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Append a Cluster Membership Variable to a Dataframe

**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**

```r
assignCluster(clusterData, origData, clusterVec)
```
### Arguments

- **clusterData**: The data matrix used in the clustering solution. The data matrix may have 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 `cutree` for clustering solutions generated by `hclust` or the cluster component of a list object created by `kmeans` or `KMeans`.

### 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

```r
data(USArrests)
USArrk3 <- KMeans(USArrests[USArrests$UrbanPop<66, ], centers=3)
assignCluster(USArrests[USArrests$UrbanPop<66, ], USArrests, USArrk3$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

```r
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", label.bars=FALSE, ...)```

```
Arguments

- **x**: a factor (or character or logical variable).
- **by**: optionally, a second factor (or character or logical variable).
- **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.
- **xlab**: an optional character string providing a label for the horizontal axis.
- **legend.title**: an optional character string providing a title for the legend.
- **ylab**: an optional character string providing a label for the vertical axis.
- **main**: an optional main title for the plot.
- **legend.pos**: position of the legend, in a form acceptable to the legend function; the default, "above", puts the legend above the plot.
- **label.bars**: if TRUE (the default is FALSE) show values of frequencies or percents in the bars.
- **...**: arguments to be passed to the barplot function.

Value

Invisibly returns the horizontal coordinates of the centers of the bars.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

barplot, legend, rainbow_hcl

Examples

```r
with(Mroz, {
  Barplot(wc)
  Barplot(wc, col="lightblue", label.bars=TRUE)
  Barplot(wc, by=hc)
  Barplot(wc, by=hc, scale="percent", label.bars=TRUE)
  Barplot(wc, by=hc, style="parallel",
           scale="percent", legend.pos="center")
})
```
**binnedCounts**

**Binned Frequency Distributions of Numeric Variables**

**Description**

Bins a numeric variable, as for a histogram, and reports the count and percentage 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**

```r
binnedCounts(x, breaks="Sturges", round.percents=2, 
               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.
- `round.percents` number of decimal places to round percentages; default is 2.
- `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`, `discreteCounts`

**Examples**

```r
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**

```r
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**

```r
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

\[
\begin{align*}
\text{colPercents} & \text{ (tab, digits=1)} \\
\text{rowPercents} & \text{ (tab, digits=1)} \\
\text{totPercents} & \text{ (tab, digits=1)}
\end{align*}
\]

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

```r
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 b0 (if there is an intercept in the model), b1, b2, 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")
}


discreteCounts  

Frequency Distributions of Numeric Variables

Description

Computes the frequency and percentage distribution of a discrete numeric variable or the distributions of the variables in a numeric matrix or data frame.

Usage

discreteCounts(x, round.percents=2, name=deparse(substitute(x)), max.values=min(round(2*sqrt(length(x))), round(10*log10(length(x))), 100))

Arguments

x  
a discrete numeric vector, matrix, or data frame.

round.percents  
number of decimal places to round percentages; default is 2.

name  
name for the variable; only used for vector argument x.

max.values  
maximum number of unique values (default is the smallest of twice the square root of the number of elements in x, 10 times the log10 of the number of elements, and 100); if exceeded, an error is reported.

Value

For a numeric vector, invisibly returns the table of counts. For a matrix or data frame, invisibly returns NULL

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

binnedCounts

Examples

set.seed(12345) # for reproducibility
discreteCounts(data.frame(x=rpois(51, 2), y=rpois(51, 10)))
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 = "",
  xlim=NULL, ylim=NULL, ...)

Arguments

- **x**: a numeric variable.
- **by**: optionally a factor (or character or logical variable) 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).
- **xlim, ylim**: two-element numeric vectors specifying the ranges of the x and y axes; if not specified, will be determined from the data; the lower limit of the y-axis should normally be 0 and a warning will be printed if it isn’t.
- **...**: other arguments to be passed to plot.

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 the horizontal and vertical axes.

Value

Returns NULL invisibly.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

Hist, link(Dotplot).
Examples

```r
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

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

Arguments

- `x` a numeric variable.
- `by` optionally a factor (or character or logical variable) 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.
**Gumbel**

**The Gumbel Distribution**

**Description**

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

**Usage**

```r
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 `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 $P(X > x)$.
Hist

Author(s)

John Fox <jfox@mcmaster.ca>

References


Examples

```r
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

```r
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 (or character or logical variable) 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
```r
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
```r
indexplot(x, groups, labels = seq_along(x), id.method = "y", type = "h",
          id.n = 0, ylab, legend="topright", title, col=palette(), ...)
```

Arguments
- **x**: a numeric variable, a matrix whose columns are numeric variables, or a numeric data frame; if `x` is a matrix or data frame, plots vertically aligned index plots for the columns.
- **labels**: point labels; if `x` is a data frame, defaults to the row names of `x`, otherwise to the case index.
- **groups**: an optional grouping variable, typically a factor (or character or logical variable).
- **id.method**: method for identifying points; see `showLabels`.
- **type**: to be passed to `plot`.
- **id.n**: number of points to identify; see `showLabels`.
- **ylab**: label for vertical axis; if missing, will be constructed from `x`; for a data frame, defaults to the column names.
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

x 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).

centers The number of clusters in the solution.

iter.max The maximum number of iterations allowed.

num.seeds The number of different starting random seeds to use. Each random seed results in a different k-means solution.

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")],  
            groups = Prestige$type, id.n=2)  
}

KMeans legend keyword (see link[graphics]legend) giving location of the legend if groups are specified; if legend=FALSE, the legend is suppressed.

title title for the legend; may normally be omitted.

col vector of colors for the groups.

... to be passed to plot.
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

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

Description

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

Usage

```r
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 is there is just one.

Value

Produces a plot; returns NULL invisibly.


mergeRows

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.
normalityTest

Examples

```r
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

```r
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

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

Value

If testing by groups, the function invisibly returns NULL; otherwise it returns an object of class "htest", 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)

}
**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)

---

**piechart**

*Draw a Piechart With Percents or Counts in the Labels*

**Description**

piechart is a front-end to the standard R pie function, with the capability of adding percents or counts to the pie-segment labels.

**Usage**

piechart(x, scale = c("percent", "frequency", "none"),
         col = rainbow_hcl(nlevels(x)), ...)

**Arguments**

- **x**
  - a factor or other discrete variable; the segments of the pie correspond to the unique values (levels) of x and are proportional to the frequency counts in the various levels.

- **scale**
  - parenthetical numbers to add to the pie-segment labels; the default is "percent".

- **col**
  - colors for the segments; the default is provided by the rainbow_hcl function in the colorspace package.

- **...**
  - further arguments to be passed to pie.

**Author(s)**

John Fox <jfox@mcmaster.ca>

**See Also**

pie, rainbow_hcl
Examples

```r
with(Duncan, piechart(type))
```

plotBoot

---

### Description

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

### Usage

```r
plotBoot(object, confint=NULL, ...)
```

#### S3 method for class 'boot'

```r
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

```r
## 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
plotMeans(x, pbinom(x, 10, 0.5), xlab="successes", discrete=TRUE, cdf=TRUE, main="Binomial Distribution Function, p=0.5, n=10")

plotMeans

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.
rcorr.adjust

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.
**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**

```r
readSAS(file, rownames=FALSE, stringsAsFactors=FALSE)
```

**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 (the default is FALSE) then columns containing character data are converted to factors.

**Value**

- a data frame

**Author(s)**

John Fox <jfox@mcmaster.ca>
readSPSS

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=FALSE, 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 (the default is FALSE) then columns containing character data are converted to factors and factors are created from SPSS value labels.
tolower  change variable names to lowercase, default TRUE.
use.value.labels  if TRUE, the default, variables with value labels in the SPSS data set will become either factors or character variables (depending on the stringsAsFactors 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).
use.haven  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 .sav file and FALSE for a .por file.

Value

a data frame

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

read_spss, read.spss
readStata  
*Read a Stata Data Set*

**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**

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

**Arguments**

- `file` path to a Stata `.dta` 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 (the default is FALSE) then columns containing character data are converted to factors and factors are created from Stata value labels.
- `convert.dates` 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 = FALSE)

event_sheets(path)

Arguments

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

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


See Also
cov

Examples

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

repeatedMeasuresPlot  Plot Means for Repeated-Measures ANOVA Designs

Description

Creates a means plot for a repeated-measures ANOVA design with one or two within-subjects factor and zero or more between-subjects factors, for data in "wide" format.

Usage

repeatedMeasuresPlot(data, within, within.names, within.levels, between.names = NULL, response.name = "score", trace, xvar, pch=15:25, lty=1:6, col=palette()[-1], plot.means=TRUE, print.tables = FALSE)
Arguments

data a data frame in wide format.
within a character vector with the names of the data columns containing the repeated measures.
within.names a character vector with one or two elements, of names of the within-subjects factor(s).
within.levels a named list whose elements are character vectors of level names for the within-subjects factors, with names corresponding to the names of the within-subjects factors; the product of the numbers of levels should be equal to the number of repeated-measures columns in within.
between.names a column vector of names of the between-subjects factors (if any).
response.name optional quoted name for the response variable, defaults to "score".
trace optional quoted name of the (either within- or between-subjects) factor to define profiles of means in each panel of the graph; the default is the within-subjects factor with the smaller number of levels, if there are two, or not used if there is one.
xvar optional quoted name of the factor to define the horizontal axis of each panel; the default is the within-subjects factor with the larger number of levels.
pch, lty vectors of symbol and line-type numbers to use for the profiles of means (i.e., levels of the trace factor); for the meaning of the defaults, see points and par.
col vector of colors for the profiles of means; the default is given by palette(), starting at the second color.
plot.means if TRUE (the default), draw a plot of means by the factors.
print.tables if TRUE (the default is FALSE), print tables of means and standard deviations of the response by the factors.

Value

A "trellis" object, which normally is just "printed" (i.e., plotted).

Author(s)

John Fox <jfox@mcmaster.ca>

See Also

Anova, OBrienKaiser

Examples

if (require(carData)){
  repeatedMeasuresPlot(
    data=OBrienKaiser,
    within=c("pre.1", "pre.2", "pre.3", "pre.4", "pre.5",
             "post.1", "post.2", "post.3", "post.4", "post.5",
             "fup.1", "fup.2", "fup.3", "fup.4", "fup.5"),
    ...
reshapeL2W

Reshape Repeated-Measures Data from Long to Wide Format

Description

A simple front-end to the standard R reshape function. The data are assumed to be in "long" format, with several rows for each subject.

Usage

reshapeL2W(data, within, id, varying, ignore)

Arguments

data a data frame in long format.
within a character vector of names of the within-subjects factors in the long form of the data; there must be at least one within-subjects factor.
id the (character) name of the variable representing the subject identifier in the long form of the data set; that is, rows with the same id belong to the same subject.
varying a character vector of names of the occasion-varying variables in the long form of the data; there must be at least one such variable, and typically there will be just one, an occasion-varying response variable.

ignore an optional character vector of names of variables in the long form of the data to exclude from the wide data set.

Details

Between-subjects variables don’t vary by occasions for each subject. Variables that aren’t listed explicitly in the arguments to the function are assumed to be between-subjects variables, and a warning is printed if their values aren’t invariant for each subject (see the ignore argument).

Within-subjects factors vary by occasions for each subject, and it is assumed that the within-subjects design is regular, completely crossed, and balanced, so that the same combinations of within-subjects factors are observed for each subject.

Occasion-varying variables, as their name implies, (potentially) vary by occasions for each subject, and include one or more “response” variables, possibly along with occasion-varying covariates; these variables can be factors as well as numeric variables.

The data are reshaped so that there is one row per subject, with columns for the between-subjects variables, and each occasion-varying variable as multiple columns representing the combinations of levels of the within-subjects factors. The names of the columns for the occasion-varying variables are composed from the combinations of levels of the within-subjects factors and from the names of the occasion-varying variables. If a subject in the long form of the data set lacks any combination of levels of within-subjects factors, he or she is excluded (with a warning) from the wide form of the data.

Value

a data frame in “wide” format, with one row for each subject, columns representing the between-subjects factors, and columns for the occasion-varying variable(s) for each combination of within-subjects factors.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also


Examples

if (require(carData)){
  OBW <- reshapeL2W(O'BrienKaiserLong,
                   within=c("phase", "hour"),
                   id="id", varying="score")
  brief(OBW)
  # should be the same as O'BrienKaiser in the carData package:
  all.equal(O'BrienKaiser, OBW, check.attributes=FALSE)
}
Reshape Repeated-Measures Data from Wide to Long Format

Description

The data are assumed to be in "wide" format, with a single row for each subject, and different columns for values of one or more repeated-measures variables classified by one or more within-subjects factors.

Usage

reshapeW2L(data, within, levels, varying, ignore, id = "id")

Arguments

data : wide version of data set.
within : a character vector of names for the crossed within-subjects factors to be created in the long form of the data.
levels : a named list of character vectors, each element giving the names of the levels for a within-subjects factor; the names of the list elements are the names of the within-subjects factor, given in the within argument.
varying : a named list of the names of variables in the wide data set specifying the occasion-varying variables to be created in the long data set; each element in the list is named for an occasion-varying variable and is a character vector of column names in the wide data for that occasion-varying variable.
ignore : a character vector of names of variables in the wide data to be dropped in the long form of the data.
id : the (character) name of the subject ID variable to be created in the long form of the data, default "id".

Details

Between-subjects variables don’t vary by occasions for each subject. Variables that aren’t listed explicitly in the arguments to the function are assumed to be between-subjects variables. The values of these variables are duplicated in each row pertaining to a given subject.

Within-subjects factors vary by occasions for each subject, and it is assumed that the within-subjects design is regular, completely crossed, and balanced, so that the same combinations of within-subjects factors are observed for each subject. There are typically one or two within-subject factors.

Occasion-varying variables, as their name implies, (potentially) vary by occasions for each subject, and include one or more "response" variables, possibly along with occasion-varying covariates; these variables can be factors as well as numeric variables. Each occasion-varying variable is encoded in multiple columns of the wide form of the data and in a single column in the long form. There is typically one occasion-varying variable, a response variable.

There is one value of each occasion-varying variable for each combination of levels of the within-subjects factors. Thus, the number of variables in the wide data for each occasion-varying variable
must be equal to the product of levels of the within-subjects factors, with the levels of the within-subjects factors varying most quickly from right to left in the within argument.

Value

a data frame in "long" format, with multiple rows for each subject (equal to the number of combinations of levels of the within-subject factors) and one column for each between-subjects and occasion-varying variable.

Author(s)

John Fox <jfox@mcmaster.ca>

See Also


Examples

if (require(carData)){
  OBrienKaiserL <- reshapeW2L(OBrienKaiser, within=c("phase", "hour"),
    levels=list(phase=c("pre", "post", "fup"), hour=1:5),
    varying=list(score=c("pre.1", "pre.2", "pre.3", "pre.4", "pre.5",
      "post.1", "post.2", "post.3", "post.4", "post.5",
      "fup.1", "fup.2", "fup.3", "fup.4", "fup.5")),
    brief(OBrienKaiserL, c(15, 15))
  m1 <- tapply(score ~ phase + hour + treatment + gender, mean, data=OBrienKaiserL)
  m2 <- tapply(score ~ phase + hour + treatment + gender, mean, data=subset(OBrienKaiserLong, hour==1))
  all.equal(m1, m2) # should be equal
}

if (require(carData)){
  OBrienKaiserL2 <- reshapeW2L(OBrienKaiser, within="phase",
    levels=list(phase=c("pre", "post", "fup")),
    ignore=c("pre.2", "pre.3", "pre.4", "pre.5",
      "post.2", "post.3", "post.4", "post.5",
      "fup.2", "fup.3", "fup.4", "fup.5"),
    varying=list(score=c("pre.1", "post.1", "fup.1")),
    brief(OBrienKaiserL2, c(6, 6))
  m1 <- tapply(score ~ phase + treatment + gender, mean, data=OBrienKaiserL2)
  m2 <- tapply(score ~ phase + treatment + gender, mean,
    data=subset(OBrienKaiserLong, hour==1))
  all.equal(m1, m2) # should be equal
}
**stepwise**  

*Stepwise Model Selection*

**Description**

This function is a front end to the `stepAIC` function in the **MASS** package.

**Usage**

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

**Arguments**

- `mod`: a model object of a class that can be handled by `stepAIC`.
- `direction`: 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.
- `criterion`: for selection. Either "BIC" (the default) or "AIC". Note that `stepAIC` labels the criterion in the output as "AIC" regardless of which criterion is employed.
- `...`: arguments to be passed to `stepAIC`.

**Value**

The model selected by `stepAIC`.

**Author(s)**

John Fox <jfox@mcmaster.ca>

**References**


**See Also**

`stepAIC`
Examples

```r
# 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)[c(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))
p
```

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

```r
summarySandwich(model, ...)
```

## S3 method for class 'lm'

```r
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 hccm or vcovHAC

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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