stored in a file of type `.dta`, into an R data frame; it provides a front end to the [read.dta13](#) function in the **readstata13** package.

Usage

```
readStata(file, rownames=FALSE, stringsAsFactors=default.stringsAsFactors(),
          convert.dates=TRUE)
```

Arguments

<code>file</code>	path to a Stata <code>.dta</code> file.
<code>rownames</code>	if TRUE (the default is FALSE), the first column in the data set contains row names, which should be unique.
<code>stringsAsFactors</code>	if TRUE then columns containing character data are converted to factors and factors are created from Stata value labels; the default is taken from <code>default.stringsAsFactors()</code> .
<code>convert.dates</code>	if TRUE (the default) then Stata dates are converted to R dates.

Value

a data frame

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[read.dta13](#)

readXL

Read an Excel File

Description

readXL reads an Excel file, either of type .xls or .xlsx into an R data frame; it provides a front end to the [read_excel](#) function in the **readxl** package. [excel_sheets](#) is re-exported from the **readxl** package and reports the names of spreadsheets in an Excel file.

Usage

```
readXL(file, rownames = FALSE, header = TRUE, na = "", sheet = 1,
        stringsAsFactors = default.stringsAsFactors())
```

```
excel_sheets(path)
```

Arguments

<code>file, path</code>	path to an Excel file.
<code>rownames</code>	if TRUE (the default is FALSE), the first column in the spreadsheet contains row names (which must be unique—i.e., no duplicates).
<code>header</code>	if TRUE (the default), the first row in the spreadsheet contains column (variable) names.
<code>na</code>	character string denoting missing data; the default is the empty string, "".
<code>sheet</code>	number of the spreadsheet in the file containing the data to be read; the default is 1.
<code>stringsAsFactors</code>	if TRUE then columns containing character data are converted to factors; the default is taken from <code>default.stringsAsFactors()</code> .

Value

a data frame

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[read_excel](#), [excel_sheets](#)

reliability

Reliability of a Composite Scale

Description

Calculates Cronbach's alpha and standardized alpha (lower bounds on reliability) for a composite (summated-rating) scale. Standardized alpha is for the sum of the standardized items. In addition, the function calculates alpha and standardized alpha for the scale with each item deleted in turn, and computes the correlation between each item and the sum of the other items.

Usage

```
reliability(S)

## S3 method for class 'reliability'
print(x, digits=4, ...)
```

Arguments

S	the covariance matrix of the items; normally, there should be at least 3 items and certainly no fewer than 2.
x	reliability object to be printed.
digits	number of decimal places.
...	not used: for compatibility with the print generic."

Value

an object of class reliability, which normally would be printed.

Author(s)

John Fox <jfox@mcmaster.ca>

References

N. Cliff (1986) Psychological testing theory. Pp. 343–349 in S. Kotz and N. Johnson, eds., *Encyclopedia of Statistical Sciences, Vol. 7*. Wiley.

See Also[cov](#)**Examples**

```

if (require(car)){
  data(DavisThin)
  reliability(cov(DavisThin))
}

```

stepwise

*Stepwise Model Selection***Description**

This function is a front end to the [stepAIC](#) function in the **MASS** package.

Usage

```

stepwise(mod,
  direction = c("backward/forward", "forward/backward", "backward", "forward"),
  criterion = c("BIC", "AIC"), ...)

```

Arguments

<code>mod</code>	a model object of a class that can be handled by <code>stepAIC</code> .
<code>direction</code>	if "backward/forward" (the default), selection starts with the full model and eliminates predictors one at a time, at each step considering whether the criterion will be improved by adding back in a variable removed at a previous step; if "forward/backwards", selection starts with a model including only a constant, and adds predictors one at a time, at each step considering whether the criterion will be improved by removing a previously added variable; "backwards" and "forward" are similar without the reconsideration at each step.
<code>criterion</code>	for selection. Either "BIC" (the default) or "AIC". Note that <code>stepAIC</code> labels the criterion in the output as "AIC" regardless of which criterion is employed.
<code>...</code>	arguments to be passed to <code>stepAIC</code> .

Value

The model selected by `stepAIC`.

Author(s)

John Fox <jfox@mcmaster.ca>

References

W. N. Venables and B. D. Ripley *Modern Applied Statistics Statistics with S, Fourth Edition* Springer, 2002.

See Also

[stepAIC](#)

Examples

```
# adapted from ?stepAIC in MASS
if (require(MASS)){
data(birthwt)
bwt <- with(birthwt, {
  race <- factor(race, labels = c("white", "black", "other"))
  ptd <- factor(ptl > 0)
  ftv <- factor(ftv)
  levels(ftv)[- (1:2)] <- "2+"
  data.frame(low = factor(low), age, lwt, race, smoke = (smoke > 0),
             ptd, ht = (ht > 0), ui = (ui > 0), ftv)
})
birthwt.glm <- glm(low ~ ., family = binomial, data = bwt)
print(stepwise(birthwt.glm, trace = FALSE))
print(stepwise(birthwt.glm, direction="forward/backward"))
}
```

summarySandwich

Linear Model Summary with Sandwich Standard Errors

Description

summarySandwich creates a summary of a "lm" object similar to the standard one, with sandwich estimates of the coefficient standard errors in the place of the usual OLS standard errors, also modifying as a consequence the reported t-tests and p-values for the coefficients. Standard errors may be computed from a heteroscedasticity-consistent ("HC") covariance matrix for the coefficients (of several varieties), or from a heteroscedasticity-and-autocorrelation-consistent ("HAC") covariance matrix.

Usage

```
summarySandwich(model, ...)

## S3 method for class 'lm'
summarySandwich(model,
  type=c("hc3", "hc0", "hc1", "hc2", "hc4", "hac"), ...)
```

Arguments

model	a linear-model object.
type	type of sandwich standard errors to be computed; see hccm in the car package, and vcovHAC in the sandwich package, for details.
...	arguments to be passed to <code>hccm</code> or <code>vcovHAC</code>

Value

an object of class "summary.lm", with sandwich standard errors substituted for the usual OLS standard errors; the omnibus F-test is similarly adjusted.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

[hccm](#), [vcovHAC](#).

Examples

```
mod <- lm(prestige ~ income + education + type, data=Prestige)
summary(mod)
summarySandwich(mod)
```

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