Package: HH (via r-universe)

September 11, 2024

Type Package

Title Statistical Analysis and Data Display: Heiberger and Holland

Version 3.1-52

Date 2024-02-10

Author Richard M. Heiberger

Maintainer Richard M. Heiberger <rmh@temple.edu>

Depends R (>= 3.0.2), lattice, stats, grid, latticeExtra, multcomp, gridExtra (>= 2.0.0), graphics

Imports reshape2, leaps, vcd, colorspace, RColorBrewer, shiny (>= 0.13.1), Hmisc, abind, Rmpfr (>= 0.6.0), grDevices, methods

Suggests mvtnorm, car, Rcmdr, RcmdrPlugin.HH, microplot

Description Support software for Statistical Analysis and Data Display (Second Edition, Springer, ISBN 978-1-4939-2121-8, 2015) and (First Edition, Springer, ISBN 0-387-40270-5, 2004) by Richard M. Heiberger and Burt Holland. This contemporary presentation of statistical methods features extensive use of graphical displays for exploring data and for displaying the analysis. The second edition includes redesigned graphics and additional chapters. The authors emphasize how to construct and interpret graphs, discuss principles of graphical design, and show how accompanying traditional tabular results are used to confirm the visual impressions derived directly from the graphs. Many of the graphical formats are novel and appear here for the first time in print. All chapters have exercises. All functions introduced in the book are in the package. R code for all examples, both graphs and tables, in the book is included in the scripts directory of the package.

License GPL (>= 2)

NeedsCompilation no

Date/Publication 2024-02-11 00:00:02 UTC

Repository https://rmheiberger.r-universe.dev

RemoteUrl https://github.com/cran/HH

RemoteRef HEAD

RemoteSha dbcae2570dc57c07e1b7e709df23e4028ae8aca1

Contents

`HH-package` *Statistical Analysis and Data Display: Heiberger and Holland*

Description

Support software for Statistical Analysis and Data Display (Second Edition, Springer, ISBN 978-1-4939-2121-8, 2015) and (First Edition, Springer, ISBN 0-387-40270-5, 2004) by Richard M. Heiberger and Burt Holland. This contemporary presentation of statistical methods features extensive use of graphical displays for exploring data and for displaying the analysis. The second edition includes redesigned graphics and additional chapters. The authors emphasize how to construct and interpret graphs, discuss principles of graphical design, and show how accompanying traditional tabular results are used to confirm the visual impressions derived directly from the graphs. Many of the graphical formats are novel and appear here for the first time in print. All chapters have exercises. All functions introduced in the book are in the package. R code for all examples, both graphs and tables, in the book is included in the scripts directory of the package.

Details

The DESCRIPTION file:

Package:	HH
Type:	Package
Title:	Statistical Analysis and Data Display: Heiberger and Holland
Version:	3.1-52
Date:	2024-02-10
Author:	Richard M. Heiberger
Maintainer:	Richard M. Heiberger <rmh@temple.edu>
Depends:	R (>= 3.0.2), lattice, stats, grid, latticeExtra, multcomp, gridExtra (>= 2.0.0), graphics
Imports:	reshape2, leaps, vcd, colorspace, RColorBrewer, shiny (>= 0.13.1), Hmisc, abind, Rmpfr (>= 0.6.0), grDevices
Suggests:	mvtnorm, car, Rcmdr, RcmdrPlugin.HH, microplot
Description:	Support software for Statistical Analysis and Data Display (Second Edition, Springer, ISBN 978-1-4939-2121-
License:	GPL (>= 2)

Index of help topics:

```
AEdotplot               AE (Adverse Events) dotplot of incidence and
                        relative risk
AEdotplot.data.frame    AE (Adverse Events) dotplot of incidence and
```

	relative risk, support functions
CIplot	Illustration of the meaning of confidence levels.
Discrete4	Discrete with four levels color dataset.
EmphasizeVerticalPanels	Helper function for likertWeighted(). used for vertical spacing and horizontal borders of grouped panels.
F.curve	plot a chisquare or a F-curve.
GSremove	Remove selected GraphSheetPages in the S-Plus Windows GUI Graphsheet
HH-package	Statistical Analysis and Data Display: Heiberger and Holland
HH.regsubsets	Display tabular results for Best Subsets Regression.
HHscriptnames	Find absolute pathname of a script file for the HH book in the HH package.
InsertVerticalPanels	Expand a 3D array on the second dimension, inserting empty layers where the input vector has a '0' value. A 2D argument 'x' with 'dim(x)==c(r,c)' is first extended to 3D with 'dim(x)==c(1,r,c)', and then the result is collapsed back to 2D.
LikertPercentCountColumns	Display likert plots with percents in the first column of panels and counts in the second column of panels.
NTplot	Specify plots to illustrate Normal and t Hypothesis Tests or Confidence Intervals, including normal approximation to the binomial.
NormalAndTPower	Construct a power graph based on the NTplot.
NormalAndTplot	Specify plots to illustrate Normal and t Hypothesis Tests or Confidence Intervals.
OddsRatio	Calculate or plot the odds ratio for a 2x2 table of counts.
OneWayVarPlot	Displays a three-panel 'bwplot' of the data by group, of the group means, and of the entire dataset. This is an approximate visualization of the Mean Square lines from the ANOVA table for a one-way ANOVA model.
ResizeEtc	Display multiple independent trellis objects on the same coordinated scale.
ResizeEtc.likertPlot	Display multiple independent trellis objects, representing likert plots, on the same coordinated scale.
ToBW.likert	Change colors in a likert plot to shades of Black and White.
X.residuals	Residuals from the regression of each column of

	a data.frame against all the other columns.
ae.dotplot	AE (Adverse Events) dotplot of incidence and relative risk
ancova	Compute and plot oneway analysis of covariance
ancova-class	Class "ancova" Analysis of Covariance
ancovaplot	Analysis of Covariance Plots
anova.ancovaplot	ANOVA table for a c("ancovaplot","trellis") object.
anovaMean	ANOVA table from the group sample sizes, means, and standard deviations.
aovSufficient	Analysis of variance from sufficient statistics for groups.
arima.diag.hh	Repair design error in S-Plus arima.diag
arma.loop	Loop through a series of ARIMA models and display coordinated tables and diagnoastic graphs.
as.likert	Support functions for diverging stacked barcharts for Likert, semantic differential, and rating scale data.
as.matrix.listOfNamedMatrices	Convert a list of numeric matrices to a single matrix
as.multicomp	Support functions in R for MMC (mean-mean multiple comparisons) plots.
as.rts	Miscellaneous functions that I wish were in or consistent between S-Plus and R.
as.vector.trellis	Convert a two-dimensional trellis object into a one-dimensional trellis object. Change the order of panels in a trellis object.
axis.i2wt	specialized axis function for interaction2wt.
bivariateNormal	Plot the bivariate normal density using wireframe for specified rho.
case	case statistics for regression analysis
ci.plot	Plot confidence and prediction intervals for simple linear regression
col.hh	Initializing Trellis Displays
col3x2	col3x2 color dataset
combineLimits.trellisvector	Combine limits on a one-dimensional trellis object.
cp.calc	Rearranges and improves the legibility of the output from the stepwise function in S-Plus.
cplx	Generate a sequence spanning the xlim of a lattice window.
datasets	Datasets for Statistical Analysis and Data Display, Heiberger and Holland
dchisq.intermediate	Intermediate f and chisq functions to simplify writing for both R and S-Plus.

diag.maybe.null	Returns a value for the diagonal of NA and NULL arguments.
diagQQ	QQ plot of regression residuals.
diagplot5new	Transpose of ECDF for centered fitted values and residuals from a linear model.
do.formula.trellis.xysplom	Interprets model formulas for xysplom and extended bwplots
emptyMainLeftAxisLeftStripBottomLegend	Remove main title, left axis tick labels, left strip, bottom legend from plot and keep the vertical spacing allocated to those items.
export.eps	Exports a graph to an EPS file.
glhtWithMCP.993	Retain averaging behavior that was previously available in glht.
gof.calculation	Calculate Box-Ljung Goodness of Fit for ARIMA models in S-Plus.
grid.yaxis.hh	make x- and y-axis labels
hhpdf	R tools for writing HH2: hhpdf, hhdev.off, hhcapture, hhcode, hhpng, hhlatex
hov	Homogeneity of Variance
hovBF	Homogeneity of Variance: Brown-Forsyth method
hovPlot	Homogeneity of Variance Plot
if.R	Conditional Execution for R or S-Plus
interaction.positioned	interaction method for positioned factors.
interaction2wt	Plot all main effects and twoway interactions in a multifactor design
interval	Prediction and Confidence Intervals for glm Objects
intxplot	Interaction plot, with an option to print standard error bars.
ladder	Draw a "ladder of powers" plot, plotting each of several powers of y against the same powers of x.
latex.array	Generate the latex code for an '"array"' or '"table"' with 3, 4, or more dimensions.
latticeresids	Subroutine used by residual.plots.lattice
legendGrob2wt	place separate keys to the left of each row of a trellis
likert	Diverging stacked barcharts for Likert, semantic differential, rating scale data, and population pyramids.
likertColor	Selection of colors for Likert plots.
likertMosaic	Diverging stacked barcharts for Likert, semantic differential, rating scale data, and population pyramids based on mosaic as the plotting style.

likertWeighted	Special case wrapper for likert() when multiple columns are to have the same bar thicknesses. Uses formula with one or two conditioning variables.
lm.regsubsets	Evaluate lm model with highest adjusted R^2.
lmatPairwise	lmatPairwise
lmatRows	Find the row numbers in the lmat corresponding to the focus factor.
lmplot	Four types of residual plots for linear models.
logit	Logistic and odds functions and their inverses.
matrix.trellis	Convert a one-dimensional trellis object to a two-dimensional trellis object. This permits combineLimits and useOuterStrips to work.
mcalinfct	MCA multiple comparisons analysis (pairwise)
mmc	MMC (Mean-mean Multiple Comparisons) plots.
mmc.mean	MMC (Mean-mean Multiple Comparisons) plots from the sufficient statistics for a one-way design.
mmcAspect	Control aspect ratio in MMC plots to maintain isomeans grid as a square.
mmcPruneIsomeans	MMC plots in lattice-suppress isomeans grid lines for specified levels of the factor.
mmcisomeans	Functions used by mmcplot.
mmcplot	MMC (Mean-mean Multiple Comparisons) plots in lattice.
multicomp.order	Update a multicomp object by ordering its contrasts.
multicomp.reverse	Force all comparisons in a "multicomp" object to have the same sign.
norm.curve	plot a normal or a t-curve with both x and z axes.
normalApproxBinomial	Plots to illustrate Normal Approximation to the Binomial-hypothesis tests or confidence intervals.
npar.arma	Count the number of parameters in an ARIMA model specification.
objip	loop through all attached directories looking for pattern, possibly restricting to specified class or mode.
orthog.complete	Construct an orthogonal matrix which is an arbitrary completion of the column space of the input set of columns.
panel.acf	Panel functions for tsdiagplot.
panel.axis.right	Right-justify right-axis tick labels.
panel.bwplot.intermediate.hh	Panel functions for bwplot.
panel.bwplot.superpose	Panel function for bwplot that displays an entire box in the colors coded by groups.

panel.bwplott	Extension to S-Plus trellis to allow transposed plots.
panel.cartesian	trellis panel function, with labeled rows and columns and without strip labels.
panel.ci.plot	Default Panel Function for ci.plot
panel.confintMMC	Confidence interval panel for MMC tiebreaker plots, or confidence interval plot.
panel.dotplot.tb	Dotplot with evenly spaced tiebreakers.
panel.interaction2wt	Plot all main effects and twoway interactions in a multifactor design
panel.isomeans	isomeans grid for MMC plots.
panel.likert	Panel functions for likert that include a stackWidth argument
panel.pairs.hh	Function based on S-Plus panel.pairs to add the subpanel.scales and panel.cex arguments.
panel.xysplom	panel method for xysplom.
partial.corr	partial correlations
pdf.latex	Construct a pdf file from a "latex" file. See Hmisc::latex for concepts.
pdiscunif	Discrete Uniform Distribution
perspPlane	Helper functions for regr2.plot
plot.mmc.multicomp	MMC (Mean-mean Multiple Comparisons) plot.
plot.multicomp	Multiple comparisons plot that gives independent user control over the appearance of the significant and not significant comparisons.
position	Find or assign the implied position for graphing the levels of a factor. A new class "positioned", which inherits from "ordered" and "factor", is defined.
positioned-class	Class "positioned", extends "ordered" to specify the position for graphing the levels of a factor.
print.NormalAndTplot	Print method for Normal and t plots from NTplot.
print.TwoTrellisColumns5	Print two conformable trellis plots in adjacent columns with user control of widths.
print.latticeresids	Print a 'latticeresids' object.
print.tsdiagplot	Print a "tsdiagplot" object.
push.vp.hh	push and pop a grid viewport, turn clipping off, change scale.
pyramidLikert	Print a Likert plot as a Population Triangle
rbind.trellis	Extend matrix reshaping functions to trellis objects.
regr1.plot	plot x and y, with optional straight line fit and display of squared residuals
regr2.plot	3D plot of z against x and y, with regression

	plane fit and display of squared residuals.
regrresidplot	Draw a plot of y vs x from a linear model object, with residuals indicated by lines or squares.
resid.squares	plot squared residuals in inches to match the y-dimension
residVSfitted	Draw plots of resid ~ y.hat and sqrt(abs(resid)) ~ y.hat
residual.plots	Residual plots for a linear model.
residual.plots.lattice	Construct four sets of regression plots: Y against X, residuals against X, partial residuals against X, partial residuals against each X adjusted for all the other X columns.
rowPcts	Row and columns percents
seqplot	Time series plot.
seqplotForecast	seqplot with confidence bands for the forecast region.
strip.background0	Turn off the coloring in the trellis strip labels. Color 0 is the background color.
strip.useOuterStrips.first	Functions based on strip.default for use with the useOuterScales function.
strip.xysplom	strip function that is able to place the correlation or regression coefficient into the strip label.
sufficient	Calculates the mean, standard deviation, and number of observations in each group of a data.frame that has one continuous variable and two factors.
summary.arma.loop	summary and print and subscript methods for tsdiagplot and related objects.
toCQxR	Reshape a 3-way array to a 2-way data.frame that can can be used with a trellis conditioning formula to get the three-way behavior. Used with likertWeighted().
tsacfplots	Coordinated time series and ACF and PCF plots.
tsdiagplot	Times series diagnostic plots for a structured set of ARIMA models.
useOuterScales	Put scales for axes only on the bottom and left panels of a lattice display, and give fine control over the placement of strips
useOuterStripsT2L1	Three-factor generalization of latticeExtra::useOuterStrips
vif	Calculate the Variance Inflation Factor
xysplom	scatterplot matrix with potentially different sets of variables on the rows and columns.
z.test	Z test for known population standard deviation

data display, scatterplot matrix, (MMC Mean–mean Multiple Comparison) plots, interaction plots, ANCOVA plots, regression diagnostics, time series, ARIMA models, boxplots

Author(s)

Richard M. Heiberger

Maintainer: Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2004). *Statistical Analysis and Data Display: An Intermediate Course with Examples in S-Plus, R, and SAS*, First Edition. Springer Texts in Statistics. Springer. https://link.springer.com/book/10.1007/978-1-4757-4284-8.

See Also

ancovaplot, ci.plot, interaction2wt, ladder, case.lm, NTplot for Normal and t plots, hov, resid.squares, MMC, AEdotplot, likert, tsacfplots, tsdiagplot

demo(package="HH")

Examples

```
## In addition to the examples for each function,
## there are seven interactive shiny apps in the HH package:
## Not run:
if (interactive())   NTplot(mean0=0, mean1=1, shiny=TRUE)
if (interactive())   shiny::runApp(system.file("shiny/bivariateNormal", package="HH"))
if (interactive())  shiny::runApp(system.file("shiny/bivariateNormalScatterplot", package="HH"))
if (interactive())   shiny::runApp(system.file("shiny/PopulationPyramid", package="HH"))
if (interactive())   shiny.CIplot(height = "auto")
if (interactive())   shiny::runApp(system.file("shiny/AEdotplot", package="HH"))
if (interactive())   shiny::runApp(system.file("shiny/likert", package="HH"))

## End(Not run)
```

---

ae.dotplot *AE (Adverse Events) dotplot of incidence and relative risk*

Description

A two-panel display of the most frequently occurring AEs in the active arm of a clinical study. The first panel displays their incidence by treatment group, with different symbols for each group. The second panel displays the relative risk of an event on the active arm relative to the placebo arm, with 95% confidence intervals for a 2×2 table. By default, the AEs are ordered by relative risk so that events with the largest increases in risk for the active treatment are prominent at the top of the display. See the Details section for information on changing the sort order.

Usage

```
ae.dotplot(ae, ...)

ae.dotplot.long(xr,
                A.name = levels(xr$RAND)[1], B.name = levels(xr$RAND)[2],
                col.AB = c("red","blue"), pch.AB = c(16, 17),
                main.title = paste("Most Frequent On-Therapy Adverse Events",
                                   "Sorted by Relative Risk"),
                main.cex = 1,
                cex.AB.points = NULL, cex.AB.y.scale = 0.6,
           position.left = c(0, 0, 0.7, 1), position.right = c(0.61, 0, 0.98, 1),
                key.y = -0.2, CI.percent=95)

logrelrisk(ae, A.name, B.name, crit.value=1.96)

panel.ae.leftplot(x, y, groups, col.AB, ...)

panel.ae.rightplot(x, y, ..., lwd=6, lower, upper, cex=.7)

panel.ae.dotplot(x, y, groups, ..., col.AB, pch.AB, lower, upper) ## R only

aeReshapeToLong(aewide)
```

Arguments

ae	For ae.dotplot, either a data.frame containing the Adverse Event data in long format as described by the detail for xr below, or a data.frame containing the Adverse event data in wide format as described by the detail for aewide below. For logrelrisk, a data.frame containing the first 4 columns of xr described below.
...	For ae.dotplot, all the arguments listed in the calling sequence for ae.ddotplot.long and possibly standard panel function arguments. For the other functions, just standard panel function arguments.
xr	• RAND: treatment as randomized (factor). • PREF: adverse event symptom name (factor). • SN: number of patients in treatment group. • SAE: number of patients in each group for whom the event PREF was observed. • PCT: SAE/SN as a percent. • relrisk: Relative risk defined as PCT for the B treatment divided by PCT for the A treatment. • logrelrisk: natural logarithm of relrisk. • ase.logrelrisk: asymptotic standard error of logrelrisk. • logrelriskCI.lower, logrelriskCI.upper: confidence interval for

- logrelrisk.
- relriskCI.lower, relriskCI.upper: back transform of the CI for the log relative risk into the relative risk scale.

aewide
- Event: adverse event symptom name (factor).
- N.A, N.B: number of patients in treatment groups A and B.
- AE.A, AE.B: number of patients in treatment groups A and B for whom the event Event was observed.
- PCT.A, PCT.B: AE.A/N.A and AE.B/N.B as a percent.
- Relative.Risk: Relative risk defined as PCT.B divided by PCT.A.
- logrelrisk: natural logarithm of relrisk.
- ase.logrelrisk: asymptotic standard error of logrelrisk.
- logrelriskCI.lower, logrelriskCI.upper: confidence interval for
- logrelrisk.
- relriskCI.lower, relriskCI.upper: back transform of the CI for the log relative risk into the relative risk scale.

A.name, B.name
: Names of treatment groups (in x$RAND).

col.AB, pch.AB, cex.AB.points
: color, plotting character and character expansion for the individual points on the left plot.

cex.AB.y.scale
: Character expansion for the left tick labels (the symptom names).

main.title, main.cex
: Main title and character expansion for the combined plot in ae.dotplot.

cex
: The character expansion for the points in the left and right plots.

position.left, position.right
: position of the left and right plots. This argument is use in S-Plus only, not in R. See the discussion of position in print.trellis,

key.y
: Position of the key (legend) in the combined plot. This is the y argument of the key. See the discussion of the key argument to xyplot in xyplot.

crit.value
: Critical value used to compute confidence intervals on the log relative risk. Defaults to 1.96. User is responsible for specifying both crit.value and CI.percent consistently.

CI.percent
: Confidence percent associated with the crit.value Defaults to 95. User is responsible for specifying both crit.value and CI.percent consistently.

x, y, groups, lwd
: standard panel function arguments.

lower, upper
: xr$logrelriskCI.lower and xr$logrelriskCI.upper inside the panel functions.

Details

The second panel shows relative risk of an event on the active arm (treatment B) relative to the placebo arm (treatment A), with 95% confidence intervals for a 2×2 table. Confidence intervals on the log relative risk are calculated using the asymptotic standard error formula given as Equation 3.18 in Agresti A., Categorical Data Analysis. Wiley: New York, 1990.

By default the ae.dotplot function sorts the events by relative risk. To change the sort order, you must redefine the ordering of the ordered factor PREF. See the examples below.

Value

`logrelrisk` takes an input data.frame of the form `x` described in the argument list and returns a data.frame consisting of the input argument with additional columns as described in the argument `xr`. The result column of symptom names `PREF` is an ordered factor, with the order specified by the relative risk.

`ae.leftplot` returns a `"trellis"` object containing a horizontal dotplot of the percents against each of the symptom names.

`ae.rightplot` returns a `"trellis"` object containing a horizontal plot on the log scale of the relative risk confidence intervals against each of the symptom names.

`ae.dotplot` calls both `ae.leftplot` and `ae.rightplot` and combines their plots into a single display with a single set of left axis labels, a main title, and a key. The value returned invisibly is a list of the full left trellis object and the right trellis object with its left labels blanked out. Printing the value will not usually be interesting as the main title and key are not included. It is better to call `ae.dotplot` directly, perhaps with a change in some of the positioning arguments.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Ohad Amit, Richard M. Heiberger, and Peter W. Lane. (2008) "Graphical Approaches to the Analysis of Safety Data from Clinical Trials". *Pharmaceutical Statistics*, **7**, 1, 20–35. https://onlinelibrary.wiley.com/doi/10.1002/pst.254

See Also

`AEdotplot` for a three-panel version that also has an associated shiny app.

Examples

```
## variable names in the input data.frame aeanonym
## RAND   treatment as randomized
## PREF   adverse event symptom name
## SN     number of patients in treatment group
## SAE    number of patients  in each group for whom the event PREF was observed
##
## Input sort order is PREF/RAND

data(aeanonym)
head(aeanonym)

## Calculate log relative risk and confidence intervals (95% by default).
## logrelrisk sets the sort order for PREF to match the relative risk.
aeanonymr <- logrelrisk(aeanonym) ## sorts by relative risk
head(aeanonymr)

## construct and print plot on current graphics device
ae.dotplot(aeanonymr,
```

```
           A.name="TREATMENT A (N=216)",
           B.name="TREATMENT B (N=431)")
## export.eps(h2("stdt/figure/aerelrisk.eps"))
## This looks great on screen and exports badly to eps.
## We recommend drawing this plot directly to the postscript device:
##
## trellis.device(postscript, color=TRUE, horizontal=TRUE,
##                colors=ps.colors.rgb[
##                  c("black", "blue", "red", "green",
##                    "yellow", "cyan","magenta","brown"),],
##                onefile=FALSE, print.it=FALSE,
##                file=h2("stdt/figure/aerelrisk.ps"))
## ae.dotplot(aeanonymr,
##            A.name="TREATMENT A (N=216)",
##            B.name="TREATMENT B (N=431)")
## dev.off()

## To change the sort order, redefine the PREF factor.
## For this example, to plot alphabetically, use the statement
aeanonymr$PREF <- ordered(aeanonymr$PREF, levels=sort(levels(aeanonymr$PREF)))
ae.dotplot(aeanonymr,
           A.name="TREATMENT A (N=216)",
           B.name="TREATMENT B (N=431)",
           main.title="change the main title to reflect the new sort order")

## Not run:
## to restore the order back to the default, use
relrisk <- aeanonymr[seq(1, nrow(aeanonymr), 2), "relrisk"]
PREF <- unique(aeanonymr$PREF)
aeanonymr$PREF <- ordered(aeanonymr$PREF, levels=PREF[order(relrisk)])
ae.dotplot(aeanonymr,
           A.name="TREATMENT A (N=216)",
           B.name="TREATMENT B (N=431)",
           main.title="back to the original sort order")

## smaller artifical example with the wide format
aewide <- data.frame(Event=letters[1:6],
                     N.A=c(50,50,50,50,50,50),
                     N.B=c(90,90,90,90,90,90),
                     AE.A=2*(1:6),
                     AE.B=1:6)
aewtol <- aeReshapeToLong(aewide)
xr <- logrelrisk(aewtol)
ae.dotplot(xr)

## End(Not run)
```

AEdotplot *AE (Adverse Events) dotplot of incidence and relative risk*

Description

A three-panel display of the most frequently occurring AEs in the active arm of a clinical study. The first panel displays their incidence by treatment group, with different symbols for each group. The second panel displays the relative risk of an event on the active arm relative to the placebo arm, with 95% confidence intervals for a 2×2 table. By default, the AEs are ordered by relative risk so that events with the largest increases in risk for the active treatment are prominent at the top of the display. By setting the argument `sortbyRelativeRisk=FALSE`, the AEs retain the order specified by the levels of the factor. The third panel displays the numerical values of number of patients for each treatment, number of adverse events for each treatment, and relative risk. The third panel can be suppressed by the `print` method.

Usage

```
  AEdotplot(xr, ...)

  ## S3 method for class 'formula'
AEdotplot(xr, groups=NULL, data=NULL,
          sortbyRelativeRisk=TRUE,
          ...,
          sub=list(deparse(this.call[1:4],
                           width.cutoff=500), cex=.7))
```

Arguments

`xr`	For the formula method, a formula of the form `AE ~ nAE/nTRT | OrgSys`, where the condition variable is optional. For the formula method only, the variable names are not restricted. See `AEdotplot.data.frame` for the support methods.
`groups`	Variable containing the treatment levels.
`data`	`data.frame` containing at least four variables: containing the AE name as a factor, the treatment level as a factor, the number of observed AE in that treatment level, the number of patients in that treatment group. It may also contain a fifth variable containing a condition variable used to split the `data.frame` into partitions. It may be used to partition the plot, for example by organ system or by gender. The treatment factor must have exactly two levels. Each AE name must appear exactly once for each level of the treatment.
`sortbyRelativeRisk`	logical. If `TRUE`, then make the Adverse Events an ordered factor ordering by relative risk. If `FALSE`, then make the Adverse Events an ordered factor retaining the order of the input levels.
`sub`	Subtitle for the plot. The default value is the command that generates the plot.
`...`	Any of the arguments (such as the sorting options) listed in the calling sequence for the methods documented in `AEdotplot.data.frame`.

Details

The first panel is an ordinary dotplot of the percent of AE observed for each treatment by AE.

The second panel shows relative risk of an event on the Treatment B arm (usually the active compound) relative to the Treatment A arm (usually the placebo), with 95% confidence intervals for a 2×2 table. Confidence intervals on the log relative risk are calculated using the asymptotic standard error formula given as Equation 3.18 in Agresti A., *Categorical Data Analysis.* Wiley: New York, 1990.

By default the `AEdotplot` function sorts the events by relative risk. To retain the sort order implied by the `levels` of the AE factor, specify the argument `sortbyRelativeRisk=FALSE`. To control the sort order, make the AE factor in the input dataset an `ordered` factor and specify the levels in the order you want.

The third panel shows the numerical values of the number and percent of observed events on each arm and the relative risk. The display of third panel can be suppressed by specifying the `panel.widths` argument. See the discussion of the `panel.widths` in `AEdotplot.data.frame`.

Value

The primary interest is in the display of the plot.

The function returns an `AEdotplot` object which is a list of three `trellis` objects, one for the the Percent plot, one for the Relative Risk plot, and one for the Text plot containing the table of input values. The object has attributes

1. `main` and `sub` hold the main and subtitles. Each must be a list containing the text in the first component.
2. `ae.key` is a key as described in `xyplot`.
3. `n.events` is a vector containing the number of events in each subpanel.
4. `panel.widths` is a vector of relative widths of the three components of the graph. The numbers must sum to one. Zero values are permitted. The first width includes the left axis and the Percent plot. The second is the Relative Risk plot, and the third is the plot of the table values.
5. `AEtable` is a table containing the data plotted on its row.

Note

Ann Liu-Ferrara was a beta tester for the shiny app.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Ohad Amit, Richard M. Heiberger, and Peter W. Lane. (2008) "Graphical Approaches to the Analysis of Safety Data from Clinical Trials". *Pharmaceutical Statistics*, **7**, 1, 20–35. https://onlinelibrary.wiley.com/doi/10.1002/pst.254

See Also

`AEdotplot.data.frame`

Examples

```
## formula method.  See ?AEdotplot.data.frame for other methods.
data(AEdata)
head(AEdata)

AEdotplot(AE ~ nAE/nTRT, groups = TRT, data = AEdata)           ## sort by Relative Risk
AEdotplot(AE ~ nAE/nTRT | OrgSys, groups = TRT, data = AEdata)  ## conditioned on Organ System

## Not run:
AEdotplot(AE ~ nAE/nTRT, groups = TRT, data = AEdata, sortbyVar="PCT")             ## PCT A
AEdotplot(AE ~ nAE/nTRT, groups = TRT, data = AEdata, sortbyVar="PCT", sortbyVarBegin=2) ## PCT B
AEdotplot(AE ~ nAE/nTRT, groups = TRT, data = AEdata, sortbyRelativeRisk=FALSE)    ## levels(AE)
AEdotplot(AE ~ nAE/nTRT | OrgSys, groups = TRT, data = AEdata, sortbyVar="ase.logrelrisk")

## End(Not run)


## Not run:
AEdotplot(AE ~ nAE/nTRT | OrgSys, groups = TRT,
          data = AEdata[c(AEdata$OrgSys %in% c("GI","Resp")),])

## test sortbyRelativeRisk=FALSE
ABCD.12345 <- AEdata[1:12,]
head(ABCD.12345)
AEdotplot(AE ~ nAE/nTRT | OrgSys, groups=TRT, data=ABCD.12345)
AEdotplot(AE ~ nAE/nTRT | OrgSys, groups=TRT, data=ABCD.12345, sort=FALSE)

## suppress third panel
tmp <- AEdotplot(AE ~ nAE/nTRT, groups = TRT, data = AEdata)
print(tmp, AEtable=FALSE)

## End(Not run)

## Not run:
  ## run the shiny app
 if (interactive())  shiny::runApp(system.file("shiny/AEdotplot", package="HH"))

## End(Not run)
```

`AEdotplot.data.frame` *AE (Adverse Events) dotplot of incidence and relative risk, support functions*

Description

Support functions for the `AEdotplot`.

Usage

```
  ## S3 method for class 'data.frame'
AEdotplot(xr, ...,
          conditionVariable=NULL,
          conditionName=deparse(substitute(xr)),
          useCondition=!is.null(conditionVariable),
          sub=list(conditionName, cex=.7))

  ## S3 method for class 'AElogrelrisk'
AEdotplot(xr,
          A.name=paste(levels(xr$RAND)[1], " (n=", xr$SN[1], ")", sep=""),
          B.name=paste(levels(xr$RAND)[2], " (n=", xr$SN[2], ")", sep=""),
          col.AB=c("red","blue"), pch.AB=c(16,17),
           main=if (sortbyRelativeRisk)
          list("Most Frequent On-Therapy Adverse Events Sorted by Relative Risk",
                  cex=1)
           else
              list("Most Frequent On-Therapy Adverse Events", cex=1),
          cex.AB.points=NULL, cex.AB.y.scale=.6, cex.x.scale=.6,
          panel.widths=c(.55, .22, .23),
          key.y=-.2, CI.percent=95,
          conditionName=deparse(substitute(xr)),
          sortbyRelativeRisk=TRUE,
          ...,
          sub=list(conditionName, cex=.7),
          par.strip.text=list(cex=.7))

  ## S3 method for class 'AEtable'
AEdotplot(xr, ..., useCondition=TRUE,
                             sub="sub for AEsecond")

  ## S3 method for class 'AEdotplot'
print(x, ...,
      main=attr(x, "main"),
      sub=attr(x,"sub"),
      ae.key=attr(x, "ae.key"),
      panel.widths=attr(x,"panel.widths"),
      AEtable=TRUE)

  ## S3 method for class 'AEdotplot'
c(..., panel.widths=attr(aedp[[1]], "panel.widths"),
                        par.strip.text=list(cex=.7))

  AElogrelrisk(ae,
               A.name=levels(ae$RAND)[1],
               B.name=levels(ae$RAND)[2],
               crit.value=1.96,
               sortbyRelativeRisk=TRUE, ...,
```

```
                          sortbyVar=c("PREF", ## Event name
                            "PCT",            ## Percent
                            "SN",             ## Number of Patients
                            "SAE",            ## Number of Observed Events
                            "relrisk",        ## Relative Risk (RR)
                           "ase.logrelrisk", ## Asymptotic Standard Error(log(RR))
                            "relriskCI.lower", ## Confidence Interval Bounds
                            "relriskCI.upper"),
                        sortbyVarBegin=1)   ## 1 for A treatment, 2 for B treatment

  AEmatchSortorder(AEstandard,
                   AEsecond,
                   AEsecond.AEtable=attr(AEsecond, "AEtable"),
                   levels.order=
                      lapply(attr(AEstandard,"AEtable"),
                             function(AEsubtable) levels(AEsubtable$PREF)),
                main.second=list(paste("Most Frequent On-Therapy Adverse Events",
                                       "Sorted to Match First Table"),
                                 cex=1))

  ## S3 method for class 'AEdotplot'
update(object, ...)
```

Arguments

ae	For AElogrelrisk, a data.frame containing at least the first 4 columns of xr.
xr	For the formula method documented in AEdotplot, a formula of the form AE ~ nAE/nTRT | OrgSys, where the condition variable is optional. For the formula method only, the variable names are not restricted. For the other methods, xr is a data.frame containing the Adverse Event data in long format. It must have variables named RAND: treatment as randomized (factor with exactly two levels). PREF: adverse event symptom name (factor). SN: number of patients in treatment group. SAE: number of patients in each group for whom the event PREF was observed. If the xr object is a AElogrelrisk object, then it must also have variables PCT: SAE/SN as a percent. relrisk: Relative risk defined as PCT for the B treatment divided by PCT for the A treatment. logrelrisk: natural logarithm of relrisk. ase.logrelrisk: asymptotic standard error of logrelrisk. logrelriskCI.lower, logrelriskCI.upper: confidence interval for logrelrisk. relriskCI.lower, relriskCI.upper: back transform of the CI for the log relative risk into the relative risk scale.
sortbyRelativeRisk	logical. If TRUE, then make the Adverse Events an ordered factor ordering by relative risk. If FALSE, then make the Adverse Events an ordered factor retaining the order of the input levels.

`conditionVariable`
: Vector of same length as number of rows in `xr`, it may be one of the columns in `xr` in which case its full name in the form xr$varname must be used. It will be used to split the `data.frame` into partitions. It may be used to partition the plot, for example by organ system or by gender.

`conditionName`
: Character. Name to be used in `left.strip`.

`useCondition`
: logical. If `FALSE`, then a non-`NULL` `ConditionVariable` won't be used.

`x`
: object to be printed.

`panel.widths`
: Vector of three non-negative numerics that sum to 1. These are the widths of each of the three panels in the output plot. The left panel contains the AE names as y-tick labels and the Percent plot. The middle panel contains the Relative Risk plot. The right panel contains a table of the numerical values of number of patients for each treatment, number of adverse events for each treatment, and relative risk. Setting the third value to 0 suppresses the table of numerical values from the display.

`AEtable`
: logical. For the `print.AEdotplot` function. If `TRUE` (the default), display all three panels. If `FALSE`, then display only the Percent and Relative Risk plots.

`main, sub`
: Main title and subtitle for the combined plot in `AEdotplot`.

`main.second`
: Main title for second plot whose sort order has been changed to match the first plot.

`A.name, B.name`
: Names of treatment groups (in `x$RAND`).

`col.AB, pch.AB, cex.AB.points`
: color, plotting character and character expansion for the individual points on the left plot.

`cex.AB.y.scale`
: Character expansion for the left tick labels (the Adverse Effects names).

`cex.x.scale`
: Character expansion for the x-axis tick labels.

`key.y`
: Position of the key (legend) in the combined plot. This is the `y` argument of the `key`. See the discussion of the `key` argument to `xyplot` in `xyplot`

`.`

`ae.key`
: is a key as described in `xyplot`.

`AEstandard, AEsecond, AEsecond.AEtable, levels.order`
: Arguments that force the Adverse Events in the panels of `AEsecond` to have the same sort order `levels.order` of `PREF` as the panels of `AEstandard`. `AEstandard` and `AEsecond` are two `"AEdotplot"` objects with the same set of panels and the same Adverse Events in corresponding panels. `AEsecond.AEtable` is the `AEtable` object from `AEsecond`. `levels.order` is the new order for `AEsecond`; normally the same order as in `AEprimary`.

`crit.value`
: Critical value used to compute confidence intervals on the log relative risk. Defaults to 1.96. User is responsible for specifying both `crit.value` and `CI.percent` consistently.

`CI.percent`
: Confidence percent associated with the `crit.value` Defaults to 95. User is responsible for specifying both `crit.value` and `CI.percent` consistently.

...	For AEdotplot and AEdotplot.data.frame, all the arguments listed in the calling sequence for AEddotplot.AErelrisk.. For c.AEdotplot, one or more "AEdotplot" objects. For print.AEdotplot, the ... arguments are ignored.
sortbyVar	Specify which variable will be used to provide the sort order in the plot. The names are the internal names for the variables.
sortbyVarBegin	1 for A treatment, 2 for B treatment.
object	An AEdotplot object. The update method updates the components of each of the constituent trellis objects. It does not update the "main" and "sub" attributes (nor any other attribute) of the AEdotplot object.
par.strip.text	Default value for strip labels. See xyplot for details.

Details

The first panel is an ordinary dotplot of the percent of AE observed for each treatment by AE.

The second panel shows relative risk of an event on the Treatment B arm (usually the active compound) relative to the Treatment A arm (usually the placebo), with 95% confidence intervals for a 2×2 table. Confidence intervals on the log relative risk are calculated using the asymptotic standard error formula given as Equation 3.18 in Agresti A., *Categorical Data Analysis.* Wiley: New York, 1990.

By default the AEdotplot function sorts the events by relative risk. To retain the sort order implied by the levels of the AE factor, specify the argument sortbyRelativeRisk=FALSE. To control the sort order, make the AE factor in the input dataset an ordered factor and specify the levels in the order you want.

The third panel shows the numerical values of the number and percent of observed events on each arm and the relative risk. The display of third panel can be suppressed by specifying the panel.widths argument.

Value

The primary interest is in the display of the plot.

The function returns an AEdotplot object which is a list of three trellis objects, one for the the Percent plot, one for the Relative Risk plot, and one for the Text plot containing the table of input values. The object has attributes

1. main and sub hold the main and subtitles. Each must be a list containing the text in the first component.
2. ae.key is a key as described in xyplot.
3. n.events is a vector containing the number of events in each subpanel.
4. panel.widths is a vector of relative widths of the three components of the graph. The numbers must sum to one. Zero values are permitted. The first width includes the left axis and the Percent plot. The second is the Relative Risk plot, and the third is the plot of the table values.
5. AEtable is a table containing the data plotted on its row.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Ohad Amit, Richard M. Heiberger, and Peter W. Lane. (2008) "Graphical Approaches to the Analysis of Safety Data from Clinical Trials". *Pharmaceutical Statistics*, **7**, 1, 20–35. https://onlinelibrary.wiley.com/doi/10.1002/pst.254

See Also

AEdotplot

Examples

```
## Not run:
## variable names in the input data.frame aeanonym
## RAND   treatment as randomized
## PREF   adverse event symptom name
## SN     number of patients in treatment group
## SAE    number of patients  in each group for whom the event PREF was observed
## OrgSys Organ System
##
## Input sort order is PREF/RAND

data(aeanonym)
head(aeanonym)

## variable names are hard-wired in the program
## names(aeanonym) <- c("RAND", "PREF", "SAE", "SN", "OrgSys")


## Calculate log relative risk and confidence intervals (95
## AElogrelrisk sets the sort order for PREF to match the relative risk.
aeanonymr <- AElogrelrisk(aeanonym) ## PREF sorted by relative risk
head(aeanonymr)
class(aeanonymr$PREF)
levels(aeanonymr$PREF)

AEdotplot(aeanonym)

AEdotplot(aeanonym, sort=FALSE)

AEdotplot(aeanonym, conditionVariable=aeanonym$OrgSys)

aefake <- rbind(cbind(aeanonym, group="ABC"), cbind(aeanonym, group="DEF"))
aefake$SAE[67:132] <- sample(aefake$SAE[67:132])
aefake$OrgSys.group <- with(aefake, interaction(OrgSys, group))

## fake 2
KEEP <- aefake$OrgSys %in% c("GI","Resp")
AEfakeGR <- AEdotplot(aefake[KEEP,], conditionVariable=aefake$OrgSys.group[KEEP],
            sub=list("ABC and DEF have different sort orders for PREF", cex=.7))
AEfakeGR ## ABC and DEF have different sort orders for PREF

AEfakeGR1 <- AEdotplot(aefake[KEEP & (1:132) <= 66,],
```

```
                        conditionVariable=aefake$OrgSys.group[KEEP & (1:132) <= 66])
AEfakeGR2 <- AEdotplot(aefake[KEEP & (1:132) >= 67,],
                        conditionVariable=aefake$OrgSys.group[KEEP & (1:132) >= 67])

AEfakeGR1
AEfakeGR2

AEfakeMatched <- AEmatchSortorder(AEfakeGR1, AEfakeGR2)
update(do.call(c, AEfakeMatched),
       main="ABC sorted by Relative Risk; DEF matches ABC order")

## End(Not run)
## Please see  ?AEdotplot  for examples using the formula method
##
## Many more examples are in demo("AEdotplotManyExamples")
```

---

ancova *Compute and plot oneway analysis of covariance*

Description

Compute and plot oneway analysis of covariance. The result object is an ancova object which consists of an ordinary aov object with an additional `trellis` attribute. The `trellis` attribute is a `trellis` object consisting of a series of plots of `y ~ x`. The left set of panels is conditioned on the levels of the factor groups. The right panel is a superpose of all the groups.

Usage

```
ancova(formula, data.in = NULL, ...,
       x, groups, transpose = FALSE,
       display.plot.command = FALSE,
       superpose.level.name = "superpose",
       ignore.groups = FALSE, ignore.groups.name = "ignore.groups",
       blocks, blocks.pch = letters[seq(levels(blocks))],
       layout, between, main,
       pch=trellis.par.get()$superpose.symbol$pch)

panel.ancova(x, y, subscripts, groups,
 transpose = FALSE, ...,
 coef, contrasts, classes,
 ignore.groups, blocks, blocks.pch, blocks.cex, pch)

## The following are ancova methods for generic functions.
## S3 method for class 'ancova'
anova(object, ...)

## S3 method for class 'ancova'
predict(object, ...)
```

```
## S3 method for class 'ancova'
print(x, ...) ## prints the anova(x) and the trellis attribute

## S3 method for class 'ancova'
model.frame(formula, ...)

## S3 method for class 'ancova'
summary(object, ...)

## S3 method for class 'ancova'
plot(x, y, ...) ## standard lm plot.  y is always ignored.

## S3 method for class 'ancova'
coef(object, ...)
```

Arguments

formula	A formula specifying the model.
data.in	A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.
...	Arguments to be passed to aov, such as subset or na.action.
x	Covariate in ancova, needed for plotting when the formula does not include x. "aov" object in print.ancova, to match the argument of the print generic function. Variable to plotted in "panel.ancova".
groups	Factor. Needed for plotting when the formula does not include groups after the conditioning bar "|".
transpose	S-Plus: The axes in each panel of the plot are transposed. The analysis is identical, just the axes displaying it have been interchanged. R: no effect.
display.plot.command	The default setting is usually what the user wants. The alternate value TRUE prints on the console the command that draws the graph. This is strictly for debugging the ancova command.
superpose.level.name	Name used in strip label for superposed panel.
ignore.groups	When TRUE, an additional panel showing all groups together with a common regression line is displayed.
ignore.groups.name	Name used in strip label for ignore.groups panel.
pch	Plotting character for groups.
blocks	Additional factor used to label points in the panels.
blocks.pch	Alternate set of labels used when a blocks factor is specified.
blocks.cex	Alternate set of cex used when a blocks factor is specified.

`layout` The layout of multiple panels. The default is a single row. See details.

`between` Space between the panels for the individual group levels and the superpose panel including all groups.

`main` Character with a main header title to be done on the top of each page.

`y, subscripts` In `"panel.ancova"`, see `panel.xyplot`.

`object` An `"aov"`

object. The functions using this argument are methods for the similarly named generic functions.

`coef, contrasts, classes`
Internal variables used to communicate between `ancova` and `panel.ancova`. They keep track of the constant or different slopes and intercepts in each panel of the plot.

Details

The `ancova` function does two things. It passes its arguments directly to the `aov` function and returns the entire `aov` object. It also rearranges the data and formula in its argument and passes that to the `xyplot` function. The `trellis` attribute is a `trellis` object consisting of a series of plots of `y ~ x`. The left set of panels is conditioned on the levels of the factor `groups`. The right panel is a superpose of all the groups.

Value

The result object is an `ancova` object which consists of an ordinary `aov` object with an additional `trellis` attribute. The default print method is to print both the `anova` of the object and the `trellis` attribute.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

`ancova-class` `aov` `xyplot`. See `ancovaplot` for a newer set of functions that keep the graph and the `aov` object separate.

Examples

```
data(hotdog)

## y ~ x                    ## constant line across all groups
ancova(Sodium ~ Calories,     data=hotdog, groups=Type)
```

```
## y ~ a                      ## different horizontal line in each group
ancova(Sodium ~            Type, data=hotdog, x=Calories)

## This is the usual usage
## y ~ x + a  or  y ~ a + x  ## constant slope, different intercepts
ancova(Sodium ~ Calories + Type, data=hotdog)
ancova(Sodium ~ Type + Calories, data=hotdog)

## y ~ x * a  or  y ~ a * x  ## different slopes, and different intercepts
ancova(Sodium ~ Calories * Type, data=hotdog)
ancova(Sodium ~ Type * Calories, data=hotdog)

## y ~ a * x ## save the object and print the trellis graph
hotdog.ancova <- ancova(Sodium ~ Type * Calories, data=hotdog)
attr(hotdog.ancova, "trellis")


## label points in the panels by the value of the block factor
data(apple)
ancova(yield ~ treat + pre, data=apple, blocks=block)

## Please see
##      demo("ancova")
## for a composite graph illustrating the four models listed above.
```

`ancova-class` *Class "ancova" Analysis of Covariance*

Description

Analysis of Covariance. The class is an extension of "aov" and "lm". It is identical to the "aov" for a single factor and a single covariate plus an attribute which contains a `"trellis"` object. Four different models are included in the class. See ancova for the examples.

Objects from the Class

A virtual Class: No objects may be created from it.

Extends

Class `"aov"`, directly. Class `"lm"`, by class "aov", distance 2. Class `"mlm"`, by class "aov", distance 2, with explicit test and coerce. Class `"oldClass"`, by class "aov", distance 3. Class `"oldClass"`, by class "aov", distance 4, with explicit test and coerce.

Methods

No methods defined with class "ancova" in the signature. S3-type methods are `"anova.ancova"`, `"coef.ancova"`, `"coefficients.ancova"`, `"model.frame.ancova"`, `"plot.ancova"`, `"predict.ancova"`, `"print.ancova"`, `"summary.ancova"`. `"plot.ancova(x)"` plots a standard lm plot of `x`. `"print.ancova(x)"` prints the `anova(x)` and the trellis attribute. The remaining methods use `NextMethod`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

ancova

---

ancovaplot *Analysis of Covariance Plots*

Description

Analysis of Covariance Plots. Any of the ancova models
y ~ x * t
y ~ t * x
y ~ x + t
y ~ t + x
y ~ x , groups=t
y ~ t, x=x
y ~ x * t, groups=b
y ~ t * x, groups=b
y ~ x + t, groups=b
y ~ t + x, groups=b

Usage

```
ancovaplot(object, ...)
## S3 method for class 'formula'
ancovaplot(object, data, groups=NULL, x=NULL, ...,
           formula=object,
           col=rep(tpg$col,
             length=length(levels(as.factor(groups)))),
           pch=rep(c(15,19,17,18,16,20, 0:14),
             length=length(levels(as.factor(groups)))),
           slope, intercept,
           layout=c(length(levels(cc)), 1),
           col.line=col, lty=1,
           superpose.panel=TRUE,
           between=if (superpose.panel)
                      list(x=c(rep(0, length(levels(cc))-1), 1))
                   else
```

```
                    list(x=0),
            col.by.groups=FALSE ## ignored unless groups= is specified
            )

panel.ancova.superpose(x, y, subscripts, groups,
                       slope, intercept,
                       col, pch, ...,
                       col.line, lty,
                       superpose.panel,
                       col.by.groups,
                       condition.factor,
                       groups.cc.incompatible,
                       plot.resids=FALSE,
                       print.resids=FALSE,
                       mean.x.line=FALSE,
                       col.mean.x.line="gray80")
```

Arguments

formula, object	formula specifying the aov model. The function modifies it for the xyplot specification.
data	data.frame
groups	If the treatment factor is included in the formula, then groups is not needed. By default groups will be set to the treatment factor, but the user may specify another factor for groups, usually a blocking factor. The pch will follow the value of groups. If the treatment is not included in the formula, then groups is required.
x	Covariate. Required by ancovaplot.formula if the covariate is not included in the formula. For panel.ancova.superpose, see panel.superpose.
...	Other arguments to be passed to xyplot.
col, pch	Standard **lattice** arguments. pch follows the value of groups. When col.by.groups is TRUE, then col follow the value of groups. When col.by.groups is FALSE, then col follows the value of the treatment factor, and is constant in each panel.
slope, intercept	Vector, the length of the number of treatment levels, containing slope and intercept of the abline in each panel. This is by default calculated based on the formula. The user may override each independently.
layout, between	Standard **lattice** arguments.
col.line, lty	Standard **lattice** arguments. By default, they follow the value of the treatment factor in the formula. col.line is recycled to the number of panels in the plot.
y, subscripts	See panel.xyplot.
superpose.panel	logical. if TRUE (the default), there is an additional panel on the right containing the superposition of the points and lines for all treatment levels.
col.by.groups	logical. See the discussion in argument col.

`condition.factor`, `groups.cc.incompatible`
: These are both internal variables. `condition.factor` contains a copy of the treatment factor. `groups.cc.incompatible` is a logical which is set to `TRUE` when the `groups` argument is explicitly set by the user.

`plot.resids`, `print.resids`, `mean.x.line`, `col.mean.x.line`
: logical, logical, logical or numeric, color name. When `plot.resids==TRUE` then vertical line segments connecting the data points and the fitted line are drawn. The other two arguments are interpreted only when `plot.resids==TRUE`. When `print.resids==TRUE` then the values of the residuals are printed on the console. When `is.numeric(mean.x.line)` then a vertical reference line is drawn at the specified value, which will normally be specified by the user as the mean of the full set of x values. The reference line will have color specified by `col.mean.x.line`.

Details

```
ancova=aov specification   xyplot specification   abline
 y ~ x * t                 y ~ x | t, groups=t     lm(y[t] ~ x[t])   ## separate lines
 y ~ t * x                 y ~ x | t, groups=t     lm(y[t] ~ x[t])   ## separate lines
 y ~ x + t                 y ~ x | t, groups=t     lm(y ~ x + t)     ## parallel lines
 y ~ t + x                 y ~ x | t, groups=t     lm(y ~ x + t)     ## parallel lines
 y ~ x , groups=t          y ~ x | t, groups=t     lm(y ~ x)         ## single regression line
 y ~ t, x=x                y ~ x | t, groups=t     mean(t)           ## separate horizontal lines
 y ~ x * t, groups=b       y ~ x | t, groups=b     lm(y[t] ~ x[t])   ## sep lines, pch&col follow b
 y ~ t * x, groups=b       y ~ x | t, groups=b     lm(y[t] ~ x[t])   ## sep lines, pch&col follow b
 y ~ x + t, groups=b       y ~ x | t, groups=b     lm(y ~ x + t)     ## par lines, pch&col follow b
 y ~ t + x, groups=b       y ~ x | t, groups=b     lm(y ~ x + t)     ## par lines, pch&col follow b
```

Value

`ancovaplot` returns a `c("ancova","trellis")` object. `panel.ancova.superpose` is an ordinary **lattice** `panel` function.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

See the older ancova.

Examples

```
data(hotdog, package="HH")
ancovaplot(Sodium ~ Calories + Type, data=hotdog)
ancovaplot(Sodium ~ Calories * Type, data=hotdog)
ancovaplot(Sodium ~ Calories, groups=Type, data=hotdog)
ancovaplot(Sodium ~ Type, x=Calories, data=hotdog)

## Please see demo("ancova", package="HH") to coordinate placement
## of all four of these plots on the same page.

ancovaplot(Sodium ~ Calories + Type, data=hotdog, plot.resids=TRUE)
```

---

anova.ancovaplot *ANOVA table for a c("ancovaplot","trellis") object.*

Description

ANOVA table for a c("ancovaplot","trellis") object.

Usage

```
## S3 method for class 'ancovaplot'
anova(object, ...)
aov.ancovaplot(object, warn=TRUE)
aovStatement(object, ...)
## S3 method for class 'ancovaplot'
aovStatement(object, ...)
aovStatementAndAnova(object, ...)
## S3 method for class 'ancovaplot'
aovStatementAndAnova(object, ...)
## S3 method for class 'ancovaplot'
model.tables(x, ...)
```

Arguments

object, x	c("ancovaplot","trellis") object.
warn, ...	warn is logical with default TRUE. See the Details section for the interpretation of warn. When ... is received by aov.ancovaplot, it is evaluated if it is warn and ignored for all other values. When ... is received by model.tables it is interpreted normally.

Details

The aov.ancovaplot modifies the call item into an aov call with the same formula and data. If there are groups in the call specified as a name, the groups factor is included in the constructed aov call only if there are both a factor and a covariate in the right-hand-side of the formula. In that

case they the groups will be interpreted as a block factor and will be placed first. If the groups are specified as a vector of values in the call, the groups are ignored with a warning. If there is only one term in the right-hand-side, then the groups factor will not be placed into the aov formula. In this case, there will be a warning if the argument warn is TRUE, and no warning if the warn argument is FALSE.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

ancovaplot

---

anovaMean *ANOVA table from the group sample sizes, means, and standard deviations.*

Description

Oneway ANOVA table from the summary information consisting of group sample sizes, means, and standard deviations. The full dataset is not needed.

Usage

```
anovaMean(object, n, ybar, s, ..., ylabel = "ylabel")
```

Arguments

object	level names
n	sample size for each level
ybar	sample mean for each level
s	sample standard deviation for each level
...	other arguments (not used)
ylabel	name of response variable

Value

Analysis of variance table, identical to the ANOVA table that would have been produced by anova.lm if the original data, rather than the summary data, had been available.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

anova.lm, plot.mmc.multicomp

Examples

```
## pulmonary data used in Hsu and Peruggia paper defining the mean-mean plot
## See ?plot.mmc.multicomp for details on the dataset.

data(pulmonary)

anovaMean(pulmonary$smoker,
          pulmonary$n,
          pulmonary$FVC,
          pulmonary$s,
          ylabel="pulmonary")
```

`aovSufficient` *Analysis of variance from sufficient statistics for groups.*

Description

Analysis of variance from sufficient statistics for groups. For each group, we need the factor level, the response mean, the within-group standard deviation, and the sample size. The correct ANOVA table is produced. The residuals are fake. The generic `vcov` and `summary.lm` don't work for the variance of the regression coefficients in this case. Use `vcovSufficient`.

Usage

```
aovSufficient(formula, data = NULL,
              projections = FALSE, qr = TRUE, contrasts = NULL,
              weights = data$n, sd = data$s,
              ...)

vcovSufficient(object, ...)
```

Arguments

`formula`, `data`, `projections`, `qr`, `contrasts`, `...`	See `aov`.
`weights`	See `lm`.
`sd`	vector of within-group standard deviations.
`object`	`"aov"` object constructed by `aovSufficient`. It also works with regular `aov` objects.

Value

For `aovSufficient`, an object of class c("aov", "lm"). For `vcovSufficient`, a function that returns the covariance matrix of the regression coefficients.

Note

The residuals are fake. They are all identical and equal to the MLE standard error (`sqrt(SumSq.res/df.tot)`). They give the right ANOVA table. They may cause confusion or warnings in other programs. The standard errors and t-tests of the coefficients are not calculated by `summary.lm`. Using the `aov` object from `aovSufficient` in `glht` requires the `vcov.` and `df` arguments.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`MMC` and `aov`.

Examples

```
## This example is from Hsu and Peruggia

## This is the R version
## See ?mmc.mean for S-Plus

if.R(s={},
r={

data(pulmonary)
pulmonary
pulmonary.aov <- aovSufficient(FVC ~ smoker,
                               data=pulmonary)
summary(pulmonary.aov)

## Not run:
pulmonary.mmc <- mmc(pulmonary.aov,
                     linfct=mcp(smoker="Tukey"),
                     df=pulmonary.aov$df.residual,
                     vcov.=vcovSufficient)
mmcplot(pulmonary.mmc, style="both")

## orthogonal contrasts
pulm.lmat <- cbind("npnl-mh"=c( 1, 1, 1, 1,-2,-2), ## not.much vs lots
                   "n-pnl"  =c( 3,-1,-1,-1, 0, 0), ## none vs light
                   "p-nl"   =c( 0, 2,-1,-1, 0, 0), ## {} arbitrary 2 df
                   "n-l"    =c( 0, 0, 1,-1, 0, 0), ## {} for 3 types of light
                   "m-h"    =c( 0, 0, 0, 0, 1,-1)) ## moderate vs heavy
dimnames(pulm.lmat)[[1]] <- row.names(pulmonary)
pulm.lmat

pulmonary.mmc <- mmc(pulmonary.aov,
                     linfct=mcp(smoker="Tukey"),
                     df=pulmonary.aov$df.residual,
                     vcov.=vcovSufficient,
                     focus.lmat=pulm.lmat)
```

```
mmcplot(pulmonary.mmc, style="both", type="lmat")

## End(Not run)
})
```

`arima.diag.hh` *Repair design error in S-Plus arima.diag*

Description

Repair design error in S-Plus `arima.diag`.

Usage

```
arima.diag.hh(z, acf.resid = TRUE,
              lag.max = round(max(gof.lag + n.parms + 1, 10 * log10(n))),
              gof.lag = 15, resid = FALSE,
              std.resid = TRUE, plot = TRUE, type = "h", ...,
              x=eval(parse(text = series.name)))
```

Arguments

`z`, `acf.resid`, `lag.max`, `gof.lag`, `resid`, `std.resid`, `plot`, `type`, `...`	This function is a no-op in R. The arguments are not used.
`x`	The time series. This must be specified when arima.diag is called from inside another function.

Details

Repairs design flaw in S-Plus `arima.diag`. The location of the time series is hardwired one level up, so it can't be found when `arima.diag` is not one level down from the top.

This function is a no-op in R.

Value

This function is a no-op in R. It returns `NA`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`tsdiagplot` in both systems and `arima.diag` in S-Plus.

`arma.loop` *Loop through a series of ARIMA models and display coordinated tables and diagnoastic graphs.*

Description

Loop through a series of ARIMA models and display coordinated tables and diagnostic graphs. The complete example from the Heiberger and Teles article, also included in the Heiberger and Holland book, is illustrated.

Usage

```
arma.loop(x,
          model,             ## S-Plus
          order, seasonal,   ## R
          series=deparse(substitute(x)), ...)

diag.arma.loop(z,
               x=stop("The time series x is needed in S-Plus when p=q=0."),
               lag.max = 36, gof.lag = lag.max)

rearrange.diag.arma.loop(z)
```

Arguments

`x`	Time series vector. In S-Plus, `x` must be an `"rts"`.
`model`	A valid S-Plus `model` for `arima.mle`.
`order, seasonal`	A valid R `order` and `seasonal` for `arima`.
`series`	Character string describing the time series.
`...`	Additional arguments for `arima.mle` or `arima`.
`z`	For `diag.arma.loop`, an "arma.loop" object. For `rearrange.diag.arma.loop`, an "diag.arma.loop" object.
`lag.max`	Maximum lag for the acf and pacf plots.
`gof.lag`	Maximum lag for the gof plots.

Details

S-Plus and R have different functions, with different input argument names and different components in their value.

Value

`arma.loop`: `"arma.loop"` object which is a matrix of lists, each containing an arima model.

`diag.arma.loop`: `"diag.arma.loop"` object which is a matrix of lists, each containing the standard diagnostics for one arima model.

`rearrange.diag.arma.loop`: List of matrices, each containing all the values for a specific diagnostic measure collected from the set of arima models.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

References

"Displays for Direct Comparison of ARIMA Models" The American Statistician, May 2002, Vol. 56, No. 2, pp. 131-138. Richard M. Heiberger, Temple University, and Paulo Teles, Faculdade de Economia do Porto.

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

`tsdiagplot`

Examples

```
## see tsdiagplot for the example
```

`as.likert` *Support functions for diverging stacked barcharts for Likert, semantic differential, and rating scale data.*

Description

Constructs class="likert" objects to be used by the plot.likert methods.

Usage

```
is.likert(x)

as.likert(x, ...)
## Default S3 method:
as.likert(x, ...)
## S3 method for class 'data.frame'
as.likert(x, ...)
## S3 method for class 'formula'
as.likert(x, ...)  ## doesn't work yet
## S3 method for class 'ftable'
as.likert(x, ...)
## S3 method for class 'table'
as.likert(x, ...)
## S3 method for class 'matrix'
```

```
as.likert(x,
          ReferenceZero=NULL,
          ...,
          rowlabel=NULL, collabel=NULL,
          xlimEqualLeftRight=FALSE,
          xTickLabelsPositive=TRUE,
          padding=FALSE,
          reverse.left=TRUE)
## S3 method for class 'listOfNamedMatrices'
as.likert(x, ...)
## S3 method for class 'array'
as.likert(x, ...)

## S3 method for class 'likert'
rev(x)

is.likertCapable(x, ...)
```

Arguments

x	For the as.likert methods, a numeric object stored as a vector, matrix, two-dimensional table, two-dimensional ftable, two-dimensional structable (as defined in the vcd package), or list of named matrices. For functions is.likert and is.likertCapable, any object. This is the only required argument.
rowlabel, collabel	names(dimnames(x)), where x is the argument to the as.likert functions. These will become the xlab and ylab of the likert plot.
...	other arguments. They will be ignored by the as.likert method.
ReferenceZero	Please see discussion of this argument in likert.
xlimEqualLeftRight	Logical. The default is FALSE. If TRUE, then the left and right x limits are set to negative and positive of the larger of the absolute value of the original x limits.
xTickLabelsPositive	Logical. The default is TRUE. If TRUE, then the tick labels on the negative side are displayed as positive values.
padding, reverse.left	padding is FALSE for likert and TRUE for likertMosaic. reverse.left is TRUE for likert and FALSE for likertMosaic. likert is based on barchart and requires that the sequencing of negative values be reversed. likertMosiac is based on mosaic and needs padding on left and right to fill the rectangle implied by the convex hull of the plot.

Details

Please see likert for information on the plot for which as.likert prepares the data.

Value

For the as.likert methods, a likert object, which is a matrix with additional attributes that are needed to make the barchart method used by the plot.likert methods work with the data. Columns for respondents who disagree have negated values. Any NA values in the argument x are changed to 0. The column of the original data for respondents who neither agree nor disagree is split into two columns, each containing halved values—one positive and one negative. Negative columns come first in the sequence of "No Opinion"(negative)–"Strongly Disagree", followed by "No Opinion"(positive)–"Strongly Agree". There are four attributes: "even.col" indicating whether there were originally an even number of columns, "n.levels" the original number of levels, "levels" the original levels in the original order, "positive.order" The sequence in which to display the rows in order to make the right hand sides progress with high values on top.

is.likert returns a TRUE or FALSE value.

is.likertCapable returns a TRUE or FALSE value if the argument can used as an argument to one of the plot.likert methods.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Richard M. Heiberger, Naomi B. Robbins (2014)., "Design of Diverging Stacked Bar Charts for Likert Scales and Other Applications", Journal of Statistical Software, 57(5), 1–32, doi:10.18637/jss.v057.i05.

Naomi Robbins <naomi@nbr-graphs.com>, "Visualizing Data: Challenges to Presentation of Quality Graphics—and Solutions", Amstat News, September 2011, 28–30.

Naomi B. Robbins and Richard M. Heiberger (2011). Plotting Likert and Other Rating Scales. In JSM Proceedings, Section on Survey Research Methods. Alexandria, VA: American Statistical Association.

Luo, Amy and Tim Keyes (2005). "Second Set of Results in from the Career Track Member Survey," Amstat News. Arlington, VA: American Statistical Association.

See Also

likert

Examples

```
## Please see ?likert to see these functions used in context.

tmp2 <- array(1:12, dim=c(3,4), dimnames=list(B=LETTERS[3:5], C=letters[6:9]))
as.likert(tmp2)  ## even number of levels.

is.likert(tmp2)
is.likert(as.likert(tmp2))
```

`as.matrix.listOfNamedMatrices` *Convert a list of numeric matrices to a single matrix*

Description

Convert a list of numeric matrices to a single matrix. This function is used to improve legibility of the printed object. The `as.matrix.listOfNamedMatrices` display is easier to read when the rownames are very long, as in the example illustrated here. Because the default print of the matrix repeats the rownames several times, with only a few columns of the data shown in each repetition, the actual matrix structure of the data values is obscured.

Usage

```
## S3 method for class 'listOfNamedMatrices'
as.matrix(x, abbreviate = TRUE, minlength = 4, ...)
is.listOfNamedMatrices(x,  xName=deparse(substitute(x)))
## S3 method for class 'listOfNamedMatrices'
as.data.frame(x, ...)
as.listOfNamedMatrices(x,  xName=deparse(substitute(x)), ...)
## S3 method for class 'listOfNamedMatrices'
x[...]
## S3 method for class 'array'
as.listOfNamedMatrices(x, xName=deparse(substitute(x)), ...)
## S3 method for class 'list'
as.listOfNamedMatrices(x, xName=deparse(substitute(x)), ...)
## S3 method for class 'MatrixList'
as.listOfNamedMatrices(x, xName=deparse(substitute(x)), ...)
## S3 method for class 'listOfNamedMatrices'
print(x, ...)

as.MatrixList(x)
## S3 method for class 'array'
as.MatrixList(x)
## S3 method for class 'MatrixList'
print(x, ...)

as.likertDataFrame(x, xName=deparse(substitute(x)))
## S3 method for class 'listOfNamedMatrices'
as.likertDataFrame(x, xName=deparse(substitute(x)))
## S3 method for class 'array'
as.likertDataFrame(x, xName=deparse(substitute(x)))
```

Arguments

x	Named list of numeric matrices. All matrices in the list should have the same number of columns and the same column names. The names of the list items will normally be long; NA, as introduced by the addNA, is a valid name. The row names will normally be long. The number of rows and their names will normally differ across the matrices. Each named item in the list may be a vector, matrix, array, data.frame, two-dimensional table, two-dimensional ftable, or two-dimensional structable. For the as.MatrixList methods, an array.
...	Other arguments. Not used.
abbreviate	Logical. If TRUE, then use the abbreviate function on the item names and row names.
minlength	the minimum length of the abbreviations.
xName	Name of the argument in its original environment.

Value

The result of as.listOfNamedMatrices is a list with class=c("listOfNamedMatrices", "list").

The result of as.matrix.listOfNamedMatrices is an rbind of the individual matrices in the argument list x. The rownames of the result matrix are constructed by pasting the abbreviation of the list item names with the abbreviation of the individual matrix rownames. The original names are retained as the "Subtables.Rows" attribute.

The result of is.listOfNamedMatrices is logical value.

print.listOfNamedMatrices prints as.matrix.listOfNamedMatrices of its argument and returns the original argument.

as.data.frame.listOfNamedMatrices(x, ...) is an unfortunate kluge. The result is the original x that has NOT been transformed to a data.frame. A warning message is generated that states that the conversion has not taken place. This kluge is needed to use "listOfNamedMatrices" objects with the Commander package because Rcmdr follows its calls to the R data function with an attempt, futile in this case, to force the resulting object to be a data.frame.

The as.MatrixList methods construct a list of matrices from an array. Each matrix has the first two dimensions of the array. The result list is itself an array defined by all but the first two dimensions of the argument array.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

likert

Examples

```
data(ProfChal)

tmp <- data.matrix(ProfChal[,1:5])
```

```
rownames(tmp) <- ProfChal$Question
ProfChal.list <- split.data.frame(tmp, ProfChal$Subtable)

## Original list of matrices is difficult to read because
## it is displayed on too many lines.
ProfChal.list[2:3]

## Single matrix with long list item names and long row names
## of argument list retained as an attribute.
as.listOfNamedMatrices(ProfChal.list[2:3], minlength=6)

## Not run:
## NA as a dimname value
tmp <- structure(c(0, 0, 0, 6293, 18200, 2122,
                   0, 0, 0, 2462, 7015, 5589,
                   6908, 5337, 842, 0, 0, 0),
                 .Dim = c(3L, 2L, 3L),
                 .Dimnames = list(c("A", "B", "C"),
                                  c("D", "E"),
                                  c("F", "G", NA)))
tmp
as.MatrixList(tmp)

## End(Not run)

## Not run:
sapply(as.MatrixList(tmp3), as.likert, simplify=FALSE)  ## odd number of levels.

data(NZScienceTeaching)
likert(Question ~ ., NZScienceTeaching)
likert(Question ~ . | Subtable, data=NZScienceTeaching)
likert(Question ~ . | Subtable, data=NZScienceTeaching,
       layout=c(1,2), scales=list(y=list(relation="free")))



## End(Not run)
```

`as.multicomp` *Support functions in R for MMC (mean–mean multiple comparisons) plots.*

Description

MMC plots: In R, functions used to interface the `glht` in R to the MMC functions designed with S-Plus `multicomp` notation. These are all internal functions that the user doesn't see.

Usage

```
## S3 method for class 'mmc.multicomp'
```

```
print(x, ..., width.cutoff=options()$width-5)

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

## print.multicomp.hh(x, digits = 4, ..., height=T) ## S-Plus only

## S3 method for class 'multicomp.hh'
print(x, ...) ## R only


as.multicomp(x, ...)

## S3 method for class 'glht'
as.multicomp(x,       ## glht object
           focus=x$focus,
           ylabel=deparse(terms(x$model)[[2]]),
           means=model.tables(x$model, type="means",
                              cterm=focus)$tables[[focus]],
           height=rev(1:nrow(x$linfct)),
           lmat=t(x$linfct),
           lmat.rows=lmatRows(x, focus),
           lmat.scale.abs2=TRUE,
           estimate.sign=1,
           order.contrasts=TRUE,
           contrasts.none=FALSE,
           level=0.95,
           calpha=NULL,
           method=x$type,
           df,
           vcov.,
           ...
           )

as.glht(x, ...)

## S3 method for class 'multicomp'
as.glht(x, ...)
```

Arguments

x	"glht" object for as.multicomp. A "mmc.multicomp" object for print.mmc.multicomp. A "multicomp" object for as.glht and print.multicomp.
...	other arguments.
focus	name of focus factor.
ylabel	response variable name on the graph.
means	means of the response variable on the focus factor.

`lmat`, `lmat.rows` mmc

`lmat.scale.abs2`
: logical, almost always `TRUE`. If it is not `TRUE`, then the contrasts will not be properly placed on the MMC plot.

`estimate.sign`
: numeric. 1: force all contrasts to be positive by reversing negative contrasts. -1: force all contrasts to be negative by reversing positive contrasts. Leave contrasts as they are constructed by `glht`.

`order.contrasts`, `height`
: logical. If `TRUE`, order contrasts by `height` (see `mmc`).

`contrasts.none`
: logical. This is an internal detail. The "contrasts" for the group means are not real contrasts in the sense they don't compare anything. `mmc.glht` sets this argument to `TRUE` for the `none` component.

`level`
: Confidence level. Defaults to 0.95.

`calpha`
: R only. User-specified critical point. See `confint.glht`.

`df`, `vcov.`
: R only. Arguments forwarded through `glht` to `modelparm`.

`method`
: R only. See `type` in `confint.glht`.

`width.cutoff`
: See `deparse`.

Details

The `mmc.multicomp` `print` method displays the confidence intervals and heights on the MMC plot for each component of the `mmc.multicomp` object.

`print.multicomp` displays the confidence intervals and heights for a single component.

Value

`as.multicomp` is a generic function to change its argument to a `"multicomp"` object.

`as.multicomp.glht` changes an `"glht"` object to a `"multicomp"` object. If the model component of the argument `"x"` is an `"aov"` object then the standard error is taken from the `anova(x$model)` table, otherwise from the `summary(x)`. With a large number of levels for the focus factor, the `summary(x)` function is exceedingly slow (80 minutes for 30 levels on 1.5GHz Windows XP). For the same example, the `anova(x$model)` takes a fraction of a second.

Note

The multiple comparisons calculations in R and S-Plus use completely different functions. MMC plots in R are based on `glht`. MMC plots in S-Plus are based on `multicomp`. The MMC plot is the same in both systems. The details of gettting the plot differ.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

See Also

mmc, glht.

`as.vector.trellis` *Convert a two-dimensional trellis object into a one-dimensional trellis object. Change the order of panels in a trellis object.*

Description

`as.vector.trellis` converts a two-dimensional trellis object into a one-dimensional trellis object. `reorder.trellis` changes the order of the `panel.args` component in a trellis object. These are are mostly used as utilities by `matrix.trellis`.

Usage

```
## S3 method for class 'trellis'
as.vector(x, mode = "any")
## S3 method for class 'trellis'
reorder(x, X, ...)
```

Arguments

`x`	`trellis` object.
`mode`	We are hijacking the `mode` argument. It is used here for the names of the panels.
`...`	Other arguments are ignored.
`X`	Subscript vector specifying the new order of the panels.

Value

trellis object with `length(dim(x)) == 1`. `as.vector` retains the original order of the panels. `reorder` changes the order to the one specified by using the `X` argument as a subscript.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
tmp <- data.frame(a=letters[c(1:3,1:3,1:3)],
                  b=1:9,
                  d=1:9,
                  e=LETTERS[c(4,4,4,5,5,5,6,6,6)])
tmp
a6 <- xyplot(b ~ d | a*e, data=tmp, pch=19)
a6
dim(a6)
a62 <- as.vector(a6)
a62
dim(a62)
a63 <- reorder(a6, c(1,4,7, 2,5,8, 3,6,9))
a63
dim(a63)
a64 <- matrix.trellis(a63, nrow=3, ncol=3, dimnames=dimnames(a6), byrow=TRUE)
a64
dim(a64)
```

---

axis.i2wt *specialized axis function for interaction2wt.*

Description

Labels the bottom axis with the x-factor name for each column. Labels the right axis with the response variable name in all rows.

Usage

```
axis.i2wt(side, scales, ...)
```

Arguments

`side, scales, ...`
: See `axis.default`.

Author(s)

Richard M. Heiberger, with asssistance from Deepayan Sarkar.

See Also

`interaction2wt`

`bivariateNormal` *Plot the bivariate normal density using wireframe for specified rho.*

Description

Plot the bivariate normal density using wireframe for specified rho. There is a shiny app that allows this to be done dynamically.

Usage

```
bivariateNormal(rho = 0, layout = c(3, 3), lwd = 0.2,
                angle = c(22.5, 67.5, 112.5, 337.5, 157.5, 292.5, 247.5, 202.5),
                 col.regions = trellis.par.get("regions")$col, ...)
```

Arguments

`rho`	Correlation between x and y.
`layout`, `lwd`	Standard **lattice** arguments.
`angle`	This is used as the `z` component of the `screen` argument to `panel.wireframe`.
`col.regions`, `...`	See `wireframe`.

Details

The default setting shows the view as seen from a series of eight angles. To see just a single view, see the example.

Value

`"trellis"` object.

Note

Based on the `galaxy` example on pages 204–205 in *S & S-PLUS Trellis Graphics User's Manual*, Richard A. Becker and William S. Cleveland (1996), https://www.stat.auckland.ac.nz/~ihaka/courses/120/trellis.user.pdf

Author(s)

Richard M. Heiberger (rmh@temple.edu)

Examples

```
bv8 <- bivariateNormal(.7)  ## all views on one page
bv8
update(bv8[3], layout=c(1,1)) ## one panel
## Not run:
  if (interactive())
    shiny::runApp(file.path(system.file(package="HH"), "shiny/bivariateNormal")) ## 3D
  if (interactive())
   shiny::runApp(system.file("shiny/bivariateNormalScatterplot", package="HH")) ## scatterplot

## End(Not run)
```

`ci.plot` *Plot confidence and prediction intervals for simple linear regression*

Description

The data, the least squares line, the confidence interval lines, and the prediction interval lines for a simple linear regression (`lm(y ~ x)`) are displayed. Tick marks are placed at the location of xbar, the x-value of the narrowest interval.

Usage

```
ci.plot(lm.object, ...)

## S3 method for class 'lm'
ci.plot(lm.object,
        xlim=range(data[, x.name]),
        newdata,
        conf.level=.95,
        data=model.frame(lm.object),
        newfit,
        ylim,
        pch=19,
        lty=c(1,3,4,2),
        lwd=2,
        main.cex=1,
        main=list(paste(100*conf.level,
          "% confidence and prediction intervals for ",
          substitute(lm.object), sep=""), cex=main.cex), ...
        )
```

Arguments

`lm.object`	Linear model for one `y` and one `x` variable.
`xlim`	`xlim` for plot. Default is based on data from which `lm.object` was constructed.

newdata	data.frame containing data for which predictions are wanted. The variable name of the column must be identical to the name of the predictor variable in the model object. Defaults to a data.frame containing a vector spanning the range of observed data. User-specified values are appended to the default vector.
conf.level	Confidence level for intervals, defaults to .95
data	data extracted from the lm.object
newfit	Constructed data.frame containing the predictions,confidence interval, and prediction interval for the newdata.
ylim	ylim for plot. Default is based on the constructed prediction interval.
pch	Plotting character for observed points.
lty, lwd	Line types and line width for fit and intervals.
main.cex	Font size for main title.
main	Main title for plot
...	Additional arguments to be passed to panel function.

Value

"trellis" object containing the plot.

Note

The predict.lm functions in S-Plus and R differ. The S-Plus function can produce both confidence and prediction intervals with a single call. The R function produces only one of them in a single call. Therefore the default calculation of newfit within the function depends on the system.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

lm, predict.lm

Examples

```
tmp <- data.frame(x=rnorm(20), y=rnorm(20))
tmp.lm <- lm(y ~ x, data=tmp)
ci.plot(tmp.lm)
```

CIplot *Illustration of the meaning of confidence levels.*

Description

Illustration of the meaning of confidence levels. Generate sets of confidence intervals for independent randomly generated sets of normally distributed numbers. Low confidence levels give narrow intervals that are less likely to bracket the true value. Higher confidence levels increase the probability of bracketing the true value, and are also much wider and therefore less precise. The shiny app can animate how the increase in confidence level and width leads to a consequent decrease in precision.

Usage

```
CIplot(n.intervals = 100,
       n.per.row = 40,
       pop.mean = 0,
       pop.sd = 1,
       conf.level = 0.95,
       ...)

confintervaldata(n.intervals = 100,
                 n.per.row = 40,
                 pop.mean = 0,
                 pop.sd = 1,
                 conf.level = 0.95,
                 seed,
                 ...)

confinterval.matrix(x,
                    conf.level = attr(x, "conf.level"),
                    ...)

confintervalplot(x.ci,
                 n.intervals = nrow(x.ci),
                 pop.mean = attr(x.ci, "pop.mean"),
                 pop.sd = attr(x.ci, "pop.sd"),
                 n.per.row = attr(x.ci, "n.per.row"),
                 xlim, ylim, ...)

shiny.CIplot(height = "auto")
```

Arguments

n.intervals	Number of sets of observations to generate. Each set leads to one confidence interval on the plot.
n.per.row	Number of observations in each set.

pop.mean, pop.sd
: Population mean and standard deviation for generated set of n.per.row independent normally distributed random numbers.

conf.level
: Confidence level of each of the n.per.row confidence intervals calculated from the generated datasets.

seed
: Standard argument to rnorm.

x
: Output matrix from confintervaldata.

x.ci
: Output data.frame from confinterval.matrix.

xlim, ylim
: Standard xyplot arguments.

height
: Height of graph on web page in pixels.

...
: Additional arguments. For CIplot, seed will be forwarded to confintervaldata, and xlim and ylim will be forwarded to confintervalplot. Any other additional arguments will be ignored.

Details

The shiny app has sliders for the n.intervals, n.per.row, pop.mean, pop.sd, and conf.level. Changes in the conf.level slider, either manually by animation, use the same set of generated data to show how increasing the confidence level increases the width of the confidence interval and consequently decreases the precision of the interval estimator.

Value

CIplot and confintervalplot return a "trellis" plot containing a plot of Confidence Intervals.

confintervaldata returns a matrix of n.intervals rows by n.per.row columns of independent normally distributed random numbers. The matrix has a set of attributes recording the arguments to the function.

confinterval.matrix returns a data.frame of n.intervals with three columns containing the lower bound, center, and upper bound of the confidence interval for each row of its input matrix. The data.frame has a set of attributes recording the arguments to the function.

shiny.CIplot returns a shiny app object which, when printed, runs a shiny app displaying the Confidence Interval plot and several slider controls.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
## A. from the console

## example 1
CIplot()

## example 2
## Not run:
CIplot(n.intervals=100,
```

```
        n.per.row=40,
        pop.mean=0,
        pop.sd=1,
        conf.level=.95)

## End(Not run)

## example 3
## Not run:
tmp.data <- confintervaldata()
tmp.ci <- confinterval.matrix(tmp.data)
confintervalplot(tmp.ci)

## End(Not run)

## example 4
## Not run:
tmp.data <- confintervaldata(n.intervals=100,
                             n.per.row=40,
                             pop.mean=0,
                             pop.sd=1,
                             conf.level=.95)
tmp.ci <- confinterval.matrix(tmp.data)
confintervalplot(tmp.ci)

## End(Not run)


## B. shiny, initiated from the console

## example 5
## Not run:
  if (interactive())
    shiny.CIplot()

## End(Not run)

## example 6
## Not run:
  if (interactive())
    shiny.CIplot(height=800)  ## px
  ## take control of the height of the graph in the web page

## End(Not run)
```

---

col.hh *Initializing Trellis Displays*

Description

Initialization of an R display device with the graphical parameters that rmh prefers.

Usage

```
col.hh()
```

Value

List of graphical parameters to be used in the `theme` argument to the `trellis.device` or `trellis.par.set` functions.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`trellis.device`, `trellis.par.get`

Examples

```
## Not run:
trellis.device(theme="col.hh") ## Open a device with the theme

trellis.device(theme=col.hh()) ## Open a device with the theme

trellis.par.set(theme=col.hh())## Add theme to already open device

## End(Not run)
```

`col3x2` *col3x2 color dataset*

Description

col3x2 color dataset.

Usage

```
data("col3x2")
```

Format

The format is: chr [1:6] "#1B9E77" "#D95F02" "#7570B3" "#66C2A5" "#FC8D62" "#8DA0CB"

Details

3x2 color scheme. These colors look like a 3x2 color array when run through the vischeck simulator to see how they look for the three most common color vision deficiencies: Deuteranope, Protanope, Tritanope.

References

About 10% of the population have color deficient vision. Your job is make your graphs legible to everyone. Download ImageJ from https://imagej.net/Downloads and VischeckJ from http://vischeck.com and follow the instructions in those sites. This program will allow you to simulate color deficient vision on your computer.

On my Mac, I need to doubleclick ij.jar to open the program. Then open the "Vischeck Panel" on the Plugins menu and navigate to a png file with the "File Open" menu. Click on each of the three types of color deficiency.

Examples

```
data(col3x2)
col3x2

## Not run:
library(RColorBrewer)
library(lattice)
col3x2 <- c(brewer.pal(n=3, "Dark2"), brewer.pal(n=3, "Set2"))
col3x2
## save(col3x2, file="col3x2.rda") ## data(col3x2, package="HH")

## End(Not run)

## Not run:
barchart(~ 1:6, col=col3x2, lwd=0, origin=0, horizontal=FALSE,
         scales=list(x=list(at=1:6, labels=col3x2)))


tmp <- array(c(1, rep(0,6)), c(1,3,2,6),
             dimnames=list("",
                           c("green","orange","blue"),
                           c("Dark2","Set2"),
                           col3x2))

useOuterStrips(barchart(tmp, col=col3x2,
                        between=list(x=1, y=1),
                        scales=list(x=list(at=-1)),
                        main="col3x2", xlab="")) +
  layer(panel.text(x=.5, y=1.45, labels=col3x2[panel.number()]))


## End(Not run)
```

`combineLimits.trellisvector` *Combine limits on a one-dimensional trellis object.*

Description

Combine limits on a one-dimensional trellis object.

Usage

```
combineLimits.trellisvector(x, margin.x = 1:2, margin.y = 1:2,
                            layout = x$layout,
                            ncol=x$layout[1], nrow=x$layout[2],
                            condlevels = x$condlevels[[1]], ...)
```

Arguments

x	trellis object.
margin.x, margin.y	See combineLimits.
layout	See xyplot.
condlevels	Character. Names of each panel of the result. Defaults to the names of the panels of the argument.
...	Other arguments are ignored.
nrow, ncol	See matrix.trellis. These arguments default to the levels of x$layout if it is non-null. Otherwise nrow==1 and ncol==dim(x).

Details

The one-dimensional object is converted to a two-dimensional object which is forwarded to the standard combineLimits function. The result is converted back to a one-dimensional object.

Value

One-dimensional trellis object with combined xlim and ylim values across all panels.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

combineLimits

Examples

```
tmp <- data.frame(a=1:3,
                  b=c(4,5,7),
                  c=5:7,
                  d=c(8, 9, 12),
                  e=9:11)
tmp

a2 <- xyplot(a + b ~ c + d + e, data=tmp, outer=TRUE,
             scales=list(relation="free"), main="a2")
a2
dim(a2)
combineLimits.trellisvector(a2)
```

```
a21 <- combineLimits.trellisvector(update(a2, layout=c(3,2)))
a21
dim(a21)
```

`cp.calc` *Rearranges and improves the legibility of the output from the stepwise function in S-Plus.*

Description

Rearranges and improves the legibility of the output from the `stepwise` function in S-Plus. The output can be used for the Cp plot. `cp.calc` works only in S-Plus. Use `regsubsets` in R. The example below works in both languages.

Usage

```
cp.calc(sw, data, y.name)

## S3 method for class 'cp.object'
print(x, ...)

## S3 method for class 'cp.object'
x[..., drop = TRUE]
```

Arguments

`sw`	Output from the S-Plus `stepwise` function.
`data`	Dataset name from which `"sw"` was calculated.
`y.name`	Name of response variable for which `"sw"` was calculated.
`x`	Object of class `"cp.object"`.
`...`	Additional arguments to `"["` or `"print"`.
`drop`	Argument to the `print` function.

Value

`"cp.object"`, which is a data.frame containing information about each model that was attempted with additional attributes: `tss` total sum of squares, `n` number of observations, `y.name` response variable, `full.i` row name of full model. The columns are

`p`	number of parameters in the model
`cp`	Cp statistic
`aic`	AIC statistic
`rss`	Residual sum of squares
`r2`	R^2
`r2.adj`	Adjusted R^2
`xvars`	X variables
`sw.names`	Model name produced by `stepwise`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Examples

```
## This example is from Section 9.15 of Heiberger and Holland (2004).
data(usair)
if.R(s={usair <- usair}, r={})

splom(~usair, main="U.S. Air Pollution Data with SO2 response", cex=.5)
## export.eps(hh("regb/figure/regb.f1.usair.eps"))

usair$lnSO2 <- log(usair$SO2)
usair$lnmfg <- log(usair$mfgfirms)
usair$lnpopn <- log(usair$popn)

usair[1:3,]   ## lnSO2 is in position 8, SO2 is in position 1
              ## lnmfg is in position 9, lnpopn is in position 10

splom(~usair[, c(8,2,9,10,5:7)],
              main="U.S. Air Pollution Data with 3 log-transformed variables",
              cex=.5)
## export.eps(hh("regb/figure/regb.f2.usair.eps"))

if.R(s={
  usair.step <- stepwise(y=usair$lnSO2,
                         x=usair[, c(2,9,10,5:7)],
                         method="exhaustive",
                         plot=FALSE, nbest=2)
  ## print for pedagogical purposes only.  The plot of cp ~ p is more useful.
  ## The line with rss=1e35 is a stepwise() bug, that we reported to S-Plus.
  print(usair.step, digits=4)
  usair.cp <- cp.calc(usair.step, usair, "lnSO2")
  ## print for pedagogical purposes only.  The plot of cp ~ p is more useful.
  usair.cp
  tmp <- (usair.cp$cp <= 10)
  usair.cp[tmp,]

  old.par <- par(mar=par()$mar+c(0,1,0,0))
  tmp <- (usair.cp$cp <= 10)
  plot(cp ~ p, data=usair.cp[tmp,], ylim=c(0,10), type="n", cex=1.3)
  abline(b=1)
  text(x=usair.cp$p[tmp], y=usair.cp$cp[tmp],
       row.names(usair.cp)[tmp], cex=1.3)
  title(main="Cp plot for usair.dat, Cp<10")
  par(old.par)
```

```
## export.eps(hh("regb/figure/regb.f3.usair.eps"))
},r={
  usair.regsubset <- leaps::regsubsets(lnSO2~lnmfg+lnpopn+precip+raindays+temp+wind,
                                       data=usair, nbest=2)
  usair.subsets.Summary <- summaryHH(usair.regsubset)
  tmp <- (usair.subsets.Summary$cp <= 10)
  usair.subsets.Summary[tmp,]
  plot(usair.subsets.Summary[tmp,], statistic='cp', legend=FALSE)

  usair.lm7 <- lm.regsubsets(usair.regsubset, 7)
  anova(usair.lm7)
  summary(usair.lm7)
})

vif(lnSO2 ~ temp + lnmfg + lnpopn + wind + precip + raindays, data=usair)

vif(lnSO2 ~ temp + lnmfg + wind + precip, data=usair)

usair.lm <- lm(lnSO2 ~ temp + lnmfg + wind + precip, data=usair)
anova(usair.lm)
summary(usair.lm, corr=FALSE)
```

`cplx` *Generate a sequence spanning the xlim of a lattice window.*

Description

Generate a sequence of `length` points spanning the `current.panel.limits()$xlim` of a lattice window.

Usage

```
cplx(length)
```

Arguments

`length`	Integer number of points.

Value

One-column matrix containing `length` rows. The first value is the x-value at the left side of the window. The last value is the x-value at the right side of the window. The in between points are evenly spaced.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

scale

Examples

```
cplx(11)
```

---

datasets *Datasets for Statistical Analysis and Data Display, Heiberger and Holland*

Description

Most of the datasets are described in the book *Statistical Analysis and Data Display*.

For ProfChal, see plot.likert.

AudiencePercent is from personal communication by the market researcher who did the study.

SFF8121 is student evaluations of my class compared to the average of all graduate classes in the Spring 2010 semester. Personal communication from the Temple University Office of the Provost to me.

ProfDiv is "Profit-and-Dividend Status of 348 Corportations in the United States for the period from 1929 to 1935" from Brinton WC (1939), *Graphic Presentation*. Brinton Associates. http://www.archive.org/details/graphicpresentat00brinrich.

NZScienceTeaching is from New Zealand Ministry of Research Science and Technology(2006), "Staying in Science." This URL is no longer valid. http://www.morst.govt.nz/Documents/publications/researchrep

PoorChildren is from "Poor Children, Working Parents", Analysis of data from the CensusBureau's American Community Survey. Comparison of Census areas of 100,000 or more people, based on samples from 2005 to 2009.

Source: Data from the U.S. Census Bureau's American Community Survey; analysis by Andrew A. Beveridge, QueensCollege. Copyright 2011 The New York Times Company

https://archive.nytimes.com/www.nytimes.com/imagepages/2011/12/03/opinion/03blow-ch.html?ref=opinion

https://www.nytimes.com/2011/12/03/opinion/blow-newts-war-on-poor-children.html?_r=1

Naomi Robbins and I discuss the PoorChildren example in the Forbes online column: https://www.forbes.com/sites/naomirobbins/2011/12/20/alternative-to-charles-blows-figure-in-newts-war-on-p

```
demo(PoorChildren, package="HH")
```

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

`dchisq.intermediate` *Intermediate f and chisq functions to simplify writing for both R and S-Plus.*

Description

Intermediate f and chisq functions to simplify writing for both R and S-Plus.

Usage

```
dchisq.intermediate(x, df, ncp=0, log=FALSE)
pchisq.intermediate(q, df, ncp=0, lower.tail=TRUE, log.p=FALSE)
qchisq.intermediate(p, df, ncp=0, lower.tail=TRUE, log.p=FALSE)
df.intermediate(x, df1, df2, ncp=0, log=FALSE)
pf.intermediate(q, df1, df2, ncp=0, lower.tail=TRUE, log.p=FALSE)
qf.intermediate(p, df1, df2, ncp=0, lower.tail=TRUE, log.p=FALSE)
```

Arguments

`x`, `p`, `q`, `df`, `df1`, `df2`, `ncp`, `log`, `log.p`, `lower.tail`
: See `pchisq` and `pf`. Some arguments don't exist in S-Plus. That is why these functions are needed.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

`diag.maybe.null` *Returns a value for the diagonal of NA and NULL arguments.*

Description

Returns the argument for the diagonal of NA and NULL arguments. For all other arguments, it calls the regular `diag` function.

Usage

```
diag.maybe.null(x, ...)
```

Arguments

x	matrix, vector, NA,
...	Other arguments to diag.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

diag.

Examples

```
diag.maybe.null(NULL)
diag.maybe.null(NA)
diag.maybe.null(1:5)
```

---

diagplot5new *Transpose of ECDF for centered fitted values and residuals from a linear model.*

Description

Transpose of ECDF (Empirical CDF) for centered fitted values and residuals from a linear model.

Usage

```
diagplot5new(linearmodel, ..., pch = 19)
```

Arguments

linearmodel	"lm" object.
pch, ...	Arguments to xyplot.

Details

This is an implementation in xyplot of the "r-f spread" plot.

Value

"trellis" object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

William Cleveland (1993), *Visualizing Data*, Hobart Press.

Examples

```
## See ?residVSfitted
## Not run:
data(fat)
fat.lm <- lm(bodyfat ~ abdomin, data=fat)
diagplot5new(fat.lm)

## End(Not run)
```

`diagQQ` *QQ plot of regression residuals.*

Description

QQ plot of regression residuals. The `panel.qqmathline` is displayed.

Usage

```
diagQQ(lm.object, ...)
```

Arguments

`lm.object`	`"lm"` object.
`...`	Additional arguments to `qqmath`.

Value

`"trellis"` object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`qqmath`

Examples

```
## See ?residVSfitted
## Not run:
data(fat)
fat.lm <- lm(bodyfat ~ abdomin, data=fat)
diagQQ(fat.lm)

## End(Not run)
```

Discrete4 *Discrete with four levels color dataset.*

Description

Discrete with four levels color dataset. These colors look like four distinct colors when run through the vischeck simulator to see how they look for the three most common color vision deficiencies: Deuteranope, Protanope, Tritanope.

Usage

```
data("Discrete4")
```

Format

The format is: chr [1:4] "#E31A1C" "#1F78B4" "#FB9A99" "#A6CEE3"

Details

4x1 color scheme

Examples

```
data(Discrete4)
## Not run:
library(RColorBrewer)
library(lattice)
Discrete4 <- brewer.pal(n=12, "Paired")[c(6,2,5,1)]
Discrete4
## save(Discrete4, file="Discrete4.rda") ## data(Discrete4, package="HH")
##
barchart(~ 1:4, col=Discrete4, lwd=0, origin=0, horizontal=FALSE,
         xlab="Colors", scales=list(x=list(labels=Discrete4), y=list(labels=NULL)),
         main=paste("These colors look like four distinct colors when run through",
                    "the vischeck simulator to see how they look for the three most",
                  "common color vision deficiencies: Deuteranope, Protanope, Tritanope.",
                    sep="\n"))

## End(Not run)
```

`do.formula.trellis.xysplom` *Interprets model formulas for xysplom and extended bwplots*

Description

Interprets a model formula in the context of its data.frame.

Usage

```
do.formula.trellis.xysplom(formula, data, na.action = na.pass)
```

Arguments

`formula`	model formula
`data`	data.frame
`na.action`	see `na.action`

Value

A list containing three data.frames and three formula, one for each.

`x`	`data.frame` containing the variables on the right-hand side of the model formula.
`y`	`data.frame` containing the variables on the left-hand side of the model formula.
`g`	`data.frame` containing the variables, if any, after the conditioning bar `|` of the model formula.
`x.formula`	`formula` containing the right-hand side of the model formula.
`y.formula`	`formula` containing the left-hand side of the model formula.
`g.formula`	`formula` containing the formula after the conditioning bar `|` of the model formula.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`formula`, `na.action`

Examples

```
tmp <- data.frame(y=1, x=2, z=3, g=4)
do.formula.trellis.xysplom( y ~ x + z | g, data=tmp)
```

`EmphasizeVerticalPanels` *Helper function for likertWeighted(). used for vertical spacing and horizontal borders of grouped panels.*

Description

Helper function for `likertWeighted()` used for vertical spacing and horizontal borders of grouped panels. Horizontal rules between panels are suppressed by default by `likertWeighted` unless `y.between` is non-zero. See examples.

Usage

```
EmphasizeVerticalPanels(x, y.between)
```

Arguments

`x`	`"trellis"` object, normally one constructed by `likertWeighted`.
`y.between`	The `between=list(y=numericvector)` argument applied to a trellis object.

Value

Revised `trellis` object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`likertWeighted`

Examples

```
tmp1 <- array(1:60, c(5, 4, 3), list(letters[1:5],letters[6:9],letters[10:12]))
tmp2 <- toCQxR(tmp1)
colnames(tmp2)

likertWeighted(~ . | group + row, tmp2)

likertWeighted(~ . | group + row, tmp2, h.resize.panels=1:5,
               between=list(y=c(0,0,3,0)),
               h.resizePanels=1:5,
               ylab=c("Bottom","Top"),
               xlab.top=c("First","Second","Third"),
               auto.key.title="Response Level",
               main="Three Questions by Five Levels of Classification")

likertObject <- likertWeighted(~ . | group + row, tmp2)
```

```
likertObject

EmphasizeVerticalPanels(likertObject, y.between=c(0,0,1,0))
```

`emptyMainLeftAxisLeftStripBottomLegend`
Remove main title, left axis tick labels, left strip, bottom legend from plot and keep the vertical spacing allocated to those items.

Description

Remove main title, left axis tick labels, left strip, bottom legend from plot and keep the vertical spacing allocated to those items. This function is used to prepare a trellis object to be placed next to another trellis object. The current object will have much of its annotation removed with the intent of sharing annotation with the other object. This is motivated by the `ProfChal` example in `plot.likert`.

Usage

```
emptyMainLeftAxisLeftStripBottomLegend(x)
```

Arguments

`x`	A `"trellis"` object.

Details

We manipulate the items inside the trellis object.

Value

A `"trellis"` object with the stated items replaced by non-printing values. The vertical spacing of the original object is retained.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

The manipulations are similar to those in the `c.trellis` and related functions in the `latticeExtra` package.

See Also

`plot.likert`

Examples

```
## This is a small example.
## See ?plot.likert for the complete example including motivation.
##
require(grid)
require(lattice)
require(latticeExtra)
require(HH)

data(ProfChal)

tmp <- data.matrix(ProfChal[,1:5])
rownames(tmp) <- ProfChal$Question
ProfChal.list <- split.data.frame(tmp, ProfChal$Subtable)

Empl <- ProfChal.list[[2]]

pct   <- likert(Empl, as.percent="noRightAxis", xlab="Percent")
pct
count <- likert(Empl, rightAxis=TRUE,
                xlab="Count", ylab.right="Row Count Totals",
                scales=list(x=list(at=c(0, 100, 200))))
count
countEmptied <- HH:::emptyMainLeftAxisLeftStripBottomLegend(count)
countEmptied

tmp <- update(resizePanels(c(pct, countEmptied, y.same=TRUE, layout=c(2,1)), w=c(.8, .2)),
              scales=list(y=list(alternating=3, limits=count$y.limits),
                          x=list(at=list(pct$x.scales$at, count$x.scales$at),
                                 labels=list(pct$x.scales$labels,
                                             count$x.scales$labels))),
              xlab=c(" ", pct$xlab, " ", count$xlab),
              between=list(x=1))
tmp
```

`export.eps` *Exports a graph to an EPS file.*

Description

Exports a graph from the current device in R, or the `graphsheet` in S-Plus, to an `EPS` file.

Usage

```
export.eps(FileName.in, Name.in="GSD2", ...)
```

Arguments

`FileName.in`	name of file to be created.

Name.in	Name of graphsheet in S-Plus, ignored in R.
...	other arguments in R, ignored in S-Plus.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

dev2.

Examples

```
## Not run:
  if (interactive()) {
    trellis.device()
    plot(1:10)
    export.eps("abcd.eps")
  }

## End(Not run)
```

---

extra *Miscellaneous functions that I wish were in or consistent between S-Plus and R.*

Description

Miscellaneous functions that I wish were in or consistent between S-Plus and R.

Usage

```
as.rts(x, ...)

title.trellis(main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
    line = NA, outer = FALSE, axes=NULL, ...)

title.grob(main=NULL, y=.99, gp=gpar(cex=1.5))

## S3 method for class 'arima.model'
as.character(x, ...)

arima.model(x)

coefArimaHH(object, ...)

.arima.info.names.not.ordered (model)
```

Arguments

x	vector or time series
...	Additional arguments.
main, sub, xlab, ylab, line, outer, axes	See title.
model	A time series model specification in the S-Plus notation.
object	"arima" object in S-Plus.
y, gp	See grid.text in R.

Value

The result object of arima.model has class "arima.model"

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

arma.loop

F.curve *plot a chisquare or a F-curve.*

Description

Plot a chisquare or a F-curve. Shade a region for rejection region or do-not-reject region. F.observed and chisq.observed plots a vertical line with arrowhead markers at the location of the observed xbar and outlines the area corresponding to the p-value.

Usage

```
F.setup(df1=1,
        df2=Inf,
        ncp=0,
        log.p=FALSE,
        xlim.in=c(0, 5),
        ylim.in=range(c(0, 1.1*df.intermediate(x=seq(.5,1.5,.01),
                       df1=df1, df2=df2, ncp=ncp, log=log.p))),
        main.in=main.calc, ylab.in="F density",
        ...)

F.curve(df1=1,
        df2=Inf,
        ncp=0,
        log.p=FALSE,
```

```
          alpha=.05,
          critical.values=f.alpha,
          f=seq(0, par()$usr[2], length=109),
          shade="right", col=par("col"),
          axis.name="f",
          ...)

F.observed(f.obs, col="green",
           df1=1,
           df2=Inf,
           ncp=0,
           log.p=FALSE,
           axis.name="f",
           shade="right",
           shaded.area=0,
           display.obs=TRUE)

chisq.setup(df=1,
           ncp=0,
           log.p=FALSE,
         xlim.in=c(0, qchisq.intermediate(p=1-.01, df=df, ncp=ncp, log.p=log.p)),
        ylim.in=range(c(0, 1.1*dchisq.intermediate(x=seq(max(0.5,df-2),df+2,.01),
                        df=df, ncp=ncp, log=log.p))),
           main.in=main.calc, ylab.in="Chisq density",
           ...)

chisq.curve(df=1,
            ncp=0,
            log.p=FALSE,
            alpha=.05,
            critical.values=chisq.alpha,
            chisq=seq(0, par()$usr[2], length=109),
            shade="right", col=par("col"),
            axis.name="chisq",
            ...)

chisq.observed(chisq.obs, col="green",
               df=1,
               ncp=0,
               log.p=FALSE,
               axis.name="chisq",
               shade="right",
               shaded.area=0,
               display.obs=TRUE)
```

Arguments

xlim.in, ylim.in	Initial settings for xlim, ylim. The defaults are calculated for the degrees of freedom.
df, df1, df2, ncp, log.p	Degrees of freedom, non-centrality parameter, probabilities are given as log(p). See pchisq and pf.
alpha	Probability of a Type I error. alpha is a vector of one or two values. If one value, it is the right alpha. If two values, they are the c(left.alpha, right.alpha).
critical.values	Critical values. Initial values correspond to the specified alpha levels. A scalar value implies a one-sided test on the right side. A vector of two values implies a two-sided test.
main.in, ylab.in	Main title, default ylab.
shade	Valid values for shade are "right", "left", "inside", "outside", "none". Default is "right" for one-sided critical.values and "outside" for two-sided critical values.
col	color of the shaded region and the area of the shaded region.
shaded.area	Numerical value of the area. This value may be cumulated over two calls to the function (one call for left, one call for right). The shaded.area is the return value of the function. The calling program is responsible for the cumulation.
display.obs	Logical. If TRUE, print the numerical value of the observed value, plot a vertical abline at the value, and use it for showing the p-value. If FALSE, don't print or plot the observed value; just use it for showing the p-value.
f, chisq	Values used to draw curve. Replace them if more resolution is needed.
f.obs, chisq.obs	Observed values of statistic. p-values are calculated for these values.
axis.name	Axis name.
...	Other arguments which are ignored.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
old.omd <- par(omd=c(.05,.88, .05,1))
chisq.setup(df=12)
chisq.curve(df=12, col='blue')
chisq.observed(22, df=12)
par(old.omd)

old.omd <- par(omd=c(.05,.88, .05,1))
chisq.setup(df=12)
chisq.curve(df=12, col='blue', alpha=c(.05, .05))
par(old.omd)
```

```
old.omd <- par(omd=c(.05,.88, .05,1))
F.setup(df1=5, df2=30)
F.curve(df1=5, df2=30, col='blue')
F.observed(3, df1=5, df2=30)
par(old.omd)

old.omd <- par(omd=c(.05,.88, .05,1))
F.setup(df1=5, df2=30)
F.curve(df1=5, df2=30, col='blue', alpha=c(.05, .05))
par(old.omd)
```

`glhtWithMCP.993` *Retain averaging behavior that was previously available in glht.*

Description

For some ANOVA models with two or more factors, we need to average over interaction terms. These functions use an older version of glht.mcp and mcp2matrix to do that averaging.

Usage

```
glhtWithMCP.993(model, linfct, ...)
mcp2matrix.993(model, linfct)
```

Arguments

`model`, `linfct`, `...`
: See `glht`

Details

`mcp2matrix` is taken from from `multcomp_0.993-2.tar.gz/R/mcp.R`.

`glhtWithMCP.993` is based on `glht.mcp` in `multcomp_1.0-0/R/glht.R` with the call to `mcp2matrix` replaced by a call to `mcp2matrix.993`.

Value

See `glht`

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`mmc`

`gof.calculation` *Calculate Box–Ljung Goodness of Fit for ARIMA models in S-Plus.*

Description

Calculate Box–Ljung Goodness of Fit for ARIMA models in S-Plus. In R we use the `Box.test` function.

Usage

```
gof.calculation(acf.list, gof.lag, n, n.parms)
```

Arguments

`acf.list`	An `"acf"` object.
`gof.lag`	The number of model parameters is the number of lags to use for computing the Portmanteau goodness of fit statistic
`n`	Number of residuals in model.
`n.parms`	Number of AR and MA parameters in the model.

Details

This function is isolated from the S-Plus `arima.diag` function. It is used only in S-Plus.

Value

See the `gof` value described in `arima.diag` in S-Plus.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

`arima.diag` in S-Plus.

Examples

```
if.R(s={
co2.arima <- arima.mle(co2, list(list(order=c(0,1,1)),
                                 list(order=c(0,1,1), period=12)))
co2.acf <- acf(resid(co2.arima), plot=FALSE, lag=40)
co2.gof <- gof.calculation(co2.acf, 36, length(co2), 2)
xyplot(p.value ~ lag, data=co2.gof, panel=panel.gof,
       ylim=range(0, co2.gof$p.value))
},r={})
```

grid.yaxis.hh *make x- and y-axis labels*

Description

uses modified older version of grid functions. Includes optional specification of the axis labels.

Usage

```
grid.yaxis.hh(at = NULL, label = TRUE, main = TRUE, gp = gpar(),
              draw = TRUE, vp = NULL, labels)

make.yaxis.hh.labels(at, main, labels = at)

grid.xaxis.hh(at = NULL, label = TRUE, main = TRUE, gp = gpar(),
              draw = TRUE, vp = NULL, labels)

make.xaxis.hh.labels(at, main, labels = at)
```

Arguments

at, label, main, gp, draw, vp	See link[grid]{grid.xaxis}.
labels	label values if you don't want the defaults

Value

See link[grid]{grid.xaxis}.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

link[grid]{grid.xaxis}

GSremove — *Remove selected GraphSheetPages in the S-Plus Windows GUI Graphsheet*

Description

Remove selected GraphSheetPages in the S-Plus Windows GUI Graphsheet. This does the same task as right-click/delete on the tabs of the GraphSheet.

Usage

```
GSremove(pages, sheet = "GSD2$Page")
```

Arguments

pages	Page numbers in the tabs at the bottom of the Graphsheet.
sheet	Defaults to GSD2, the first name that is used when the graphsheet or trellis.device function is used.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

graphsheet in S-Plus.

Examples

```
## Not run:
trellis.device()
plot(1:10); plot(11:20); plot(21:30)
GSremove(c(1,3))

## End(Not run)
```

HH.regsubsets — *Display tabular results for Best Subsets Regression.*

Description

Print a tabular display of the results of Best Subsets Regression. This is an alternate display for the object from the regsubsets function. This function is based on regsubsets. The functions described here are designed for the HH package in R and use the leaps package in R. The leaps package is not in S-Plus, hence these functions do not work in the HH package for S-Plus.

Usage

```
`summaryHH`(object, ...)

## S3 method for class 'regsubsets'
summaryHH(object,
           names = abbreviate(dimnames(incidence)[[2]], minlength = abbrev),
           abbrev = 1, min.size = 1, max.size = dim(sumry$which)[2],
           statistic = c("bic", "cp", "adjr2", "rsq", "rss", "stderr"),
           las = par("las"),
           cex.subsets = 1, ..., main=statistic)

## S3 method for class 'summaryHH.regsubsets'
plot(x, ...,
           statistic="adjr2", legend=FALSE,
           col="darkgray", cex=1, pch=16,
           col.text="black", cex.text=1, col.abline="darkgray")
```

Arguments

object	An object of class "regsubsets".
x	An object of class "summaryHH.regsubsets".
statistic	Name of statistic to be plotted for each model.
...	Other arguments to be passed down to subsets.regsubsets and plot.
names	Abbreviations of variable names.
abbrev	minimum number of letters in each abbreviation.
min.size	minimum size subset to plot; default is 1.
max.size	maximum size subset to plot; default is number of predictors.
legend	logical variable, TRUE if the legend should be printed. If the legend is printed, the execution halts until the user clicks an empty space in the graph where the legend should be placed.
las	Orientation for model names on graph.
cex.subsets	can be used to change the relative size of the characters used to plot the regression subsets; default is 1.
main	"main" title for graph.
col, cex, pch	par values for dot locating statistic.
col.text, cex.text	par values for abbreviations of models on plot.
col.abline	par parameters for abline when the statistic is cp.

Value

summaryHH produces a table of models, with p, rsq, rss, adjr2, cp, bic, stderr for each. plot.summaryHH.regsubset plots the specified statistic from the summary. All the others are support functions.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

regsubsets

---

hhpdf *R tools for writing HH2: hhpdf, hhdev.off, hhcapture, hhcode, hhpng, hhlatex*

Description

R tools for writing HH2: hhpdf, hhdev.off, hhcapture, hhcode, hhpng, hhlatex. These functions in the HH package are placeholders used by the `scripts` files. See details.

Usage

```
hhpdf(file, ...)

hhdev.off(...)

hhcapture(file, text, echo=TRUE, print.eval=TRUE)

hhcode(file, text)

hhpng(file, ...)

hhlatex(file="", ...)
```

Arguments

`file`	Output file name. Ignored.
`text`	Multi-line character string. It will be displayed on the console by `hhcode`, and will be executed and the resulting value displayed on the console by `hhcapture`.
`...`	Ignored.
`echo`, `print.eval`	See `source`.

Details

The files in `HHscriptnames()` contain R code for all examples and figures in the book. The examples can all be directly executed by the user. The code examples all use these functions.

The versions of these functions here are essentially placeholders. Functions `hhpdf`, `hhpng`, and `hhdev.off` are no-ops and return `NULL`. As a consequence, the code between them will execute and display on the default graphics device. Function `hhcapture` sources its text argument and prints the

output to the console. Function hhcode prints its text argument to the console. Function hhlatex prints the latex source to the console and returns NULL.

While writing the book, these placeholder functions are replaced by more elaborate functions with the same names that write the graphs onto pdf or png files, the console output to text files, and the latex code to a file.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

HHscriptnames *Find absolute pathname of a script file for the HH book in the HH package.*

Description

Find absolute pathname of a script file for the HH book in the **HH** package.

Usage

```
HHscriptnames(chapternumbers=NULL, edition=2)

WindowsPath(x, display=TRUE)
```

Arguments

chapternumbers	A number or letter name for a chapter in the HH book. For the Second edition, the valid values are from the set c(1:18, LETTERS[1:15]). For the First edition, the valid values are from the set c(1:18). The argument may be a vector of one or more items. The file basename for the corresponding chapter is also accepted. If the chapternumbers is NULL (the default) then the directory containing the script files for the edition is returned.
edition	Either 2 or 1, for the second or first edition of the book *Statistical Analysis and Data Display*.
x	A vector or matrix of pathnames as generated by R, with "/" as the separator character.
display	Logical. With the default TRUE, the WindowsPath function prints the pathname on the console with a single \ character as the separator suitable for copy and paste into a Windows program and returns its result invisibly. With FALSE the WindowsPath function does not print anything; it returns its result visibly.

Value

For HHscriptnames, matrix of full pathnames to script files in the HH package.

For WindowsPath, a vector or matrix of full pathnames with all "/" characters changed to "\\" (which displays as \ by the cat function). When display is TRUE the function also prints at the console the pathnames with a single \ character suitable for copy and paste into a Windows program.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Examples

```
## Not run:
  ## All Operating Systems

  ## Second Edition
  HHscriptnames()
  HHscriptnames(6)
  HHscriptnames("6")
  HHscriptnames("oway")

  HHscriptnames("H")
  HHscriptnames("RApx")

  HHscriptnames(c(1:18, LETTERS[1:15]))

  ## with Windows pathname separators
  WindowsPath(HHscriptnames())
  WindowsPath(HHscriptnames(6))
  WindowsPath(HHscriptnames(6), display=FALSE)
  WindowsPath(HHscriptnames(6:8))
  WindowsPath(HHscriptnames(6:8), display=FALSE)

  ## First Edition
  HHscriptnames(6, edition=1)

## End(Not run)
```

---

hov *Homogeneity of Variance*

Description

Oneway analysis of variance makes the assumption that the variances of the groups are equal. Brown and Forsyth, 1974 present the recommended test of this assumption. The Brown and Forsyth test statistic is the F statistic resulting from an ordinary one-way analysis of variance on the absolute deviations from the median.

Usage

```
hov(x, data=NULL, method = "bf") ## x is a formula

## users will normally use the formula above and will not call the
## method directly.
hov.bf(x, group,  ## x is the response variable
       y.name = deparse(substitute(x)),
       group.name = deparse(substitute(group)))
```

Arguments

x	Formula appropriate for oneway anova in hov. Response variable in hov.bf.
data	data.frame
method	Character string defining method. At this time the only recognized method is "bf" for the Brown–Forsyth method.
group	factor.
y.name	name of response variable, defaults to variable name in formula.
group.name	name of factor, defaults to variable name in formula.

Value

"htest" object for the hov test.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Brown, M.~B. and Forsyth, A.~B. (1974). *Robust tests for equality of variances*. *Journal of the American Statistical Association*, 69:364–367.

See Also

aov, hovPlot

Examples

```
data(turkey)

hov(wt.gain ~ diet, data=turkey)
hovPlot(wt.gain ~ diet, data=turkey)
```

hovBF *Homogeneity of Variance: Brown–Forsyth method*

Description

Homogeneity of Variance: Brown–Forsyth method

Usage

```
hovBF(x, data=NULL, ..., na.rm = TRUE)
hovplotBF(x, data, ..., na.rm = TRUE,
          main = "Brown-Forsyth Homogeneity of Variance", plotmath = TRUE)
```

Arguments

x	Model formula with one response variable and one factor.
data	data.frame
...	Other arguments. hovplotBF sends them on to the panel function. hovBF ignores them.
na.rm	A logical value indicating whether 'NA' values should be stripped before the computation proceeds. See median.
main	main title for the plot.
plotmath	Logical. When TRUE (the default) the strip labels use plotmath. When FALSE the strip labels use ASCII.

Value

hovplotBF returns a three-panel trellis object. hovBF returns an htest object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Brown, M.~B. and Forsyth, A.~B. (1974). "Robust tests for equality of variances." *Journal of the American Statistical Association*, 69:364–367.

Examples

```
data(batch)
batch1.aov <- aov(Calcium ~ Batch, data=batch)
anova(batch1.aov)
hovBF(Calcium ~ Batch, data=batch)
hovplotBF(Calcium ~ Batch, data=batch)
```

if.R *Conditional Execution for R or S-Plus*

Description

`if.R` uses the `is.R` function to determine whether to execute the expression in the `r` argument or the expression in the `s` argument. `is.R`, copied from the now defunct base R function, returns `TRUE` if running under R and returns `FALSE` otherwise (initially designed for S/S-PLUS).

Usage

```
if.R(r, s)

is.R()
```

Arguments

`r`	Any R expression, including a group of expressions nested in braces. Assignments made in this expression are available to the enclosing function.
`s`	Any S-Plus expression, including a group of expressions nested in braces. Assignments made in this expression are available to the enclosing function.

Details

Not all functions are in both implementations of the S language. In particular, panel functions for `lattice` in R (based on `grid` graphics) are very different from panel functions for `trellis` (based on the older graphics technology) in S-Plus.

`is.R` is copied from the now defunct base R function of the same name.

Value

For `if.R` the result of the executed expression.

`is.R` returns `TRUE` if we are using R and `FALSE` otherwise.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`R.Version`

Examples

```
if.R(r={"This is R."},
     s={"This is S-Plus"})

is.R()
```

InsertVerticalPanels	*Expand a 3D array on the second dimension, inserting empty layers where the input vector has a* `0` *value. A 2D argument* `x` *with* `dim(x)==c(r,c)` *is first extended to 3D with* `dim(x)==c(1,r,c)`*, and then the result is collapsed back to 2D.*

Description

Expand a 3D array on the second dimension, inserting empty layers where the input vector has a `0` value. A 2D argument `x` with `dim(x)==c(r,c)` is first extended to 3D with `dim(x)==c(1,r,c)`, and then the result is collapsed back to 2D.

Usage

```
InsertVerticalPanels(x, expansion, newRowheights=5, newValue=NA)
```

Arguments

`x`	Three-dimensional array, for example, one defined as a set of matrices for the `likert` and related functions. `x[1,,]` and more generally `x[i,,]` will be an argument to `likert`.
`expansion`	Vector of `0` and `1`, with `1` indicating an existing layer in dimension 2, and `0` a placeholder for where a new layer in dimension 2 should be inserted.
`newRowheights`	Value to be used for inserted row by `likertWeighted` function.
`newValue`	Value to be inserted in all positions of inserted layer.

Value

Array similarly structured to the input array `x`, but with more layers on the second dimension. The `"rowheights"` attribute gives the `rowheights` used by `EmphasizeVerticalPanels`. The `newRows` gives the row (second dimension) numbers in the result that are the generated values. All data items in the `newRows` will have value in the `newValue` argument.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

EmphasizeVerticalPanels

Examples

```
x <- array(1:24, c(3, 4, 2),
               dimnames = list(letters[1:3], LETTERS[4:7], letters[8:9]))
x

expansion <- c(1, 1, 0, 1, 0, 1)
result <- InsertVerticalPanels(x, expansion)
result

Pop.labels1 <- result[1,, ]
Pop.labels1[ attr(result, "newRows"),] <- " "

Pop.labels2 <- result[2,, ]
Pop.labels2[ attr(result, "newRows"),] <- " "

Pct.labels1 <- format(round(HH::rowPcts(result[1,, ])))
Pct.labels1[ attr(result, "newRows"),] <- " "

Pct.labels2 <- format(round(HH::rowPcts(result[2,, ])))
Pct.labels2[ attr(result, "newRows"),] <- " "
```

---

interaction.positioned

interaction method for positioned factors.

Description

This is intended to be a method for `interaction` for positioned factors. Since `interaction` is not currently implemented as a generic, `interaction.positioned` is a standalone function. The result is assigned a `position`. The position for each interaction level is the position of the corresponding `a` factor plus a scaled level of the `b` factor. The default scale is .1.

Usage

```
interaction.positioned(...,  ## exactly two factors
             drop = FALSE, sep = ".",
             b.offset=0,
             b.scale=.1)
```

Arguments

`...`	exactly two factors. The first factor `a` is used as the major factor in sort order. The second factor `b` is used as minor factor in sort order.
`b.offset`	amount added to `position(b)` to adjust appearance.
`b.scale`	scale to relate units of `position(a)` to units of `position(b)`.
`drop, sep`	See `factor`.

Value

"positioned" object containing the ordinary interaction with a "position" attribute.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

positioned.

Examples

```
a <- positioned(letters[c(1,2,3,1,2,3)], value=c(1,4,9))
b <- positioned(LETTERS[c(4,4,4,5,5,5)], value=c(1,2))
a.b <- interaction.positioned(a, b)
a.b.2 <- interaction.positioned(a, b, b.scale=.2)
b.a <- interaction.positioned(b, a)
```

---

interaction2wt *Plot all main effects and twoway interactions in a multifactor design*

Description

The main diagonal displays boxplots for the main effects of each factor. The off-diagonals show the interaction plots for each pair of factors. The i,j panel shows the same factors as the j,i but with the trace- and x-factor roles interchanged.

Usage

```
interaction2wt(x, ...)

## S3 method for class 'formula'
interaction2wt(x, data=NULL, responselab, ...)

## Default S3 method:
interaction2wt(x,
               response.var,
               responselab = deparse(substitute(response.var)),
               responselab.expression = responselab,
               relation = list(x = "same", y = "same"),
               x.relation = relation$x,
               y.relation = relation$y,
               digits = 3,
               x.between=1,
               y.between=1,
               between,
```

```
                cex = 0.75,
                rot=c(0,0),
                panel.input = panel.interaction2wt,
                strip.input =
                 if (label.as.interaction.formula) strip.default
                 else strip.interaction2wt,
                par.strip.text.input = trellis.par.get()$add.text,
                scales.additional,
                main.in =
                  paste(responselab,
                        ": ", c("main", "simple")[1+simple],
                        " effects and 2-way interactions",
                        sep=""),
                xlab = "",
                ylab = "",
                simple=FALSE,
                box.ratio=if (simple) .32 else 1,
                label.as.interaction.formula=TRUE,
                ...,
                main.cex,
                key.cex.title=.8,
                key.cex.text=.7,
                factor.expressions=names.x,
                simple.pch=NULL,
                col.by.row=TRUE,
                col  =trellis.par.get("superpose.line")$col,
                lty  =trellis.par.get("superpose.line")$lty,
                lwd  =trellis.par.get("superpose.line")$lwd,
                alpha=trellis.par.get("superpose.line")$alpha
)
```

Arguments

Arguments when x is a formula.

x	The object on which method dispatch is carried out. For the "formula" method, a formula describing the response variable and factors. The formula is generally of the form y ~ g1 + g2 + ... There may be one or more factors in the formula. For the "default" method, data.frame of factors. This is usually constructed by formula method from the input data and the input formula.
data	For the formula method, a data frame containing values for any variables in the formula. In the R version, if not found in data, or if data is unspecified, the variables are looked for in the environment of the formula.
responselab	Character name of response variable, defaults to the name of the response variable in the formula.
responselab.expression	plotmath or character name of response variable, defaults to responselab.

...	additional arguments, primarily trellis arguments.
response.var	For the "default" method, the response variable. This is usually constructed by formula method from the input data and the input formula.
simple	logical. TRUE if simple effects are to be displayed. Arguments simple.offset, simple.scale, and col.by.row may also be needed. See panel.interaction2wt for details.
box.ratio	xyplot.

Trellis/Lattice arguments. Default values are set by the the formula method. The user may override the defaults. See also xyplot.

relation	trellis argument.
x.relation	x value of relation argument.
y.relation	y value of relation argument.
digits	doesn't do anything at the moment
x.between	x value of between argument.
y.between	y value of between argument.
between	trellis/lattice between argument. If used, between has precedence over both the x.between and y.between arguments.
cex	S-Plus: changes the size of the median dot in the boxplots. R: doesn't do anything.
panel.input	panel function. Default is panel.interaction2wt.
label.as.interaction.formula	logical. If TRUE, each panel has a single strip label of the form y ~ a | b. If FALSE, each panel has a pair of strip labels, one for the trace factor and one for the x factor.
strip.input	strip function. Default depends on the value of label.as.interaction.formula.
par.strip.text.input	par.strip.text argument.
scales.additional	additional arguments to scales argument of interaction.positioned.
main.in	Text of main title.
xlab	No effect.
ylab	No effect.
main.cex	cex for main title.
key.cex.title	cex key title. Defaults to cex for xlab.
key.cex.text	cex group names in key. Defaults to cex for axis.text.
factor.expressions	Expressions for titles of keys and xlab for each column. Defaults to the names of the factors in the input formula.
rot	Rotation of x tick labels and y tick labels. Only 0 and 90 will look good.

`simple.pch` Named list containing plotting characters for each level of one or more of the factors. `simple.pch` is used only when `simple==TRUE`. If the argument `simple.pch` is missing, then the integers for the levels of the factors are used. The characters are used for the median of the box plots in the diagonal panels. They match the trace factor of the interaction panel in the same column of the display.

`col.by.row` logical. If `TRUE` (the default), simple effects plots color the simple effects on the main diagonals in the same color as the trace levels in their row. If `FALSE`, then simple effects are colored to match the x levels in their column.

`col, lty, lwd, alpha` Arguments to `trellis.par.set(superpose.line=list())`.

Value

`"trellis"` object containing the plot.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

`panel.interaction2wt`

Examples

```
data(vulcan)

interaction2wt(wear ~ filler + pretreat + raw, data=vulcan,
               par.strip.text=list(cex=.7))

interaction2wt(wear ~ filler + pretreat + raw, data=vulcan,
               par.strip.text=list(cex=.7),
               label.as.interaction.formula=FALSE)

interaction2wt(wear ~ filler + raw, data=vulcan,
               simple=TRUE)

interaction2wt(wear ~ filler + raw, data=vulcan,
               simple=TRUE, col.by.row=FALSE)

interaction2wt(wear ~ filler + raw, data=vulcan,
               simple=TRUE, simple.scale=c(filler=.15, raw=.2),
               xlim=c(.3, 5.6))

interaction2wt(wear ~ filler + raw, data=vulcan,
```

```
               col=1:5, lwd=1:5, lty=1:5)

interaction2wt(wear ~ filler + raw, data=vulcan,
               simple=TRUE, col=1:5, lwd=1:5, lty=1:5)

interaction2wt(wear ~ filler + raw, data=vulcan,
               simple=TRUE, col=1:5, lwd=1:5, lty=1:5, col.by.row=FALSE,
               simple.pch=list(filler=LETTERS[1:5], raw=letters[6:9]), cex=2)



ToothGrowth$dose <- positioned(ToothGrowth$dose) ## modify local copy
anova(aov(len ~ supp*dose, data=ToothGrowth))
interaction2wt(len ~ supp + dose, data=ToothGrowth)


esoph$ntotal <- with(esoph, ncases + ncontrols) ## modify local copy
esoph$rate   <- with(esoph, ncases/ntotal)      ## modify local copy

position(esoph$alcgp) <- 2:5
position(esoph$tobgp) <- 2:5

interaction2wt(rate ~ agegp + alcgp + tobgp, esoph, rot=c(90,0),
               par.strip.text=list(cex=.8))

interaction2wt(rate ~ agegp + alcgp + tobgp, esoph, rot=c(90,0),
               par.strip.text=list(cex=.8),
               factor.expressions=c(
                 agegp=expression(Age~~(years)),
                 alcgp=expression(Alcohol~
                   bgroup("(",scriptstyle(frac(gm, day)),")")),
                 tobgp=expression(Tobacco~
                   bgroup("(",scriptstyle(frac(gm, day)),")"))),
               par.settings=list(
                 par.xlab.text=list(cex=.8),
                 par.ylab.text=list(cex=.8)),
               responselab.expression="Cancer\nRate",
               main=list(
"Esophogeal Cancer Rate ~ Alcohol Consumption + Tobacco Consumption",
                 cex=1.2))

esoph.aov <- aov(rate ~ agegp + alcgp + tobgp, data=esoph)
anova(esoph.aov)
```

`interval` *Prediction and Confidence Intervals for glm Objects*

Description

Prediction and Confidence Intervals for `glm` Objects

Usage

```
interval(glm.object, ...)
## S3 method for class 'glm'
interval(glm.object, linkfit.object,
         type = c("link", "response"),
         conf.level = 0.95, ...)
```

Arguments

glm.object	result from a call to the glm function.
linkfit.object	result from a call to the predict function for the glm.object with type="link", se.fit=TRUE.
type	Either "link" or "response". See predict.glm for details.
conf.level	Confidence level, for example .95 for 95%.
...	Other arguments to be passed to predict.glm.

Value

Matrix with five columns: fit, ci.low, ci.hi, pi.low, pi.hi and as many rows as predict.glm returns.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
data(spacshu)
spacshu.bin.glm <- glm(damage ~ tempF, data=spacshu, family=binomial)

## observed data
spacshu.interval          <- interval(spacshu.bin.glm)

## new data, link
spacshu.interval.link     <- interval(spacshu.bin.glm, newdata=data.frame(tempF=30:85))

## new data, response
spacshu.interval.response <- interval(spacshu.bin.glm, newdata=data.frame(tempF=30:85),
                                      type="response")
```

---

intxplot *Interaction plot, with an option to print standard error bars.*

Description

Interaction plot, with an option to print standard error bars. There is an option to offset group lines to prevent the bars from overprinting.

Usage

```
intxplot(x, data=NULL, groups.in,
          scales,
          key.length=1,
          key.lines,
          key=TRUE,
          trace.factor.name=deparse(substitute(groups.in)),
          x.factor.name=x.factor,
          xlab=x.factor.name,
          main=list(main.title, cex=main.cex),
          condition.name="condition",
          panel="panel.intxplot",
          summary.function="sufficient",
          se,
          ...,
          data.is.summary=FALSE,
          main.title=paste(
            "Interactions of", trace.factor.name, "and",
            x.factor.name,
            if (length(x[[3]]) > 1)
            paste("|", condition.name.to.use)),
          main.cex=1.5,
          col, lwd, lty, alpha)

panel.intxplot(x, y, subscripts, groups, type = "l", se, cv=1.96,
               offset.use=(!missing(groups) && !missing(se)),
               offset.scale=2*max(as.numeric(groups)),
               offset=
              as.numeric(groups[match(levels(groups), groups)]) / offset.scale,
               rug.use=offset.use,
               col, lwd, lty, alpha,
               ...)
```

Arguments

x	For intxplot, a formula with a factor as the predictor variable. For panel.intxplot, standard argument for panel functions.
data	data.frame, as used in xyplot.
groups.in	groups.in, as used in xyplot.
scales	Optional, additional arguments for the standard scales in xyplot.
key.length	Number of columns in the key.
key.lines	default value for the lines argument of key.
key	logical. If TRUE, draw the key.
trace.factor.name	Name of the grouping variable.

`x.factor.name` name of the dependent variable.

`xlab` as in `xyplot`, defaults to the name of the predictor variable from the formula.

`main` as in `xyplot`. Defaults to the `main.title` argument.

`panel` as in `xyplot`. Defaults to the `"panel.intxplot"`.

`condition.name` name of the conditioning variable.

`summary.function`
The default `sufficient` finds the mean, standard deviation, and sample size of the response variable for each level of the conditioning factor. See `sufficient`.

`se` standard errors to be passed to `panel.intxplot`. `se` Missing, logical, or a numeric vector. If missing or `FALSE`, standard errors are not plotted. If `se=TRUE` in `intxplot`, the standard errors are calculated from the sufficient statistics for each group as the group's standard deviation divided by the square root of the group's observation count. If `se` is numeric vector, it is evaluated in the environment of the sufficient statistics. the `se` argument to `panel.intxplot` must be numeric.

,

`...` In `intxplot`, arguments for `panel.intxplot`. In `panel.intxplot`, arguments for `panel.superpose`.

`data.is.summary`
logical, defaults to `FALSE` under the assumption that the input data.frame is the original data and the `intxplot` function will generate the summary information (primarily standard deviation `sd` and number of observations `nobs` for each group). When `TRUE`, the standard error calculation assumes variables `sd` and `nobs` are in the dataset.

`main.title` Default main title for plot.

`main.cex` Default character expansion for main title.

`y`, `subscripts`, `groups`, `type`
Standard arguments for panel functions.

`cv` critical value for confidence intervals. Defaults to 1.96.

`offset.use` logical. If `TRUE`, offset the endpoints of each group.

`offset.scale` Scale number indicating how far apart the ends of the groups will be placed. Larger numbers make them closer together.

`offset` Actual numbers by which the end of the groups are offset from their nominal location which is the `as.numeric` of the group levels.

`rug.use` logical. If `TRUE`, display a rug for the endpoints of each group.

`col`, `lwd`, `lty`, `alpha`
Arguments to `trellis.par.set(superpose.line=list())`.

Value

`"trellis"` object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

sufficient

Examples

```
## This uses the same data as the HH Section 12.13 rhizobium example.

data(rhiz.clover)

## interaction plot, no SE
intxplot(Npg ~ strain, groups=comb, data=rhiz.clover,
         main="Interaction Plot. No SE")

## interaction plot, individual SE for each treatment combination
## Rescaled to allow the CI bars to stay within the plot region
intxplot(Npg ~ strain, groups=comb, data=rhiz.clover, se=TRUE,
         ylim=c(17,47),
         main="Interaction Plot. Rescaled to keep CI bars within the plot region")

## Common SE based on ANOVA table. Rescaled to allow the CI bars to stay within the plot region
intxplot(Npg ~ strain, groups=comb, data=rhiz.clover,
         se=sqrt(sum((nobs-1)*sd^2)/(sum(nobs-1)))/sqrt(5),
         ylim=c(16,41),
         main=paste("Interaction Plot. Common SE based on ANOVA table.\n",
                    "Rescaled to keep CI bars within the plot region"))

## change distance between endpoints
intxplot(Npg ~ strain, groups=comb, data=rhiz.clover, se=TRUE,
         offset.scale=10, ylim=c(18,46),
         main="Interaction plot. Change distance between endpoints")

## When data includes the nobs and sd variables, data.is.summary=TRUE is needed.
intxplot(Npg ~ strain, groups=comb,
         se=sqrt(sum((nobs-1)*sd^2)/(sum(nobs-1)))/sqrt(5),
         data=sufficient(rhiz.clover, y="Npg", c("strain","comb")),
         data.is.summary=TRUE,
         ylim=c(16,41),
         main=paste("Interaction plot. When data includes the nobs and sd variables,\n",
           "'data.is.summary=TRUE' is needed"))
```

---

ladder *Draw a "ladder of powers" plot, plotting each of several powers of y against the same powers of x.*

Description

Draw a "ladder of powers" plot, plotting each of several powers of y against the same powers of x. The powers are

```
result <- data.frame(-1/x, -1/sqrt(x), log(x), sqrt(x), x, x^2)

names(result) <- c(-1, -.5, 0, .5, 1, 2)
```

Usage

```
ladder(formula.in, data=NULL,
       main.in="Ladders of Powers",
       panel.in=panel.cartesian,
       xlab=deparse(formula.in[[3]]),
       ylab=deparse(formula.in[[2]]),
       scales=list(alternating=FALSE,
         labels=FALSE, ticks=FALSE, cex=.6),
       par.strip.text=list(cex=.6),
       cex=.5, pch=16, between=list(x=.3, y=.3),
       dsx=xlab,
       dsy=ylab,
       ladder.function=ladder.f,
       strip.number=2,
       strip.names,
       strip.style=1,
       strip,
       oma=c(0,0,0,0),  ## S-Plus
       axis3.line=.61,
       layout=c(length(tmp$x.power), length(tmp$y.power)),
       axis.key.padding = 10, ## R right axis
       key.axis.padding = 10, ## R top axis
       useOuter=TRUE, ## R useOuterStrips(combineLimits(result))
       ...)

ladder3(x, y,
        dsx=deparse(substitute(x)),
        dsy=deparse(substitute(y)),
        ladder.function=ladder.f)

ladder.f(x, name.prefix="")

ladder.fstar(x, name.prefix="")

strip.ladder(which.given,
             which.panel,
             var.name,
             factor.levels,
             shingle.intervals,
             par.strip.text=trellis.par.get("add.text"),
             strip.names=c(TRUE,TRUE),
             style=1,
             ...)
```

Arguments

formula.in	A formula with exactly one variable on each side.
data	data.frame
main.in	main title for xyplot
panel.in	panel.cartesian has many arguments in addition to the arguments in panel.xyplot. Any replacement panel function must have those argument names, even if it doesn't do anything with them.
xlab, ylab	Trellis arguments, default to right- and left-sides of the formula.in.
strip	Strip function. Our default is strip.ladder (see below). The other viable argument value is FALSE.
cex, pch, between, scales, layout	arguments for xyplot.
dsx, dsy	Names to be used as level names in ladder.function for the generated factor distinguishing the powers. They default to xlab, ylab. For long variable names, an abbreviated name here will decrease clutter in the ladder of powers plot. These names are not visible in the plot when strip=FALSE.
ladder.function	function to use to create data.frame of powers of input variable.
name.prefix	Base name used for column names of powers. The default is empty (""). An alternative must include the power symbol "^", for example, "abc^".
strip.number	Number of strip labels in each panel of the display. 0: no strip labels; 1: one strip label of the form y^p ~ x^q; 2: two strip labels of the form ylab: y^p and xlab: x^q, where p and q are the powers returned by ladders; y and x are the arguments dsy and dsx.
useOuter	logical, defaults to TRUE. In R, this implies that strip.number is forced to 2 and that the resulting "trellis" object will be sent through useOuterStrips(combineLimits(result)). This argument is ignored by S-Plus.
strip.style	style argument to strip.
oma	argument to par in S-Plus.
...	other arguments to xyplot.
axis3.line	extra space to make the top axis align with the top of the top row of panels. Trial and error to choose a good value.
axis.key.padding	Extra space on right of set of panels in R.
key.axis.padding	Extra space on top of set of panels in R.
x, y	variables.
which.given, which.panel, var.name, factor.levels, shingle.intervals, par.strip.text	See strip.default.
strip.names, style	We always print the strip.names in style=1. Multicolored styles are too busy.

Details

The ladder function uses panel.cartesian which is defined differently in R (using grid graphics) and S-Plus (using traditional graphics). Therefore the fine control over appearance uses different arguments or different values for the same arguments.

Value

ladder returns a "trellis" object.

The functions ladder.fstar and ladder.f take an input vector x of non-negative values and construct a data.frame by taking the input to the powers c(-1, -.5, 0, .5, 1, 2), one column per power. ladder.f uses the simple powers and ladder.fstar uses the scaled Box–Cox transformation.

ladder.fstar	ladder.fstar	notation
(x^p - 1)/p	(x^p - 1)/p	p
(1/x - 1)/(-1)	(1/x - 1)/(-1)	-1.0
(1/sqrt(x)-1)/(-.5)	(1/sqrt(x)-1)/(-.5)	-0.5
log(x)	log(x)	0.0
((sqrt(x)-1)/.5)	((sqrt(x)-1)/.5)	0.5
x-1	x-1	1.0
(x^2 - 1)/2	(x^2 - 1)/2	2.0

ladder3 takes two vectors as arguments. It returns a data.frame with five columns:

X, Y: data to be plotted. The column X contains the data from the input x taken to all the powers and aligned with the similarly expanded column Y.

x, y: symbolic labeling of the power corresponding to X,Y.

group: result from pasting the labels in x, y with * between them.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Hoaglin, D.~C., Mosteller, F., and Tukey, J.~W., editors (1983). *Understanding Robust and Exploratory Data Analysis*. Wiley.

Box, G. E.~P. and Cox, D.~R. (1964). An analysis of transformations. *J. Royal Statist Soc B*, 26:211–252.

See Also

panel.cartesian

Examples

```
data(tv)

## default
## R: outer strip labels
ladder(life.exp ~ ppl.per.phys, data=tv,
       main="Ladder of Powers for Life Expectancy and People per Physician")

## Not run:
## one strip label
  ladder(life.exp ~ ppl.per.phys, data=tv, strip.number=1, useOuter=FALSE,
         dsx="ppp", dsy="le")

## two strip labels
  ladder(life.exp ~ ppl.per.phys, data=tv, strip.number=2, useOuter=FALSE)

## outer strip labels
ladder(life.exp ~ ppl.per.phys, data=tv, useOuter=TRUE)

## no strip labels (probably silly, but possible)
ladder(life.exp ~ ppl.per.phys, data=tv, strip.number=0, useOuter=FALSE)

## End(Not run)
```

`latex.array` *Generate the latex code for an* `"array"` *or* `"table"` *with 3, 4, or more dimensions.*

Description

Generate the latex code for an `"array"` or `"table"` with 3, 4, or more dimensions.

Usage

```
## S3 method for class 'array'
latex(object, ...,
       var.sep = "}\\tabularnewline{\\bfseries ", value.sep = ": ",
       use.ndn = TRUE, cgroup = NULL,
       ## rgroup here captures and ignores any incoming rgroup argument
       rgroup = NULL, n.rgroup = NULL,
       title = first.word(deparse(substitute(object))),
       rowlabel=title,
            rsubgroup=NULL, n.rsubgroup=NULL)

## S3 method for class 'matrix'
latex(object, ...,
        use.ndn=TRUE, cgroup=NULL,
        title=first.word(deparse(substitute(object))),
```

```
        rowlabel=title)

## S3 method for class 'table'
latex(object, ...) ## prepend c("matrix", "array") to the
        ## class of the input object, and then call latex.default
```

Arguments

object	A c("matrix", "array") or "table" object.
...	Arguments forwarded to the "default" method for latex.
use.ndn	Logical. ndn is an abbreviation for "Names of DimNames". When TRUE (the default), the rowlabel, cgroup, and rgroup values will be taken from the names(dimnames(object)).
rgroup, n.rgroup	These are the standard arguments for latex. Incoming values for rgroup and n.rgroup are ignored by latex.array and replaced with values constructed from the names of the dimnames of the third and higher dimensions of the input array object. Each item in rgroup is assigned the appropriate combination of names(dimnames(object))[-(1:2)].
rsubgroup, n.rsubgroup	These are based on the standard arguments for latex. Incoming values for rsubgroup and n.rsubgroup are applied to the rows of each rgroup.
title, rowlabel, cgroup	These are the standard arguments for latex. When use.ndn is TRUE (the default), then rowlabel is assigned the names(dimnames(object))[1] and cgroup is assigned the names(dimnames(object))[2].
value.sep	When use.ndn is TRUE (the default), and length(dim(object)) >= 3 then this string is used in the constructed rgroup values to separate the factor name from the factor level of the specified dimension, for example ABC: 5.
var.sep	When use.ndn is TRUE (the default), and length(dim(object)) >= 4 then this string is used in the in the constructed rgroup values to separate the name and level of each dimension, for example ABC: 5 ; DEF: 6. The default value is exactly what Hmisc::latex needs in order to place two or more lines (one for each dimension) in boldface.

Details

latex.matrix calls latex.default directly. When use.ndn is TRUE (the default), rowlabel and cgroup are constructed from names(dimnames(object)) unless the user explicitly specified them.

latex.array appends all two-dimensional layers object[,, one, at, a, time] into a single long "matrix", ignores any incoming rgroup and n.rgroup (with a warning), and constructs rgroup and n.rgroup to label the layers. When use.ndn is TRUE (the default), rowlabel and cgroup are constructed from names(dimnames(object)) unless the user explicitly specified them.

latex.table prepends c("matrix", "array") to the class of the "table" object, then calls the generic "latex". This step is necessary because the survey package creates objects whose class includes the value "table" but not the values c("matrix", "array"). Should this object be sent directly to latex.default, it would cause on error for any table with dimension larger than two.

Value

See latex.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

latex

Examples

```
## Not run:
## These are the recommended options.  See ?Hmisc::latex for details.
options(latexcmd='pdflatex')
options(dviExtension='pdf')
options(xdvicmd='open')  ## Macintosh, Windows,      SMP linux

## End(Not run)

## This sets up the defaults for latex to write to a pdf file
microplot::latexSetOptions()
## It is needed for R CMD check.
## It is recommended if you normally use pdflatex.
## If you want some other destination for latex, use a non-default argument.


  tmp3 <- array(1:8, c(2,2,2),
                list(letters[1:2],
                     letters[3:4],
                     letters[5:6]))

  tmp3

  ltmp3 <- latex(tmp3) ## assignment prevents display of the generated pdf file
                       ## enter the object name to display the file on screen
  ## ltmp3

  ## latex(tmp3) causes a file tmp3.tex to be created in the working directory.
  ## A user might want to keep tmp3.tex and \input{tmp3.tex} it into a longer .tex file.
  ## R CMD check doesn't like tmp3.tex to remain, so it is removed here.
  file.remove("tmp3.tex")

## Not run:
  try(  ## warning: Input rgroup and n.rgroup are ignored
    latex(tmp3, rgroup=letters[1:3], n.rgroup=c(1,1,2), file="ignorergroup.tex")
     )

  names(dimnames(tmp3)) <- LETTERS[24:26]
  latex(tmp3, file="LETTERS3.tex")
  latex(tmp3, rowlabel="Something Else", file="SomethingElse.tex")
```

```
tmp4 <- array(1:120, c(5,4,3,2),
              list(letters[1:5],
                   letters[6:9],
                   letters[10:12],
                   letters[13:14]))

tmp4
latex(tmp4, var.sep=" ; ")

names(dimnames(tmp4)) <- LETTERS[23:26]
latex(tmp4, file="LETTERS4.tex")


## with rsubgroup and n.rsubgroup
latex(tmp4, var.sep=" ; ", file="LETTERS4sub.tex",
      rsubgroup=c("Three","Two"), n.rsubgroup=c(3,2))

## with rsubgroup and n.rsubgroup and cgroup and n.cgroup
latex(tmp4, var.sep=" ; ", file="LETTERS4sub.tex",
      rsubgroup=c("Three","Two"), n.rsubgroup=c(3,2),
      cgroup=c("FGH","I"), n.cgroup=c(3,1))


tmp2 <- array(1:6, c(3,2),
              list(Rows=letters[1:3],
                   Columns=letters[4:5]))

tmp2

latex(tmp2)

## Input rgroup honored for "matrix"
latex(tmp2, rgroup=c("Two","One"), n.rgroup=c(2,1), file="rgroup.tex")

latex(tmp2, rowlabel="something else", file="something.tex")

## tableDemo is based on a table constructed from
##         survey::svytable(~ FactorA + FactorB + FactorC, Survey.Design.Object)
tableDemo <- structure(c(28, 25, 33, 12, 6, 22,  8, 12, 23, 24,  6, 32,
                         32, 31, 59, 11, 2, 33, 10,  3, 23,  7,  2, 26),
                       .Dim = c(3L, 4L, 2L),
                       .Dimnames = list(FactorA = c("a", "b", "c"),
                                        FactorB = c("d", "e", "f", "g"),
                                        FactorC = c("h", "i")),
                       class = "table")

class(tableDemo)
latex(tableDemo)

## End(Not run)
```

latticeresids *Subroutine used by residual.plots.lattice*

Description

Subroutine used by `residual.plots.lattice`

Usage

```
latticeresids(x, data,
              main = "please use an appropriate main title",
              par.strip.text, scales.cex, y.relation, ...)
```

Arguments

`x`, `data`, `main`, `par.strip.text`, `...`	**lattice** arguments. See `xyplot`.
`scales.cex`	`cex` for the `scales` argument in `xyplot`.
`y.relation`	`relation` for the `y` argument to `scales` argument in `xyplot`.

Value

`"trellis"` object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`residual.plots.lattice`

legendGrob2wt *place separate keys to the left of each row of a trellis*

Description

Each key is created and then inserted into a single grob.

Usage

```
legendGrob2wt(...)
```

Arguments

`...`	key1, key2, etc. Each key will normally be the result of a `draw.key` with `draw=FALSE`.

Value

A Grid frame object (that inherits from 'grob').

Author(s)

Richard M. Heiberger, with asssistance from Deepayan Sarkar.

See Also

interaction2wt

---

likert *Diverging stacked barcharts for Likert, semantic differential, rating scale data, and population pyramids.*

Description

Constructs and plots diverging stacked barcharts for Likert, semantic differential, rating scale data, and population pyramids.

Usage

```
likert(x, ...)
likertplot(x, ...)
## S3 method for class 'likert'
plot(x, ...)
## S3 method for class 'formula'
plot.likert(x, data, ReferenceZero=NULL, value, levelsName="",
                              scales.in=NULL,   ## use scales=
                        between=list(x=1 + (horizontal), y=.5 + 2*(!horizontal)),
                              auto.key.in=NULL, ## use auto.key=
                              panel.in=NULL,    ## use panel=
                              horizontal=TRUE,
                              par.settings.in=NULL, ## use par.settings=
                              ...,
                              as.percent = FALSE,
                              ## titles
                              ylab= if (horizontal) {
                                if (length(x)==3)
                                  deparse(x[[2]])
                                else
                                  "Question"
                              }
                              else
                             if (as.percent != FALSE) "Percent" else "Count",

                              xlab= if (!horizontal) {
```

```
            if (length(x)==3)
              deparse(x[[2]])
            else
              "Question"
          }
          else
        if (as.percent != FALSE) "Percent" else "Count",

          main = x.sys.call,

          ## right axis
          rightAxisLabels = rowSums(data.list$Nums),
          rightAxis = !missing(rightAxisLabels),
ylab.right = if (rightAxis) "Row Count Totals" else NULL,
          xlab.top = NULL,
          right.text.cex =
            if (horizontal) { ## lazy evaluation
          if (!is.null(scales$y$cex)) scales$y$cex else .8
            }
            else
              {
          if (!is.null(scales$x$cex)) scales$x$cex else .8
              },

          ## scales
          xscale.components = xscale.components.top.HH,
          yscale.components = yscale.components.right.HH,
          xlimEqualLeftRight = FALSE,
          xTickLabelsPositive = TRUE,

          ## row sequencing
          as.table=TRUE,
          positive.order=FALSE,
          data.order=FALSE,
          reverse=ifelse(horizontal, as.table, FALSE),

          ## resizePanels arguments
          h.resizePanels=sapply(result$y.used.at, length),
          w.resizePanels=sapply(result$x.used.at, length),

          ## color options
          reference.line.col="gray65",
          col.strip.background="gray97",
          key.border.white=TRUE,
          col=likertColor(Nums.attr$nlevels,
            ReferenceZero=ReferenceZero,
            colorFunction=colorFunction,
            colorFunctionOption=colorFunctionOption),
```

```
                                colorFunction="diverge_hcl",
                                colorFunctionOption="lighter"
                                )
## S3 method for class 'matrix'
plot.likert(x,
            positive.order=FALSE,
            ylab=names(dimnames(x)[1]),
            xlab=if (as.percent != FALSE) "Percent" else "Count",
            main=xName,
            reference.line.col="gray65",
            col.strip.background="gray97",
            col=likertColor(attr(x, "nlevels"),
              ReferenceZero=ReferenceZero,
              colorFunction=colorFunction,
              colorFunctionOption=colorFunctionOption),
            colorFunction="diverge_hcl",
            colorFunctionOption="lighter",
            as.percent=FALSE,
            par.settings.in=NULL,
            horizontal=TRUE,
            ReferenceZero=NULL,
            ...,
            key.border.white=TRUE,
            xName=deparse(substitute(x)),
            rightAxisLabels=rowSums(abs(x)),
            rightAxis=!missing(rightAxisLabels),
            ylab.right=if (rightAxis) "Row Count Totals" else NULL,
            panel=panel.barchart,
            xscale.components=xscale.components.top.HH,
            yscale.components=yscale.components.right.HH,
            xlimEqualLeftRight=FALSE,
            xTickLabelsPositive=TRUE,
            reverse=FALSE)

## Default S3 method:
plot.likert(x, ...)  ## calls plot.likert.matrix

## S3 method for class 'array'
plot.likert(x,
             condlevelsName=paste("names(dimnames(", xName, "))[-(1:2)]",
                                  sep=""),
             xName=deparse(substitute(x)),
             main=paste("layers of", xName, "by", condlevelsName),
             ...)

## S3 method for class 'likert'
plot.likert(x, ...)  ## See Details
```

```
## S3 method for class 'list'
plot.likert(x,  ## named list of matrices, 2D tables,
                              ## 2D ftables, or 2D structables,
                              ## or all-numeric data.frames
            condlevelsName="ListNames",
            xName=deparse(substitute(x)),
            main=paste("List items of", xName, "by", condlevelsName),
            layout=if (length(dim.x) > 1) dim.x else {
                          if (horizontal) c(1, length(x)) else c(length(x), 1)},
            positive.order=FALSE,
            strip=!horizontal,
            strip.left=horizontal,
            strip.left.values=names(x),
            strip.values=names(x),
            strip.par=list(cex=1, lines=1),
            strip.left.par=list(cex=1, lines=1),
            horizontal=TRUE,
            ...,
          rightAxisLabels=sapply(x, function(x) rowSums(abs(x)), simplify = FALSE),
            rightAxis=!missing(rightAxisLabels),
            resize.height.tuning=-.5,
            resize.height=if (missing(layout) || length(dim.x) != 2) {
              c("nrow","rowSums")
            } else {
              rep(1, layout[2])
            },
            resize.width=if (missing(layout)) {1 } else {
              rep(1, layout[1])
            },
            box.ratio=if (
              length(resize.height)==1 &&
              resize.height == "rowSums") 1000 else 2,
            xscale.components=xscale.components.top.HH,
            yscale.components=yscale.components.right.HH)

## S3 method for class 'table'
plot.likert(x, ..., xName=deparse(substitute(x)))
## S3 method for class 'ftable'
plot.likert(x, ..., xName=deparse(substitute(x)))
## S3 method for class 'structable'
plot.likert(x, ..., xName=deparse(substitute(x)))
## S3 method for class 'data.frame'
plot.likert(x, ..., xName=deparse(substitute(x)))


xscale.components.top.HH(...)
yscale.components.right.HH(...)
```

Arguments

x	For the formula method, a model formula. All terms in the formula must be the names of columns in the data.frame argument data or the special abbreviation . only on the right-hand-side. Functions of the names will not work. The right-hand-side must be either . or the sum of the names of numeric variables in data. Non-syntactic names must be in quotes (single ' or double "), but not backticks `. The . on the right-hand-side is expanded to the formula containing the sum of all remaining (after the response and the conditioning variables) numeric columns in data. An empty left-hand-side is interpreted as the rownames(data). See the examples for all possible forms of formula recognized by the likert function. Otherwise, any numeric object stored as a vector, matrix, array, data.frame, table, ftable, structable (as defined in the vcd package), or as a list of named two-dimensional objects. This is the only required argument. See the Details section for restrictions on the form of data.frame, list, ftable, and structable arguments.
data	For the formula method, a data.frame. Do not use variable names ".value" or ".variable".
ReferenceZero	Numeric scalar or NULL. The position in the range seq(0, attr(x, "nlevels")+.5, .5) where the reference line at 0 will be placed. attr(x, "nlevels") is the number of columns of the original argument x, *before* it has been coerced to a "likert" object. The default NULL corresponds to the middle level if there are an odd number of levels, and to halfway between the two middle levels if there are an even number of levels. This argument is used when the number of positive levels and the number of negative levels are not the same. For example, with 4 levels c("Disagree", "Neutral", "Weak Agree", "Strong Agree"), the argument would be specified ReferenceZero=2 indicating that the graphical split would be in the middle of the second group with label "Neutral".
value	Name of the numeric variable containing the data when the formula method is used with the long data form. The predictor in the formula will be a factor name. The name of the predictor will be used as the title in the key.
levelsName	(optional) Name of the implied factor distinguishing the columns of the response variables when the formula method is used with the wide data form. This name will be used as the title in the key.
positive.order	If FALSE, the default value, the original order of the rows is retained. This is necessary for arrays, because each panel has the same rownames. If TRUE, rows are ordered within each panel with the row whose bar goes farthest to the right at the top of a panel of horizontal bars or at the left of a panel of vertical bars. positive.order is frequently set to TRUE for lists.
data.order	formula method only. If positive.order is TRUE, this data.order variable is ignored. If FALSE, the default value, and the rows are specified by a factor, then they are ordered by their levels. If TRUE, then the rows are ordered by their order in the input data.frame.
as.percent	When as.percent==TRUE or as.percent=="noRightAxis", then the values in each row are rescaled to row percents. When as.percent==TRUE the original row totals are used as rightAxisLabels, rightAxis is set to TRUE, the

ylab.right is by default set to "Row Count Totals" (the user can change its value in the calling sequence). When as.percent=="noRightAxis", then rightAxis will be set to FALSE.

as.table Standard lattice argument. See barchart.

par.settings.in, scales.in, auto.key.in, panel.in
These are placeholders for lattice arguments that lets the user specify some lattice par.settings and still retain the ones that are prespecified in the plot.likert.default.

ylab, xlab, ylab.right, xlab.top, main
Standard lattice graph labels in barchart.

right.text.cex The right axis, as used here for the "Row Count Totals", has non-standard controls. It's cex follows the cex of the left axis, unless this argument is used to override that value. When horizontal=FALSE, then the top axis defaults to follow the bottom axis unless overridden by right.text.cex.

between Standard lattice argument.

col Vector of color names for the levels of the agreement factor. Although the colors can be specified as an arbitrary vector of color names, for example, col=c('red','blue','#4AB3F2'), usually specifying one of the diverging palettes from diverge_hcl or sequential palettes from sequential_hcl will suffice. For less intense colors, you can use the middle colors from a larger set of colors; e.g., col=sequential_hcl(11)[5:2]. See the last AudiencePercent example below for this usage.

colorFunction, colorFunctionOption
See likertColor.

reference.line.col
Color for reference line at zero.

col.strip.background
Background color for the strip labels.

key.border.white
Logical. If TRUE, then place a white border around the rect in the key, else use the col of the rect itself.

horizontal Logical, with default TRUE indicating horizontal bars, will be passed to the barchart function by the plot.likert method. In addition, it interchanges the meaning of resize.height and resize.width arguments to the likert functions applied to arrays and lists.

... other arguments. These will be passed to the barchart function by the plot.likert method. The most useful of these is the border argument which defaults to make the borders of the bars the same color as the bars themselves. A scalar alternative (border="white" being our first choice) puts a border around each bar in the stacked barchart. This works very well when the ReferenceZero line is between two levels. It gives a misleading division of the central bar when the ReferenceZero is in the middle of a level. See the example in the examples section. Arguments to the lattice auto.key=list() argument (described in barchart) will be used in the legend. See the examples.

strip.left, strip
: Logical. The default strip.left=TRUE places the strip labels on the left of each panel as in the first professional challenges example. The alternative strip.left=FALSE puts the strip labels on the top of each panel, the traditional lattice strip label position.

condlevelsName, strip.left.values, strip.values, strip.par, strip.left.par, layout
: Arguments which will be passed to ResizeEtc.

xName
: Name of the argument in its original environment.

rightAxis
: logical. Should right axis values be displayed? Defaults to FALSE unless rightAxisLabels are specified.

rightAxisLabels
: Values to be displayed on the right axis. The default values are the row totals. These are sensible for tables of counts. When the data is rescaled to percents by the as.percent=TRUE argument, then the rightAxisLabels are still defaulted to the row totals for the counts. We illustrate this usage in the ProfChal example.

resize.height.tuning
: Tuning parameter used to adjust the space between bars as specified by the resize.height argument to the ResizeEtc function.

h.resizePanels, resize.height
: Either character scalar or numeric vector. If "nrow", then the panels heights are proportional to the number of bars in each panel. If "rowSums" and there is exactly one bar per panel, then the panels heights are proportional to the total count in each bar, and see the discussion of the box.ratio argument. If a numeric vector, the panel heights are proportional to the numbers in the argument.

w.resizePanels, resize.width
: Numeric vector. The panel widths are proportional to the numbers in the argument.

box.ratio
: If there are more than one bar in any panel, then this defaults to the trellis standard value of 2. If there is exactly one bar in a panel, then the value is 1000, with the intent to minimize the white space in the panel. In this way, when as.percent==TRUE, the bar total area is the count and the bar widths are all equal at 100%. See the example below.

panel
: panel function eventually to be used by barchart.

xscale.components, yscale.components
: See yscale.components.default. xscale.components.top.HH constructs the top x-axis labels, when needed, as the names of the bottom x-axis labels. yscale.components.right.HH constructs the right y-axis labels, when needed, as the names of the left y-axis labels. The names are placed automatically by the plot.likert methods based on the value of the arguments as.percent, rightAxis, and rightAxisLabels. By default, when rightAxis != FALSE the layout.widths are set to list(ylab.right=5, right.padding=0). Otherwise, those arguments are left at their default values. They may be adjusted with an argument of the form par.settings.in= list(layout.widths=list(ylab.right=5, right.padding=0)).

Similarly, spacing for the top labels can be adjusted with an argument of the form `par.settings.in=list(layout.heights=list(key.axis.padding=6))`.

`xlimEqualLeftRight`
: Logical. The default is `FALSE`. If `TRUE` and `at` and `labels` are not explicitly specified, then the left and right x limits are set to negative and positive of the larger of the absolute value of the original x limits. When `!horizontal`, this argument applies to the y coordinate.

`xTickLabelsPositive`
: Logical. The default is `TRUE`. If `TRUE` and `at` and `labels` are not explicitly specified, then the tick labels on the negative side are displayed as positive values. When `!horizontal`, this argument applies to the y coordinate.

`reverse`
: Logical. The default is `FALSE`. If `TRUE`, the rows of the input matrix are reversed. The default is to plot the rows from top-to-bottom for horizontal bars and from left-to-write for vertical bars. `reverse`, `positive.order`, and `horizontal` are independent. All eight combinations are possible. See the `Eight sequences and orientations` section in the example for all eight.

Details

The counts (or percentages) of respondents on each row who agree with the statement are shown to the right of the zero line; the counts (or percentages) who disagree are shown to the left. The counts (or percentages) for respondents who neither agree nor disagree are split down the middle and are shown in a neutral color. The neutral category is omitted when the scale has an even number of choices. It is difficult to compare lengths without a common baseline. In this situation, we are primarily interested in the total count (or percent) to the right or left of the zero line; the breakdown into strongly or not is of lesser interest so that the primary comparisons do have a common baseline of zero. The rows within each panel are displayed in their original order by default. If the argument `positive.order=TRUE` is specified, the rows are ordered by the counts (or percentages) who agree.

Diverging stacked barcharts are also called "two-directional stacked barcharts". Some authors use the term "floating barcharts" for vertical diverging stacked barcharts and the term "sliding barcharts" for horizontal diverging stacked barcharts.

All items in a list of named two-dimensional objects must have the same number of columns. If the items have different column names, the column names of the last item in the list will be used in the key. If the dimnames of the matrices are named, the names will be used in the plot. It is possible to produce a likert plot with a list of objects with different numbers of columns, but not with the `plot.likert.list` method. These must be done manually by using the `ResizeEtc` function on each of the individual likert plots. The difficulty is that the legend is based on the last item in the list and will have the wrong number of values for some of the panels.

A single data.frame `x` will be plotted as `data.matrix(x[sapply(x, is.numeric)])`. The subscripting on the class of the columns is there to remove columns of characters (which would otherwise be coerced to NA) and factor columns (which would otherwise be coerced to integers). A data.frame with only numeric columns will work in a named list. A list of data.frame with factors or characters will be plotted by automatically removing columns that are not numeric.

`ftable` and `structable` arguments `x` will be plotted as `as.table(x)`. This changes the display sequence. Therefore the user will probably want to use `aperm` on the `ftable` or `structable` before using `plot.likert`.

The `likert` method is designed for use with `"likert"` objects created with the independent **likert** package. It is not recommended that the **HH** package and the `likert` package both be loaded at the same time, as they have incompatible usage of the exported function names `likert` and `plot.likert`. If the **likert** package is installed, it can be run without loading by using the function calls `likert::likert()` and `likert:::plot.likert()`.

Value

A `"trellis"` object containing the plot. The plot will be automatically displayed unless the result is assigned to an object.

Note

The current version of the `likert` function uses the default diverging palette from `diverge_hcl` as the default. Previous versions used the `RColorBrewer` palette `"RdBu"` as the default color palette. The previous color palette is still available with an explicit call to `likertColorBrewer`, for example

```
col=likertColorBrewer(nc, ReferenceZero=ReferenceZero,
BrewerPaletteName="RdBu", middle.color="gray90")
```

Note

Ann Liu-Ferrara was a beta tester for the shiny app.

Note

Documentation note: Most of the plots drawn by `plot.likert` have a long left-axis tick label. They therefore require a wider window than R's default of a nominal 7in $\times$ 7in window. The comments with the examples suggest aesthetic window sizes.

Technical note: There are three (almost) equivalent calling sequences for likert plots.

1. `likert(x) ## recommended`
   `likert` is an alias for `plot.likert()`.
2. `plot.likert(x)`
   `plot.likert` is both a method of `plot` for `"likert"` objects, and a generic function in its own right. There are methods of `plot.likert` for `"formula"`, `"matrix"`, `"array"`, `"table"`, and several other classes of input objects.
3. `plot(as.likert(x))`
   Both `likert` and `plot.likert` work by calling the `as.likert` function on their argument `x`. Once `as.likert` has converted its argument to a `"likert"` object, the method dispatch technology for the generic `plot.likert` is in play. The user can make the explicit call `as.likert(x)` to see what a `"likert"` object looks like, but is very unlikely to want to look a second time.

Author(s)

Richard M. Heiberger, with contributions from Naomi B. Robbins <naomi@nbr-graphs.com>.

Maintainer: Richard M. Heiberger <rmh@temple.edu>

References

Richard M. Heiberger, Naomi B. Robbins (2014)., "Design of Diverging Stacked Bar Charts for Likert Scales and Other Applications", Journal of Statistical Software, 57(5), 1–32, doi:10.18637/jss.v057.i05.

Richard Heiberger and Naomi Robbins (2011), "Alternative to Charles Blow's Figure in \"Newt's War on Poor Children\"", Forbes OnLine, December 20, 2011. https://www.forbes.com/sites/naomirobbins/2011/12/20/alternative-to-charles-blows-figure-in-newts-war-on-poor-children-2/

Naomi Robbins (2011), "Visualizing Data: Challenges to Presentation of Quality Graphics—and Solutions", Amstat News, September 2011, 28–30. http://magazine.amstat.org/blog/2011/09/01/visualizingdata/

Luo, Amy and Tim Keyes (2005). "Second Set of Results in from the Career Track Member Survey," Amstat News. Arlington, VA: American Statistical Association.

See Also

barchart, ResizeEtc, as.likert, as.matrix.listOfNamedMatrices, pyramidLikert

Examples

```
## See file HH/demo/likert-paper.r for a complete set of examples using
## the formula method into the underlying lattice:::barchart plotting
## technology.  See file HH/demo/likert-paper-noFormula.r for the same
## set of examples using the matrix and list of matrices methods.  See
## file HH/demo/likertMosaic-paper.r for the same set of examples using
## the still experimental functions built on the vcd:::mosaic as the
## underlying plotting technology

data(ProfChal)  ## ProfChal is a data.frame.
## See below for discussion of the dataset.


## Count plot
likert(Question ~ . , ProfChal[ProfChal$Subtable=="Employment sector",],
       main='Is your job professionally challenging?',
       ylab=NULL,
       sub="This plot looks better in a 9in x 4in window.")

## Percent plot calculated automatically from Count data
likert(Question ~ . , ProfChal[ProfChal$Subtable=="Employment sector",],
       as.percent=TRUE,
       main='Is your job professionally challenging?',
       ylab=NULL,
       sub="This plot looks better in a 9in x 4in window.")

## formula method
data(NZScienceTeaching)
likert(Question ~ . | Subtable, data=NZScienceTeaching,
       ylab=NULL,
       scales=list(y=list(relation="free")), layout=c(1,2))

## Not run:
```

```
## formula notation with expanded right-hand-side
likert(Question ~
       "Strongly disagree" + Disagree + Neutral + Agree + "Strongly agree" |
       Subtable, data=NZScienceTeaching,
       ylab=NULL,
       scales=list(y=list(relation="free")), layout=c(1,2))

## End(Not run)

## Not run:
## formula notation with long data arrangement
NZScienceTeachingLong <- reshape2::melt(NZScienceTeaching,
                                        id.vars=c("Question", "Subtable"))
names(NZScienceTeachingLong)[3] <- "Agreement"
head(NZScienceTeachingLong)

likert(Question ~ Agreement | Subtable, value="value", data=NZScienceTeachingLong,
       ylab=NULL,
       scales=list(y=list(relation="free")), layout=c(1,2))

## End(Not run)

## Examples with higher-dimensional arrays.
tmp3 <- array(1:24, dim=c(2,3,4),
              dimnames=list(A=letters[1:2], B=LETTERS[3:5], C=letters[6:9]))

## positive.order=FALSE is the default.  With arrays
## the rownames within each item of an array are identical.

## likert(tmp3)
likert(tmp3, layout=c(1,4))
likert(tmp3, layout=c(2,2), resize.height=c(2,1), resize.width=c(3,4))


## plot.likert interprets vectors as single-row matrices.
## http://survey.cvent.com/blog/customer-insights-2/box-scores-are-not-just-for-baseball
Responses <- c(15, 13, 12, 25, 35)
names(Responses) <- c("Strongly Disagree", "Disagree", "No Opinion",
                      "Agree", "Strongly Agree")
## Not run:
likert(Responses, main="Retail-R-Us offers the best everyday prices.",
       sub="This plot looks better in a 9in x 2.6in window.")

## End(Not run)
## reverse=TRUE  is needed for a single-column key with
## horizontal=FALSE and with space="right"
likert(Responses, horizontal=FALSE,
       aspect=1.5,
       main="Retail-R-Us offers the best everyday prices.",
       auto.key=list(space="right", columns=1,
                     reverse=TRUE, padding.text=2),
       sub="This plot looks better in a 4in x 3in window.")
```

```
## Not run:
## Since age is always positive and increases in a single direction,
## this example uses colors from a sequential palette for the age
## groups.  In this example we do not use a diverging palette that is
## appropriate when groups are defined by a characteristic, such as
## strength of agreement or disagreement, that can increase in two directions.

## Initially we use the default Blue palette in the sequential_hcl function.
data(AudiencePercent)
likert(AudiencePercent,
       auto.key=list(between=1, between.columns=2),
       xlab=paste("Percentage of audience younger than 35 (left of zero)",
                  "and older than 35 (right of zero)"),
       main="Target Audience",
       col=rev(colorspace::sequential_hcl(4)),
       sub="This plot looks better in a 7in x 3.5in window.")

## The really light colors in the previous example are too light.
## Therefore we use the col argument directly.  We chose to use an
## intermediate set of Blue colors selected from a longer Blue palette.
likert(AudiencePercent,
       positive.order=TRUE,
       auto.key=list(between=1, between.columns=2),
       xlab=paste("Percentage of audience younger than 35",
         "(left of zero) and older than 35 (right of zero)"),
       main="Brand A has the most even distribution of ages",
       col=colorspace::sequential_hcl(11)[5:2],
       scales=list(x=list(at=seq(-90,60,10),
                     labels=as.vector(rbind("",seq(-80,60,20))))),
      sub="This plot looks better in a 7in x 3.5in window.")

## End(Not run)


## Not run:
## See the ?as.pyramidLikert help page for these examples
## Population Pyramid
data(USAge.table)
USA79 <- USAge.table[75:1, 2:1, "1979"]/1000000
PL <- likert(USA79,
             main="Population of United States 1979 (ages 0-74)",
             xlab="Count in Millions",
             ylab="Age",
             scales=list(
               y=list(
                 limits=c(0,77),
                 at=seq(1,76,5),
                 labels=seq(0,75,5),
                 tck=.5))
             )
PL
as.pyramidLikert(PL)
```

```
likert(USAge.table[75:1, 2:1, c("1939","1959","1979")]/1000000,
       main="Population of United States 1939,1959,1979 (ages 0-74)",
       sub="Look for the Baby Boom",
       xlab="Count in Millions",
       ylab="Age",
       scales=list(
         y=list(
           limits=c(0,77),
           at=seq(1,76,5),
           labels=seq(0,75,5),
           tck=.5)),
       strip.left=FALSE, strip=TRUE,
       layout=c(3,1), between=list(x=.5))

## End(Not run)


Pop <- rbind(a=c(3,2,4,9), b=c(6,10,12,10))
dimnames(Pop)[[2]] <- c("Very Low", "Low", "High", "Very High")
likert(as.listOfNamedMatrices(Pop),
            as.percent=TRUE,
            resize.height="rowSums",
            strip=FALSE,
            strip.left=FALSE,
            main=paste("Area and Height are proportional to 'Row Count Totals'.",
                       "Width is exactly 100%.", sep="\n"))


## Professional Challenges example.
##
## The data for this example is a list of related likert scales, with
## each item in the list consisting of differently named rows.  The data
## is from a questionnaire analyzed in a recent Amstat News article.
## The study population was partitioned in several ways.  Data from one
## of the partitions (Employment sector) was used in the first example
## in this help file.  The examples here show various options for
## displaying all partitions on the same plot.
##
data(ProfChal)
levels(ProfChal$Subtable)[6] <- "Prof Recog" ## reduce length of label

## 1. Plot counts with rows in each panel sorted by positive counts.
##
## Not run:
likert(Question ~ . | Subtable, ProfChal,
       positive.order=TRUE,
       main="This works, but needs more specified arguments to look good")

likert(Question ~ . | Subtable, ProfChal,
       scales=list(y=list(relation="free")), layout=c(1,6),
       positive.order=TRUE,
       between=list(y=0),
```

```
       strip=FALSE, strip.left=strip.custom(bg="gray97"),
       par.strip.text=list(cex=.6, lines=5),
       main="Is your job professionally challenging?",
       ylab=NULL,
       sub="This looks better in a 10inx7in window")

## End(Not run)

ProfChalCountsPlot <-
likert(Question ~ . | Subtable, ProfChal,
       scales=list(y=list(relation="free")), layout=c(1,6),
       positive.order=TRUE,
       box.width=unit(.4,"cm"),
       between=list(y=0),
       strip=FALSE, strip.left=strip.custom(bg="gray97"),
       par.strip.text=list(cex=.6, lines=5),
       main="Is your job professionally challenging?",
       rightAxis=TRUE,  ## display Row Count Totals
       ylab=NULL,
       sub="This looks better in a 10inx7in window")
ProfChalCountsPlot


## Not run:
## 2. Plot percents with rows in each panel sorted by positive percents.
##    This is a different sequence than the counts.  Row Count Totals are
##    displayed on the right axis.
ProfChalPctPlot <-
likert(Question ~ . | Subtable, ProfChal,
       as.percent=TRUE,    ## implies display Row Count Totals
       scales=list(y=list(relation="free")), layout=c(1,6),
       positive.order=TRUE,
       box.width=unit(.4,"cm"),
       between=list(y=0),
       strip=FALSE, strip.left=strip.custom(bg="gray97"),
       par.strip.text=list(cex=.6, lines=5),
       main="Is your job professionally challenging?",
       rightAxis=TRUE,  ## display Row Count Totals
       ylab=NULL,
       sub="This looks better in a 10inx7in window")
ProfChalPctPlot

## 3. Putting both percents and counts on the same plot, both in
##    the order of the positive percents.

LikertPercentCountColumns(Question ~ . | Subtable, ProfChal,
                          layout=c(1,6), scales=list(y=list(relation="free")),
                          ylab=NULL, between=list(y=0),
                          strip.left=strip.custom(bg="gray97"), strip=FALSE,
                          par.strip.text=list(cex=.7),
                          positive.order=TRUE,
                          main="Is your job professionally challenging?")
```

```
## Restore original name
## levels(ProfChal$Subtable)[6] <- "Attitude\ntoward\nProfessional\nRecognition"

## End(Not run)

## Not run:
## 4. All possible forms of formula for the likert formula method:
data(ProfChal)
row.names(ProfChal) <- abbreviate(ProfChal$Question, 8)

likert( Question ~ . | Subtable,
       data=ProfChal, scales=list(y=list(relation="free")), layout=c(1,6))

likert( Question ~
        "Strongly Disagree" + Disagree + "No Opinion" + Agree + "Strongly Agree" | Subtable,
       data=ProfChal, scales=list(y=list(relation="free")), layout=c(1,6))

likert( Question ~ . ,
       data=ProfChal)

likert( Question ~ "Strongly Disagree" + Disagree + "No Opinion" + Agree + "Strongly Agree",
       data=ProfChal)

likert( ~ . | Subtable,
       data=ProfChal, scales=list(y=list(relation="free")), layout=c(1,6))

likert( ~ "Strongly Disagree" + Disagree + "No Opinion" + Agree + "Strongly Agree" | Subtable,
       data=ProfChal, scales=list(y=list(relation="free")), layout=c(1,6))

likert( ~ . ,
       data=ProfChal)

likert( ~ "Strongly Disagree" + Disagree + "No Opinion" + Agree + "Strongly Agree",
       data=ProfChal)


## End(Not run)

## Not run:
## 5. putting the x-axis tick labels on top for horizontal plots
##    putting the y-axis tick lables on right for vertical plots
##
## This non-standard specification is a consequence of using the right
## axis labels for different values than appear on the left axis labels
## with horizontal plots, and using the top axis labels for different
## values than appear on the bottom axis labels with vertical plots.

## Percent plot calculated automatically from Count data

tmph <-
likert(Question ~ . , ProfChal[ProfChal$Subtable=="Employment sector",],
       as.percent=TRUE,
```

```
       main='Is your job professionally challenging?',
       ylab=NULL,
       sub="This plot looks better in a 9in x 4in window.")
tmph$x.scales$labels
names(tmph$x.scales$labels) <- tmph$x.scales$labels
update(tmph, scales=list(x=list(alternating=2)), xlab=NULL, xlab.top="Percent")

tmpv <-
likert(Question ~ . , ProfChal[ProfChal$Subtable=="Employment sector",],
       as.percent=TRUE,
       main='Is your job professionally challenging?',
       sub="likert plots with long Question names look better horizontally.
With effort they can be made to look adequate vertically.",
       horizontal=FALSE,
       scales=list(y=list(alternating=2), x=list(rot=c(90, 0))),
       ylab.right="Percent",
       ylab=NULL,
       xlab.top="Column Count Totals",
       par.settings=list(
         layout.heights=list(key.axis.padding=5),
         layout.widths=list(key.right=1.5, right.padding=0))
)
tmpv$y.scales$labels
names(tmpv$y.scales$labels) <- tmpv$y.scales$labels
tmpv
tmpv$x.limits <- abbreviate(tmpv$x.limits,8)
tmpv$x.scales$rot=c(0, 0)
tmpv


## End(Not run)

## Not run:
## illustration that a border on the bars is misleading when it splits a bar.
tmp <- data.frame(a=1, b=2, c=3)
likert(~ . , data=tmp, ReferenceZero=2, main="No border. OK.")
likert(~ . , data=tmp, ReferenceZero=2, border="white",
       main="Border. Misleading split of central bar.")
likert(~ . , data=tmp, ReferenceZero=2.5, main="No border. OK.")
likert(~ . , data=tmp, ReferenceZero=2.5, border="white", main="Border. OK.")

## End(Not run)

## Not run:
  ## run the shiny app
if (interactive())  shiny::runApp(system.file("shiny/likert", package="HH"))

## End(Not run)

## The ProfChal data is done again with explicit use of ResizeEtc
## in ?HH:::ResizeEtc
```

`likertColor` *Selection of colors for Likert plots.*

Description

Selection of colors for Likert plots.

Usage

```
ColorSet(nc, ReferenceZero=NULL)
likertColor(nc, ReferenceZero=NULL,
                colorFunction=c("diverge_hcl","sequential_hcl"),
                colorFunctionOption=c("lighter","flatter","default"),
                colorFunctionArgs=
                 likertColorFunctionArgs[[colorFunctionOption, colorFunction]],
                ...)
likertColorBrewer(nc, ReferenceZero=NULL,
                  BrewerPaletteName="RdBu", middle.color="gray90")

brewer.pal.likert(n, name, middle.color)
```

Arguments

n, nc	Number of colors in the palette. If there are more levels than RColorBrewer normally handles, we automatically interpolate with colorRampPalette.
ReferenceZero	Numeric scalar or NULL. The position in the range seq(0, attr(x, "nlevels")+.5, .5) where the reference line at 0 will be placed. attr(x, "nlevels") is the number of columns of the original argument x, *before* it has been coerced to a "likert" object. The default NULL corresponds to the middle level if there are an odd number of levels, and to halfway between the two middle levels if there are an even number of levels. This argument is used when the number of positive levels and the number of negative levels are not the same. For example, with 4 levels c("Disagee", "Neutral", "Weak Agree", "Strong Agree"), the argument would be specified ReferenceZero=2 indicating that the graphical split would be in the middle of the second group with label "Neutral".
colorFunction	Function name from the **colorspace** package, either "diverge_hcl" or "sequential_hcl".
colorFunctionOption	Name of a list item defined inside the likertColor function. The item contains a list of parameters to the function identified in the colorFunction argument.
colorFunctionArgs	list of arguments to the **colorspace** function. The default selects the values by indexing into a list defined in the likertColor function using the values of the two arguments colorFunction and colorFunctionOption

. For non-default usage, see the BlueOrange example in this help page.

`...` Other arguments are ignored.

`BrewerPaletteName, name`
: RColorBrewer palette names. We default to the diverging palette RdBu. Diverging palettes are usually appropriate for two-directional scales (Agree–Disagree). Sequential palettes are often appropriate for one-directional scales (Age Ranges). Qualitative palettes are usually not appropriate for likert plots.

`middle.color` Darker middle color than the default "#F7F7F7" in the RdBu scheme.

Details

These are support functions for the `plot.likert` function. Please see `plot.likert` for details.

`likertColor` uses by default the `diverge_hcl` diverging palette defined by the argument `colorFunctionOption="lighter"`.

`likertColorBrewer` by default uses the "RdBu" diverging palette from RColorBrewer.

Value

`ColorSet` returns a vector of integers, one per each level, corresponding to the strength of the levels from Disagree to Agree. For balanced levels, such as `c("Disagree Strongly", "Disagree Weakly", "Agree Weakly", "Agree Strongly")`, corresponding to `nc=4`, `ReferenceZero=2.5`, it returns `-2 -1 1 2`. For unbalanced levels, such as `c("Disagree", "Neutral", "Agree Weakly", "Agree Strongly")`, corresponding to `nc=4`, `ReferenceZero=2`, it returns `-1 0 1 2`.

`likertColor` returns a subset of a palette constructed by either `diverge_hcl` or `sequential_hcl` in the **colorspace** package. The subset corresponds to the levels specified by `ColorSet`.

`brewer.pal.likert` returns a RColorBrewer palette.

`likertColorBrewer` returns a subset of a palette constructed by `brewer.pal.likert`. The subset corresponds to the levels specified by `ColorSet`.

Author(s)

Richard M. Heiberger, with contributions from Naomi B. Robbins <naomi@nbr-graphs.com>.

Maintainer: Richard M. Heiberger <rmh@temple.edu>

See Also

`plot.likert`

Examples

```
brewer.pal.likert(4, "RdBu")
brewer.pal.likert(5, "RdBu")
ColorSet(4)
ColorSet(4, 2)
likertColor(4)
likertColor(4, 2.5) ## same as above
likertColor(4, 2)   ## one negative level and two positive levels: default
likertColor(5, 3)[-2] ## one negative level and two positive levels: stronger negative
```

```
## Not run:
  ## Examples illustrating the six predefined likertColor palettes, and how
  ## to define additional hcl color palettes for use with the likert functions.

  data(ProfDiv)
  ProfDiv.df <- data.frame(ProfDiv)

  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE)
  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE,
         colorFunctionOption="default")
  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE,
         colorFunctionOption="flatter")
  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE,
         colorFunction="sequential_hcl")
  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE,
         colorFunction="sequential_hcl", colorFunctionOption="default")
  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE,
         colorFunction="sequential_hcl", colorFunctionOption="flatter")

  likert(ProfDiv, horizontal=FALSE, positive.order=FALSE)
  likert(ProfDiv, horizontal=FALSE, positive.order=FALSE,
         colorFunctionOption="default")
  likert(ProfDiv, horizontal=FALSE, positive.order=FALSE,
         colorFunctionOption="flatter")
  likert(ProfDiv, horizontal=FALSE, positive.order=FALSE,
         colorFunction="sequential_hcl")
  likert(ProfDiv, horizontal=FALSE, positive.order=FALSE,
         colorFunction="sequential_hcl", colorFunctionOption="default")
  likert(ProfDiv, horizontal=FALSE, positive.order=FALSE,
         colorFunction="sequential_hcl", colorFunctionOption="flatter")

  likertMosaic(ProfDiv.df)
  likertMosaic(ProfDiv.df, colorFunctionOption="default")
  likertMosaic(ProfDiv.df, colorFunctionOption="flatter")
  likertMosaic(ProfDiv.df, colorFunction="sequential_hcl")
  likertMosaic(ProfDiv.df, colorFunction="sequential_hcl",
               colorFunctionOption="default")
  likertMosaic(ProfDiv.df, colorFunction="sequential_hcl",
               colorFunctionOption="flatter")

  ## specify an hcl palette for use with the likert functions.
  BlueOrange <- likertColor(nc=4, ReferenceZero=NULL,
                            colorFunction="diverge_hcl",
                            colorFunctionArgs=
                              list(h=c(246, 40), c=96, l=c(65,90), power=1.5))
  likert( ~ . , ProfDiv.df, horizontal=FALSE, positive.order=FALSE, col=BlueOrange)

## End(Not run)
```

likertMosaic *Diverging stacked barcharts for Likert, semantic differential, rating scale data, and population pyramids based on mosaic as the plotting style.*

Description

Constructs and plots diverging stacked barcharts for Likert, semantic differential, rating scale data, and population pyramids, .based on `mosaic` as the plotting style.

Usage

```
likertMosaic(x, ...)

## S3 method for class 'formula'
likertMosaic(x, data, ReferenceZero = NULL, spacing=NULL,
                   ..., between.y = c(1.2, 0.3))

## S3 method for class 'array'
likertMosaic(x, ReferenceZero = NULL, col = NULL, main = NULL,
             ...,
             as.percent = FALSE, variable.width = NULL, positive.order = FALSE,
             Conditions = NULL,
             x.legend = list(text = list(dimnames(x)[[ndim]]),
                             columns = x.dim[ndim],
                             space = "bottom",
                             size = 2,
                             cex = 0.8,
                             between = 0.6,
                             rect= list(col = col, border = "white")),
             legend.y = 0.05,
             spacing = spacing_highlighting,
             split_vertical = c(TRUE, FALSE),
             margins = c(3, 2, 4, 22),
             keep_aspect = FALSE,
             rot_labels = c(0, 0, 90, 0),
             just_labels = c("center", "center", "center", "right"),
             labels = c(TRUE, TRUE, FALSE, TRUE),
             varnames = FALSE,
             zero_size = 0,
             gp = gpar(fill = col.extended, col = 0),
             colorFunction="diverge_hcl",
             colorFunctionOption="lighter")

## S3 method for class 'data.frame'
likertMosaic(x, ...)

## Default S3 method:
```

```
likertMosaic(x, ...) ## most likely for a vector

## S3 method for class 'list'
likertMosaic(x, ...)

## S3 method for class 'matrix'
likertMosaic(x, ...,
 split_vertical = c(FALSE, TRUE),
 rot_labels = c(90, 0, 0, 0),
 just_labels = c("left", "center", "center", "right"),
 labels = c(TRUE, FALSE))
```

Arguments

x	For the formula method, a model formula. Otherwise, any numeric object stored as a vector, matrix, array, data.frame, table, ftable, structable (as defined in the vcd package), or as a list of named two-dimensional objects. This is the only required argument. See the Details section for restrictions on the form of data.frame, list, ftable, and structable arguments.
data	For the formula method, a data.frame.
ReferenceZero	Numeric scalar or NULL. The position in the range seq(0, attr(x, "nlevels")+.5, .5) where the reference line at 0 will be placed. attr(x, "nlevels") is the number of columns of the original argument x, *before* it has been coerced to a "likert" object. The default NULL corresponds to the middle level if there are an odd number of levels, and to halfway between the two middle levels if there are an even number of levels. This argument is used when the number of positive levels and the number of negative levels are not the same. For example, with 4 levels c("Disagee", "Neutral", "Weak Agree", "Strong Agree"), the argument would be specified ReferenceZero=2 indicating that the graphical split would be in the middle of the second group with label "Neutral".
positive.order	If FALSE, the default value, the original order of the rows is retained. This is necessary for arrays, because each panel has the same rownames. If TRUE, rows are ordered within each panel with the row whose bar goes farthest to the right at the top of a panel of horizontal bars or at the left of a panel of vertical bars. positive.order is frequently set to TRUE for lists.
as.percent	When as.percent==TRUE or as.percent=="noRightAxis", then the values in each row are rescaled to row percents.
variable.width	When TRUE and as.percent==TRUE, then the area of the bars (percent along the length times the width) is proportional to the counts.
col	Colors for the bars. With the default value NULL, the colors are chosen from the default diverge_hcl diverging palette. Any color specification that R understands can be used here.
colorFunction, colorFunctionOption	See likertColor.
main	main title for the plot.

`...` Additional arguments, passed to the next method and possibly all the way to `strucplot`.

`Conditions` Factor used to divide the rows of the plot into sets of rows corresponding to levels of Condition. In the formula method, the conditions are the factors appearing after the `|` symbol.

`between.y` vertical spacing between bars. `between.y[1]` is used between levels of conditioning factors, and `between.y[2]` is used between bars within the same level of the conditioning factor.

`x.legend` Description of legend using the terminology and conventions of the `lattice` package.

`legend.y` Adjust vertical location of legend.

`spacing`, `split_vertical`, `margins`, `keep_aspect`, `rot_labels`, `just_labels`, `labels`
Please see `strucplot` for details.

`varnames`, `zero_size`, `gp`
Please see `strucplot` for details.

Details

The counts (or percentages) of respondents on each row who agree with the statement are shown to the right of the zero line; the counts (or percentages) who disagree are shown to the left. The counts (or percentages) for respondents who neither agree nor disagree are split down the middle and are shown in a neutral color. The neutral category is omitted when the scale has an even number of choices. It is difficult to compare lengths without a common baseline. In this situation, we are primarily interested in the total count (or percent) to the right or left of the zero line; the breakdown into strongly or not is of lesser interest so that the primary comparisons do have a common baseline of zero. The rows within each panel are displayed in their original order by default. If the argument `positive.order=TRUE` is specified, the rows are ordered by the counts (or percentages) who agree.

Diverging stacked barcharts are also called "two-directional stacked barcharts". Some authors use the term "floating barcharts" for vertical diverging stacked barcharts and the term "sliding barcharts" for horizontal diverging stacked barcharts.

All items in a list of named two-dimensional objects must have the same number of columns. If the items have different column names, the column names of the last item in the list will be used in the key. If the dimnames of the matrices are named, the names will be used in the plot. It is possible to produce a likert plot with a list of objects with different numbers of columns, but not with the `plot.likert.list` method. These must be done manually by using the `ResizeEtc` function on each of the individual likert plots. The difficulty is that the legend is based on the last item in the list and will have the wrong number of values for some of the panels.

A single data.frame `x` will be plotted as `data.matrix(x)`; therefore factor columns will be converted to integers and character columns will become `NA` and will be plotted as if they had value 0. A data.frame with only numeric columns will work in a named list. A data.frame with factors or characters won't work in a named list.

ftable and structable arguments `x` will be plotted as `as.table(x)`. This changes the display sequence. Therefore the user will probably want to use `aperm` on the ftable or structable before using `plot.likert`.

Value

Please see strucplot for a description of the returned object.

Note

The functions described here are currently missing the following features:

1. no axis ticks, number, nor axis label for the x axis
2. no zero reference line
3. no right-axis labels for Row Count Totals
4. no strip.left labels for grouping by Conditions
5. In Figure 8 and 9 (HH/demo/likertMosaic-paper.r), no control of the thickness of the bars
6. All bars are horizontal.
7. No borders on the overall plot nor on the panels in plots with grouping by Conditions
8. No control of between=list(x=number)
9. cex for labeling
10. border on empty boxes
11. I am using a lattice legend, not a native strucplot legend

Author(s)

Richard M. Heiberger, with contributions from Naomi B. Robbins <naomi@nbr-graphs.com>.

Maintainer: Richard M. Heiberger <rmh@temple.edu>

References

Richard M. Heiberger, Naomi B. Robbins (2014)., "Design of Diverging Stacked Bar Charts for Likert Scales and Other Applications", Journal of Statistical Software, 57(5), 1–32, doi:10.18637/jss.v057.i05.

Richard Heiberger and Naomi Robbins (2011), "Alternative to Charles Blow's Figure in \"Newt's War on Poor Children\"", Forbes OnLine, December 20, 2011. https://www.forbes.com/sites/naomirobbins/2011/12/20/alternative-to-charles-blows-figure-in-newts-war-on-poor-children-2/

Naomi Robbins (2011), "Visualizing Data: Challenges to Presentation of Quality Graphics—and Solutions", Amstat News, September 2011, 28–30. http://magazine.amstat.org/blog/2011/09/01/visualizingdata/

Luo, Amy and Tim Keyes (2005). "Second Set of Results in from the Career Track Member Survey," Amstat News. Arlington, VA: American Statistical Association.

See Also

likert, mosaic

Examples

```
## See file HH/demo/likertMosaic-paper.r for a complete set of examples.
## Not run:
  require(vcd)
  data(ProfChal)
  likertMosaic(Question ~ . | Subtable, ProfChal,
               main="Is your job professionally challenging?")
  likertMosaic(Question ~ . | Subtable, ProfChal,
               main="Is your job professionally challenging?", as.percent=TRUE)
  likertMosaic(Question ~ . | Subtable, ProfChal,
               main="Is your job professionally challenging?", as.percent=TRUE,
               positive.order=TRUE)
  likertMosaic(Question ~ . | Subtable, ProfChal,
               main="Is your job professionally challenging?", as.percent=TRUE,
               variable.width=TRUE)

  EmpRows <- ProfChal$Subtable == "Employment sector"
  ProfChal2 <- ProfChal[EmpRows, 1:5]
  rownames(ProfChal2) <- substr(ProfChal[EmpRows, "Question"], 1, 5)

  likertMosaic(ProfChal2)
  likertMosaic(ProfChal2, main="Employment")
  likertMosaic(ProfChal2, main="Employment", ReferenceZero=0)
  likertMosaic(ProfChal2, main="Employment", ReferenceZero=3.5)
  likertMosaic(ProfChal2, main="Employment", ReferenceZero=4)
  likertMosaic(ProfChal2, main="Employment", ReferenceZero=6)
  likertMosaic(ProfChal2, main="Employment", positive.order=TRUE)
  likertMosaic(ProfChal2, main="Employment", variable.width=TRUE)

  likertMosaic(~ ., data.frame(ProfChal2), main="Employment", positive.order=TRUE)

  likertMosaic(~ ., data.frame(ProfChal2), main="Employment", variable.width=TRUE)
  likert(~ ., data.frame(ProfChal2), main="Employment", variable.width=TRUE)

  data(SFF8121)
  likertMosaic(aperm(SFF8121, c(3,1,2)))


## End(Not run)
```

`LikertPercentCountColumns` *Display likert plots with percents in the first column of panels and counts in the second column of panels.*

Description

Display likert plots with percents in the first column of panels and counts in the second column of panels. Order the rows either in their original order or by the positive order of the percent display.

Usage

```
LikertPercentCountColumns(
           x, data,
           px=list( ## defaults designed for long QuestionName values
             LL=c(.00,  .50), ## and 7in x 7in window
             LP=c(.50,  .70),
            ML=c(.50,  .51),  ## arbitrary, visually center the labels and legend
             RP=c(.71,  .87),
             RL=c(.87, 1.00)),
           ...,
           QuestionName="Question",
           as.percent="Capture and then ignore this argument",
           positive.order=FALSE)
```

Arguments

x, data, positive.order	formula, data.frame, Logical. See likert.
...	other arguments that can be used for likert.
px	See as.TwoTrellisColumns5.
as.percent	Capture this argument and ignore it. The as.percent argument of likert will be TRUE in the left (Percent) column of the resulting "TwoTrellisColumns5" object and FALSE in the right (Count) column.
QuestionName	Character string containing the name of the column in data containing the values of the response variable.

Value

A "TwoTrellisColumns5" object, consisting of a list containing the constructed left, middle, and right trellis objects, and an attribute containing the px value. See as.TwoTrellisColumns5 for details.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

likert

Examples

```
## These are based on the Professional Challenges example in ?likert
data(ProfChal)

levels(ProfChal$Subtable)[6] <- "Prof Recog" ## reduce length of label

## See ?print.TwoTrellisColumns for this example using the original ordering
```

```
## Order both the plot of the count plot and the percent plot by the
## positive.order of the percent plot.

LikertPercentCountColumns(Question ~ . | Subtable, ProfChal,
                          layout=c(1,6), scales=list(y=list(relation="free")),
                          ylab=NULL, between=list(y=0),
                          strip.left=strip.custom(bg="gray97"), strip=FALSE,
                          par.strip.text=list(cex=.7),
                          positive.order=TRUE,
                          main="Is your job professionally challenging?")
## Not run:
## Retain original order of the Question variable

LikertPercentCountColumns(Question ~ . | Subtable, ProfChal,
                          layout=c(1,6), scales=list(y=list(relation="free")),
                          ylab=NULL, between=list(y=0),
                          strip.left=strip.custom(bg="gray97"), strip=FALSE,
                          par.strip.text=list(cex=.7),
                          main="Is your job professionally challenging?")

## Order both the plot of the count plot and the percent plot by the
## positive.order of the percent plot.
## Just the "Employment sector".
LPCCEs <-
LikertPercentCountColumns(Question ~ . ,
                          ProfChal[ProfChal$Subtable == "Employment sector", -7],
                          ylab=NULL, between=list(y=0),
                          par.strip.text=list(cex=.7),
                          positive.order=TRUE,
                       main="Is your job professionally challenging?\nEmployment sector",
                          px=list( ## defaults designed for long QuestionName values
                            LL=c(.00,  .50), ## and 7in x 7in window
                            LP=c(.49,  .70),
                      ML=c(.50,  .51),  ## arbitrary, visually center the labels and legend
                            RP=c(.71,  .84),
                            RL=c(.87, 1.00)))
LPCCEs$RP$x.scales$at <- c(0,100,200)
LPCCEs$RP$x.scales$labels <- c(0,100,200)
LPCCEs

## End(Not run)
```

`likertWeighted` *Special case wrapper for likert() when multiple columns are to have the same bar thicknesses. Uses formula with one or two conditioning variables.*

Description

Special case wrapper for likert() when multiple columns are to have the same bar thicknesses. Uses formula with one or two conditioning variables.

Usage

```
likertWeighted(x, ...) ## generic

## S3 method for class 'array'
likertWeighted(x, ..., C = 1, Q = 3, R = 2) ## array

## Default S3 method:
likertWeighted(x, ...) ## matrix, table, data.frame

## S3 method for class 'formula'
likertWeighted(x, data,
               xlim=c(-100, 100),
               scales=list(y=list(relation="free", cex=1.3),
                           x=list(at=seq(-100, 100, 50),
                           labels=abs(seq(-100, 100, 50)), cex=.5)),
               box.ratio=1000,
               as.percent=TRUE, rightAxis=FALSE,
               between=list(x=1, y=0),
               strip=FALSE, strip.left=FALSE,
               par.settings=list(clip=list(panel="off")),
               h.resizePanels=1,
               auto.key.title=NULL,
               auto.key.columns=dim(data)[[2]] -
          NumberOfConditioningVariables(formula), ## excludes conditioning variables
               auto.key.cex=1.2,
               auto.key.cex.title=1.2,
               auto.key.lines.title=3,
               ylab=NULL,
               axis.top=dimnames(result)[[1]], ## Questions
               axis.top.row=1,
               ...)
```

Arguments

x	For the default method, a matrix or data.frame or two-dimensional table. For the array method, a two- or-three-dimensional array. For the formula method, a formula.
formula	Standard trellis formula, usually ~ . | row + column or ~ . | row
data	A data.frame that has been constructed from a 2D object (matrix or table or data.frame) to include an additional column row, or constructed from a 3D array by toCQxR to include two additional columns group and row. The default and array methods do that construction.

`C`, `R`, `Q` Integers, one each of 1,2,3; positions of the three dimensions. Used in `array` method. See `toCQxR`.

`xlim`, `between`, `strip`, `strip.left`, `par.settings`, `ylab`
See `xyplot`

`scales` See `xyplot`. For `likertWeighted`, when scales for x is changed, scales for y must be stated also.

`box.ratio` See `panel.bwplot`.

`as.percent`, `rightAxis`, `...`, `h.resizePanels`
First see the formula method for `likertWeighted`, and then `likert`.

`auto.key.title`, `auto.key.columns`, `auto.key.cex`, `auto.key.cex.title`, `auto.key.lines.title`
Values which will be used in `trellis` argument `auto.key=list(title=auto.key.title, columns=auto.key.columns, cex=auto.key.cex, cex.title=auto.key.cex.title, lines.title=auto.key.lines.title)`

`axis.top` Label to be placed at `x=0` for top (and other specified) panel of each column.

`axis.top.row` Which rows will have `axis.top` displayed.

Value

A `likert` plot as a `"trellis"` object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`likert`

Examples

```
## simplest 2D example
tmp <- matrix(1:12, 3, 4,
              dimnames=list(c("A","B","C"),
                            c(letters[4:7]))) * c(1,2,3)
tmp
rowSums(tmp)

likertWeighted(tmp,
               h.resizePanels=rowSums(tmp),
               main="likertWeighted, simplest example,
                     defaults to Percent,
                     specified row thicknesses")

## Same example with explicit use of the formula method
## (default method does this for you).
tmpdd <- data.frame(tmp, row=row.names(tmp))
tmpdd
likertWeighted(~ . | row, tmpdd,            ## tmpdd
```

```
               h.resizePanels=rowSums(tmp), ## tmp
main="likertWeighted,
same example but with explicit formula method")

## show subgroups
likertWeighted(tmp,
               h.resizePanels=rowSums(tmp),
               between=list(y=c(0, 1)),
               ylab=c("C in its own group","A and B together"),
               main="between=list(y=c(0,1) ## standard lattice between argument
Adjacent A and B with y.between = 0 are in the same bordered group.
Adjacent B and C with y.between != 0 are in different bordered groups.")


## simplest 3D example
## This is natural when multiple questions are asked of the
## same set of respondents in a survey.
## This example simulates that situation.
##
tmp3D <- abind::abind(h=tmp, i=tmp, j=tmp, along=3)
tmp3D[1,,"i"] <- tmp3D[1,c(4,2,1,3),"h"]
tmp3D[2,,"i"] <- tmp3D[2,c(2,4,3,1),"h"]
tmp3D[3,,"i"] <- tmp3D[3,c(4,1,2,3),"h"]
tmp3D[1,,"j"] <- tmp3D[1,c(4,3,2,1),"h"]
tmp3D[2,,"j"] <- tmp3D[2,c(1,4,3,2),"h"]
tmp3D[3,,"j"] <- tmp3D[3,c(2,4,3,1),"h"]
## now
rowSums(tmp3D[,,1]) == rowSums(tmp3D[,,2])
rowSums(tmp3D[,,1]) == rowSums(tmp3D[,,3])


likertWeighted(tmp3D, h.resizePanels=rowSums(tmp3D[,,1]),
               main="simplest 3D example, array method")

likertWeighted(tmp3D, h.resizePanels=rowSums(tmp3D[,,1]),
               between=list(x=1, y=c(0, 1)),
               main="simplest 3D example, array method, with subgroups")

## Same example with explicit use of the formula method
## (array method does this for you).
tmp3Ddf <- toCQxR(tmp3D)
dimnames(tmp3Ddf)
tmp3Ddf
likertWeighted(~ . | group + row, tmp3Ddf, h.resizePanels=rowSums(tmp3D[,,1]),
               main="simplest 3D example, formula method")
```

---

lm.case *case statistics for regression analysis*

Description

Case statistics for regression analysis. `case.lm` calculates the statistics. `plot.case` plots the cases, one statistic per panel, and illustrates and flags all observations for which the standard thresholds are exceeded. `plot.case` returns an object with class `c("trellis.case", "trellis")` containing the plot and the row.names of the flagged observations. The object is printed by a method which displays the set of graphs and prints the list of flagged cases. `panel.case` is a panel function for `plot.case`.

Usage

```
case(fit, ...)
## S3 method for class 'lm'
case(fit, lms = summary.lm(fit), lmi = lm.influence(fit), ...)

## S3 method for class 'case'
plot(x, fit,
          which=c("stu.res","si","h","cook","dffits",
            dimnames(x)[[2]][-(1:8)]),  ##DFBETAS
          between.in=list(y=4, x=9),
          cex.threshold=1.2,
          main.in=list(
            paste(deparse(fit$call), collapse=""),
            cex=main.cex),
          sigma.in=summary.lm(fit)$sigma,
          p.in=summary.lm(fit)$df[1]-1,
          main.cex=NULL,
          ...)

panel.case(x, y, subscripts, rownames, group.names,
           thresh, case.large,
           nn, pp, ss, cex.threshold,
           ...)
```

Arguments

`fit`	`"lm"` object computed with `x=TRUE`
`lms`	`summary.lm(fit)`
`lmi`	`lm.influence(fit)`
`x`	In `plot.case`, the matrix output from `case.lm` containing case diagnostics on each observation in the original dataset. In `panel.case`, the x variable to be plotted
`which`	In `plot.case`, the names of the columns of x that are to be graphed.
`between.in`	`between` trellis/lattice argument.
`cex.threshold`	Multiplier for `cex` for the threshold values.
`main.in`	`main` title for `xyplot`. The default main title displays the linear model formula from `fit`.

sigma.in	standard error for the fit.
p.in	The number of degrees of freedom associated with the fitted model.
main.cex	cex for main title.
...	other arguments to xyplot
y	the y variable to be plotted.
thresh	Named list of lists. Each list contains the components threshold (y-locations where a reference line will be drawn), thresh.label (the right-axis labels for the reference lines), thresh.id (the bounds defining "Noteworthy Observations").
case.large	Named list of "Noteworthy Observations".
nn	Number of rows in original dataset.
pp	The number of degrees of freedom associated with the fitted model.
ss	Standard error for the fit.
subscripts	trellis/lattice argument, position in the reshaped dataset constructed by plot.case before calling xyplot.
rownames	row name in the original data.frame.
group.names	names of the individual statistics.

Details

lm.influence is part of S-Plus and R case.lm and plot.case are based on: Section 4.3.3 "Influence of Individual Obervations in Chambers and Hastie", *Statistical Models in S*.

Value

case.lm returns a matrix, with one row for each observation in the original dataset. The columns contain the diagnostic statistics: e (residuals), h* (hat diagonals), si* (deleted standard deviation), sta.res (standardized residuals), stu.res* (Studentized deleted resididuals), dffit (difference in fits, change in predicted y when observation i is deleted), dffits* (standardized difference in fits, standardized change in predicted y when observation i is deleted), cook* (Cook's distance), and DFBETAs* (standardized difference in regression coefficients when observation i is deleted, one for each column of the x-matrix, including the intercept).

plot.case returns a c("trellis.case", "trellis") object containing the plot (including the starred columns by default) and also retains the row.names of the flagged observations in the $panel.args.common$case.large component. The print method for the c("trellis.case", "trellis") object prints the graph and the list of flagged observations.

panel.case is a panel function for plot.case.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

lm.influence.

Examples

```
data(kidney)

kidney2.lm <- lm(clearance ~ concent + age + weight + concent*age,
                 data=kidney,
                 na.action=na.exclude)  ## recommended

kidney2.case <- case(kidney2.lm)

## this picture looks much better in portrait, specification is device dependent

plot(kidney2.case, kidney2.lm, par.strip.text=list(cex=.9),
     layout=c(2,3))
```

---

lm.regsubsets *Evaluate lm model with highest adjusted R^2.*

Description

The regsubsets function in the leaps package finds the model with the highest adjusted R^2. This function evaluates the full lm object for that model.

Usage

```
lm.regsubsets(object, model.number, ...)
```

Arguments

object	An object of class "regsubsets".
model.number	Index number generated by Rcmdr.
...	Other arguments.

Value

"lm" object for the selected model.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

lm, regsubsets

lmatPairwise *lmatPairwise*

Description

lmatPairwise

Usage

```
lmatPairwise(x, ...)
## S3 method for class 'matrix'
lmatPairwise(x, levels, ...)
## S3 method for class 'glht'
lmatPairwise(x, ...)
## S3 method for class 'mmc.multicomp'
lmatPairwise(x, ...)
## S3 method for class 'mmc'
lmatPairwise(x, ...)
```

Arguments

x	x
...	...
levels	levels

Details

details

Value

matrix

Author(s)

rmh

See Also

mmc, mcp

Examples

```
data(catalystm)
catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)
catalystm.mmc <- mmc(catalystm1.aov)
lmatPairwise(catalystm.mmc)
```

lmatRows *Find the row numbers in the lmat corresponding to the focus factor.*

Description

lmatRows finds the row numbers in the lmat (column numbers in the linfct in R) corresponding to the focus factor. See mmc for more information. These are internal functions that the user doesn't see. They are necessary when the design has more than one factor. lmatContrast converts user-specified contrasts of levels of a factor to the full lmat or linfct matrix that carries the information about other factors and their interactions and covariates.

Usage

```
lmatRows(x, focus)
## S3 method for class 'mmc.multicomp'
lmatRows(x, focus)
## S3 method for class 'multicomp'
lmatRows(x, focus)
## S3 method for class 'glht'
lmatRows(x, focus) ## R only
## S3 method for class 'lm'
lmatRows(x, focus)
lmatContrast(lmat.none, contrast.matrix)
```

Arguments

x	"lm" or "mmc.multicomp" or "multicomp" or "glht" object.
focus	The name of the term in the ANOVA table for which multiple comparisons are to be constructed.
lmat.none	lmat matrix with the S-Plus multicomp package or t(linfct) matrix with the R multcomp package. In both packages the matrix is the one used for estimating the group means.
contrast.matrix	Matrix of column contrasts for a factor. The columns are the contrasts, the rows are the levels of the factor.

Details

The MMC function are based on glht in R and on multicomp in S-Plus. The two packages have different conventions for specifying the linear contrasts. The lmatRows function gives appropriate values in each system.

Value

For lmatRows, vector of row numbers of the lmat, the matrix of linear contrasts defining the comparisons of interest. For lmatContrast, a linear contrast matrix that follows the conventions of the multiple comparisons package. It has columns for each contrast specified by the input contrast.matrix and rows as needed for the other terms in the model.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

mmc, glht.

Examples

```
## catalystm example
## See ?MMC for more on this example
data(catalystm)
catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)

catalystm.mmc <-
  if.R(r=mmc(catalystm1.aov, linfct = mcp(catalyst = "Tukey")),
       s=multicomp.mmc(catalystm1.aov, plot=FALSE))
dimnames(catalystm.mmc$mca$lmat)[[1]]
lmatRows(catalystm1.aov, focus="catalyst")

## user-specified contrasts
catalystm.lmat <- cbind("AB-D" =c( 1, 1, 0,-2),
                        "A-B"  =c( 1,-1, 0, 0),
                        "ABD-C"=c( 1, 1,-3, 1))
dimnames(catalystm.lmat)[[1]] <- levels(catalystm$catalyst)
zapsmall(lmatContrast(catalystm.mmc$none$lmat, catalystm.lmat))
```

---

lmplot *Four types of residual plots for linear models.*

Description

Four types of residual plots for linear models. The first three are redesigns of plots that `stats:::plot.lm` presents. The first two show the positive residuals in `col[2]` and the negative residuals in color `col[1]`. The third and fourth use color `col[1]`. The fourth is based on an S-Plus panel that R\ doesn't provide.

Usage

```
lmplot(lm.object, ..., main=NULL,
       col=trellis.par.get("superpose.symbol")$col[1:2],
       ylim=NULL)
```

Arguments

`lm.object`	Linear model object. See `lm` for details.
`col`	Vector of color names. Only the first two are used. If not specified, then `trellis.par.get("superpose.symbol")$col[1:2]` is used.

main	standard main title for plots.
ylim	standard **lattice** argument. It is used as specified for the residVSfitted, diagQQ, and diagplot5new plots. For the scaleLocation plot, the ylim is modified to c(0, max(abs(ylim))). The main reason for using the ylim argument is to allow visual comparison of the residuals for two different models on the same scale.
...	Other arguments, currently ignored.

Details

The trellis plots from the four functions residVSfitted, scaleLocation, diagQQ, diagplot5new are displayed on the current device in a coordinated display.

Value

A list of three trellis objects is returned invisibly, the first contains the result of residVSfitted and scaleLocation together. The second diagQQ, and the third diagplot5new.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

residVSfitted, scaleLocation, diagQQ, diagplot5new.

Examples

```
tmp <- data.frame(y=rnorm(100), x1=rnorm(100), x2=rnorm(100))
tmp.lm <- lm(y ~ x1 + x2, data=tmp)
lmplot(tmp.lm)
```

---

logit *Logistic and odds functions and their inverses.*

Description

Logistic and odds functions and their inverses.

Usage

```
logit(p)
antilogit(x)

odds(p)
antiodds(o)
```

Arguments

p	Probability value, a vector of numbers between 0 and 1, inclusive.
x	Real number, a vector of numbers between -Inf and Inf.
o	Real number, a vector of numbers between 0 and Inf.

Value

Vector of real values log(p/(1-p)) for logit. Vector of probabilities exp(x)/(1+exp(x)) for antilogit with boundary values of -Inf and Inf for x correctly handled. Vector of real values p/(1-p) for odds. Vector of probabilities o/(o+1) for antiodds with the boundary value of Inf for o correctly handled.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
logit(seq(0, 1, .1))
antilogit(logit(seq(0, 1, .1)))

odds(seq(0, 1, .1))
antiodds(odds(seq(0, 1, .1)))
```

---

matrix.trellis *Convert a one-dimensional trellis object to a two-dimensional trellis object. This permits combineLimits and useOuterStrips to work.*

Description

matrix.trellis

Usage

```
matrix.trellis(x = NA, nrow = 1, ncol = 1, byrow = FALSE, dimnames = NULL)

## S3 method for class 'trellis'
as.matrix(x, ..., row = FALSE, yname)
```

Arguments

x	x
nrow, ncol, byrow, dimnames	See matrix.
row	Logical. The default is FALSE to match the behavior of the generic as.matrix. I think TRUE usually looks better.
yname	Character. Provides the name of the generated conditioning factor.
...	Other arguments are ignored.

Details

`matrix.trellis` lets the user specify `nrow` and `ncol`. `as.matrix.trellis` produces either be a single column (by default) or a single row.

Value

`trellis` object with `length(dim(x)) == 2` and specified nrow and ncol.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
tmp <- data.frame(a=1:3,
                  b=c(4,5,7),
                  c=5:7,
                  d=c(8, 9, 12),
                  e=9:11)
tmp
a1 <- xyplot(a + b ~ c + d + e, data=tmp, outer=TRUE,
             main="a1")
a1
dim(a1)
a2 <- xyplot(a + b ~ c + d + e, data=tmp, outer=TRUE,
             scales=list(relation="free"), main="a2")
a2
dim(a2)
try(combineLimits(a2))
combineLimits.trellisvector(a2)
combineLimits.trellisvector(update(a2, layout=c(3,2)))

a21 <- matrix.trellis(a2, ncol=3, nrow=2, byrow=TRUE)
a21 <- update(a21, main="a21")
a21
dim(a21)
a21$x.scales$at
combineLimits(a21)

a22 <- update(a21, main="a22")
a22$x.scales$at <- list(FALSE, FALSE, FALSE, NULL, NULL, NULL)
a22$y.scales$at <- list(FALSE, NULL, NULL, FALSE, NULL, NULL)
a22

a23 <- useOuterStrips(combineLimits(a21))
a23 <- update(a23, main="a23")
a23
a23$condlevels
a23$condlevels <- list(letters[3:5], letters[1:2])
a23

a24 <- resizePanels(update(a23, main="a24"), h=c(3,4), w=c(3,5,3))
```

```
a24

a25 <- update(a23, xlab=letters[3:5], ylab.right=letters[1:2],
              xlab.top="column variables",
              ylab="row variables",
              scales=list(x=list(alternating=1), y=list(alternating=2)),
         main="a25: what I want\nxyplot(a + b ~ c + d + e, data=tmp, outer=TRUE)\nto produce.")
a25

as.matrix(a1)
as.matrix(a1, yname="abcd")
as.matrix(a1, yname="abcd", row=TRUE)
```

`mcalinfct` *MCA multiple comparisons analysis (pairwise)*

Description

MCA multiple comparisons analysis (pairwise). We calculate the contrast matrix for all pairwise comparisons, taking account of covariates and interactions.

Usage

```
mcalinfct(model, focus,
          mmm.data=model$model,
          formula.in=terms(model),
          linfct.Means=

          multcomp.meanslinfct(model, focus, mmm.data, formula.in,
                               contrasts.arg=model$contrasts),
          type="Tukey"
          )
```

Arguments

`model`	aov object
`focus`	name of one of the factors in the model, as a character object.
`mmm.data`	`data.frame` from which the model was estimated. Normally, the default is the correct value.
`formula.in`	`formula` of the model which was estimated. Normally, the default is the correct value. The use of the `terms` function honors the `keep.order=TRUE` if it was specified.
`linfct.Means`	Contrast matrix for the adjusted means of each level of the focus factor. Normally, the default is the correct value.
`type`	Name of the multiple comparison procedure to be used. See `contrMat`.

Value

Matrix to be used as a value for the `linfct` argument to `glht`.

Note

This function provides results similar to the `mcp(focusname="Tukey")` argument to `glht`. I think it provides better values for covariate and interaction terms.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`MMC`

Examples

```
## See the examples in HH/scripts/MMC.cc176.R
```

`mmc` *MMC (Mean–mean Multiple Comparisons) plots.*

Description

Constructs a `"mmc.multicomp"` object from the formula and other arguments. The constructed object must be explicitly plotted with the `mmcplot` function.

Usage

```
mmc(model, ...)  ## R

## S3 method for class 'glht'
mmc(model, ...)


## Default S3 method:
mmc(model,       ## lm object
    linfct=NULL,
    focus=
    if (is.null(linfct))
    {
      if (length(model$contrasts)==1) names(model$contrasts)
      else stop("focus or linfct must be specified.")
    }
    else
    {
```

```
      if (is.null(names(linfct)))
        stop("focus must be specified.")
      else names(linfct)
    },
    focus.lmat,
    ylabel=deparse(terms(model)[[2]]),
    lmat=if (missing(focus.lmat)) {
      t(linfct)
    } else {
      lmatContrast(t(none.glht$linfct), focus.lmat)
      },
    lmat.rows=lmatRows(model, focus),
    lmat.scale.abs2=TRUE,
    estimate.sign=1,
    order.contrasts=TRUE,
    level=.95,
    calpha=NULL,
    alternative = c("two.sided", "less", "greater"),
    ...
    )

multicomp.mmc(x,  ## S-Plus
              focus=dimnames(attr(x$terms,"factors"))[[2]][1],
              comparisons="mca",
              lmat,
              lmat.rows=lmatRows(x, focus),
              lmat.scale.abs2=TRUE,
              ry,
              plot=TRUE,
              crit.point,
              iso.name=TRUE,
              estimate.sign=1,
              x.offset=0,
              order.contrasts=TRUE,
              main,
              main2,
              focus.lmat,
              ...)

## S3 method for class 'mmc.multicomp'
x[..., drop = TRUE]
```

Arguments

model	"aov" object in "lm" method.
ylabel	name of the response variable.
lmat	contrast matrix as in the S-Plus multicomp. The convention for lmat in R is to use the transpose of the linfct component produced by glht. Required for

user-specified contrasts.

`lmat.rows` rows in `lmat` for the `focus` factor.

`focus` define the factor to compute contrasts of. In R this argument often can be used to simplify the call. The statement `mmc(my.aov, focus="factorA")` is interpreted as `mmc(my.aov, factorA="Tukey", `interaction_average`=TRUE, `covariate_average`=T` With `TRUE, TRUE`, `multcomp::glht` always gives the same result as the S-Plus `multcomp` function. Without the `TRUE, TRUE`, `multcomp::glht` gives a different answer when there are interactions or covariates in the model. See `glht`.

`focus.lmat` R only. Contrast matrix used in the user-specified comparisons of the `focus` factor. This is the matrix the user constructs. Row names must include all levels of the factor. Column names are the names the user assigns to the contrasts. Each column must sum to zero. See `catalystm.lmat` in the Examples section for an example. The `focus.lmat` matrix is multiplied by the `lmat` from the `none` component to create the `lmat` for the user-specified contrasts. Display the `hibrido.lmat` and `maiz2.lmat` in the maiz example below to see what is happening.

`linfct` In R, see `glht`.

`...` other arguments. `alternative` and `base` are frequently used with `glht`.

`comparisons` argument to `multicomp`

`lmat.scale.abs2`
logical, scale the contrasts in the columns of `lmat` to make the sum of the absolute values of each column equal 2.

`estimate.sign` numeric. If `0`, leave contrasts in the default lexicographic direction. If positive, force all contrasts to positive, reversing their names if needed (if contrast A-B is negative, reverse it to B-A). If negative, the force all contrasts to positive.

`order.contrasts`
sort the contrasts in the (`mca`, `none`, `lmat`) components by height on the MMC plot. This will place the contrasts in the multicomp plots in the same order as in the MMC plot.

`alternative` Direction of alternative hypothesis. See `glht` in R. S-Plus `multicomp` uses the argument `bounds` for this concept.

`level` Confidence level. Defaults to 0.95.

`crit.point, calpha`
critical value for the tests. The value from the specified `multicomp` method is used for the user-specified contrasts when `lmat` is specified. This argument is called `crit.point` with `multicomp` in S-Plus and `calpha` when used with `glht` and `confint` in R. In R, with a large number of levels for the focus factor, `calpha` should be specified. See notes below for discussion of the timing issues and the examples for an illustration how to use `calpha`.

`plot` logical, display the plot if `TRUE`.

`ry, iso.name, x.offset, main, main2`
arguments to `plot.mmc.multicomp`.

`x, drop` See `"["`.

Details

By default, if lmat is not specified, we plot the isomeans grid and the pairwise comparisons for the focus factor. By default, we plot the specified contrasts if the lmat is specified. Each contrast is plotted at a height which is the weighted average of the means being compared. The weights are scaled to the sum of their absolute values equals 2.

We get the right contrasts automatically if the aov is oneway. If we specify an lmat for oneway it must have a leading row of 0.

For any more complex design, we must study the lmat from the mca component of the result to see how to construct the lmat (with the extra rows as needed) and how to specify the lmat.rows corresponding to the rows for the focus factor.

mmc in R works from either an "glht" object or an "aov" object. multicomp.mmc in S-Plus works from an "aov" object.

Value

An "mmc.multicomp" object contains either the first two or all three of the "multicomp" components mca, none, lmat described here. Each "multicomp" component in R also contains a "glht" object.

mca	Object containing the pairwise comparisons.
none	Object comparing each mean to 0.
lmat	Object for the contrasts specified in the lmat argument.

"[.mmc.multicomp" is a subscript method.

Note

The multiple comparisons calculations in R and S-Plus use completely different functions. MMC plots in R are constructed by mmc based on glht. MMC plots in S-Plus are constructed by multicomp.mmc based on the S-Plus multicomp. The MMC plot is the same in both systems. The details of getting the plot differ.

Function mmc calls glht and confint.glht. With a large number of levels for the focus factor, the confint function is exceedingly slow (80 minutes for 30 levels on 1.5GHz Windows XP). Therefore, always specify calpha to reduce the time to under a second for the same example.

There are two plotting functions for MMC plots. mmcplot, the newer **lattice**-based function, is recommended. mmcplot, chooses better default values for it arguments and is better coordinated with the tiebreaker plot.

The older plot.mmc.multicomp, built on **base** graphics, chooses sensible defaults for its many arguments, but they still often need manual adjustment. The examples show several types of adjustments. We have changed the centering and scaling to avoid overprinting of label information. By default the significant contrasts are shown in a more intense color than the nonsignificant contrasts. We have an option to reduce the color intensity of the isomeans grid.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

Hsu, J. and Peruggia, M. (1994). "Graphical representations of Tukey's multiple comparison method." *Journal of Computational and Graphical Statistics*, 3:143–161.

See Also

mmcplot, plot.mmc.multicomp, as.multicomp

Examples

```
## Use mmc with R.
## Use multicomp.mmc with S-Plus.

## data and ANOVA
## catalystm example
data(catalystm)

bwplot(concent ~ catalyst, data=catalystm,
       scales=list(cex=1.5),
       ylab=list("concentration", cex=1.5),
       xlab=list("catalyst",cex=1.5))


catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)
summary(catalystm1.aov)

catalystm.mca <-
glht(catalystm1.aov, linfct = mcp(catalyst = "Tukey"))
confint(catalystm.mca)
plot(catalystm.mca)                       ## multcomp plot
mmcplot(catalystm.mca, focus="catalyst") ## HH plot

## pairwise comparisons
catalystm.mmc <-
  mmc(catalystm1.aov, focus="catalyst")
catalystm.mmc

## Not run:
## these three statements are identical for a one-way aov
  mmc(catalystm1.aov)  ## simplest
  mmc(catalystm1.aov, focus="catalyst") ## generalizes to higher-order designs
  mmc(catalystm1.aov, linfct = mcp(catalyst = "Tukey")) ## glht arguments

## End(Not run)

mmcplot(catalystm.mmc, style="both")
```

```
## User-Specified Contrasts
## Row names must include all levels of the factor.
## Column names are the names the user assigns to the contrasts.
## Each column must sum to zero.
catalystm.lmat <- cbind("AB-D" =c( 1, 1, 0,-2),
                        "A-B"  =c( 1,-1, 0, 0),
                        "ABD-C"=c( 1, 1,-3, 1))
dimnames(catalystm.lmat)[[1]] <- levels(catalystm$catalyst)
catalystm.lmat

catalystm.mmc <-
mmc(catalystm1.aov,
       linfct = mcp(catalyst = "Tukey"),
       focus.lmat=catalystm.lmat)
catalystm.mmc

mmcplot(catalystm.mmc, style="both", type="lmat")


## Not run:
## Dunnett's test
## weightloss example
data(weightloss)
bwplot(loss ~ group, data=weightloss,
       scales=list(cex=1.5),
       ylab=list("Weight Loss", cex=1.5),
       xlab=list("group",cex=1.5))

weightloss.aov <- aov(loss ~ group, data=weightloss)
summary(weightloss.aov)

group.count <- table(weightloss$group)

tmp.dunnett <-
  glht(weightloss.aov,
       linfct=mcp(group=contrMat(group.count, base=4)),
       alternative="greater")
mmcplot(tmp.dunnett, main="contrasts in alphabetical order", focus="group")

tmp.dunnett.mmc <-
  mmc(weightloss.aov,
      linfct=mcp(group=contrMat(group.count, base=4)),
      alternative="greater")
mmcplot(tmp.dunnett.mmc,
     main="contrasts ordered by average value of the means\nof the two levels in the contrasts")

tmp.dunnett.mmc

## End(Not run)

## Not run:
```

```
## two-way ANOVA
## display example

data(display)

interaction2wt(time ~ emergenc * panel.ordered, data=display)

displayf.aov <- aov(time ~ emergenc * panel, data=display)
anova(displayf.aov)

## multiple comparisons
## MMC plot
displayf.mmc <- mmc(displayf.aov, focus="panel")
displayf.mmc

## same thing using glht argument list
displayf.mmc <-
  mmc(displayf.aov,
      linfct=mcp(panel="Tukey", `interaction_average`=TRUE, `covariate_average`=TRUE))

mmcplot(displayf.mmc)


panel.lmat <- cbind("3-12"=c(-1,-1,2),
                    "1-2"=c( 1,-1,0))
dimnames(panel.lmat)[[1]] <- levels(display$panel)
panel.lmat

displayf.mmc <-
  mmc(displayf.aov, focus="panel", focus.lmat=panel.lmat)

## same thing using glht argument list
displayf.mmc <-
  mmc(displayf.aov,
      linfct=mcp(panel="Tukey", `interaction_average`=TRUE, `covariate_average`=TRUE),
      focus.lmat=panel.lmat)

mmcplot(displayf.mmc, type="lmat")

## End(Not run)

## Not run:
## split plot design with tiebreaker plot
##
## This example is based on the query by Tomas Goicoa to R-news
## http://article.gmane.org/gmane.comp.lang.r.general/76275/match=goicoa
## It is a split plot similar to the one in HH Section 14.2 based on
## Yates 1937 example.  I am using the Goicoa example here because its
## MMC plot requires a tiebreaker plot.


data(maiz)
```

```
interaction2wt(yield ~ hibrido+nitrogeno+bloque, data=maiz,
               par.strip.text=list(cex=.7))
interaction2wt(yield ~ hibrido+nitrogeno, data=maiz)

maiz.aov <- aov(yield ~ nitrogeno*hibrido + Error(bloque/nitrogeno), data=maiz)

summary(maiz.aov)
summary(maiz.aov,
        split=list(hibrido=list(P3732=1, Mol17=2, A632=3, LH74=4)))

try(glht(maiz.aov, linfct=mcp(hibrido="Tukey")))  ## can't use 'aovlist' objects in glht

## R glht() requires aov, not aovlist
maiz2.aov <- aov(terms(yield ~ bloque*nitrogeno + hibrido/nitrogeno,
                       keep.order=TRUE),
                 data=maiz)
summary(maiz2.aov)

## There are many ties in the group means.
## These are easily seen in the MMC plot, where the two clusters
## c("P3747", "P3732", "LH74") and c("Mol17", "A632")
## are evident from the top three contrasts including zero and the
## bottom contrast including zero.  The significant contrasts are the
## ones comparing hybrids in the top group of three to ones in the
## bottom group of two.

## We have two graphical responses to the ties.
## 1. We constructed the tiebreaker plot.
## 2. We construct a set of orthogonal contrasts to illustrate
##    the clusters.

## pairwise contrasts with tiebreakers.
maiz2.mmc <- mmc(maiz2.aov,
                 linfct=mcp(hibrido="Tukey", interaction_average=TRUE))
mmcplot(maiz2.mmc, style="both")  ## MMC and Tiebreaker


## orthogonal contrasts
## user-specified contrasts
hibrido.lmat <- cbind("PPL-MA" =c(2, 2,-3,-3, 2),
                      "PP-L"   =c(1, 1, 0, 0,-2),
                      "P47-P32"=c(1,-1, 0, 0, 0),
                      "M-A"    =c(0, 0, 1,-1, 0))
dimnames(hibrido.lmat)[[1]] <- levels(maiz$hibrido)
hibrido.lmat

maiz2.mmc <-
  mmc(maiz2.aov, focus="hibrido", focus.lmat=hibrido.lmat)
maiz2.mmc

## same thing using glht argument list
maiz2.mmc <-
  mmc(maiz2.aov, linfct=mcp(hibrido="Tukey",
```

```
      `interaction_average`=TRUE), focus.lmat=hibrido.lmat)

  mmcplot(maiz2.mmc, style="both", type="lmat")

## End(Not run)
```

---

mmc.mean *MMC (Mean–mean Multiple Comparisons) plots from the sufficient statistics for a one-way design.*

Description

Constructs a "mmc.multicomp" object from the sufficient statistics for a one-way design. The object must be explicitly plotted. This is the S-Plus version. See ?aovSufficient for R

Usage

```
multicomp.mean(group, n, ybar, s, alpha=.05,  ## S-Plus
               ylabel="ylabel", focus.name="focus.factor", plot=FALSE,
               lmat, labels=NULL, ...,
               df=sum(n) - length(n),
               sigmahat=(sum((n-1)*s^2) / df)^.5)

multicomp.mmc.mean(group, n, ybar, s, ylabel, focus.name,  ## S-Plus
                   lmat,
                   ...,
                   comparisons="mca",
                   lmat.rows=seq(length=length(ybar)),
                   ry,
                   plot=TRUE,
                   crit.point,
                   iso.name=TRUE,
                   estimate.sign=1,
                   x.offset=0,
                   order.contrasts=TRUE,
                   method="tukey",
                   df=sum(n)-length(n),
                   sigmahat=(sum((n-1)*s^2)/df)^.5)
```

Arguments

group	character vector of levels
n	numeric vector of sample sizes
ybar	vector of group means
s	vector of group standard deviations

alpha	Significance levels of test
ylabel	name of response variable
focus.name	name of factor
plot	logical. Should the "mmc.multicomp" object be automatically plotted? ignored in R.
lmat	lmat from multicomp in S-Plus or t(linfct) from glht in R.
labels	labels argument for multicomp in S-Plus. Not used in R.
method	method for critical point calculation. This corresponds to method in S-Plus multicomp and to type in R glht
df	scalar, residual degrees of freedom
sigmahat	sqrt(MSE) from the ANOVA table
...	other arguments
comparisons	argument to S-Plus multicomp only.
estimate.sign, order.contrasts, lmat.rows	See lmat.rows in mmc.
ry	See argument ry.mmc in plot.mmc.multicomp.
crit.point	See argument crit.point in S-Plus multicomp. The equivalent is not in glht.
iso.name, x.offset	See plot.mmc.multicomp.

Value

multicomp.mmc.mean returns a "mmc.multicomp" object.

multicomp.mean returns a "multicomp" object.

Note

The multiple comparisons calculations in R and S-Plus use completely different functions. MMC plots in R are constructed by mmc based on glht. MMC plots in S-Plus are constructed by multicomp.mmc based on the S-Plus multicomp. The MMC plot is the same in both systems. The details of getting the plot differ.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

Hsu, J. and Peruggia, M. (1994). "Graphical representations of Tukey's multiple comparison method." *Journal of Computational and Graphical Statistics*, 3:143–161.

See Also

mmc

Examples

```
## This example is from Hsu and Peruggia

## This is the S-Plus version
## See ?aovSufficient for R

if.R(r={},
s={

data(pulmonary)
pulmonary.aov <- aovSufficient(FVC ~ smoker,
                               data=pulmonary)
summary(pulmonary.aov)


## multicomp object
pulmonary.mca <-
multicomp.mean(pulmonary$smoker,
               pulmonary$n,
               pulmonary$FVC,
               pulmonary$s,
               ylabel="pulmonary",
               focus="smoker")


pulmonary.mca
## lexicographic ordering of contrasts, some positive and some negative
plot(pulmonary.mca)



pulm.lmat <- cbind("npnl-mh"=c( 1, 1, 1, 1,-2,-2), ## not.much vs lots
                   "n-pnl"  =c( 3,-1,-1,-1, 0, 0), ## none vs light
                   "p-nl"   =c( 0, 2,-1,-1, 0, 0), ## {} arbitrary 2 df
                   "n-l"    =c( 0, 0, 1,-1, 0, 0), ## {} for 3 types of light
                   "m-h"    =c( 0, 0, 0, 0, 1,-1)) ## moderate vs heavy
dimnames(pulm.lmat)[[1]] <- row.names(pulmonary)
pulm.lmat


## mmc.multicomp object
pulmonary.mmc <-
multicomp.mmc.mean(pulmonary$smoker,
                   pulmonary$n,
                   pulmonary$FVC,
                   pulmonary$s,
                   ylabel="pulmonary",
                   focus="smoker",
```

```
                    lmat=pulm.lmat,
                    plot=FALSE)


old.omd <- par(omd=c(0,.95, 0,1))

## pairwise comparisons
plot(pulmonary.mmc, print.mca=TRUE, print.lmat=FALSE)

## tiebreaker plot, with contrasts ordered to match MMC plot,
## with all contrasts forced positive and with names also reversed,
## and with matched x-scale.
plotMatchMMC(pulmonary.mmc$mca)

## orthogonal contrasts
plot(pulmonary.mmc)

## pairwise and orthogonal contrasts on the same plot
plot(pulmonary.mmc, print.mca=TRUE, print.lmat=TRUE)

par(old.omd)
})
```

`mmcAspect` *Control aspect ratio in MMC plots to maintain isomeans grid as a square.*

Description

Control aspect ratio in MMC plots to maintain isomeans grid as a square.

Usage

```
mmcAspect(trellis)
```

Arguments

`trellis`	A `trellis` object. If there is more than one panel, the first panel will be used.

Value

New numeric aspect ratio that will force the isomeans grid to be a square rotated to have vertical and horizontal diagonals.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`mmcplot`

`mmcisomeans` *Functions used by mmcplot.*

Description

Functions used by mmcplot.

Usage

```
mmcisomeans(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1),
            type = "mca", xlim = NULL, ylim = NULL, ...,
            axis.right=2.2,
            ylab=paste(
              mmc$none$ylabel, "means",
              " | ",
              mmc$none$focus, "level"),
            ylab.right=NULL,
            xlab="contrast value",
            contrast.label=TRUE,
            means.height=TRUE)

mmcmatch(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1),
         type = "mca", xlim = NULL, ylim = NULL, ...,
         axis.right=2.2,
         ylab=NULL,
         ylab.right=NULL,
         xlab="contrast value",
         contrast.label=TRUE,
         xlim.match=(type != "none"))

mmcboth(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1),
        type = "mca", h = c(0.7, 0.3), xlim = NULL, ylim = NULL, ...,
        ylab.right=NULL, MMCname="MMC", Tiebreakername="Tiebreaker")
```

Arguments

`mmc`	mmc object or other object as indicated by method.
`type`	One of `c("mca", "lmat", "linfct", "none")`. For the default `"mca"`, an MMC plot is drawn of the pairwise contrasts. For `"lmat"` or `"linfct"`, an MMC plot is drawn of the contrasts specified to `mmc` in the `lmat` or `linfct` argument. For `"none"`, a confidence interval plot for the group means is drawn.
`h`	h argument for `resizePanels`.
`xlim, ylim, xlab, ylab, ylab.right`	Standard `xyplot` arguments.
`col, lwd, lty`	Standard `xyplot` arguments applied to the line segments representing the contrasts.

...	Other arguments, to be forwarded to methods.
axis.right	Value used internally for par.settings=list(layout.widths=list(axis.right=axis.right)). The user may need to set this in two circumstances. First, if the contrast names overflow the right edge of the plotting window, then use a larger value than the default. Second, if there is a ylab.right and it is too far away from the figure, then use a smaller value than the default.
contrast.label	Logical. The default TRUE means place the word contrasts at the bottom of the right axis under the tick labels. FALSE means don't place anything there.
MMCname, Tiebreakername	Panel names when mmcplot is used with style="both".
xlim.match	Logical. If TRUE, use xlim based on the contrasts in the mca component. If FALSE, use xlim based on the values of the estimates in the current component.
means.height	Logical, with default value TRUE. When TRUE, then display the values of the group means as the left axis tick labels.

Value

A "trellis" object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

See mmc for the references.

See Also

mmc for the discussion of the MMC. mmcplot for the user calls that get executed by the functions documented here.

Examples

```
## Not run:
  ## these examples exercise all optional arguments
data(catalystm)
catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)

catalystm.glht <-
   glht(catalystm1.aov, linfct = mcp(catalyst = "Tukey"))
confint(catalystm.glht)

plot(catalystm.glht)  ## this is the multcomp:::plot.glht

mmcplot(catalystm.glht)  ## mmcplot.glht sends its argument to HH:::as.multicomp.glht with
## the default arguments (estimate.sign = 1, order.contrasts = TRUE) unless overridden:
##
```

```
mmcplot(catalystm.glht, order.contrasts=FALSE, estimate.sign=0, main="B'")

catalystm.lmat <- cbind("AB-D" =c(1, 1, 0,-2),
                        "A-B"  =c(1,-1, 0, 0),
                        "ABD-C"=c(1, 1,-3, 1))
dimnames(catalystm.lmat)[[1]] <- levels(catalystm$catalyst)
catalystm.mmc <-
   mmc(catalystm1.aov,
       linfct = mcp(catalyst = "Tukey"),
       focus.lmat=catalystm.lmat)

mmcplot(catalystm.mmc, type="mca",  style="confint")
mmcplot(catalystm.mmc, type="lmat", style="confint")
mmcplot(catalystm.mmc, type="none", style="confint")
mmcplot(catalystm.mmc, type="none", style="confint", xlim.match=FALSE,
        main="xlim.match=FALSE is default for none confint")
mmcplot(catalystm.mmc, type="none", style="confint", xlim.match=TRUE, main="out of bounds")

mmcplot(catalystm.mmc$mca,  style="confint")
mmcplot(catalystm.mmc$lmat, style="confint")
mmcplot(catalystm.mmc$none, style="confint")

plot(catalystm.mmc) ## HH:::plot.mmc.multicomp method

mmcplot(catalystm.mmc)

mmcplot(catalystm.mmc)
mmcplot(catalystm.mmc, style="isomeans")
mmcplot(catalystm.mmc, style="confint")
mmcplot(catalystm.mmc, style="both")

mmcplot(catalystm.mmc, style="isomeans", type="mca")
mmcplot(catalystm.mmc, style="isomeans", type="lmat")
mmcplot(catalystm.mmc, style="isomeans", type="linfct")
mmcplot(catalystm.mmc, style="isomeans", type="none")
mmcplot(catalystm.mmc, style="isomeans", type="none", xlim.match=FALSE)

mmcplot(catalystm.mmc, style="confint",  type="mca")
mmcplot(catalystm.mmc, style="confint",  type="lmat")
mmcplot(catalystm.mmc, style="confint",  type="linfct")
mmcplot(catalystm.mmc, style="confint",  type="none")
mmcplot(catalystm.mmc, style="confint",  type="none", xlim.match=FALSE)

mmcplot(catalystm.mmc, style="both",     type="mca")
mmcplot(catalystm.mmc, style="both",     type="lmat")
mmcplot(catalystm.mmc, style="both",     type="linfct")
mmcplot(catalystm.mmc, style="both",     type="none")
mmcplot(catalystm.mmc, style="both",     type="none", xlim.match=FALSE)

mmcplot(catalystm.mmc$mca)
mmcplot(catalystm.mmc$mca$glht)
mmcplot(catalystm.mmc$none)
mmcplot(catalystm.mmc$none$glht)
```

```
mmcplot(catalystm.mmc$lmat)
mmcplot(catalystm.mmc$lmat$glht)

mmcplot(catalystm.mmc, type="none")
mmcplot(catalystm.mmc, type="none", xlim.match=FALSE)
mmcplot(catalystm.mmc$none)

## End(Not run)
```

`mmcplot` *MMC (Mean-mean Multiple Comparisons) plots in lattice.*

Description

MMC (Mean–mean Multiple Comparisons) plots in lattice

Usage

```
mmcplot(mmc, ...)
## S3 method for class 'mmc'
mmcplot(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1), ...,
                 style=c("isomeans", "confint", "both"),
                 type=c("mca", "lmat", "linfct", "none"))
## S3 method for class 'glht'
mmcplot(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1),
                 focus=mmc$focus, ...)
## S3 method for class 'mmc.multicomp'
mmcplot(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1), ...)
## S3 method for class 'multicomp'
mmcplot(mmc, col=c("black","red"), lwd=c(1,1), lty=c(2,1), ...)
## Default S3 method:
mmcplot(mmc, ...)
```

Arguments

`mmc`	mmc object or other object as indicated by method.
`col`, `lwd`, `lty`	Standard `xyplot` arguments applied to the line segments representing the contrasts.
`focus`	Name of the factor for which the `glht` object was constructed.
`...`	Other arguments to be passed on to the functions called by the methods.
`style`	Style of graph: The default `isomeans` is the standard MMC plot with the isomeans grid. `confint` is a confidence interval plot, similar to the plot produced by `multcomp:::plot.glht`. `both` prints both the `isomeans` and the `confint` plot as two panels of a `trellis` structure. When the underlying sets of means are close to each other, there will of necessity be overprinting in the `isomeans` panel and the `confint` panel will be needed as a tiebreaker. By default the `xlim` for the `confint` style will match the `xlim` of the corresponding `isomeans` plot.

type	mca for the default paired-comparisons plot. lmat or linfct for a user-specified set of contrasts. none for confidence intervals on the set of group means (that is, no comparisons).

Value

A trellis object containing the graphs.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

See mmc for the references.

See Also

mmc for the discussion of the MMC and for many examples. The functions mmcisomeans, mmcmatch, mmcboth are the internal functions that do the actual work of plotting.

Examples

```
data(catalystm)
catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)
catalystm.mmc <-
   mmc(catalystm1.aov, linfct = mcp(catalyst = "Tukey"))
mmcplot(catalystm.mmc)
mmcplot(catalystm.mmc, style="both", MMCname="catalyst")
```

---

mmcPruneIsomeans *MMC plots in lattice—suppress isomeans grid lines for specified levels of the factor.*

Description

MMC plots in lattice—suppress isomeans grid lines for specified levels of the factor.

Usage

```
mmcPruneIsomeans(mmc, keep=NULL)
```

Arguments

mmc	An "mmc.multicomp" object.
keep	Index vector of rows of mmc$none$table that will be kept in the display.

Value

A modified "mmc.multicomp" object.

See Also

mmc

Examples

```
## needed
## Not run:
## See file hh/scripts/hh2/tway.R for the complete example.
## A better example is needed for the .Rd documentation.
## possibly based on filmcoat temperature | pressure example.
data(rhiz.clover)
c(1,2,5,10,11,12)
rhiz.clover$cs <- with(rhiz.clover, interaction(comb, strain))
rhiz.clover.cs.aov <- aov(Npg ~ cs, data=rhiz.clover)
rhiz.clover.cs.aov
cs.mmc <- mmc(rhiz.clover.cs.aov, linfct=mcp(cs="Tukey"),
              calpha=qtukey( .95, 6,  48)/sqrt(2))
dlmat2 <- dimnames(cs.mmc$mca$lmat)[[2]]
cl.index <- grep("clover\\.[[:print:]]*clover\\.", dlmat2, value=TRUE)
cl.index
clover.lmat <- cs.mmc$mca$lmat[, cl.index] ## suppress "clover+alfalfa" contrasts
dimnames(clover.lmat)[[1]]
dimnames(clover.lmat)[[1]] <- levels(rhiz.clover$cs)
clover.lmat[1,] <- -colSums(clover.lmat[-1, ])
clover.lmat
csc.mmc <- mmc(rhiz.clover.cs.aov, linfct=mcp(cs="Tukey"),
               focus.lmat=clover.lmat,
               calpha=qtukey( .95, 6,  48)/sqrt(2))
## this example needs a window 11 inches high and 14 inches wide
mmcplot(csc.mmc, type="lmat", style="both")

## suppress "clover+alfalfa" means
csc.mmc.clover <- mmcPruneIsomeans(csc.mmc, keep = c(1,2,5,10,11,12))
csc.mmc.clover
## this example needs a window 11 inches high and 14 inches wide
mmcplot(csc.mmc.clover, type="lmat", style="both")

## End(Not run)
```

---

multicomp.order *Update a multicomp object by ordering its contrasts.*

Description

Update a multicomp object by ordering its contrasts. The default sort.by = "height" matches the order in the MMC plot. An alternate sort.by = "estimate" matches the order of the half-normal plot. Or the argument sort.order can be used to specify any other order.

Usage

```
multicomp.order(mca, sort.by = "height", sort.order = NULL)

multicomp.label.change(x, old="adj", new="new", how.many=2)

## S3 method for class 'multicomp'
multicomp.label.change(x, old="adj", new="new", how.many=2)

## S3 method for class 'mmc.multicomp'
multicomp.label.change(x, old="adj", new="new", how.many=2)
```

Arguments

mca	"multicomp" object. This is the result of multicomp in S-Plus or the result from applying as.multicomp to a "glht" object in R.
sort.by	Either "height" or "estimate".
sort.order	Vector of indices by which the contrasts are to be sorted. When sort.order in non-NULL, it is used.
x	"multicomp" object.
old	character string to be removed from contrast names.
new	replacement character string to be inserted in contrast names.
how.many	number of times to make the replacement.

Value

The result is a "multicomp" object containing the same contrasts as the argument.
multicomp.order sorts the contrasts (and renames them consistently) according to the specifications.
multicomp.label.change changes the contrast names according to the specifications.

When sort.by=="height", sort the contrasts by the reverse order of the heights. This provides a "multicomp" object that will be plotted by plot.multicomp in the same order used by mmcplot or the older plot.mmc.multicomp. If there is not "height" component, the original "multicomp" object is returned.

When sort.by=="estimate", sort the contrasts by the reverse order of the contrast estimates. This provides the same order as the half-normal plot.

When sort.order in non-NULL, sort the contrasts in that order.

Note

S-Plus use the multicomp functions and R uses the multcomp package.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

See Also

MMC, as.glht in R, multicomp.reverse

Examples

```
## continue with the example in mmc in R, or multicomp.mmc in S-Plus
data(catalystm)

catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)

if.R(r={
catalystm.mca <-
   glht(catalystm1.aov, linfct = mcp(catalyst = "Tukey"))
print(confint(catalystm.mca))

catalystm.mmc <-
   mmc(catalystm1.aov, linfct = mcp(catalyst = "Tukey"))
## the contrasts have been ordered by height (see ?MMC),
## which in this example corresponds to sort.order=c(1,2,4,3,5,6),
## and reversed, to make the contrast Estimates positive.
print(as.glht(catalystm.mmc$mca))

## ## For consistency with the S-Plus example,
## ## we change all factor level "A" to "control".
## as.glht(multicomp.label.change(catalystm.mmc$mca, "A", "control"))
},s={
catalystm.mca <-
   multicomp(catalystm1.aov, method="Tukey")
print(catalystm.mca)

catalystm.mmc <-
   multicomp.mmc(catalystm1.aov, method="Tukey", plot=FALSE)
## the contrasts have been ordered by height (see ?MMC),
## which in this example corresponds to sort.order=c(1,2,4,3,5,6),
## and reversed, to make the contrast Estimates positive.
print(catalystm.mmc$mca)

## S-Plus multicomp already uses simple names.  This function is
## therefore used in more complex two-way ANOVA examples.  We illustrate
## here by changing all factor level "A" to "control".
print(multicomp.label.change(catalystm.mmc$mca, "A", "control"))
})
```

`multicomp.reverse` *Force all comparisons in a "multicomp" object to have the same sign.*

Description

Force all comparisons in a `"multicomp"` object to have the same sign. If the contrast `"A-B"` has a negative estimate, reverse it show the contrast `"B-A"` with a positive estimate. If a contrast name does not include a minus sign `"-"` and the contrast is reversed, then an informative message is printed.

Usage

```
multicomp.reverse(y, estimate.sign = 1, ...)
```

Arguments

`y`	`"multicomp"` object
`estimate.sign`	If `estimate.sign==1`, reverse the negatives. If `estimate.sign==-1`, reverse the positives. Both the names of the comparisons and the numerical values are reversed. If `estimate.sign==0`, return the argument.
`...`	other arguments not used.

Value

The result is a `"multicomp"` object containing the same contrasts as the argument but with the sign of the contrasts changed as needed.

Note

S-Plus use the `multicomp` functions and R uses the `multcomp` package.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

See Also

`MMC`, `multicomp.order`

Examples

```
## see example in multicomp.order
```

`norm.curve` *plot a normal or a t-curve with both x and z axes.*

Description

Plot a normal curve or a t-curve with both x (with `mean` and `se` as specified) and z or t (mean=0, se=1) axes. Shade a region for rejection region, acceptance region, confidence interval. The density axis is marked in units appropriate for the z or t axis. The existence of any of the arguments `se`, `sd`, `n` forces dual `x` and (`z` or `t`) scales. When none of these arguments are used, the main title defaults to `"Standard Normal Density N(0,1)"` and only the `z` scale is printed. A second density curve, appropriate for an alternative hypothesis is displayed when the argument `axis.name="z1"` is specified. The shaded area is printed on the plot.

When the optional argument `df.t` is specified, then a t-distribution with `df.t` degrees of freedom is plotted.

`norm.observed` plots a vertical line with arrowhead markers at the location of the observed xbar.

`normal.and.t.dist` is a driver function that uses all the others. It's primary function is drawing a plot. It returns an invisible list containing the values it calculated and displayed on the graph.

`norm.curve` draws the curves and filled areas as requested by the `normal.and.t.dist` function. Any `out of bounds` errors (for example, with `normal.and.t.dist(deg.free=1)`) are suppressed with `par(err=-1)` by this function and restored to the previous value when the `norm.curve` function completes.

Usage

```
normal.and.t.dist(mu.H0          = 0,
                  mu.H1          = NA,
                  obs.mean       = 0,
                  std.dev        = 1,
                  n              = NA,
                  deg.freedom    = NA,
                  alpha.left     = alpha.right,
                  alpha.right    = .05,
                  Use.mu.H1      = FALSE,
                  Use.obs.mean   = FALSE,
                  Use.alpha.left = FALSE,
                  Use.alpha.right= TRUE,
                  hypoth.or.conf = 'Hypoth',
                  xmin           = NA,
                  xmax           = NA,
                  gxbar.min      = NA,
                  gxbar.max      = NA,
                  cex.crit       = 1.2,
```

```
                    polygon.density= -1,
                    polygon.lwd    = 4,
                    col.mean       = 'limegreen',
                    col.mean.label = 'limegreen',
                    col.alpha      = 'blue',
                    col.alpha.label= 'blue',
                    col.beta       = 'red',
                    col.beta.label = 'red',
                    col.conf       = 'palegreen',
                    col.conf.arrow = 'darkgreen',
                    col.conf.label = 'darkgreen'
                    )

  norm.setup(xlim=c(-2.5,2.5),
             ylim = c(0, 0.4)/se,
             mean=0,
             main=main.calc,
             se=sd/sqrt(n), sd=1, n=1,
             df.t=NULL,
             Use.obs.mean=TRUE,
              ...)

  norm.curve(mean=0, se=sd/sqrt(n),
            critical.values=mean + se*c(-1, 1)*z.975,
            z=if(se==0) 0 else
                do.call("seq", as.list(c((par()$usr[1:2]-mean)/se, length=109))),
            shade, col="blue",
            axis.name=ifelse(is.null(df.t) || df.t==Inf, "z", "t"),
            second.axis.label.line=3,
            sd=1, n=1,
            df.t=NULL,
            axis.name.expr=axis.name,
            Use.obs.mean=TRUE,
            col.label=col,
            hypoth.or.conf="Hypoth",
            col.conf.arrow=par("col"),
            col.conf.label=par("col"),
            col.crit=ifelse(hypoth.or.conf=="Hypoth", 'blue', col.conf.arrow),
            cex.crit=1.2,
            polygon.density=-1,
            polygon.lwd=4,
            col.border=ifelse(is.na(polygon.density), FALSE, col),
            ...)

  norm.observed(xbar, t.xbar, t.xbar.H1=NULL,
                col="green",
                p.val=NULL, p.val.x=par()$usr[2]+ left.margin,
                t.or.z=ifelse(is.null(deg.free) || deg.free==Inf, "z", "t"),
```

```
                t.or.z.position=par()$usr[1]-left.margin,
                cex.small=par()$cex*.7, col.label=col,
                xbar.negt=NULL, cex.large=par()$cex,
                left.margin=.15*diff(par()$usr[1:2]),
                sided="", deg.free=NULL)

norm.outline(dfunction, left, right, mu.H0, se, deg.free=NULL,
             col.mean="green")
```

Arguments

xlim, ylim, xmin, xmax, gxbar.min, gxbar.max	xlim, ylim. Defaults to correct values for standard Normal(0,1). User must set values for other mean and standard error.
mean	Mean of the normal distribution in xbar-scale, used in calls to dnorm.
se	standard error of the normal distribution in xbar-scale, used in calls to dnorm.
sd, std.dev, n	standard deviation and sample size of the normal distribution in x-scale. These may be used as an alternate way of specifying the standard error se.
df.t, deg.freedom	Degrees of freedom for the t distribution. When df.t is NULL, the normal distribution is used.
critical.values	Critical values in xbar-scale. A scalar value implies a one-sided test. A vector of two values implies a two-sided test.
main	Main title.
z	z-values (standardized to N(0,1)) used as base of plot.
shade	Valid values for shade are "right", "left", "inside", "outside", "none". Default is "right" for one-sided critical.values and "outside" for two-sided critical values.
col	color of the shaded region.
col.label, col.alpha, col.alpha.label	color of the area of the shaded rejection region and its label.
col.beta, col.beta.label	color of the area of the shaded region For Type II error and its label.
hypoth.or.conf	"Hypoth" or "Conf"
col.conf	Color of plot within confidence limits.
col.conf.arrow	Color of arrow denoting confidence limits.
col.conf.label	Color of label giving confidence level.
col.mean.label	Color of label for observed mean.
col.crit, cex.crit	Color and cex of critical values.
axis.name, axis.name.expr	defaults to "z" for the standard normal scale centered on the null hypothesis value of the mean or to "t" for the t distribution with df.t degrees of freedom. For alternative hypotheses, the user must specify either "z1" or "t1" for the

standard normal scale, or t distibution with `df.t` degrees of freedom, centered on the alternate hypothesis value of the mean. The `axis.name.expr` allows R users to say `expression(z[1])` to get real subscripts.

`second.axis.label.line`
: Defaults to `3`. Normally not needed. When two curves are drawn, one normal and one t, then the second curve needs a different label for the y-axis. Set this value to 4 to avoid overprinting.

`xbar`, `obs.mean` xbar-value of the observed data.

`t.xbar` t-value of the observed data under the null hypothesis.

`...` Other arguments which are ignored.

`Use.obs.mean` Logical. If `TRUE`, then include `"mean"` on the plot.

`alpha.right`, `alpha.left`
: Area in tail of curve.

`Use.alpha.right`, `Use.alpha.left`
: Logical. If `TRUE`, then include the specified α on the plot.

`t.xbar.H1` t-value under alternate hypothesis.

`p.val` under specified hypothesis

`p.val.x`, `t.or.z.position`
: location on x-axis to put label

`t.or.z` label for axis.

`cex.small` cex for left margin labels of axis.

`xbar.negt` location in data scale of negative t- or z-value corresponding to observed x-value. Used for two-sided p-values.

`cex.large` cex for labels in top margin.

`left.margin` distance to the left of `par()$usr[1]`.

`sided` type of test.

`deg.free` degrees of freedom or `NULL`.

`dfunction` `"dnorm"` or `"dt"`

`left` left end of interval

`right` right end of interval

`mu.H0`, `mu.H1` mean under the null hypothesis and alternative hypothesis.

`Use.mu.H1` Logical. If `TRUE`, then include `mu.H1` on the plot.

`col.mean` Color of outline.

`polygon.density`, `polygon.lwd`, `col.border`
: `density`, `lwd`, `border` arguments to `polygon`. `polygon.density` is -1 by default to give a solid color filled region. Setting `polygon.density` to a positive value (we recommend 10) gives a diagonally-hatched area appropriate for printing the graph on a black and white printer.

Value

An invisible list containing the calculated values of probabilities and critical values in the data scale, the null hypothesis z- or t-scale, and the alternative hypothesis z- or t-scale, as specified. The components are: `beta.left`, `beta.middle`, `beta.right`, `crit.val`, `crit.val.H1`, `crit.val.H1.left`, `crit.val.left`, `crit.val.left.z`, `crit.val.z`, `obs.mean.H0.p.val`, `obs.mean.H0.side`, `obs.mean.H0.z`, `obs.mean.H1.z`, `obs.mean.x.neg`, `obs.mean.x.pos`, `obs.mean.z.pos`, `standard`, `standard.error`, `standard.normal`

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
normal.and.t.dist()
normal.and.t.dist(xmin=-4)
normal.and.t.dist(std.dev=2)
normal.and.t.dist(std.dev=2, Use.alpha.left=TRUE, deg.free=6)
normal.and.t.dist(std.dev=2, Use.alpha.left=TRUE, deg.free=6, gxbar.max=.20)
normal.and.t.dist(std.dev=2, Use.alpha.left=TRUE, deg.free=6,
                  gxbar.max=.20, polygon.density=10)
normal.and.t.dist(std.dev=2, Use.alpha.left=FALSE, deg.free=6,
                  gxbar.max=.20, polygon.density=10,
                  mu.H1=2, Use.mu.H1=TRUE,
                  obs.mean=2.5, Use.obs.mean=TRUE, xmin=-7)
normal.and.t.dist(std.dev=2, hypoth.or.conf="Conf")
normal.and.t.dist(std.dev=2, hypoth.or.conf="Conf", deg.free=8)

old.par <- par(oma=c(4,0,2,5), mar=c(7,7,4,2)+.1)

norm.setup()
norm.curve()

norm.setup(xlim=c(75,125), mean=100, se=5)
norm.curve(100, 5, 100+5*(1.645))
norm.observed(112, (112-100)/5)
norm.outline("dnorm", 112, par()$usr[2], 100, 5)

norm.setup(xlim=c(75,125), mean=100, se=5)
norm.curve(100, 5, 100+5*(-1.645), shade="left")

norm.setup(xlim=c(75,125), mean=100, se=5)
norm.curve(mean=100, se=5, col='red')

norm.setup(xlim=c(75,125), mean=100, se=5)
norm.curve(100, 5, 100+5*c(-1.96, 1.96))

norm.setup(xlim=c(-3, 6))
norm.curve(critical.values=1.645, mean=1.645+1.281552, col='green',
           shade="left", axis.name="z1")
norm.curve(critical.values=1.645, col='red')
```

```
norm.setup(xlim=c(-6, 12), se=2)
norm.curve(critical.values=2*1.645, se=2, mean=2*(1.645+1.281552),
           col='green', shade="left", axis.name="z1")
norm.curve(critical.values=2*1.645, se=2, mean=0,
           col='red', shade="right")


par(mfrow=c(2,1))
norm.setup()
norm.curve()
mtext("norm.setup(); norm.curve()", side=1,  line=5)
norm.setup(n=1)
norm.curve(n=1)
mtext("norm.setup(n=1); norm.curve(n=1)", side=1,  line=5)
par(mfrow=c(1,1))


par(mfrow=c(2,2))

## naively scaled,
## areas under the curve are numerically the same but visually different
norm.setup(n=1)
norm.curve(n=1)
norm.observed(1.2, 1.2/(1/sqrt(1)))
norm.setup(n=2)
norm.curve(n=2)
norm.observed(1.2, 1.2/(1/sqrt(2)))
norm.setup(n=4)
norm.curve(n=4)
norm.observed(1.2, 1.2/(1/sqrt(4)))
norm.setup(n=10)
norm.curve(n=10)
norm.observed(1.2, 1.2/(1/sqrt(10)))
mtext("areas under the curve are numerically the same but visually different",
      side=3, outer=TRUE)

## scaled so all areas under the curve are numerically and visually the same
norm.setup(n=1, ylim=c(0,1.3))
norm.curve(n=1)
norm.observed(1.2, 1.2/(1/sqrt(1)))
norm.setup(n=2, ylim=c(0,1.3))
norm.curve(n=2)
norm.observed(1.2, 1.2/(1/sqrt(2)))
norm.setup(n=4, ylim=c(0,1.3))
norm.curve(n=4)
norm.observed(1.2, 1.2/(1/sqrt(4)))
norm.setup(n=10, ylim=c(0,1.3))
norm.curve(n=10)
norm.observed(1.2, 1.2/(1/sqrt(10)))
mtext("all areas under the curve are numerically and visually the same",
      side=3, outer=TRUE)
```

```
par(mfrow=c(1,1))


## t distribution
mu.H0 <- 16
se.val <- .4
df.val <- 10
crit.val <- mu.H0 - qt(.95, df.val) * se.val
mu.alt <- 15
obs.mean <- 14.8

alt.t <- (mu.alt - crit.val) / se.val
norm.setup(xlim=c(12, 19), se=se.val, df.t=df.val)
norm.curve(critical.values=crit.val, se=se.val, df.t=df.val, mean=mu.alt,
           col='green', shade="left", axis.name="t1")
norm.curve(critical.values=crit.val, se=se.val, df.t=df.val, mean=mu.H0,
           col='gray', shade="right")
norm.observed(obs.mean, (obs.mean-mu.H0)/se.val)

## normal
norm.setup(xlim=c(12, 19), se=se.val)
norm.curve(critical.values=crit.val, se=se.val, mean=mu.alt,
           col='green', shade="left", axis.name="z1")
norm.curve(critical.values=crit.val, se=se.val, mean=mu.H0,
           col='gray', shade="right")
norm.observed(obs.mean, (obs.mean-mu.H0)/se.val)



## normal and t
norm.setup(xlim=c(12, 19), se=se.val, main="t(6) and normal")
norm.curve(critical.values=15.5, se=se.val, mean=16.3,
           col='gray', shade="right")
norm.curve(critical.values=15.5, se.val, df.t=6, mean=14.7,
           col='green', shade="left", axis.name="t1", second.axis.label.line=4)
norm.curve(critical.values=15.5, se=se.val, mean=16.3,
           col='gray', shade="none")

norm.setup(xlim=c(12, 19), se=se.val, main="t(6) and normal")
norm.curve(critical.values=15.5, se=se.val, mean=15.5,
           col='gray', shade="right")
norm.curve(critical.values=15.5, se=se.val, df.t=6, mean=15.5,
           col='green', shade="left", axis.name="t1", second.axis.label.line=4)
norm.curve(critical.values=15.5, se=se.val, mean=15.5,
           col='gray', shade="none")



par(old.par)
```

NormalAndTplot *Specify plots to illustrate Normal and t Hypothesis Tests or Confidence Intervals.*

Description

Specify plots to illustrate Normal and t Hypothesis Tests or Confidence Intervals.

Usage

```
NormalAndTplot(mean0, ...)
## Default S3 method:
NormalAndTplot(mean0=0,
             mean1=NA,
             xbar=NA,
             df=Inf, n=1,
             sd=1,
            xlim=c(-3, 3)*sd/sqrt(n) + range(c(mean0, mean1, xbar), na.rm=TRUE),
             ylim, alpha.right=.05, alpha.left=0,
             float=TRUE, ntcolors="original",
             digits=4, digits.axis=digits, digits.float=digits,
             distribution.name=c("normal","z","t","binomial"),
             type=c("hypothesis", "confidence"),
             zaxis=FALSE, z1axis=FALSE,
             cex.z=.5, cex.xbar=.5, cex.y=.5, cex.prob=.6, cex.top.axis=1,
             cex.left.axis=1, cex.pb.axis=1,
             cex.xlab=1, cex.ylab=1.5, cex.strip=1,
             main=NA, xlab, ylab,
             prob.labels=(type=="hypothesis"),
             xhalf.multiplier=1,
             yhalf.multiplier=1,
             cex.main=1,
             key.axis.padding=4.5,
             number.vars=1,
             sub=NULL,
             NTmethod="default",
             power=FALSE,
             beta=FALSE,
              ...)
## S3 method for class 'htest'
NormalAndTplot(mean0, type="hypothesis", xlim=NULL, mean1=NA, ...,
             xbar, sd, df, n, alpha.left, alpha.right, ## ignored
             distribution.name, sub ## these input arguments will be ignored
             )
```

Arguments

mean0 Null hypothesis μ_0. When graphing a confidence interval, mean0 will be used for xbar should xbar itself have the value NA. For the htest method, mean0 is

an "htest" object. See NTplot for more information.

mean1 Alternative hypothesis μ_1.

xbar Observed $\bar{x}$.

sd Standard deviation in the data scale σ for normal-, or s for t-distribution.

df Degrees of freedom for t-distribution.

n Number of observations per group.

main, xlab, ylab, xlim, ylim, sub
Standard xyplot arguments. Default values are constructed if these arguments are missing. The input value main=NA forces a new constructed main instead of using the main coming in through the htest methods.

... Additional xyplot arguments.

number.vars Number of variables. 1 for a one-sample test, 2 for two-sample tests and paired tests.

alpha.left, alpha.right
For type="hypothesis", the sum of these two numbers is the probability of the Type I Error α. When both of these numbers are positive, there is a two-sided test. Note that it is not required that they be equal. If one of the numbers is 0, then it is a one-sided test. For type="confidence", 1 minus the sum of these two numbers is the confidence level.

float Logical. If TRUE, then the probabilities α, β, power, and p-values or the confidence value are displayed on the graph. If FALSE, these values are not displayed.

ntcolors Vector of colors used in the graph. The default value is "original" and two named alternatives are "stoplight" and "BW". The sets of colors associated with these three named sets are shown in a dontrun section of the examples. The user can enter any other color scheme by specifying a vector of ten named colors. The names are: col.alpha, col.notalpha, col.beta, col.power, col.pvalue, col.pvaluetranslucent, col.critical, col.border, col.text, col.conf.

digits.axis, digits.float, digits
digits.axis is the number of significant digits for the top axis. digits.float is the number of significant digits for the floating probability values on the graph. digits is a convenience argument to set both digits.axis and digits.float at the same time. These number is passed to the format function.

distribution.name
Name of distribution.

type "hypothesis" for a Hypothesis Test graph, or "confidence" for a Confidence Interval graph.

zaxis, z1axis Logical or list. Should the z-axis centered on μ_0, or the z_1-axis centered on μ_1, be displayed? The list version of the argument must have two components at and labels as specified in panel.axis.

cex.z, cex.xbar, cex.y, cex.prob, cex.top.axis, cex.left.axis, cex.pb.axis, cex.xlab, cex.ylab, cex.strip, cex.main
cex.z is the cex value for the z and z_1 axes on the plot. cex.prob is the cex value for the floating probabilities on the graph. cex.top.axis is the cex value

for the top axis values. cex.main is the cex value for the main title. cex.xbar and cex.y are the cex values for the horizontal and vertical axes of the plot. cex.left.axis and cex.pb.axis are the cex values for the power or beta (Type II error) values and the μ_1 value in the power and beta plots. cex.xlab, cex.ylab, and cex.strip are the cex values for xlab, ylab, and strip labels.

key.axis.padding
: tuning constant to create additional room above the graph for a larger cex.main to fit.

prob.labels
: logical. If TRUE label the floating probability values with their name, such as α. If FALSE, then don't label them. The default is TRUE for type="hypothesis" and FALSE for type="confidence".

xhalf.multiplier, yhalf.multiplier
: Numerical tuning constants to control the width and height of the floating probability values. Empirically, we need a smaller value for the **shiny** app then we need for direct writing onto a graphic device.

NTmethod
: Character string used when shiny=TRUE. It is normally calculated by the methods. NTmethod tells shiny how to use or ignore the df and n sliders.

  "htest" objects by default are interpreted as a single observation (n=1) of a t-statistic with df degrees of freedom. The slider will let the user change the df, but not the n.

  "power.htest" objects are interpreted as a set of n obervations per group and df is calculated as $(n-1)$ for single-sample tests and as $2(n-1)$ for two-sample tests. The slider will let the user change n and will calculate the revised df.

  For the normal approximation to the binomial (distribution.name="binomial"), only n is meaningful. The df is always ignored.

  For the default situation of t, determined by the initially specified sample size $n > 1$, the degrees of freedom is calculated as $(n-1)$ for single-sample tests and as $2(n-1)$ for two-sample tests. The default z, is initially specified by a sample size $n = 1$.

  In all cases except the "binomial", the user can change the interpretation of the n and df sliders. The interpretation when both n and df are under user control is not always obvious.

power, beta
: Logical. If TRUE, then display that graph, else don't display it. Passed forward to powerplot.

Details

The graphs produced by this single function cover most of the first semester introductory Statistics course. The htest method plots the results of the stats::t.test function.

NormalAndTplot is built on xyplot. Most of the arguments detailed in xyplot documentation work to control the appearance of the plot.

Value

"trellis" object.

Note

This function is built on **lattice** and **latticeExtra**. It supersedes the similar function `normal.and.t.dist` built on base graphics that is used in many displays in the book by Erich Neuwirth and me: *R through Excel*, Springer (2009). https://link.springer.com/book/10.1007/978-1-4419-0052-4. Many details, particularly the alternate color scheme and the concept of floating probability labels, grew out of discussions that Erich and I have had since the book was published. The method for `"htest"` objects incorporates ideas that Jay Kerns and I developed at the 2011 UseR! conference. This version incorporates some ideas suggested by Moritz Heene.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

NTplot

Examples

```
   NTplot(mean0=0, mean1=2,  xbar=1.8,  xlim=c(-3, 5))
   NTplot(mean0=0, mean1=2,  xbar=1.8,  xlim=c(-3, 5), distribution.name="t", df=4)
   NTplot(mean0=100, sd=12, mean1=113,  xbar=105,  xlim=c(92, 120), n=20)
   NTplot(mean0=100, sd=12, mean1=113,  xbar=105,  xlim=c(92, 120), n=20,
          zaxis=TRUE, z1axis=TRUE)
   NTplot(mean0=100, sd=12,  xbar=105,  xlim=c(92, 108), n=20, ntcolors="stoplight")
   NTplot(xbar=95, sd=10, xlim=c(65, 125), type="confidence",
          alpha.left=.025, alpha.right=.025)


x <- rnorm(12, mean=.78)
x.t <- t.test(x)
NTplot(x.t)
NTplot(x.t, type="confidence")
x.tg <- t.test(x, alternative="greater")
NTplot(x.tg)

y <- rnorm(12, mean=-.05)
xy.t <- t.test(x, y)
NTplot(xy.t)
NTplot(xy.t, type="confidence")

## Not run:
  if (interactive())
    NTplot(shiny=TRUE)  ## with any other arguments for initialization of the shiny app.

## End(Not run)

## Not run:
   ##  The partially transparent colors are:
   black127="#0000007F" ## HH:::ColorWithAlpha("black")
   green127="#00FF007F" ## HH:::ColorWithAlpha("green")
```

```
   blue127 ="#0000FF7F" ## HH:::ColorWithAlpha("blue")


## this is the default set of colors that are assigned when
## ntcolors="original" or when ntcolors is not specified
c(col.alpha = "blue",
  col.notalpha = "lightblue",
  col.beta = "red",
  col.power = "pink",
  col.pvalue = "green",
  col.pvaluetranslucent = green127,
  col.critical = "gray50",
  col.border = black127,
  col.text = "black",
  col.conf = "lightgreen")

  NTplot(                )
  NTplot(mean1 = 2,      )
  NTplot(           xbar=1)
  NTplot(mean1 = 2, xbar=1)
  NTplot(type="confidence")


## this is the set of colors that are assigned when ntcolors="stoplight"
c(col.alpha = "red",
  col.notalpha = "honeydew2",
  col.beta = "orange",
  col.power = "pink",
  col.pvalue = "blue",
  col.pvaluetranslucent = blue127,
  col.critical = "gray50",
  col.border = black127,
  col.text = "black",
  col.conf = "lightgreen")

  NTplot(                   ntcolors="stoplight")
  NTplot(mean1 = 2,         ntcolors="stoplight")
  NTplot(           xbar=1, ntcolors="stoplight")
  NTplot(mean1 = 2, xbar=1, ntcolors="stoplight")
  NTplot(type="confidence", ntcolors="stoplight")

## this is the set of colors that are assigned when ntcolors="BW"
c(col.alpha             = "gray35",
  col.notalpha          = "gray85",
  col.beta              = "gray15",
  col.power             = "gray40",
  col.pvalue            = "gray50",
  col.pvaluetranslucent = HH:::ColorWithAlpha("gray65"),
  col.critical          = "gray15",
  col.border            = "gray75",
  col.text              = "black",
  col.conf              = "gray45")
```

```
  NTplot(                   ntcolors="BW")
  NTplot(mean1 = 2,         ntcolors="BW")
  NTplot(           xbar=1, ntcolors="BW")
  NTplot(mean1 = 2, xbar=1, ntcolors="BW")
  NTplot(type="confidence", ntcolors="BW")


## End(Not run)

## Not run:
## mean1 and xbar
  NTplot(mean0=0, mean1=2,  xbar=1.8,  xlim=c(-3, 5))
  NTplot(mean0=0, mean1=-2, xbar=-1.8, xlim=c(-5, 3),
         alpha.left=.05,  alpha.right=0)
  NTplot(mean0=0, mean1=2,  xbar=2.1,  xlim=c(-3, 5),
         alpha.left=.025, alpha.right=.025)
  NTplot(mean0=0, mean1=-2, xbar=-2.1, xlim=c(-5, 3),
         alpha.left=.025, alpha.right=.025)

## mean1
  NTplot(mean0=0, mean1=2,  xbar=NA, xlim=c(-3, 5))
  NTplot(mean0=0, mean1=-2, xbar=NA, xlim=c(-5, 3),
         alpha.left=.05,  alpha.right=0)
  NTplot(mean0=0, mean1=2,  xbar=NA, xlim=c(-3, 5),
         alpha.left=.025, alpha.right=.025)
  NTplot(mean0=0, mean1=-2, xbar=NA, xlim=c(-5, 3),
         alpha.left=.025, alpha.right=.025)

## xbar
  NTplot(mean0=0, mean1=NA, xbar=1.8,  xlim=c(-3, 5))
  NTplot(mean0=0, mean1=NA, xbar=-1.8, xlim=c(-5, 3),
         alpha.left=.05,  alpha.right=0)
  NTplot(mean0=0, mean1=NA, xbar=2.1,  xlim=c(-3, 5),
         alpha.left=.025, alpha.right=.025)
  NTplot(mean0=0, mean1=NA, xbar=-2.1, xlim=c(-5, 3),
         alpha.left=.025, alpha.right=.025)

## t distribution
## mean1 and xbar
  NTplot(mean0=0, mean1=2,  xbar=1.8,  xlim=c(-3, 5),
         distribution.name="t", df=4)
  NTplot(mean0=0, mean1=-2, xbar=-1.8, xlim=c(-5, 3),
         alpha.left=.05,  alpha.right=0, distribution.name="t", df=4)
  NTplot(mean0=0, mean1=2,  xbar=2.1,  xlim=c(-3, 5),
         alpha.left=.025, alpha.right=.025, distribution.name="t", df=4)
  NTplot(mean0=0, mean1=-2, xbar=-2.1, xlim=c(-5, 3),
         alpha.left=.025, alpha.right=.025, distribution.name="t", df=4)

## mean1
  NTplot(mean0=0, mean1=2,  xbar=NA, xlim=c(-3, 5),
         distribution.name="t", df=4)
  NTplot(mean0=0, mean1=-2, xbar=NA, xlim=c(-5, 3),
         alpha.left=.05,  alpha.right=0, distribution.name="t", df=4)
```

```
  NTplot(mean0=0, mean1=2,  xbar=NA, xlim=c(-3, 5),
         alpha.left=.025, alpha.right=.025, distribution.name="t", df=4)
  NTplot(mean0=0, mean1=-2, xbar=NA, xlim=c(-5, 3),
         alpha.left=.025, alpha.right=.025, distribution.name="t", df=4)

## xbar
  NTplot(mean0=0, mean1=NA, xbar=1.8,  xlim=c(-3, 5),
         distribution.name="t", df=4)
  NTplot(mean0=0, mean1=NA, xbar=-1.8, xlim=c(-5, 3),
         alpha.left=.05,  alpha.right=0, distribution.name="t", df=4)
  NTplot(mean0=0, mean1=NA, xbar=2.1,  xlim=c(-3, 5),
         alpha.left=.025, alpha.right=.025, distribution.name="t", df=4)
  NTplot(mean0=0, mean1=NA, xbar=-2.1, xlim=c(-5, 3),
         alpha.left=.025, alpha.right=.025, distribution.name="t", df=4)

## confidence intervals

  NTplot(mean0=0, xlim=c(-3, 4), type="confidence")
  NTplot(xbar=01, xlim=c(-3, 4), type="confidence")
  NTplot(mean0=0, xlim=c(-4, 3), type="confidence",
         alpha.left=.05,  alpha.right=0)
  NTplot(mean0=0, xlim=c(-3, 3), type="confidence",
         alpha.left=.025, alpha.right=.025)
  NTplot(mean0=95, sd=10, xlim=c(65, 125), type="confidence",
         alpha.left=.025, alpha.right=.025)
  NTplot(mean0=95, sd=10, xlim=c(65, 125), type="confidence",
         alpha.left=.025, alpha.right=.025,
         distribution="t", df=10)


## End(Not run)
```

NormalAndTPower *Construct a power graph based on the NTplot.*

Description

Construct a power graph based on the NTplot. The exported function powerplot calls NormalAndTPower to construct a power curve or beta curve (operating characteristic curve) (or both) from its argument and catenates it to the original graph. The unexported function NormalAndTPower does the construction.

Usage

```
powerplot(nt, ...)

## S3 method for class 'NormalAndTplot'
powerplot(nt, power=TRUE, beta=FALSE, ...,
                          hh=if (power && beta) c(6,2,2) else c(6,2))
```

```
NormalAndTPower(nt,
                which=c("power","beta"),
                digits=4,
                digits.top.axis=digits, digits.left=digits,
                col.power=attr(nt, "color")["col.power"],
                col.beta=attr(nt, "color")["col.beta"],
                cex.pb.axis=1, cex.left.axis=1, cex.xbar=1,
                lwd.reference=4, lwd.line=2,
                main=which, ...)
```

Arguments

nt	For the generic powerplot, an object. For the NormalAndTplot method, a "NormalAndTplot" object from NTplot.
power, beta	Logical. If TRUE, then display that graph, else don't display it. Used by powerplot.
which	Which graph is to be displayed? "power" for the power curve, or "beta" for the operating characteristic curve. Used by NormalAndTPower.
...	Additional arguments passed on to methods.
hh	The h argument for resizePanels.
digits.top.axis, digits.left, digits, cex.pb.axis, cex.left.axis, cex.xbar	digits.top.axis is the number of significant digits for the top axis. digits.left is the number of significant digits for the observed power or beta on the left axis. digits is a convenience argument to set both digits.axis and digits.left at the same time. These number is passed to the format function. cex.top.axis is the cex value for the top axis values. cex.left.axis is the cex value for the observed power or beta on the left axis. cex.xbar is the cex value for the horizontal axis.
col.power, col.beta	Colors used for the crosshairs on the power and beta panels. The default values are the colors used for the power and beta regions of the NTplot panel.
lwd.reference, lwd.line	lwd values for the power or beta panel. lwd.line is used for the power curve or beta curve. lwd.reference is used for the crosshairs.
main	Main title for graph.

Value

"trellis" object.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

Examples

```
nt <- NTplot(mean0=2, mean1=4, sd=3, n=20, xlim=c(-.1, 6.1), xbar=3.5)
powerplot(nt)

## Not run:
tt <- NTplot(mean0=2, mean1=4, sd=3, n=20, xlim=c(-.1, 6.1), xbar=3.5, df=4, distribution.name="t")
powerplot(tt)

ntc <- NTplot(xbar=2, sd=3, n=20, xlim=c(-.1, 4.1), type="confidence",
              alpha.left=.025, alpha.right=.025)
ntc
try(powerplot(ntc))

## End(Not run)
```

---

normalApproxBinomial *Plots to illustrate Normal Approximation to the Binomial—hypothesis tests or confidence intervals.*

Description

Plots to illustrate Normal Approximation to the Binomial—hypothesis tests or confidence intervals.

Usage

```
normalApproxBinomial(p0= if (number.vars==1) .5 else 0,
                     p1=NA, p2=NA,
                     p.hat=if (number.vars==1) .75 else 0,
                     n=1,
                     xlim=if (number.vars==1) c(0,1) else c(-1,1),
                     ylim=c(0, 5),
                     type=c("hypothesis","confidence"),
                     alpha.left=if (type=="hypothesis") 0 else .025,
                     alpha.right=if (type=="hypothesis") .05 else .025,
                     xlab=if (number.vars==1)
                            "w = p = population proportion"
                          else
                            "w = p[1] - p[2] :: population proportions", ...,
                     number.vars=if (!is.na(p1) && !is.na(p2)) 2 else 1)
```

Arguments

p0	Null hypothesis value of p.
p1	Alternate hypothesis value of p for one-sample cases. Second sample value of p for two-sample cases.
p2	Second sample value of p.
p.hat	Observed value of p.

n	Number of observations (for example, number of coins tossed).
xlim, ylim, xlab	Standard xyplot arguments...
type	"hypothesis" for a Hypothesis Test graph, or "confidence" for a Confidence Interval graph.
..., alpha.left, alpha.right	Additional arguments forwarded to NTplot.
number.vars	Number of variables. 1 for a one-sample test, 2 for two-sample tests and paired tests.

Details

This is a wrapper function for the plots in NTplot.

Value

"trellis" object.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

Examples

```
NTplot(distribution.name="binomial", n=20, ylim=c(0,4.2), p1=.8)
NTplot(distribution.name="binomial", n=20, type="confidence", ylim=c(0,4.2))
## Not run:
NTplot(distribution.name="binomial", n=20, zaxis=TRUE, z1axis=TRUE,
       p1=.8678, ylim=c(0, 5.2))
NTplot(p0=.4, p.hat=.65, p1=.7, distribution.name="binomial", n=15)
NTplot(p.hat=.65, distribution.name="binomial", n=15, type="confidence")

## End(Not run)
## Not run:  ## these are interactive and won't work in R CMD check
  if (interactive())
    NTplot(distribution.name="binomial", n=20, ylim=c(0,4.2), p1=.8, shiny=TRUE)
  if (interactive())
    NTplot(p0=.4, p.hat=.65, p1=.7, distribution.name="binomial", n=15, shiny=TRUE)
  if (interactive())
    NTplot(p.hat=.65, distribution.name="binomial", n=15, type="confidence", shiny=TRUE)

## End(Not run)
```

npar.arma *Count the number of parameters in an ARIMA model specification.*

Description

Count the number of parameters in an ARIMA model specification. When `arima==FALSE`, just the AR and MA parameters are counted. When `arima==TRUE`, then the number of difference parameters are also included.

Usage

```
npar.arma(x, arima=FALSE)
npar.sarma(model, arima=FALSE)
npar.rarma(arma, arima=FALSE)
```

Arguments

`x`	An `"arima"` object in S-Plus or a `"Arima"` object in R.
`model`	A `model` specification in the S-Plus style.
`arma`	A `arma` specification in the R style
`arima`	Logical. `TRUE` is number of differencings is to be counted.

Value

A scalar number giving the count.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

Examples

```
co2.arima <-
  if.R(s=
       arima.mle(co2, list(list(order=c(0,1,1)),
                           list(order=c(0,1,1), period=12)))
       ,r=
       arima(co2,
             order=c(0,1,1),
             seasonal=list(order=c(0,1,1), period=12))
       )

npar.arma(co2.arima)

npar.arma(co2.arima, arima=TRUE)

npar.sarma(list(list(order=c(0,1,1)),
                list(order=c(0,1,1), period=12)))
```

```
npar.sarma(list(list(order=c(0,1,1)),
                list(order=c(0,1,1), period=12)),
           arima=TRUE)

if.R(s={},
     r=npar.rarma(co2.arima$arma)
)
if.R(s={},
     r=npar.rarma(co2.arima$arma,
           arima=TRUE)
)
```

NTplot *Specify plots to illustrate Normal and t Hypothesis Tests or Confidence Intervals, including normal approximation to the binomial.*

Description

Specify plots to illustrate Normal and t Hypothesis Tests or Confidence Intervals, including normal approximation to the binomial.

Usage

```
NTplot(mean0, ...)
## Default S3 method:
NTplot(mean0=0, ..., shiny=FALSE,
        distribution.name = c("normal","z","t","binomial"))
## S3 method for class 'htest'
NTplot(mean0, ..., shiny=FALSE, NTmethod="htest")
## S3 method for class 'power.htest'
NTplot(mean0, ..., shiny=FALSE, xbar=NA, ## these input values are used
        mean1, n, df, sd, distribution.name, sub, ## these input values ignored
        alpha.left, alpha.right, number.vars) ## these input values ignored
        ## NTplot(NTplot(htest.object), n=20) ## allows override of arguments
## S3 method for class 'NormalAndTplot'
NTplot(mean0, ..., shiny=FALSE)
```

Arguments

mean0	For the default method, mean0 is either missing or a numeric argument for the mean under the null hypothesis. For the htest method, mean0 is an htest object from the t.test or the z.test function. For the NormalAndTplot method mean0 is a "NormalAndTplot" object from a previous use of the NTplot function. For the power.htest method, mean0 is a power.htest object from the power.t.test function.
xbar	See NormalAndTplot.

`...` Other arguments, selected from the options for the default method `NormalAndTplot`. Three named color schemes are available: the default `ntcolors="original"`, `ntcolors="stoplight"`, and `ntcolors="BW"`. Their definitions, along with information on specifying other color schemes, are shown in `NormalAndTplot`.

`shiny` Logical. If `TRUE`, a `shiny` app is started to provide an interactive graphics device in a web-browser. If `FALSE`, a plot is drawn on the current graphics device. For short browser windows (`height < 800` pixels), you may adjust the pixel height of the plot in the last user input field on the `Fonts` tab.

`htest` logical. `TRUE` for `"htest"` objects.

`mean1, n, df, sd, sub, alpha.left, alpha.right, number.vars`
These variables are ignored here. They are captured so they won't interfere with similarly named variables that are generated in the `power.htest` method.

`distribution.name`
Ignored by `htest` and `power.htest` methods. Otherwise passed on to the next method.

`NTmethod` Character string used when `shiny=TRUE`. It is normally calculated by the methods. `NTmethod` tells `shiny` how to use or ignore the `df` and `n` sliders. See the extended discussion in `NormalAndTplot`.

Details

The graphs produced by this single function cover most of the first semester introductory Statistics course. All options of the `t.test`, `power.t.test`, and `z.test` are accepted and displayed.

`NTplot` is built on `xyplot`. Most of the arguments detailed in `xyplot` documentation work to control the appearance of the plot.

The shiny app (called when the argument `shiny=TRUE`) provides animated sliders for the means, standard deviation, xlimits, significance levels, df, and n. The df and n are rounded to integers for the sliders (relevant for `htest` and `power.htest` objects). Checkboxes and Radio buttons are available for various display options

When you have a graph on the shiny window that you wish to keep, click on the "Display Options" tab, and then on the "Display Call" radio button. The main shiny window will show an R command which will reproduce the current plot. Pick it up with the mouse and drop it into an R console window.

To get out of the shiny window and return to an interactive R console, move the cursor back to the console window and interrupt the shiny call, usually by entering `Ctrl-C` or `ESC`.

Value

`"trellis"` object. The object can be plotted or fed back into the `NTplot` function with argument `shiny=TRUE` to allow interactive graphical investigation of the hypothesis test or confidence interval. The attributes of the object\ `NTobj <- NTplot()\ attr(NTobj, "scales")` and `attr(NTobj, "prob")` make the data values and probability values accessible for further R computations. The `"call"` attribute `cat(attr(NT.object, "call"), "\n")` displays a statement that can be copied back into R to reproduce the graph. The `cat()` is needed to unescape embedded quotes. The `"call.list"` attribute `attr(NT.object, "call.list")` is a list that can be used with `do.call` to reproduce the graph. `do.call(NTplot, attr(NT.object, "call.list"))`. This is usually not needed by the user because the simpler statement `NTplot(NT.object)` does it for you.

Note

This function is built on **lattice** and **latticeExtra**. It supersedes the similar function `normal.and.t.dist` built on base graphics that is used in many displays in the book by Erich Neuwirth and me: *R through Excel*, Springer (2009). https://link.springer.com/book/10.1007/978-1-4419-0052-4. Many details, particularly the alternate color scheme and the concept of floating probability labels, grew out of discussions that Erich and I have had since the book was published. It incorporates ideas that Jay Kerns and I developed at the 2011 UseR! conference. This version incorporates some ideas suggested by Moritz Heene.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

`NormalAndTplot`, `print.NormalAndTplot`.

Examples

```
x1 <- rnorm(12)
x2 <- rnorm(12, mean=.5)

NT.object <- NTplot(mean0=0, mean1=1)
NT.object
attr(NT.object, "scales")
attr(NT.object, "prob")
cat(attr(NT.object, "call"), "\n") ## the cat() is needed to unescape embedded quotes.

NTplot(t.test(x1, x2))
NTplot(power.t.test(power = .90, delta = 1, alternative = "one.sided"))

## Not run:
## 22 distinct calls are shown in
demo(NTplot, ask=FALSE)

## End(Not run)

## Not run:  ## these are interactive and do not work in static checking of the code
  if (interactive())
    NTplot(mean0=0, mean1=1, shiny=TRUE)
  if (interactive())
    NTplot(shiny=TRUE, px.height=475) ## default value is 575
  if (interactive())
    NTplot(t.test(x1, x2), shiny=TRUE, mean1=1)
  if (interactive())
    NTplot(power.t.test(power = .90, delta = 1, alternative = "one.sided"), shiny=TRUE)
  if (interactive())
    NTplot(NT.object, shiny=TRUE)

## run the shiny app
if (interactive())  shiny::runApp(system.file("shiny/NTplot", package="HH"))
```

```
## End(Not run)
```

---

objip *loop through all attached directories looking for pattern, possibly restricting to specified class or mode.*

Description

Loop `objects()` through all attached directories (items in the `search()` list) looking for a regular expression pattern.

Usage

```
objip(pattern, where = search(), all.names=FALSE, mode="any", class,
      ls.function=if (mode != "any" || !missing(class)) "ls.str" else "ls")
```

Arguments

`pattern`	Character string containing a regular expression that is used to list only a subset of the objects. Only names matching 'pattern' are returned.
`where`	an object defining a database in the search list.
`all.names`	In R, a logical that is passed to the `ls` function. If 'TRUE', all object names are returned. If 'FALSE', names which begin with a '.' are omitted.
`mode, class`	See `ls.str` and `mode` for storage mode of an object. See `class` for object classes.
`ls.function`	Either `ls` or `ls.str`. If either `mode` or `class` is specified then the default is `ls.str`. If neither is specified then the default is `ls`.

Value

A list of 0 or more character vectors. Each character vector has the name of one of the items in the `search()` list. Each character vector contains the names of the objects in the specified environment which match the `pattern`. If there are no matching names in an environment, then the corresponding character vector is removed from the result.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`ls`,

Examples

```
objip("qq")
objip("^qq")
objip("qq$")
## Not run:
## R only
objip("rowSums", all.names=TRUE)

## list all objects in the second and third attached packages
search()
objip()[2:3]

## End(Not run)
```

OddsRatio *Calculate or plot the odds ratio for a 2x2 table of counts.*

Description

Calculate or plot the odds ratio for a 2x2 table of counts. The plot shows the confidence intervals on the probability of row2 for fixed odds ratio and specified probability for row1.

Usage

```
OddsRatio(x, alpha = 0.05)

plotOddsRatio(x,
              ylab="prob(col1 | row1)",
              xlab="prob(col1 | row2)",
              alpha=c(.50, .05),
              col=trellis.par.get("superpose.line")$col,
              lwd=trellis.par.get("superpose.line")$lwd,
              lwd.reference=1,
              ...)

plotOddsRatio.base(x,
 ylab = "prob(col1 | row1)", xlab = "prob(col1 | row2)",
 alpha = c(0.05, 0.5),
 legend.x=1.05,
 oma=c(0,0,0,5), ...)
```

Arguments

x	2 x 2 table of counts
alpha	Significance levels of test. OddsRatio requires a single number in the range [0,1]. plotOddsRatio accepts more than one number on the range [0,1] and draws confidence lines at each value.

xlab, ylab	x- and y-labels for the plot Sensible defaults are generated.
col, lwd	Colors and linewidths to be used in the graph.
lwd.reference	linewidth for reference line.
...	other arguments, currently ignored.
legend.x	x position of left-hand side of legend.
oma	outer margin par()$oma, needed to make room for legend.

Value

plotOddsRatio returns a lattice object.

The older plotOddsRatio.base draws a plot with base graphics and invisibly returns the same list as OddsRatio returns for the first value of alpha.

OddsRatio returns the list:

p1, p2	proportion of each row total observed in the first column.
omega1, omega2	odds for each row, p/(1-p)
psihat	odds ratio, omega2/omega1
s.ln.psihat	standard deviation of ln(psihat)
ci.ln.psihat	confidence interval for ln(psihat) using normal approximation
ci.psihat	confidence interval for psihat calculated ase p(ci.ln.psihat)
prob1	seq(0,1,.05), set of p1 values for plotting.
odds1	p1/(1-p1)
odds2	odds for the second row needed to retain psihat with the specified odds1, calculated as odds1*psihat.
ci.odds2	confidence interval for odds2
prob2	odds2 / (odds2+1)
ci.prob2	ci.odds2 / (ci.odds2+1)

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Examples

```
data(glasses)

## draw the iso-odds ratio plot with 50% CI and 95% CI,
plotOddsRatio(glasses)

## return the 95% CI information
OddsRatio(glasses)

## draw the iso-odds ratio plot with 50% CI and 95% CI,
## invisibly return the 95% CI information
plotOddsRatio.base(glasses)
```

`OneWayVarPlot` *Displays a three-panel* `bwplot` *of the data by group, of the group means, and of the entire dataset. This is an approximate visualization of the Mean Square lines from the ANOVA table for a one-way ANOVA model.*

Description

Displays a three-panel `bwplot` of the data by group, of the group means, and of the entire dataset. This is an approximate visualization of the Mean Square lines from the ANOVA table for a one-way ANOVA model. The groups are centered using medians by default. Means, and anything else, is an option.

Usage

```
OneWayVarPlot(x, data, ...,
              main="Variability of Groups, Centers of Groups, and all Data",
              centerFunctionName="median",
              center=TRUE)
```

Arguments

`x`	Model formula with one response variable and one factor.
`data`	`data.frame`
`...`	Other arguments to be forwarded to the panel function.
`main`	`main` title for graph.
`centerFunctionName`	Name of centering function, with `"median"` as the default. `"mean"` is another option.
`center`	Logical. If `TRUE`, the default, the bwplots are centered by subtracting their center (by default the median). If `FALSE` the bwplots are plotted at their observed values.

Value

Three-panel `trellis` object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
data(batch)
OneWayVarPlot(Calcium ~ Batch, data = batch)
```

`orthog.complete` *Construct an orthogonal matrix which is an arbitrary completion of the column space of the input set of columns.*

Description

Construct an orthogonal matrix which is an arbitrary completion of the column space of the input set of columns.

Usage

```
orthog.complete(x, normalize=TRUE, abs2.rows=1:nrow(x),
                Int=TRUE, drop.Int=Int)

orthog.construct(y, x, x.rows, normalize=FALSE)
```

Arguments

`x`	For `orthog.complete`, an n-row matrix of one or more columns. For `orthog.construct`, a set of contrasts for a factor.
`y`	matrix of coefficients specifying the linear combinations estimated. This will usually be the `lmat` from an S-Plus `"multicomp"` object or the `linfct` component from an R `"glht"` object.
`normalize`, `abs2.rows`, `x.rows`	The default normalizes the sum of squares of the rows in `abs2.rows` or `x.rows` to 1. The optional value `normalize="abs2"` scales the rows in `abs2.rows` or `x.rows` to make the sum of all positive value equal 1 and the sum of all negative values equal -1. Together, the sum of the absolute values of the specified rows in each column is 2.
`Int`	logical. Default `TRUE` means make all columns orthogonal to the constant column (Intercept in regression terminology). The alternative is to use only the columns in the input matrix `x`.
`drop.Int`	logical. The default is to drop the constant column and to keep all columns when the constant is not automatically generated.

Details

This function is based on `qr.Q`. The input matrix `x` has `n` rows and an arbitrary non-zero number of columns. The result is an `n` by `n` orthogonal matrix. By default the first column of the result is constant and is not returned. The second column of the result is orthogonal to the first result column. Together the first two result columns span the space of the constant column and the first input column. The third result column is orthogonal to the first two result columns and the the three result columns together span the space of the constant column and the first two inout columns. Similarly for the remaining result columns. Result columns beyond the number of input columns are constructed as an arbitrary orthogonal completion.

If the input columns are orthogonal to each other and to the constant column, then the result columns are rescaled versions of the input columns.

Optionally (`drop.Int=FALSE`), the constant column can be returned.

By default the columns are scaled to have sum of squares equal 1. If `normalize="abs2"`, they are scaled to make the sum of all positive value equal 1 and the sum of all negative values equal -1. Together, the sum of the absolute values of each column is 2.

If the input is a set of columns from a contrast matrix for a design that has multiple terms, the `abs2.rows` argument is used to specify which rows are to be included in the normalization. These will normally be rows associated with one of the main effects.

Value

Matrix of orthogonal columns.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

MMC

Examples

```
zapsmall(
orthog.complete(cbind("4-12"=c(-1,-1, 0, 2),
                      "1-2" =c( 1,-1, 0, 0)))
)

zapsmall(
orthog.complete(cbind("4-12"=c(-1,-1, 0, 2),
                      "1-2" =c( 1,-1, 0, 0)),
                drop.Int=FALSE)
)
```

```
zapsmall(
orthog.complete(cbind("4-12"=c(-1,-1, 0, 2),
                      "1-2" =c( 1,-1, 0, 0)),
                normalize="abs2")
)


## used in MMC plots
tmp <- data.frame(y=rnorm(12),
                  a=factor(c("u","u","u","u",
                             "v","v","v","v",
                             "w","w","w","w")))
tmp.aov <- aov(y ~ a, data=tmp)
lmat <- if.R(
  s=multicomp(tmp.aov, focus="a")$lmat,
  r={lmat.reduced <- t(glht(tmp.aov, linfct=mcp(a="Tukey"))$linfct)
     rbind(lmat.reduced, AU=-apply(lmat.reduced[-1,], 2, sum))
    })
zapsmall(lmat)

lmat.complete <- orthog.complete(lmat, abs2.rows=-1,
                                 normalize="abs2",
                                 drop.Int=FALSE)[,1:3]
zapsmall(lmat.complete)
if.R(r=zapsmall(lmat.complete[-4,]),
     s={})
```

`panel.acf` *Panel functions for tsdiagplot.*

Description

Panel functions for `tsdiagplot`.

Usage

```
panel.acf(..., n.used)
panel.std.resid(...)
panel.gof(...)
```

Arguments

`...`	standard arguments to panel functions.
`n.used`	number of lags. THis number is needed to calculate the confidence interval which is `2//sqrt(n.used)`.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

tsdiagplot

---

panel.axis.right *Right-justify right-axis tick labels.*

Description

panel.axis.right is almost identical to panel.axis. axis.RightAdjustRight is almost identical to axis.default. The only difference is that these functions right-justify right-axis tick labels.

Usage

```
panel.axis.right(side = c("bottom", "left", "top", "right"),
                 at = pretty(scale.range),
                 labels = TRUE, draw.labels = TRUE,
                 check.overlap = FALSE, outside = FALSE, ticks = TRUE,
                 half = !outside,
                 which.half = switch(side, bottom = "lower",
                                     left = "upper", top = "upper",
                                     right = "lower"),
                 tck = as.numeric(ticks),
                 rot = if (is.logical(labels)) 0 else c(90, 0),
                 text.col = axis.text$col, text.alpha = axis.text$alpha,
                 text.cex = axis.text$cex, text.font = axis.text$font,
                 text.fontfamily = axis.text$fontfamily,
                 text.fontface = axis.text$fontface,
                 text.lineheight = axis.text$lineheight,
                 line.col = axis.line$col, line.lty = axis.line$lty,
                 line.lwd = axis.line$lwd, line.alpha = axis.line$alpha)

axis.RightAdjustRight(side = c("top", "bottom", "left", "right"),
                      scales, components, as.table,
                      labels = c("default", "yes", "no"),
                      ticks = c("default", "yes", "no"),
                      ...,

                      prefix = lattice.lattice.getStatus("current.prefix"))
```

Arguments

side, at, labels, draw.labels, check.overlap, outside, ticks, half, which.half
: See panel.axis and axis.default

tck, rot, text.col, text.alpha, text.cex, text.font, text.fontfamily
: See panel.axis and axis.default

text.fontface, text.lineheight, line.col, line.lty, line.lwd, line.alpha
: See panel.axis and axis.default

scales, components, as.table, ..., prefix
: See axis.default

Author(s)

Deepayan Sarkar Deepayan.Sarkar@R-project.org wrote panel.axis and axis.default. David Winsemius wrote the modification panel.axis.right. Richard Heiberger rmh@temple.edu wrote the modification axis.RightAdjustRight. Richard Heiberger is maintaining this distribution of both functions.

See Also

panel.axis

---

panel.bwplot.intermediate.hh

Panel functions for bwplot.

Description

Panel function for bwplot that give the user control over the placement of the boxes. When used with a positioned factor, the boxes are placed according to the position associated with the factor.

Usage

```
panel.bwplot.intermediate.hh(x, y, horizontal = TRUE,
          pch, col, lwd,
          ...)
```

Arguments

x, y, pch, col, lwd, horizontal
: see xyplot and panel.bwplot.

...
: Extra arguments, if any, for 'panel.bwplot'.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*, Second Edition. Springer Texts in Statistics. Springer. ISBN 978-1-4939-2121-8.

See Also

panel.xyplot, xyplot, interaction2wt, position

Examples

```
## see examples at
## Not run:
  demo("bwplot.examples", package="HH")

## End(Not run)
```

---

panel.bwplot.superpose

Panel function for bwplot that displays an entire box in the colors coded by groups.

Description

Panel function for bwplot that displays an entire box (central dot, box, umbrella, outliers) in the same color, coded by the groups argument. The function is based on panel.superpose.

Usage

```
panel.bwplot.superpose(x, y, ...,
                       groups=groups,
                       col=rep(trellis.par.get("superpose.symbol")$col,
                               length=length(groups)),
                       pch=trellis.par.get("box.dot")$pch,
                       panel.groups=panel.bwplot.groups)

panel.bwplot.groups(..., col, pch, fill, fill.alpha=NULL, group.number)
```

Arguments

x, y	Standard arguments to a **lattice** panel function. When x has class positioned (see position), the position will be forwarded by panel.bwplot.superpose to panel.bwplot.groups.
...	Additional **lattice** arguments.
groups	Factor to be used for color coding entire boxes: central dot, rectangle, umbrella, and outlier symbol.

col — Colors to be assigned to the levels of the group. The default colors are taken from `trellis.par.get("superpose.symbol")$col`.

pch — Standard **lattice** arguments. The pch describes the central dot. The outlier dots are specified in the `plot.symbol` component of `trellis.par.get`.

fill, fill.alpha — These are related to the similarly named arguments in `panel.bwplot`. The `fill` argument is ignored. It is there to capture the automatically generated `fill` argument. The default`NULL` value of `fill.alpha` implies that there is no background color for the boxes. The user can set `fill.alpha` to a number between 0 and 1. The boxes will be shaded in a lighter version of their color as implied by the `groups` argument. The value 0 gives a transparent fill, and the value one makes the box the full opaque color.

panel.groups, group.number — See `panel.superpose` for details.

Details

`panel.bwplot.superpose` is the user-level function. `panel.bwplot.groups` is the `panel.groups` function called by `panel.superpose`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`position`, `panel.bwplot.intermediate.hh`, `panel.superpose`

Examples

```
tmp <- data.frame(Response=rnorm(20), Group=factor(rep(LETTERS[1:3], c(5,7,8))))

bwplot(Group ~ Response, data=tmp,
       main="Default panel.bwplot, groups ignored", groups=Group)

bwplot(Group ~ Response, data=tmp,
       main="panel.bwplot.superpose",
       groups=Group, panel=panel.bwplot.superpose)

bwplot(Group ~ Response, data=tmp,
       main="panel.bwplot.superpose with fill specified",
       groups=Group, panel=panel.bwplot.superpose,
       fill.alpha=.33)


bwplot(Group ~ Response, data=tmp,
       main="panel.bwplot.superpose, with color specified",
       groups=Group, panel=panel.bwplot.superpose,
       col=c("forestgreen","blue", "brown"))
```

```
Test <- data.frame(id=rep(letters, each=4),
                   Week=rep(c(0,1,3,6), 26),
                   Treatment=rep(factor(c("A","B"), levels=c("A","B")), each=52),
                   y=rep(1:4, 52) + rep(4:5, each=52) + rnorm(104),
                   stringsAsFactors=FALSE)
Test$WeekTrt <- with(Test, interaction(Week, Treatment))
position(Test$Week) <- unique(Test$Week)
position(Test$WeekTrt) <- as.vector(outer(position(Test$Week), c(-.2, .2), `+`))

tapply(Test$y, Test[c("Week", "Treatment")], median)

bwplot( y ~ WeekTrt, groups = Treatment, data = Test,
      main="default panel.bwplot, groups ignored")

bwplot( y ~ WeekTrt, groups = Treatment, data = Test,
      panel=panel.bwplot.superpose,
      scales=list(x=list(limits=c(-1, 7))),
      main="Minimal use of panel.bwplot.superpose")

bwplot( y ~ WeekTrt, groups = Treatment, data = Test,
       panel=panel.bwplot.superpose,
       scales=list(x=list(limits=c(-1, 7), at=position(Test$Week))),
       box.width=.3,
       xlab="Week",
       pch=c(17, 16),
       key=list(col=trellis.par.get()$superpose.symbol$col[1:2],
           border=TRUE, title="Treatment", cex.title=1, columns=2,
           text=list(levels(Test$Treatment)),
           points=list(pch=c(17, 16))),
       par.settings=list(plot.symbol=list(pch=c(17, 16), cex=.5)),
       main="panel.bwplot.superpose with additional annotations")


bwplot( y ~ WeekTrt, groups = Treatment, data = Test,
       panel=panel.bwplot.superpose,
       scales=list(x=list(limits=c(-1, 7), at=position(Test$Week))),
       box.width=.3,
       xlab="Week",
       pch=c(17, 16),
       key=list(col=trellis.par.get()$superpose.symbol$col[1:2],
           border=TRUE, title="Treatment", cex.title=1, columns=2,
           text=list(levels(Test$Treatment)),
           points=list(pch=c(17, 16))),
       par.settings=list(plot.symbol=list(pch=c(17, 16), cex=.5)),
       main="panel.bwplot.superpose with fill and more complex panel.groups",
       panel.groups = function(...) {
           panel.stripplot(...)
           panel.bwplot.groups(...)
       },
       fill.alpha=.33,
       jitter.data = TRUE)
```

panel.bwplott *Extension to S-Plus trellis to allow transposed plots.*

Description

Extension to S-Plus trellis to allow transposed plots. All x - and y-components of the trellis object are interchanged. This function is not needed in R as lattice has a horizontal argument in its definitions.

Usage

```
panel.bwplott(x, y, box.ratio = 1,
              font = box.dot$font, pch = box.dot$pch, cex = box.dot$cex,
              col = box.dot$col, ..., transpose=FALSE)
```

Arguments

x, y, box.ratio, font, pch, cex, col, ...	See panel.bwplot.
transpose	logical. If FALSE, the plot is printed in the default orientation. If TRUE, the x- and y-components of the trellis object are interchanged. This has the effect, for example, of displaying vertical boxplots instead of the default horizontal boxplots.

Value

The function is used for its side effect of drawing boxplots in a trellis panel.

Note

This function is not needed in R. If it is used and

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

xyplot.

`panel.cartesian` *trellis panel function, with labeled rows and columns and without strip labels.*

Description

trellis panel function, with labeled rows and columns and without strip labels. Designed for use with the ladder of powers plot.

Usage

```
panel.cartesian(x, y,
                x.label=unique(panel.labels[,"x"]),
                y.label=unique(panel.labels[,"y"]),
                group.label.side="",
                axis3.line=1,
                xg.label, yg.label, g.cex=.7,
                rescale=list(x=TRUE,y=TRUE), ...,
                browser.on=FALSE)
```

Arguments

x, y	x and y as for any other panel function
x.label	labels for the columns of the scatterplot matrix
y.label	labels for the rows of the scatterplot matrix
axis3.line	The x.label doesn't always show up in the right place. This allows the user to adjust it's position.
group.label.side	c("","left","top"), when the plotting formula is conditioned on a group factor, the levels of the group are displayed in the margins of the plot. The appearance depends on the setting of the trellis between argument. Getting it to look good for any given plot requires experimentation. Since it is redundant with the information in the strip labels, leaving it at the default "" is often the best thing to do.
xg.label	group labels for rows of the scatterplot matrix
yg.label	group labels for rows of the scatterplot matrix
g.cex	cex for the group labels
rescale	alternate way to get something similar to relation="free"
...	other arguments
browser.on	logical, normally FALSE. This is a debugging tool. When TRUE, the browser() is turned on at various critical points.

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

ladder, xysplom

Examples

```
data(rent)  ## Weisberg's file alr162

rent.lm <- lm(rnt.alf ~ rnt.till + cow.dens + lime, data=rent)
rent$resid.rent <- resid(rent.lm)

xysplom(resid.rent ~ rnt.till + cow.dens | lime, data=rent,
        layout=c(2,2))

xysplom(resid.rent ~ rnt.till + cow.dens | lime, data=rent,
        layout=c(2,2),
        xlab="", ylab="",
        x.label="", y.label="",
        group.label.side="",
        par.strip.text=list(cex=1.2),
        panel=panel.cartesian,
        axis3.line=2.4,
        scales=list(
          relation="same",
          alternating=FALSE, labels=FALSE, ticks=FALSE),
        between=list(x=1, y=3))

xysplom(resid.rent ~ rnt.till + cow.dens | lime, data=rent,
        layout=c(2,2),
        xlab="", ylab="",
        x.label="", y.label="",
        group.label.side="",
        par.strip.text=list(cex=1.2),
        panel=panel.cartesian,
        axis3.line=3.6,
        scales=list(
          relation="same",
          alternating=FALSE, labels=FALSE, ticks=FALSE),
        rescale=list(x=FALSE, y=FALSE),
        between=list(x=1, y=3))

xysplom(resid.rent ~ rnt.till + cow.dens | lime, data=rent,
        layout=c(2,2),
        xlab="", ylab="",
        x.label="", y.label="",
        group.label.side="",
        par.strip.text=list(cex=1.2),
```

```
        panel=panel.cartesian,
        axis3.line=3.6,
        scales=list(
          relation="free",
          alternating=FALSE, labels=FALSE, ticks=FALSE),
        between=list(x=1, y=3))

tmp <-
xysplom(resid.rent ~ rnt.till + cow.dens | lime, data=rent,
        layout=c(2,2),
        xlab="", ylab="",
        y.label="resid",
        group.label.side="top",
        par.strip.text=list(cex=1.2),
        panel=panel.cartesian,
        axis3.line=3.6,
        scales=list(alternating=FALSE, labels=FALSE, ticks=FALSE),
        rescale=list(x=FALSE, y=FALSE),
        between=list(x=4, y=5))
if.R(r=tmp$par.settings <- list(layout.widths=list(right.padding=4)),
     s={})
tmp
```

`panel.ci.plot` *Default Panel Function for ci.plot*

Description

This is the default panel function for `ci.plot`.

Usage

```
panel.ci.plot(x, y, newdata, newfit = newfit, ...)
```

Arguments

`x`	Observed values of predictor variable.
`y`	Observed values of response variable.
`newdata`	`x` values for which predictions are calculated.
`newfit`	`data.frame` containing six components: `"fit"`, `"se.fit"`, `"residual.scale"`, `"df"`, `"ci.fit"`, `"pi.fit"`. In S-Plus these are the output from the `predict.lm` function. In R they are a rearrangement of the output of the `predict.lm` function.
`...`	other arguments passed to `panel.xyplot`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

ci.plot, xyplot, lm

---

panel.confintMMC *Confidence interval panel for MMC tiebreaker plots, or confidence interval plot.*

Description

Confidence interval panel for MMC tiebreaker plots, or confidence interval plot.

Usage

```
panel.confintMMC(x, y, subscripts, ..., col, lwd, lty, lower, upper,
                 contrast.name, right.text.cex = 0.8,
                 contrast.height=FALSE)
```

Arguments

x	means
y	When called from mmcisomeans, the heights associated with the contrasts. When called from mmcmatch, integers from one to the number of means.
subscripts	Index into the contrast.names.
...	Additional arguments are ignored.
col, lty, lwd	Standard **lattice** arguments.
lower	Vector of lower bounds for the intervals.
upper	Vector of upper bounds for the intervals.
contrast.name	Names of the contrasts.
right.text.cex	The right axis has non-standard controls.
contrast.height	Logical. The alternate TRUE means display the values of the contrast heights as the left axis tick labels.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

See mmc for the references and examples.

panel.dotplot.tb *Dotplot with evenly spaced tiebreakers.*

Description

Dotplot with evenly spaced tiebreakers. Multiple hits on a specific x value are stacked.

Usage

```
panel.dotplot.tb(x, y, factor=.1,
                 jitter.data=TRUE, horizontal=TRUE,
                 max.freq=max(sapply(subsets, length)),
                 ...)
```

Arguments

x, y	See xyplot.
factor	jitter factor, see xyplot. Increment is factor/max.freq where max.freq is the maximum number of duplicates of any x value in any y group.
jitter.data, horizontal	Always TRUE.
max.freq	maximum number of observation at any combination of response values, factor levels, and group levels. If the formula includes one or more conditioning factors, then the user is responsible for providing a value for max.freq.
...	Other arguments for xyplot.

Details

Creates (possibly grouped) Dotplot of x against y. y is the 'factor'.

Warning

If the formula includes one or more conditioning factors, then the user is responsible for providing a value for max.freq. The default behavior is a different max.freq for each panel in a multi-panel display.

Author(s)

Richard M. Heiberger

Maintainer: Richard M. Heiberger <rmh@temple.edu>

Examples

```
x <- c(1,1,2,2,2,5,4,2,1,5)
y <- factor(letters[rep(1:2, 5)])

dotplot(x, panel=panel.dotplot.tb)
dotplot(x, panel=panel.dotplot.tb, factor=.2)
dotplot(y ~ x, panel=panel.dotplot.tb)
dotplot(y ~ x, panel=panel.dotplot.tb, cex=1.5, factor=.15)



quiz <- data.frame(scores=sample(10, 360, replace=TRUE),
                   date=rep(rep(c("0902", "0916", "0930"), c(40,40,40)), 3),
                   section=rep(
                     c("Stat1-3", "Stat1-5", "Stat1-8"),
                     c(120,120,120)))

dotplot(date ~ scores | section, data=quiz,
        panel=panel.dotplot.tb, factor=.5)

dotplot(date ~ scores | section, data=quiz,
        panel=panel.dotplot.tb, factor=.5,
        layout=c(1,3), between=list(y=1),
        main='Three quizzes for three sections of Stat 1')


## If the formula includes one or more conditioning factors, then the
## user is responsible for providing a value for the argument max.freq
##
a <- rep(1, 10)
z <- c(1,1,2,2,2,3,2,3,1,1)
g <- LETTERS[c(1,1,1,1,1,2,2,2,2,2)]

print(split=c(1,1,2,1), more=TRUE,
dotplot( a ~ z | g, panel=panel.dotplot.tb,
        factor=.6, cex=1.5, layout=c(2,1),
        main="different scaling in each panel")
)

print(split=c(2,1,2,1), more=FALSE,
dotplot( a ~ z | g, panel=panel.dotplot.tb, max.freq=3,
        factor=.6, cex=1.5, layout=c(2,1),
        main="same scaling in each panel")
)
```

`panel.interaction2wt` *Plot all main effects and twoway interactions in a multifactor design*

Description

This is the panel function for `interaction2wt`. The main diagonal displays boxplots for the main effects of each factor. The off-diagonals show the interaction plots for each pair of factors. The `i,j` panel shows the same factors as the `j,i` but with the trace- and x-factor roles interchanged.

Usage

```
panel.interaction2wt(x, y, subscripts,
                     responselab, trace.values,
                     factor.levels, factor.position,
                     fun = mean,
                     se,
                     type="l",
                     ...,
                     box.ratio,
                     simple=FALSE,
                     simple.offset,
                     simple.scale,
                     simple.pch,
                     data.x,
                     col.by.row=TRUE,
                     col  =trellis.par.get("superpose.line")$col,
                     lty  =trellis.par.get("superpose.line")$lty,
                     lwd  =trellis.par.get("superpose.line")$lwd,
                     alpha=trellis.par.get("superpose.line")$alpha
)

strip.interaction2wt(which.given, which.panel, var.name,
                     factor.levels, shingle.intervals,
                     strip.names = c(TRUE, TRUE), style = 1, ...)
```

Arguments

`panel.interaction2wt` arguments:

`x`	levels of x-factor
`y`	Summary value of response variable at each level of x- and trace-factors.
`subscripts`	used to get the right set of response values for the summary statistics on the off-diagonals
`responselab`	Character name of response variable, defaults to the name of the response variable.
`trace.values`	levels of trace-factor
`fun`	Summary function, defaults to `mean`
`se`	standard errors to be passed to `panel.intxplot`. Missing, logical, or a numeric vector. If `se` is missing or `FALSE`, or if `simple` is `FALSE`, then standard errors are not plotted. If `TRUE`, the standard errors are calculated from the sufficient statistics for each group as the group's standard deviation divided by the square

root of the group's observation count. If a numeric vector, it is evaluated in the environment of the sufficient statistics.

,

`type` See `panel.xyplot`.

,

`box.ratio` passed to `panel.bwplot.intermediate.hh`

,

`...` extra arguments, primarily color, to be passed to `panel.bwplot.intermediate.hh`

`factor.position`
"position" attribute of factor.

`simple` logical. If `TRUE`, then simple effects are to be displayed.

`simple.offset, simple.scale`
named list of offset and scale for the response and trace factors.
See `interaction.positioned` for their use.

`simple.pch` Named list containing plotting characters for each level of one or more of the factors. `simple.pch` is used only when `simple==TRUE`. If the argument `simple.pch` is missing, then the integers for the levels of the factors are used. The characters are used for the median of the box plots in the diagonal panels. They match the trace factor of the interaction panel in the same column of the display.

`data.x` `data.frame` containing factors from the input data.frame

`col.by.row` logical. If `TRUE` (the default), simple effects plots color the simple effects on the main diagonals in the same color as the trace levels in their row. If `FALSE`, then simple effects are colored to match the x levels in their column.

`col, lty, lwd, alpha`
Arguments to `trellis.par.set(superpose.line=list())`.

`strip.interaction2wt` arguments

`which.given, which.panel, var.name, factor.levels, shingle.intervals`
see documentation for `strip.default`

.

`strip.names` Force `strip.names=TRUE`

`style` force `style=1`

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

interaction2wt, panel.bwplot.intermediate.hh

Examples

```
## Not run:
tmp <- data.frame(y=rnorm(48),
                  A=factor(rep(1:2, 24)),
                  B=factor(rep(rep(1:3, each=2), 8)),
                  C=factor(rep(rep(1:4, each=6), 2)))
interaction2wt(y ~ A+B+C, data=tmp,
               key.in=list(x=-3), ## key.in is ignored by R
               xlim=c(.4, 4.5))
interaction2wt(y ~ B+C, data=tmp, key.in=list(x=-2), xlim=c(.4, 4.5))
position(tmp$B) <- c(1, 2.4, 3.8)
interaction2wt(y ~ B+C, data=tmp, key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ B+C, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ C+B, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ B+C, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               simple.pch=list(C=c(16,17,18,19)),
               key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ C+B, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               simple.pch=list(C=c(16,17,18,19)),
               key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ C+B, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               simple.pch=list(A=c(1:2), B=c(3:5), C=c(16,17,18,19)),
               key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ C+B, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               simple.pch=list(A=c(1:2)),
               key.in=list(x=-2), xlim=c(.4, 4.5))
interaction2wt(y ~ B+C, data=tmp, simple=TRUE,
               simple.scale=list(B=.18, C=.27),  box.ratio=.2,
               simple.pch=list(B=c(16,17,18)),
               key.in=list(x=-2), xlim=c(.4, 4.5),
               se=TRUE)

## End(Not run)
```

---

panel.isomeans *isomeans grid for MMC plots.*

Description

isomeans grid for MMC plots.

Usage

```
panel.isomeans(ybar,
               lty.iso=7,
               col.iso='darkgray',
               lwd.iso=1,
               lty.contr0=2,
               col.contr0='darkgray',
               lwd.contr0=1,
               ...,
               col, lwd, lty ## capture potentially ambiguous name
               )
```

Arguments

`ybar`	Vector of means.
`lty.iso`, `col.iso`, `lwd.iso`	color, line type, line width for the isomeans grid.
`lty.contr0`, `col.contr0`, `lwd.contr0`	color, line type, line width for the vertical contrast=0 line.
`...`	ignore any additional arguments
`col`, `lwd`, `lty`	ignore these arguments. They are captured here to avoid ambiguity with `col.iso` and `lty.iso`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

See `mmc` for the references and examples.

`panel.likert` *Panel functions for likert that include a stackWidth argument*

Description

`panel.barchart2` is based on `panel.barchart`
The changes are
* the heights in each horizontal stacked bar are constant.
* the widths in each vertical stacked bar are constant.
* the panel.barchart heights and widths are based on the box.width argument.

* the panel.barchart2 heights and widths when stack==TRUE are also based on the new stackWidth argument.

panel.likert calls panel.barchart2

scaling of stackWidth:
stackWidth <- stackWidth/mean(stackWidth) ## and maybe smaller with another /2

Usage

```
panel.barchart2(x, y, box.ratio = 1, box.width = box.ratio/(1 + box.ratio),
    horizontal = TRUE, origin = NULL, reference = TRUE, stack = FALSE,
    groups = NULL,
    col = if (is.null(groups)) plot.polygon$col else superpose.polygon$col,
   border = if (is.null(groups)) plot.polygon$border else superpose.polygon$border,
    lty = if (is.null(groups)) plot.polygon$lty else superpose.polygon$lty,
    lwd = if (is.null(groups)) plot.polygon$lwd else superpose.polygon$lwd,
    ..., identifier = "barchart",
          stackWidth=NULL)

panel.likert(..., horizontal=TRUE, reference.line.col="gray65")
```

Arguments

x, y, box.ratio, box.width, horizontal, origin, reference, stack, groups, col	See panel.barchart.
border, lty, lwd, identifier	See panel.barchart.
...	Extra arguments, if any, for panel.barchart.
stackWidth	Heights in each horizontal stacked bar, when stack=TRUE, are constant and specified by this argument. We recommend starting with stackWidth <- stackWidth/mean(stackWidth) and adjusting as seems appropriate.
reference.line.col	See likert.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

likert

panel.pairs.hh *Function based on S-Plus panel.pairs to add the subpanel.scales and panel.cex arguments.*

Description

Function based on S-Plus panel.pairs to add the subpanel.scales and panel.cex arguments. In R, this is an alias for panel.pairs.

Usage

```
panel.pairs.hh(x, y, z, subscripts, pscales, subpanel = panel.splom,
           varnames = dimnames(x)[[2]], ...,
           subpanel.scales, panel.cex=par()$cex)
```

Arguments

x, y, z, subscripts, pscales, subpanel, varnames, ...	See splom in S-Plus.
subpanel.scales	Controls the size of the tick labels in the diagonal panel.
panel.cex	Controls the size of the variable names in the diagonal panel.

Value

"trellis" object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

splom in S-Plus.

Examples

```
if.R(s={
     longley <- data.frame(longley.x, Employed = longley.y)
     },r={
     data(longley)
     })

if.R(s=
     splom( ~ longley, pch=16, cex=.55,
           superpanel=panel.pairs.hh, subpanel.scales=list(cex=.8),
           pscales=2,
           panel.cex=.8)
```

```
    ,r=
    splom( ~ longley, pch=16,
          pscales=2,
          varname.cex=.8,
          axis.text.cex=.5)
  )
```

`panel.xysplom` *panel method for xysplom.*

Description

panel method for xysplom. It has a `corr` argument that is removed before sending the information on to panel.xyplot.

Usage

```
panel.xysplom(corr, ...)
```

Arguments

`corr`	logical. If `TRUE`, display the correlation and/or the regression coefficient for `lm(y ~ x)` for each panel in an additional strip label.
`...`	Remaining arguments to `panel.xyplot`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`xysplom`

`partial.corr` *partial correlations*

Description

The partial correlation of x and y conditioning on z is the ordinary correlation of the residuals from the regression of x on z and the regression of y on z.

Usage

```
partial.corr(vars, cond)
```

Arguments

vars	matrix of data.frame of all the variables to be correlated.
cond	matrix of data.frame of all the variables to be conditioned on.

Value

matrix of partial correlations of the numeric variables in the argument vars conditioning on the numeric variables in cond.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
if.R(r=
partial.corr(longley[,1:3], longley[,4:6])
,s=
partial.corr(longley.x[,1:3], longley.x[,4:6])
)
```

---

pdf.latex *Construct a pdf file from a "latex" file. See Hmisc::latex for concepts.*

Description

Construct a "pdf" file from a "latex" file. See latex for concepts.

Usage

```
pdf.latex(latex.object, ..., file, overwrite = TRUE, copy.mode = TRUE, copy.date = TRUE)
```

Arguments

latex.object	Result from a call to Hmisc::latex().
...	Optional arguments to Hmisc::dvi()
file	File name in getwd() to place resulting pdf file.
overwrite	If the file already exists, TRUE means replace it.
copy.mode, copy.date	If TRUE copy file mode and date from temporary directory to getwd().

Value

Filename of class "dvi"

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

latex

Examples

```
## you will normally need these options.  See ?Hmisc::latex for details.
options(latexcmd='pdflatex')
options(dviExtension='pdf')
options(xdvicmd='open')  ## Macintosh, Windows,      SMP linux

## Not run:
## these examples place files in your current working directory

## matrix
tmp <- array(1:20, c(4,5), list(LETTERS[1:4], LETTERS[5:9]))
tmp

pdf.latex(latex(tmp)) ## for matrix, accept the default structure.tex and structure.pdf filenames.

pdf.latex(latex(tmp, title="tmp")) ## specify name of .tex and .pdf file.



## 3D array
tmp3 <- array(1:40, c(4,5,2), list(LETTERS[1:4], LETTERS[5:9], LETTERS[10:11]))
tmp3

pdf.latex(latex(tmp3)) ## for array, the default base filename is the
                       ##  name of the argument, hence tmp3.tex and tmp3.pdf

pdf.latex(latex(tmp3, title="somethingelse")) ## or specify somethingelse

## End(Not run)
```

---

pdiscunif *Discrete Uniform Distribution*

Description

Discrete Uniform Distribution

Usage

```
pdiscunif(q, size)
qdiscunif(p, size)
ddiscunif(q, size)
rdiscunif(n, size)
```

Arguments

size	parameter of distribution. Numbers from 1 to size are equally likely.
q	Quantiles.
p	Probability.
n	number of items in the random sample.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
q <- seq(-.5, 7.5, .5)

pp <- pdiscunif(q, 6)

## xyplot(pp ~ q,
##        scales=list(
##        x=list(at=floor(min(q)):ceiling(max(q))),
##        y=list(at=seq(0, 1, .1))))

qq <- qdiscunif(pp, 6)

dd <- ddiscunif(q, 6)

cbind(q, pp, qq, dd)

rdiscunif(12, 6)
```

---

perspPlane *Helper functions for regr2.plot*

Description

Helper functions for regr2.plot.

Usage

```
perspPlane(x, y, z, persp.out, ...)
perspFloor(x, y, z, persp.out, ...)
perspBack.wall.x(x, y, z, persp.out, ...)
perspBack.wall.y(x, y, z, persp.out, ...)
```

Arguments

x, y, z	Arguments to trans3d in R, or perspp in S-Plus.
persp.out	Result from previous call to persp.
...	Additional arguments to persp.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

regr2.plot

---

plot.hov *Homogeneity of Variance Plot*

Description

Oneway analysis of variance makes the assumption that the variances of the groups are equal. Brown and Forsyth, 1974 present the recommended test of this assumption. The Brown and Forsyth test statistic is the F statistic resulting from an ordinary one-way analysis of variance on the absolute deviations from the median. The hovPlot function graphs the components of the Brown and Forsyth test statistic.

Usage

```
hovPlot(x, data=NULL, method = "bf",  ## x is a formula
        transpose = TRUE, ...)

## users will normally use the formula above and will not call the
## method directly.
hovPlot.bf(x, group,  ## x is the response variable
           y.name = deparse(substitute(x)),
           group.name = deparse(substitute(group)),
           transpose = TRUE, ...)

## users will normally use the formula above and will not call the
## panel function directly.
panel.hov(..., transpose = TRUE)
```

Arguments

x	Formula appropriate for oneway anova in hovPlot. Response variable in hovPlot.bf.
data	data.frame
method	Character string defining method. At this time the only recognized method is "bf" for the Brown-Forsyth method.

transpose	Always TRUE in R. Normally TRUE in S-Plus to force vertical boxplots.
group	factor.
y.name	name of response variable, defaults to variable name in formula.
group.name	name of factor, defaults to variable name in formula.
...	additional arguments.

Value

"trellis" object with three panels containing boxplots for each group: The observed data "y", the data with the median subtracted "y-med(y)", and the absolute deviations from the median "abs(y-med(y))" The Brown and Forsyth test statistic is the F statistic resulting from an ordinary one-way analysis of variance on the data points in the third panel.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Brown, M.~B. and Forsyth, A.~B. (1974). *Robust tests for equality of variances*. *Journal of the American Statistical Association*, 69:364–367.

See Also

aov, hov

Examples

```
data(turkey)

hov(wt.gain ~ diet, data=turkey)
hovPlot(wt.gain ~ diet, data=turkey)
```

---

plot.mmc.multicomp *MMC (Mean–mean Multiple Comparisons) plot.*

Description

MMC (Mean–mean Multiple Comparisons) plot. The plot method documented here is no longer recommended for R; use mmcplot instead. This method is still necessary for S-Plus.

Usage

```
## S3 method for class 'mmc.multicomp'
plot(x,
     xlab="contrast value",
     ylab=none$ylabel,
     focus=none$focus,
     main= main.method.phrase,
     main2=main2.method.phrase,
     main.method.phrase=
       paste("multiple comparisons of means of", ylab),
     main2.method.phrase=paste("simultaneous ",
       100*(1-none$alpha),"% confidence limits, ",
       method, " method", sep="" ),
     ry.mmc=TRUE,
     key.x=par()$usr[1]+ diff(par()$usr[1:2])/20,
     key.y=par()$usr[3]+ diff(par()$usr[3:4])/3,
     method=if (is.null(mca)) lmat$method else mca$method,
     print.lmat=(!is.null(lmat)),
     print.mca=(!is.null(mca) && (!print.lmat)),
     iso.name=TRUE,
     x.offset=0,
     col.mca.signif="red",  col.mca.not.signif="black",
     lty.mca.signif=1,  lty.mca.not.signif=6,
     lwd.mca.signif=1,  lwd.mca.not.signif=1,
     col.lmat.signif="blue", col.lmat.not.signif="black",
     lty.lmat.signif=1, lty.lmat.not.signif=6,
     lwd.lmat.signif=1, lwd.lmat.not.signif=1,
     lty.iso=7, col.iso="darkgray", lwd.iso=1,
     lty.contr0=2, col.contr0="darkgray", lwd.contr0=1,
     decdigits.ybar=2,
     ...
     )
```

Arguments

x	mmc.multicomp object
xlab	"contrast value". An alternate "" can help unclutter a figure when several MMC plots are displayed together.
ylab	name of response variable
focus	define the factor to compute contrasts of.
main, main2	main and second line of title of plot
main.method.phrase, main2.method.phrase	default expressions for title of plot
ry.mmc	range of values on the y-axis. It is similar to par("ylim"), but not the same as additional calculations are needed to maintain the isomeans grid as a square.
key.x, key.y	location of the key displayed when iso.name=FALSE.

method	method used to construct contrasts and confidence intervals. See the type argument to glht for the list.
print.lmat	logical. If TRUE, then display the user-specified contrasts.
print.mca	logical. If TRUE, then display the pair-wise contrasts.
iso.name	logical. If TRUE, label the isomeans grid with the factor levels. If FALSE, label the isomeans grid with sequential numbers and display a key relating the numbers to the factor levels.
x.offset	amount to move the vertical 0 line to the left or right to reduce overprinting of labels and plotted lines.
col.mca.signif, lty.mca.signif, lwd.mca.signif	color, line type, line width for significant pairwise contrasts.
col.mca.not.signif, lty.mca.not.signif, lwd.mca.not.signif	color, line type, line width for non-significant pairwise contrasts.
col.lmat.signif, lty.lmat.signif, lwd.lmat.signif	color, line type, line width for significant user-specified contrasts.
col.lmat.not.signif, lty.lmat.not.signif, lwd.lmat.not.signif	color, line type, line width for non-significant user-specified contrasts.
lty.iso, col.iso, lwd.iso	color, line type, line width for the isomeans grid.
lty.contr0, col.contr0, lwd.contr0	color, line type, line width for the vertical contrast=0 line.
decdigits.ybar	number of decimal digits in the left-axis labels.
...	other arguments, currently ignored.

Note

plot.mmc.multicomp chooses sensible defaults for its many arguments. They will often need manual adjustment. The examples show several types of adjustments. We have changed the centering and scaling to avoid overprinting of label information. By default the significant contrasts are shown in a more intense color than the nonsignificant contrasts. We have an option to reduce the color intensity of the isomeans grid.

When there is overprinting of labels (a consequence of level means being close together), a tiebreaker plot may be needed. See ?MMC for an example.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, Richard M. and Holland, Burt (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

Hsu, J. and Peruggia, M. (1994). "Graphical representations of Tukey's multiple comparison method." *Journal of Computational and Graphical Statistics*, 3:143–161.

See Also

mmc, plotMatchMMC, mmcplot.

Examples

```
data(catalystm)
catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)
summary(catalystm1.aov)

## See ?MMC to see why these contrasts are chosen
catalystm.lmat <- cbind("AB-D" =c( 1, 1, 0,-2),
                        "A-B"  =c( 1,-1, 0, 0),
                        "ABD-C"=c( 1, 1,-3, 1))
dimnames(catalystm.lmat)[[1]] <- levels(catalystm$catalyst)


catalystm.mmc <-
if.R(r={mmc(catalystm1.aov, linfct = mcp(catalyst = "Tukey"),
            focus.lmat=catalystm.lmat)}
    ,s={multicomp.mmc(catalystm1.aov, focus.lmat=catalystm.lmat,
                      plot=FALSE)}
)

## Not run:
## pairwise contrasts, default settings
plot(catalystm.mmc, print.lmat=FALSE)

## End(Not run)

## Centering, scaling, emphasize significant contrasts.
## Needed in R with 7in x 7in default plot window.
## Not needed in S-Plus with 4x3 aspect ratio of plot window.
plot(catalystm.mmc, x.offset=2.1, ry.mmc=c(50,58), print.lmat=FALSE)

## user-specified contrasts
plot(catalystm.mmc, x.offset=2.1, ry.mmc=c(50,58))

## reduce intensity of isomeans grid, number isomeans grid lines
plot(catalystm.mmc, x.offset=2.1, ry.mmc=c(50,58),
     lty.iso=2, col.iso='darkgray', iso.name=FALSE)

## both pairwise contrasts and user-specified contrasts
plot(catalystm.mmc, x.offset=2.1, ry.mmc=c(50,58), lty.iso=2,
     col.iso='darkgray', print.mca=TRUE)

## Not run:
## newer mmcplot
mmcplot(catalystm.mmc)
mmcplot(catalystm.mmc, type="lmat")

## End(Not run)
```

`plot.multicomp` *Multiple comparisons plot that gives independent user control over the appearance of the significant and not significant comparisons.*

Description

Multiple comparisons plot that gives independent user control over the appearance of the significant and not significant comparisons. In R, both `plot.multicomp` `plot.multicomp.hh` coerce their argument to an `"glht"` object and plots that with the appropriate `plot` method. In R, `plot.multicomp.adjusted` replaces the bounds calculated by `multcomp:::confint.glht` with bounds based on a common standard error for a set of anova tables that are partitioned for the simple effects on an analysis conditioned on the levels of one of the factors. In S-Plus, `plot.multicomp.hh` augments the standard `plot.multicomp` to give additional user arguments to control the appearance of the plot.

`plotMatchMMC` uses the `plot.multicomp.hh` code. `plotMatchMMC` must immediately follow a plot of an `mmc.multicomp` object and is applied to either the `$mca` or `$lmat` component of the `mmc.multicomp` object. `plotMatchMMC` is used as a tiebreaker plot for the `MMC` plot. `plotMatchMMC` matches the horizontal scaling of the `MMC` plot and displays the individual contrasts in the same order as the `MMC` plot. See `mmc` for examples.

These functions are no longer recommended. Use `mmcplot` instead.

Usage

```
## S3 method for class 'multicomp'
plot(x, ...) ## R only

## S3 method for class 'multicomp.hh'
plot(x, ylabel = x$ylabel, href = 0, uniform = TRUE,
           plt.in = c(0.2, 0.9, 0.1, 0.9),
           x.label.adj=1,
           xrange.include=href,
           xlim,
           comparisons.per.page=21,
           col.signif=1, col.not.signif=1,
           lty.signif=4, lty.not.signif=4,
           lwd.signif=1, lwd.not.signif=1,
           ...,
           xlabel.print=TRUE, y.axis.side=2, ylabel.inside=FALSE)

plotMatchMMC(x, ...,
             xlabel.print=FALSE,
             cex.axis=par()$cex.axis,
             col.signif='red', main="",
             ylabel.inside=FALSE,
             y.axis.side=4,
             adjusted=FALSE)
```

Arguments

x	A "multicomp" object. plotMatchMMC will also accept a mmc.multicomp object. It will use the lmat component if there is one, otherwise it will use the mca component.
ylabel	Y label on graph.
y.axis.side	Y labels are on the left by default when plotting a "multicomp" object. We move them to the right when matching the x-axis of an MMC plot.
...	other arguments to plot.multicomp.
ylabel.inside	Logical value, if FALSE (the default), the plotMatchMMC right-axis labels are in the margin. If TRUE, the right-axis labels are in the figure area. Setting the argument to TRUE makes sense when plotting the lmat component of an mmc.multicomp object.
href	reference line for the intervals. The default is 0. S-Plus only.
xrange.include	xlim will be extended to include these values. S-Plus only.
uniform	S-Plus only. Logical value, if TRUE and the plots fill more than one page, the scale will be uniform across pages.
plt.in	S-Plus only. Value for par("plt") to make better use of the space on the plotting page.
x.label.adj	S-Plus only. This is the par("adj") applied to the x-location of the y.labels on the multicomp plot.
xlim	x-range of the plot.
comparisons.per.page	The default S-Plus plot.multicomp hardwires this to 21, which allows for all pairwise comparisons of 7 levels taken 2 at a time. The HH plot.multicomp makes it a variable. Use it together with plt.in to make better use of the space on the plot. S-Plus only.
lty.signif, lwd.signif	Line type, and line width for significant comparisons. S-Plus only.
col.signif	Color for significant comparisons. S-Plus only for plot.multicomp. Both R and S-Plus for plotMatchMMC.
col.not.signif, lty.not.signif, lwd.not.signif	Color, line type, and line width for non-significant comparisons. S-Plus only.
xlabel.print	logical. When TRUE, the caption under the plot is printed. When FALSE, the caption under the plot is not printed. It is helpful to set this to FALSE when the multicomp plot is used as a tiebreaker plot for the MMC plot. S-Plus only.
cex.axis	cex for axis ticklabels.
main	Main title for plot.
adjusted	Logical. When TRUE, HH:::plot.multicomp.adjusted is used to replace the standard confidence bounds calculated by multcomp:::confint.glht, with bounds calculated by as.multicomp.glht with a rescaled critical value based on rescaling the standard error. This rescaling is used to construct a common standard error for a set of anova tables that are partitioned for the simple effects on an analysis conditioned on the levels of one of the factors. See the clover.commonstrMS.clov.mmc example in file hh("scripts/Ch12-tway.r").

Value

`plot.multicomp` plots a `"multicomp"` object. In S-Plus, this masks the standard `plot.multicomp` in order to provide additional arguments for controlling the appearance. It defaults to the standard appearance. In R, it coerces its argument to a `"glht"` object and plots that with the appropriate `plot` method.

Note

The multiple comparisons calculations in R and S-Plus use completely different packages. Multiple comparisons in R are based on `glht`. Multiple comparisons in S-Plus are based on `multicomp`. The MMC plot in the HH package is the same in both systems. The details of getting the plot differ.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Heiberger, R. M. and Holland, B. (2006). "Mean–mean multiple comparison displays for families of linear contrasts." *Journal of Computational and Graphical Statistics*, 15:937–955.

See Also

`mmc` in both languages, `glht`.

Examples

```
## data and ANOVA
data(catalystm)

catalystm1.aov <- aov(concent ~ catalyst, data=catalystm)
summary(catalystm1.aov)

catalystm.mca <-
if.R(r=glht(catalystm1.aov, linfct = mcp(catalyst = "Tukey")),
     s=multicomp(catalystm1.aov, plot=FALSE))
if.R(s=plot(catalystm.mca),
     r=plot(confint(catalystm.mca, calpha=qtukey(.95, 4, 12)/sqrt(2))))
       ## calpha is strongly recommended in R with a large number of levels
       ## See ?MMC for details.
```

position	*Find or assign the implied position for graphing the levels of a factor. A new class "positioned", which inherits from "ordered" and "factor", is defined.*

Description

The default values for plotting a factor x are the integers `1:length(levels(x))`. These functions provide a way of specifying alternate plotting locations for the levels.

Usage

```
position(x)

position(x) <- value

## S3 method for class 'positioned'
is.numeric(x, ...)
## S3 method for class 'positioned'
as.numeric(x, ...)
## S3 method for class 'positioned'
x[..., drop=FALSE]
## S3 method for class 'positioned'
is.na(x)
as.positioned(x)
as.position(x)
is.positioned(x)
positioned(x, ..., value)
## S3 method for class 'positioned'
print(x, ...)
## S3 method for class 'positioned'
unique(x, incomparables = FALSE, ...)
unpositioned(x, ...)
```

Arguments

x	numeric vector or factor
value	numerical values to be associated with `levels(x)`. The `length(value)` must equal `length(levels(as.factor(x)))`.
...	other arguments.
drop	See `Extract`.
incomparables	See `unique`.

Value

`position(x) <- value` first forces its argument to be an ordered factor and then assigns the `value` to the `"position"` attribute of the ordered factor. The result is assigned class `"positioned"` and returned.

`position(x)` returns the position values associated with `levels(x)`. If `x` is a positioned factor, then the `"position"` attribute is returned. If `x` is a factor, then the integers `1:length(levels(x))` are returned. For anything else, `as.numeric(x)` is returned.

`as.position(x)` returns a numeric vector the length of the original vector. If `x` inherits from `"factor"`, then the values in the vector are the values in `position(x)` subscripted by the levels of the factor. If `x` is numeric, then `x` itself is returned.

`unpositioned(x)` removes the `"position"` attribute and removes the `"positioned"` value from the the `class` of the object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`panel.interaction2wt`, `factor`.

Examples

```
## ordered with character levels defaults to
## integer position of specified levels
tmp <- ordered(c("mm","cm","m","m","mm","cm"),
               levels=c("mm","cm","m")) ## size order
tmp
as.numeric(tmp)
levels(tmp)
position(tmp)
as.position(tmp)
as.positioned(tmp)
positioned(tmp)
unpositioned(tmp)
unique(tmp)

## position is assigned to ordered in specified order
tmp <- ordered(c("cm","mm","m","m","mm","cm"),
               levels=c("mm","cm","m")) ## size order
levels(tmp)
position(tmp) <- c(-3, -2, 0) ## log10 assigned in size order
tmp
as.numeric(tmp)
levels(tmp)
position(tmp)
as.position(tmp)
as.positioned(tmp)
positioned(tmp)
unpositioned(tmp)
```

```
unique(tmp)

## numeric stays numeric
tmp <- c(0.010, 0.001, 1.000, 1.000, 0.001, 0.010)
tmp
as.numeric(tmp)
levels(tmp)
position(tmp)
as.position(tmp)
as.positioned(tmp)
positioned(tmp)
unpositioned(tmp)
unique(tmp)

## factor with numeric levels, position is integer position in size order
tmp <- factor(c(0.010, 0.001, 1.000, 1.000, 0.001, 0.010))
tmp
as.numeric(tmp)
levels(tmp)
position(tmp)
as.position(tmp)
as.positioned(tmp)
positioned(tmp)
unpositioned(tmp)
unique(tmp)

## ordered with numeric levels, position is numeric value in size order
tmp <- ordered(c(0.010, 0.001, 1.000, 1.000, 0.001, 0.010))
tmp
as.numeric(tmp)
levels(tmp)
position(tmp)
as.position(tmp)
as.positioned(tmp)
positioned(tmp)
unpositioned(tmp)
unique(tmp)


## factor with numeric levels
## position is assigned in size order
tmp <- factor(c(0.010, 0.001, 1.000, 1.000, 0.001, 0.010))
levels(tmp)
position(tmp) <- c(-3, -2, 0) ## log10 assigned in size order
tmp
as.numeric(tmp)
levels(tmp)
position(tmp)
as.position(tmp)
as.positioned(tmp)
positioned(tmp)
unpositioned(tmp)
unique(tmp)
```

```
## boxplots coded by week
tmp <- data.frame(Y=rnorm(40, rep(c(20,25,15,22), 10), 5),
                  week=ordered(rep(1:4, 10)))
position(tmp$week) <- c(1, 2, 4, 8)

bwplot(Y ~ week, horizontal=FALSE,
       scales=list(x=list(limits=c(0,9),
                          at=position(tmp$week),
                          labels=position(tmp$week))),
       data=tmp, panel=panel.bwplot.intermediate.hh)


#### You probably don't want to use the next two examples.
#### You need to be aware of their behavior.
##
## factor with character levels defaults to
## integer position of sorted levels.
## you probably DON'T want to do this!
tmp <- factor(c("cm","mm","m","m","mm","cm")) ## default alphabetic order
tmp
as.numeric(tmp)
levels(tmp)   ## you probably DON'T want to do this!
position(tmp) ## you probably DON'T want to do this!
as.numeric(tmp)
##
## position is assigned to factor in default alphabetic order.
## you probably DON'T want to do this!
tmp <- factor(c("cm","mm","m","m","mm","cm"))
levels(tmp)
position(tmp) <- c(-3, -2, 0) ## assigned in default alphabetic order
tmp
as.numeric(tmp)
levels(tmp)   ## you probably DON'T want to do this!
position(tmp) ## you probably DON'T want to do this!
as.numeric(tmp)
```

`positioned-class` *Class "positioned", extends "ordered" to specify the position for graphing the levels of a factor.*

Description

The default values for plotting a factor `x` are the integers `1:length(levels(x))`. This class and its functions provide a way of specifying alternate plotting locations for the levels.

Objects from the Class

A virtual Class: No objects may be created from it.

Extends

Class "ordered", directly. Class "factor", by class "ordered", distance 2. Class "oldClass", by class "ordered", distance 3.

Methods

No methods defined with class "positioned" in the signature. S3-type methods are "[.positioned", as.double.positioned, as.numeric.positioned, as.positioned, is.numeric.positioned, is.positioned, positioned, print.positioned, unique.positioned.
Although interaction.positioned should be a method, it isn't because interaction is not a generic and can't easily be made one since the name interaction.plot conflicts.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

position.

---

print.latticeresids *Print a* latticeresids *object.*

Description

Print a latticeresids object.

Usage

```
## S3 method for class 'latticeresids'
print(x, ...,
           A321.left=0, A321.bottom=0.27,
           A4.left=0, A4.top=0.30,
           position=list(
             A321=c(A321.left,     A321.bottom, 1, 1     ),
             A4  =c(A4.left,       0,           1, A4.top)),
           panel.width=NULL,
           which=1:4)
```

Arguments

x	A latticeresids object.
A321.left, A321.bottom, A4.left, A4.top, position	The first three rows are on the same x scale (the scales of the independent variables). The arguments with "A321" in their name are used to construct the position argument to print.trellis for the first three rows. The fourth row is on a different x scale (the scales of each independent variable adjusted for all the other x variables). The arguments with "A4" in their name are used to construct the position argument to print.trellis for the fourth row. The two sets of rows {1,2,3} and {4} may have different widths for their left axis tick labels. The arguments A321.left and A4.left along with absolute dimensions for panel.width ("cm" or "in", not "npc") can be hand-tailored to make the columns line up precisely. See the example.
panel.width	the panel.width argument of print.trellis.
which	Vector of row numbers which are to be printed. If not all four printed, consider adjusting the A321.bottom and A4.top values.
...	Other arguments for print.

Details

The four trellis objects, one for each type of plot, are printed as a single four-row lattice object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

residual.plots.lattice

---

print.NormalAndTplot *Print method for Normal and t plots from NTplot.*

Description

Print method for Normal and t plots from NTplot.

Usage

```
## S3 method for class 'NormalAndTplot'
print(x, tablesOnPlot=TRUE, plot=TRUE,
                scales=FALSE, prob=FALSE, call=FALSE,
                ..., cex.table=.7, digits=attr(x, "call.list")$digits,
                position.2=.17)
```

Arguments

x	A "NormalAndTplot" object.
tablesOnPlot	Logical. If TRUE, display the tables in the attr(x, "scales") and attr(x, "prob") on the plot.
plot	Logical. If TRUE, display the graph on the plot.
scales, prob	Logical. If TRUE, display the specified attribute on the R Console.
call	Logical. If TRUE, display an R statement on the R console.
...	Other arguments are ignored.
cex.table, digits	cex and digits for the tablesOnPlot display of the attr(x, "scales") and attr(x, "prob") tables.
position.2	When tablesOnPlot=TRUE, the graph occupies the top of the device beginning at position.2. This is the second value in the position argument of print.trellis.

Value

The argument is returned invisibly.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

NTplot, NormalAndTplot.

---

print.tsdiagplot *Print a "tsdiagplot" object.*

Description

Print a "tsdiagplot" object.

Usage

```
## S3 method for class 'tsdiagplot'
print(x, ..., portrait=FALSE)
print1.tsdiagplot(x)
print2.tsdiagplot(x)
```

Arguments

x	a "tsdiagplot" object
...	Optional arguments to print. The only ...\ argument that is used is pages. If pages is not used or pages==1, then use print1.tsdiagplot. If pages!=1, then use print2.tsdiagplot.
portrait	logical. If FALSE, arrange the panels for a landscape orientation (pdf with width=12 inches looks good). If TRUE, arrange the panels for a portrait orientation (pdf with height=13 inches looks good).

Details

A "tsdiagplot" object is a collection of several "trellis" objects. We provide two options for printing them.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

tsdiagplot

---

print.TwoTrellisColumns

Print two conformable trellis plots in adjacent columns with user control of widths.

Description

Print two conformable trellis plots in adjacent columns with user control of widths. Left y ticklabels and left.strip are removed from the right-hand plot.

Usage

```
as.TwoTrellisColumns5(left,  ## left  is the left trellis object
                      right, ## right is the right trellis object
                      ## Both left and right must have identical
                      ## settings for number and size of vertical panels,
                      ## left-axis labels, number of lines in main, sub, legend.
                      ...,
                      pw=c(.3, .30, .01, .30, .09),
                      px=list(
                        LL=c(0, pwc[1]),
                        LP=pwc[1:2],
                        ML=pwc[2:3],
                        RP=pwc[3:4],
```

```
                        RL=pwc[4:5]),
                      pwc=cumsum(pw),
                      strip.left=TRUE,
                      y.tck=c(0,0)
                      )

## S3 method for class 'TwoTrellisColumns5'
print(x, px=attr(x, "px"), ...)

leftLabels.trellis(x)
rightLabels.trellis(x)
panelOnly.trellis(x, strip.left=FALSE, y.tck=0)
mainSubLegend.trellis(x)
emptyRightAxis(x)
```

Arguments

left, right	Conformable "trellis" objects. Both must have the identical settings for number and size of vertical panels, left-axis labels, number of lines in main, sub, legend.
x	"trellis" object.
px	These are used x-values used in the position argument of the print.trellis function. The default (constructed from the pw argument) makes the Left and Right panels the same width and the Middle containing the y-axis is given the remainder. Overlapping is permitted. The appearance depends on the width of the graphics device.
pw, pwc	pw vector of five positive numbers that sum to 1. These are the relative widths of the five sections of the result: LeftLabels, LeftPanel, MainSubLegend, RightPanel, RightLabels. pwc is the cumulative sum of pw. pwc is expanded in the px argument to the x values used in the position argument of the print.trellis function.
strip.left	See barchart.
y.tck	A vector of one or two numeric values. This will be used as the y tck value for the right column of panels. See 'tck' in barchart for details.
...	Other arguments are ignored.

Details

as.TwoTrellisColumns5 constructs a "TwoTrellisColumns5" object, which is a list of five trellis objects named "LL", "LP","ML", "RP", "RL". LL is the left labels from the left input object. LP is the panels from the left input object. ML is the middle labels from the left object; these are the main title, sub title, and legend. RP is the panels from the right input object. RL is the right labels from the right input object.

print.TwoTrellisColumns5 is a print method for a "TwoTrellisColumns5" object. It takes left-to-right positioning information from the "px" attribute of its argument x or from an input argument. The numbers are used as the "x" information for the position argument to the print.trellis method.

`emptyLeftAxis`,`leftLabels.trellis`,`rightLabels.trellis`,`panelOnly.trellis`, `mainSubLegend.trellis`,`emptyLeftStrip`,`emptyRightAxis` are functions which blank out the various components of the trellis argument and retains their vertical spacing.

Value

A "`TwoTrellisColumns5`" object, consisting of a list containing the constructed left, middle, and right trellis objects, and an attribute containing the `px` value.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`likert` for the details on the motivating example.

Examples

```
## These are based on the Professional Challenges example in ?likert
data(ProfChal)
levels(ProfChal$Subtable)[6] <- "Prof Recog" ## reduce length of label

## initial ordering of Question factor
PCC <- likert(Question ~ . | Subtable, ProfChal, ylab=NULL,
              rightAxis=TRUE,
              layout=c(1,6),
              strip=FALSE,
              strip.left=strip.custom(bg="gray97"),
              par.strip.text=list(cex=.7),
              scales=list(y=list(relation="free")),
              main="Is your job professionally challenging?")

## initial ordering of Question factor
PCP <- likert(Question ~ . | Subtable, ProfChal, ylab=NULL,
              as.percent=TRUE,
              layout=c(1,6),
              strip=FALSE,
              strip.left=strip.custom(bg="gray97"),
              par.strip.text=list(cex=.7),
              scales=list(y=list(relation="free")),
              main="Is your job professionally challenging?")

## Not run:
## default equal widths of the two panels
as.TwoTrellisColumns5(PCP, PCC)  ## 11in x 7in

## make left panel twice as wide as right panel
as.TwoTrellisColumns5(PCP, PCC, pw=c(.3, .4, .01, .2, .09))  ## 11in x 7in
##                                  --------------------    ## sum to 1.00
```

```
## make left panel twice as wide as right panel, and control position of main and legend
as.TwoTrellisColumns5(PCP, PCC,  ## 11in x 7in
                      px=list(
                        LL=c(.00,  .30),
                        LP=c(.30,  .70),
                        ML=c(.60,  .61),  ## arbitrary,
                                          ## visually center the labels and legend
                        RP=c(.71,  .91),
                        RL=c(.91, 1.00)))

## End(Not run)

## Size that works in default 7x7 window.  7x7 is not recommended for
## this example because most of the space is used for labeling and not
## much for the panels containing the data.  Use the px values for the
## 11x7 illustrated above in the dontrun section.

as.TwoTrellisColumns5(PCP, PCC,  ## 7in x 7in
                      px=list(
                        LL=c(.00,  .50),
                        LP=c(.50,  .70),
                        ML=c(.50,  .51),  ## arbitrary,
                                          ## visually center the labels and legend
                        RP=c(.71,  .87),
                        RL=c(.87, 1.00)))

## Ordering the rows by the lengths of the positive bars and also
## put percents and counts on the same plot.
## The easiest way is to use the LikertPercentCountColumns function:

LikertPercentCountColumns(Question ~ . | Subtable, ProfChal,
                          layout=c(1,6), scales=list(y=list(relation="free")),
                          ylab=NULL, between=list(y=0),
                          strip.left=strip.custom(bg="gray97"), strip=FALSE,
                          par.strip.text=list(cex=.7),
                          positive.order=TRUE,
                          main="Is your job professionally challenging?")

## Not run:

## Ordering the rows by the lengths of the positive bars and also
## putting percents and counts on the same plot requires coordination.
## The easiest way is to order the original tables of counts by the
## order of the percent plot.

percentPlot <- likert(Question ~ . | Subtable, ProfChal,
                      as.percent=TRUE,
                      layout=c(1,6), scales=list(y=list(relation="free")),
                      ylab=NULL, between=list(y=0),
                      strip.left=strip.custom(bg="gray97"), strip=FALSE,
                      par.strip.text=list(cex=.7),
                      positive.order=TRUE,
                      main="Is your job professionally challenging?")
```

```
## percentPlot
pct.order <- percentPlot$y.limits[[1]]

ProfChal2 <- ProfChal
ProfChal2$Question <- factor(ProfChal2$Question, levels=rev(pct.order))

countPlot   <- likert(Question ~ . | Subtable, ProfChal2,
                      layout=c(1,6),
                      rightAxis=TRUE,
                      scales=list(y=list(relation="free"),
                                  x=list(at=c(0, 250, 500))),
                      ylab=NULL, between=list(y=0),
                      strip.left=strip.custom(bg="gray97"), strip=FALSE,
                      par.strip.text=list(cex=.7),
                      main="Is your job professionally challenging?")
## countPlot
levels(ProfChal$Subtable)[6] <-
      "Attitude\ntoward\nProfessional\nRecognition" ## Restore original label

## Size that works in default 7x7 window.  7x7 is not recommended for
## this example because most of the space is used for labeling and not
## much for the panels containing the data.  Use the px values for the
## 11x7 illustrated above in the dontrun section.

as.TwoTrellisColumns5(percentPlot, countPlot,  ## 7in x 7in
                      px=list(
                        LL=c(.00,  .50),
                        LP=c(.50,  .70),
                        ML=c(.50,  .51),  ## arbitrary,
                                          ## visually center the labels and legend
                        RP=c(.71,  .87),
                        RL=c(.87, 1.00)))

## End(Not run)
```

---

push.vp.hh *push and pop a grid viewport, turn clipping off, change scale.*

Description

push and pop a grid viewport, turn clipping off, change scale.

Usage

```
push.vp.hh(scale = 100)
pop.vp.hh()
```

Arguments

scale	argument to the unit function.

Details

Used in panel.cartesian to ease labeling the rows and columns of a scatterplot matrix.

Value

An object of class "unit".

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

viewport, unit, panel.cartesian

---

pyramidLikert *Print a Likert plot as a Population Triangle*

Description

Prints a likert plot in the traditional format for a population pyramid, with the Left and Right sides in separate panels, with the x-tick marks on the left side made positive, and with the y-axis in the Middle.

Usage

```
## S3 method for class 'pyramidLikert'
print(x, ...,
                     panel.width=.48,
                     px=list(
                       L=c(0, panel.width),
                       R=c(1-panel.width, 1),
                       M=c(panel.width, 1-panel.width)),
                    keepLegend=(length(x$legend$bottom$args$text) > 2),
                    xlab.top=list(
                      L=list(x$legend$bottom$args$text[1]),
                      R=list(x$legend$bottom$args$text[2]),
                      M=list(x$ylab, just=1)))

as.pyramidLikert(x, ...,
                  panel.width=.48,
                  px=list(
                    L=c(0, panel.width),
                    R=c(1-panel.width, 1),
                    M=c(panel.width, 1-panel.width)),
                  keepLegend=(length(x$legend$bottom$args$text) > 2),
                  xlab.top=list(
```

```
                    L=list(x$legend$bottom$args$text[1]),
                    R=list(x$legend$bottom$args$text[2]),
                    M=list(x$ylab, just=1)))
```

Arguments

x	a single-panel 'trellis' object.
...	Other arguments are ignored.
panel.width	Numeric scalar between 0 and 0.5. Common width of left and right panels. The default value .48 value works well for the USAge.table example. This number is expanded in the px argument to the x values used in the position argument of the print.trellis function.
px	x values used in the position argument of the print.trellis function. The default makes the Left and Right panels the same width and the Middle containing the y-axis is given the remainder.
keepLegend	If TRUE and x contains a bottom legend, then it is printed along with the Middle section containing the y-axis. If FALSE or there is no bottom legend, then the bottom legend is not printed.
xlab.top	A vector of three labels. The default is designed for a population triangle with two levels (usually, Male on one side and Female on the other). The Left and Right labels are taken from the first two labels in the legend. The Middle value is the variable name for the y-axis.

Details

This is a print method for population triangles. It is designed for a likert plot with one left-side level and one right-side level. It works for any single-panel "trellis" object, in the sense that it produces a plot.

Value

The input argument x.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

likert

Examples

```
data(USAge.table)  ## from latticeExtra
USA79 <- USAge.table[75:1, 2:1, "1979"]/1000000
PL <- plot(as.likert(USA79),
                    main="Population of United States 1979 (ages 0-74)",
                    xlab="Count in Millions",
                    ylab="Age",
```

```
                      scales=list(
                        y=list(
                          limits=c(0,77),
                          at=seq(1,76,5),
                          labels=seq(0,75,5),
                          tck=.5))
                         )
PL
as.pyramidLikert(PL)

likert(USAge.table[75:1, 2:1, c("1939","1959","1979")]/1000000,
       main="Population of United States 1939,1959,1979 (ages 0-74)",
       sub="Look for the Baby Boom",
       xlab="Count in Millions",
       ylab="Age",
       scales=list(
         y=list(
           limits=c(0,77),
           at=seq(1,76,5),
           labels=seq(0,75,5),
           tck=.5)),
       strip.left=FALSE, strip=TRUE,
       layout=c(3,1), between=list(x=.5))

## Not run:
  ## run the shiny app
if (interactive())  shiny::runApp(system.file("shiny/PopulationPyramid", package="HH"))

## End(Not run)

## For additional examples, see demo(PoorChildren, package="HH")
```

`rbind.trellis` *Extend matrix reshaping functions to trellis objects.*

Description

Extend matrix reshaping functions to trellis objects. See the details section for comparisons with similar functions in the **lattice** package.

Usage

```
transpose(x)
## S3 method for class 'trellis'
transpose(x)
## Default S3 method:
transpose(x)
## S3 method for class 'trellis'
aperm(a, perm, ...)
```

```
## S3 method for class 'trellis'
rbind(..., deparse.level=1,
      combineLimits=TRUE, useOuterStrips=TRUE)
## S3 method for class 'trellis'
cbind(..., deparse.level=1,
      combineLimits=TRUE, useOuterStrips=TRUE)
```

Arguments

`...`, `x`, `a`	A set of `trellis` objects.
`perm`	Permutation vector, see `aperm` for details.
`combineLimits`, `useOuterStrips`	logical. If `TRUE` (the default), use the similarly named **latticeExtra** functions before returning the result.
`deparse.level`	See `cbind` for details. These functions ignore this argument and always use the `names(list(...))`, if non-`NULL`, for the labels. If `NULL`, then the first `length(list(...))` uppercase letters are used.

Details

`transpose.trellis` tries to capture and modify all potentially relevant trellis components. `transpose.trellis` is more comprehensive than the similar `t.trellis` which adjusts only the `perm.cond` component.

`aperm.trellis` does not attempt to check all potentially relevant trellis components. It does not adjust `layout.heights`, `layout.widths`, or `between` It may show strange axis positions or strip positions for any non-standard arrangement, for example, for any trellis object that has already been through `latticeExtra::combineLimits`.

Value

trellis object constructed from arguments with new dim and layout.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
F <- xyplot((1:15) ~ (1:15) | rep(factor(letters[3:5]), each=5))
G <- xyplot((1:18) ~ (1:18) | rep(factor(letters[3:5]), each=6))
rbind(AAA=F, BBB=G)
cbind(AAA=F, BBB=G)

tmp <- data.frame(y=1:24,
                  x=1:24,
                  a=rep(letters[1:2], each=12),
                  b=rep(letters[3:5], each=4, times=2),
                  c=rep(letters[6:9], times=6))

t3 <- xyplot(y ~ x | c*b*a, data=tmp,
             panel=function(x, y, ...) panel.text(x, y, y),
```

```
             scales=list(alternating=FALSE))
## t3
t3u <- update(t3, layout=c(4*3, 2), between=list(x=c(0,0,0,1)), main="t3")
useOuterStripsT2L1(t3u)

## Not run:
## update(t3, layout=c(24, 1))

t3.321 <- aperm(t3, c(3,2,1))
update(t3.321, main="t3.321", layout=c(6,4), between=list(x=c(0,1))) ## 2*3,4

try(transpose(t3))   ## requires a one- or two-dimensional trellis object.

t3.123 <- aperm(t3, c(1,2,3)) ## identity operation
t3.132 <- aperm(t3, c(1,3,2))
t3.213 <- aperm(t3, c(2,1,3))
t3.231 <- aperm(t3, c(2,3,1))
t3.312 <- aperm(t3, c(3,1,2))
t3.321 <- aperm(t3, c(3,2,1))

u3.123 <- update(t3.123, main="t3.123", layout=c(12,2),
                 between=list(x=c(0,0,0,1))) ## 4*3,2
u3.132 <- update(t3.132, main="t3.132", layout=c(8,3),
                 between=list(x=c(0,0,0,1))) ## 4*2,3
u3.213 <- update(t3.213, main="t3.213", layout=c(3,8),
                 between=list(y=c(0,0,0,1)), par.strip.text=list(cex=.8)) ## 3,4*2
u3.231 <- update(t3.231, main="t3.231", layout=c(6,4),
                 between=list(x=c(0,0,1))) ## 2*3,4
u3.312 <- update(t3.312, main="t3.312", layout=c(2,12),
                 between=list(y=c(0,0,0,1)), par.strip.text=list(cex=.6)) ## 2,3*4
u3.321 <- update(t3.321, main="t3.321", layout=c(6,4),
                 between=list(x=c(0,1))) ## 2*3,4

u5 <- tempfile("u5", fileext = ".pdf")
pdf(u5, width=17, height=22)
print(u3.123, split=c(1,1,2,3), more=TRUE)
print(u3.132, split=c(2,1,2,3), more=TRUE)
print(u3.213, split=c(1,2,2,3), more=TRUE)
print(u3.231, split=c(2,2,2,3), more=TRUE)
print(u3.312, split=c(1,3,2,3), more=TRUE)
print(u3.321, split=c(2,3,2,3), more=FALSE)
dev.off()

try(transpose(t3.123)) ## layout is a matrix, but dim is not.

## End(Not run)

## Not run:
t2 <- xyplot(y ~ x | b*c, data=tmp,
             panel=function(x, y, ...) panel.text(x, y, y),
             scales=list(alternating=FALSE))
t2
```

```
## aperm(t2, 1:2) ## identity

transpose(t2)
aperm(t2, 2:1)

t1a <- xyplot(y ~ x | b, data=tmp[tmp$a=="a",])
t1b <- xyplot(y ~ x | b, data=tmp[tmp$a=="b",])
t1a
t1b

rbind(t1a, t1b)
rbind(AAA=t1a, BBB=t1b)

cbind(t1a, t1b)
cbind(AAA=t1a, BBB=t1b)

## End(Not run)
```

`regr1.plot` *plot x and y, with optional straight line fit and display of squared residuals*

Description

Plot `x` and `y`, with optional fitted line and display of squared residuals. By default the least squares line is calculated and used. Any other straight line can be specified by placing its coefficients in `coef.model`. Any other fitted model can be calculated by specifying the `model` argument. Any other function of one variable can be specified in the `alt.function` argument. At most one of the arguments `model`, `coef.model`, `alt.function` can be specified.

Usage

```
regr1.plot(x, y,
           model=lm(y~x),
           coef.model,
           alt.function,
           main="put a useful title here",
           xlab=deparse(substitute(x)),
           ylab=deparse(substitute(y)),
           jitter.x=FALSE,
           resid.plot=FALSE,
           points.yhat=TRUE,
           pch=16,
           ..., length.x.set=51,
           x.name,
           pch.yhat=16,
           cex.yhat=par()$cex*.7,
           err=-1)
```

Arguments

x	x variable
y	y variable
model	Defaults to the simple linear model lm(y ~ x). Any model object with one x variable, such as the quadratic lm(y ~ x + I(x^2)) can be used.
coef.model	Defaults to the coefficients of the model argument. Other intercept and slope coefficients for a straight line (for example, c(3,5)) can be entered to illustrate the sense in which they are not "least squares".
alt.function	Any function of a single argument can be placed here. For example, alt.function=function(x) {3 + 2*x + 3*x^2}. All coefficients must be specified.
main, xlab, ylab	arguments to plot.
jitter.x	logical. If TRUE, the x is jittered before plotting. Jittering is often helpful when there are multiple y-values at the same level of x.
resid.plot	If FALSE, then do not plot the residuals. If "square", then call resid.squares to plot the squared residuals. If TRUE (or anything else), then call resid.squares to plot straight lines for the residuals.
points.yhat	logical. If TRUE, the predicted values are plotted.
...	other arguments.
length.x.set	number of points used to plot the predicted values.
x.name	If the model argument used a different name for the independent variable, you might need to specify it.
pch	Plotting character for the observed points.
pch.yhat	Plotting character for the fitted points.
cex.yhat	cex for the fitted points.
err	The default -1 suppresses warnings about out of bound points.

Note

This plot is designed as a pedagogical example for introductory courses. When resid.plot=="square", then we actually see the set of squares for which the sum of their areas is minimized by the method of "least squares".

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Smith, W. and Gonick, L. (1993). *The Cartoon Guide to Statistics*. HarperCollins.

See Also

resid.squares

Examples

```
data(hardness)

## linear and quadratic regressions
hardness.lin.lm  <- lm(hardness ~ density,                data=hardness)
hardness.quad.lm <- lm(hardness ~ density + I(density^2), data=hardness)

anova(hardness.quad.lm)  ## quadratic term has very low p-value

par(mfrow=c(1,2))

regr1.plot(hardness$density, hardness$hardness,
           resid.plot="square",
           main="squared residuals for linear fit",
           xlab="density", ylab="hardness",
           points.yhat=FALSE,
           xlim=c(20,95), ylim=c(0,3400))

regr1.plot(hardness$density, hardness$hardness,
           model=hardness.quad.lm,
           resid.plot="square",
           main="squared residuals for quadratic fit",
           xlab="density", ylab="hardness",
           points.yhat=FALSE,
           xlim=c(20,95), ylim=c(0,3400))

par(mfrow=c(1,1))
```

---

regr2.plot *3D plot of z against x and y, with regression plane fit and display of squared residuals.*

Description

3D plot of z against x and y, with regression plane fit and display of squared residuals.

Usage

```
regr2.plot(x, y, z,
           main.in="put a useful title here",
           resid.plot=FALSE,
           plot.base.plane=TRUE,
           plot.back.planes=TRUE,
           plot.base.points=FALSE,
           eye=NULL,                    ## S-Plus
```

```
            theta=0, phi=15, r=sqrt(3), ticktype="detailed", ## R
            ...)
```

Arguments

x, y, z	See persp.
main.in	main title for plot.
resid.plot	Argument to resid.squares.
plot.base.plane, plot.back.planes, plot.base.points	Should these items be plotted?
eye	S-Plus only. See persp.
theta, phi, r, ticktype	R only. See persp.
...	Other arguments to persp.

Value

"Viewing Transformation" for projecting 3D coordinates (x,y,z) into the 2D plane. See persp for details.

Note

This plot is designed as a pedagogical example for introductory courses. When resid.plot=="square", then we actually see the set of squares for which the sum of their areas is minimized by the method of "least squares". The demo called in the examples section shows the geometry of regression coefficients, the change in predicted y when x1 is changed one unit holding all other x variables constant.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

Smith, W. and Gonick, L. (1993). *The Cartoon Guide to Statistics*. HarperCollins.

See Also

resid.squares, regr1.plot, persp

Examples

```
data(fat)
regr2.plot(fat[,"abdomin"], xlab="abdomin",
           fat[,"biceps"],  ylab="biceps",
           fat[,"bodyfat"], zlab="bodyfat",
           resid.plot="square",
           eye=c(335.5, 115.65, 171.9),   ## used only in S-Plus
           theta=140, phi=35, r=sqrt(15), ## used only in R
           box=is.R(),
           plot.back.planes=FALSE,
           main="Least-squares with two X-variables")

## Not run:
  demo("regr2", package="HH", ask=FALSE)
  ## run the file manually to see the individual steps.

## End(Not run)
```

`regrresidplot` *Draw a plot of y vs x from a linear model object, with residuals indicated by lines or squares.*

Description

Draw a plot of response vector y vs predictor variable x from a linear model object all of whose predictors are a function of x, with residuals indicated by lines or squares.

Usage

```
regrresidplot(x, y, resid.plot = FALSE, fit.line=TRUE,
              lm.object = lm(y ~ x), x.name = names(lm.object$model)[2],
              col = trellis.par.get()$plot.symbol$col,
              col.yhat = NULL, col.fit = "gray80", col.resid = "gray40", ...)

panel.residSquare(x, y, yhat, resid.plot = FALSE, col = "black", ...)
```

Arguments

`x`	Predictor variable. Must be a vector or a single column.
`y`	Response variable. Must be a vector or a single column.
`yhat`	Predicted value of y based on the model in `lm.object` over the `xlim` range of the plot.
`resid.plot`	Logical or character. Should the residuals from `lm.object` be plotted, and how? Default is `FALSE`. Alternatives are `TRUE` for lines and `"square"` for squares.
`fit.line`	Logical. Should the fitted regression line from `lm.object` be plotted? Default `TRUE`.

lm.object	Linear model object of y against some function of x. The default value is the simple linear regression of lm(y ~ x).
x.name	Name of x-variable to be used in the construction of the fitted values.
col	Color of observed points.
col.yhat	Color of fitted points. Default is NULL.
col.fit	Color of fitted line.
col.resid	Color of residuals, either lines or squares depending on the value of resid.plot.
...	Additional arguments to the panel functions.

Value

regrresidplot returns a "trellis" object. panel.residSquare is a panel function with no useful returned value.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
data(fat)
fat.lm <- lm(bodyfat ~ abdomin, data=fat)

AA <- regrresidplot(fat$abdomin, fat$bodyfat, xlim=c(70,185), ylim=c(0,50))
BB <- regrresidplot(fat$abdomin, fat$bodyfat, xlim=c(70,185), ylim=c(0,50),
                    resid.plot="line")
CC <- regrresidplot(fat$abdomin, fat$bodyfat, xlim=c(70,185), ylim=c(0,50),
                    resid.plot="square")

update(between=list(y=1),
       c("Residuals Not Displayed"=AA,
         "Residual Lines"=BB,
         "Residual Squares"=CC, layout=c(1,3)))
```

---

resid.squares *plot squared residuals in inches to match the y-dimension*

Description

plot squared residuals in inches to match the y-dimension

Usage

```
resid.squares(x, y, y.hat, resid.plot = "square", ...)
```

Arguments

x	x values
y	observed y values
y.hat	predicted y values
resid.plot	If "square", then plot the squared residuals. If TRUE (or anything else), then plot straight lines for the residuals.
...	Other graphics arguments.

Details

The goal is to get real squares on the screen or paper. The trick is to play games with the aspect ratio. We find the number of inches that each vertical residual occupies. We then find the number of x-units that corresponds to, and plot a rectangle with height=height in the y-data units and with width=the number of x-units that we just calculated.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

regr1.plot

Examples

```
data(hardness)

hardness.lin.lm  <- lm(hardness ~ density, data=hardness)

plot(hardness ~ density, data=hardness, xlim=c(22,73), ylim=c(0,3400))
abline(hardness.lin.lm)
resid.squares(hardness$density, hardness$hardness,
              predict(hardness.lin.lm))

plot(hardness ~ density, data=hardness, xlim=c(22,73), ylim=c(0,3400))
abline(hardness.lin.lm)
resid.squares(hardness$density, hardness$hardness,
              predict(hardness.lin.lm), resid.plot = "line")
```

`residual.plots` *Residual plots for a linear model.*

Description

Residual plots for a linear model. Four sets of plots are produced: (1) response against each of the predictor variables, (2) residuals against each of the predictor variables, (3) partial residuals for each predictor against that predictor ("partial residuals plots", and (4) partial residuals against the residuals of each predictor regressed on the other predictors ("added variable plots").

Usage

```
residual.plots(lm.object, X=dft$x,
               layout=c(dim(X)[2],1),
               par.strip.text=list(cex=.8),
               scales.cex=.6,
               na.action=na.pass,
               y.relation="free",
               ...)
```

Arguments

`lm.object`	An object inheriting from `"lm"`. It may be necessary for the `lm.object` to be constructed with arguments `x=TRUE, y=TRUE`.
`X`	The x matrix of predictor variables used in the linear model `lm.object`.
`layout, par.strip.text`	trellis or lattice arguments.
`scales.cex`	`cex` argument forwarded to the scales argument of `xyplot`.
`na.action`	A function to filter missing data. See `lm`.
`y.relation`	See `relation` in the discussion of the `scales` argument in `xyplot`.
`...`	Other arguments for `xysplom` or `xyplot`.

Value

A list of four trellis objects, one for each of the four sets of plots. The objects are named `"y.X"`, `"res.X"` `"pres.X"`, `"pres.Xj"`. The default "printing" of the result will produce four pages of plots, one set per page. They are often easier to read when all four sets appear as separate rows on one page (this usually requires an oversize device), or two rows are printed on each of two pages.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

residual.plots.lattice

Examples

```
if.R(s={
     longley <- data.frame(longley.x, Employed = longley.y)
     },r={
     data(longley)
     })

longley.lm <- lm( Employed ~ . , data=longley, x=TRUE, y=TRUE)
## 'x=TRUE, y=TRUE' are needed to pass the S-Plus CMD check.
## They may be needed if residual.plots() is inside a nested set of
## function calls.

tmp <- residual.plots(longley.lm)

## print two rows per page
print(tmp[[1]], position=c(0, 0.5, 1, 1.0), more=TRUE)
print(tmp[[2]], position=c(0, 0.0, 1, 0.5), more=FALSE)
print(tmp[[3]], position=c(0, 0.5, 1, 1.0), more=TRUE)
print(tmp[[4]], position=c(0, 0.0, 1, 0.5), more=FALSE)

## print as a single trellis object
ABCD <- do.call(rbind, lapply(tmp, as.vector))
dimnames(ABCD)[[1]] <- dimnames(tmp[[1]])[[1]]
ABCD
```

---

residual.plots.lattice

Construct four sets of regression plots: Y against X, residuals against X, partial residuals against X, partial residuals against each X adjusted for all the other X columns.

Description

Construct four sets of regression plots. Response variable Y against each X_j, residuals e against each X_j, partial residuals plots of e^j against each X_j, added variable plots of e^j against the residuals of each X_j adjusted for the other X columns. The slopes shown in the panels of both bottom rows are equal to the regression coefficients.

Usage

```
residual.plots.lattice(lm.object, X=dft$x, layout=c(dim(X)[2],1),
                       par.strip.text=list(cex=.8),
                       scales.cex=.6,
                       na.action=na.pass,
                       y.relation="same",
                       ...)
```

Arguments

lm.object	lm.object
X	Identify the variables in each of the x, y, group positions in a formula object. See do.formula.trellis.xysplom for more detail.
layout, par.strip.text, ...	**lattice** arguments. See xyplot.
scales.cex	cex for the scales argument in xyplot.
na.action	See na.action.
y.relation	relation for the y argument to scales argument in xyplot.

Value

"trellis" object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

residual.plots, print.latticeresids

Examples

```
data(longley)
longley.lm <- lm( Employed ~ . , data=longley, x=TRUE, y=TRUE)
residual.plots.lattice(longley.lm)

## Not run:
  longleyResid <- tempfile("longleyResid", fileext = ".pdf")
  pdf(longleyResid, height=9, width=14)
  print(residual.plots.lattice(longley.lm, pch=19),
        A4.left=.0125, panel.width=list(5,"cm"))
  dev.off()

## End(Not run)
```

`residVSfitted` *Draw plots of resid ~ y.hat and sqrt(abs(resid)) ~ y.hat*

Description

Draw plots of `resid ~ y.hat` and `sqrt(abs(resid)) ~ y.hat`. This is a pair of **lattice** functions that duplicate the first and third panels of `stats:::plot.lm`.

Usage

```
residVSfitted(linearmodel, groups = (e >= 0), ...)
scaleLocation(linearmodel, groups = (e >= 0), ...)
```

Arguments

`linearmodel`	"`lm`" object.
`groups`	This is the standard `groups` argument for `xyplot`. The default value is one symbol and color for positive residuals and a different symbol and color for negative residuals.
`...`	Additional arguments to `xyplot`.

Value

"`trellis`" object.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
data(fat)
fat.lm <- lm(bodyfat ~ abdomin, data=fat)

A <- residVSfitted(fat.lm, pch=c(25,24),
                   fill=trellis.par.get("superpose.symbol")$col[1:2])
B <- scaleLocation(fat.lm, pch=c(25,24),
                   fill=trellis.par.get("superpose.symbol")$col[1:2])
BA <- c("Scale-Location"=B,
        "Residuals vs Fitted"=update(A, scales=list(y=list(at=-100, alternating=3))),
        layout=c(1,2))
BA

BAu <-
  update(BA,
         ylab=c(B$ylab, A$ylab),
         ylab.right=c(B$ylab.right, A$ylab.right),
         xlab.top=NULL,
```

```
          between=list(y=1),
          par.settings=list(layout.widths=list(ylab.right=6))
          )

C <- diagQQ(fat.lm)

D <- diagplot5new(fat.lm)

print(BAu, split=c(1,1,2,1), more=TRUE)

print(update(c("Normal Q-Q"=C), xlab.top=NULL, strip=TRUE),
      ## split=c(2,1,2,2),
      position=c(.5, .54, 1, 1),  ## .54 is function of device and size
      more=TRUE)

print(update(D, xlab.top=NULL,
             strip=strip.custom(factor.levels=D$xlab.top),
             par.strip.text=list(lines=1.3)),
      ## split=c(2,2,2,2),
      position=c(.5, 0, 1, .57),  ## .57 is function of device and size
      more=FALSE)
## the .54 and .57 work nicely with the default quartz window on Mac OS X.
```

`ResizeEtc` *Display multiple independent trellis objects on the same coordinated scale.*

Description

This function is a wrapper for several of the functions in the `latticeExtra` package.

Usage

```
ResizeEtc(c.list,
          condlevelsName,
          x.same, y.same,
          layout,
          strip=TRUE,
          strip.left=TRUE,
          strip.values, strip.left.values,
          strip.par, strip.left.par,  ## only the second is effective
                                      ## when both are specified
          resize.height, resize.width,
          main,
          ...)
```

Arguments

c.list	combination of two or more trellis objects from c.trellis. If c.list has names, the names will appear in the strips.
condlevelsName	Name of the dimname of the items in the c.list.
x.same, y.same	If TRUE, force all panels to have the same x.limits or y.limits.
layout	Standard lattice layout argument.
strip, strip.left	standard lattice arguments described in barchart.
strip.values, strip.left.values	strip names for the panels. Only the second is effective when both are specified.
strip.par, strip.left.par	par.strip.text. Only the second is effective when both are specified.
resize.height, resize.width	h and w arguments to resizePanels.
main	Main title for resulting combined plot.
...	Other arguments to barchart.

Value

"trellis" object combining each of the individual plots in the c.list argument according to the specifications in the other arguments.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

c.trellis, plot.likert

Examples

```
## see the examples in ?HH:::plot.likert

require(grid)
require(lattice)
require(latticeExtra)
require(HH)

## This is the same example as in ?HH:::plot.likert
## Here, it is done with explicit use of ResizeEtc.

data(ProfChal)
tmp <- data.matrix(ProfChal[,1:5])
rownames(tmp) <- ProfChal$Question

AA <- likert(tmp[1,], box.width=unit(.4,"cm"), positive.order=TRUE)
BB <- likert(tmp[2:6,], box.width=unit(.4,"cm"), positive.order=TRUE)
```

```
CC <- likert(tmp[7:10,], box.width=unit(.4,"cm"), positive.order=TRUE)
DD <- likert(tmp[11:12,], box.width=unit(.4,"cm"), positive.order=TRUE)
EE <- likert(tmp[13:14,], box.width=unit(.4,"cm"), positive.order=TRUE)
FF <- likert(tmp[15:16,], box.width=unit(.4,"cm"), positive.order=TRUE)

BB

## print(AA, more=TRUE,  split=c(1,1,3,2))
## print(BB, more=TRUE,  split=c(2,1,3,2))
## print(CC, more=TRUE,  split=c(3,1,3,2))
## print(DD, more=TRUE,  split=c(1,2,3,2))
## print(EE, more=TRUE,  split=c(2,2,3,2))
## print(FF, more=FALSE, split=c(3,2,3,2))

ResizeEtc(c.list=c(AA,BB,CC,DD,EE,FF),
          layout=c(1,6), main="Not yet good enough")

Group <- levels(ProfChal$Subtable)

ResizeEtc(c.list=c(AA,BB,CC,DD,EE,FF),
          condlevelsName='Group',
          x.same=TRUE,
          layout=c(1,6),
          strip.left.values=Group,
          strip.left.par=list(cex=.7, lines=5),
          resize.height=c(1,5,4,2,2,2)+.5,
          main=list("Is your job professionally challenging?", x=unit(.65, "npc")))
```

`ResizeEtc.likertPlot` *Display multiple independent trellis objects, representing likert plots, on the same coordinated scale.*

Description

This is a method for `ResizeEtc` intended for use with `"likert"` plots that allows positive values on the negative side of the axis.

Usage

```
## S3 method for class 'likertPlot'
ResizeEtc(c.list,
          x,
          x.pl.nonames,
          horizontal,
          ...)
```

Arguments

c.list	combination of two or more trellis objects from c.trellis. If c.list has names, the names will appear in the strips.
x	List of two-dimensional objects with the same columns. See plot.likert.list for details.
x.pl.nonames	List of "likert" objects corresponding to the items in argument x. The items in x.pl.nonames are unnamed.
horizontal	Standard argument for barchart.
...	Other arguments to ResizeEtc.

Value

The result is a "trellis" object. It is essentially the same object returned by ResizeEtc with possibly adjusted x tick-labels to put positive labels on the negative axis. If horizontal==FALSE, then the possible adjusted labels are the y tick-labels.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

ResizeEtc, likert.

---

rowPcts *Row and columns percents*

Description

Row and columns percents.

Usage

```
rowPcts(x, ...)
colPcts(x, ...)
```

Arguments

x	numerical matrix
...	Additional arguments for rowSums

Value

Calculate percents by row or column. The rowSums or colSums are stored in the Sums attribute of the result.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

rowSums

Examples

```
tmp <- matrix(1:12, 3, 4,
              dimnames=list(c("A","B","C"),
                            c(letters[4:7])))
tmp
rowPcts(tmp)
colPcts(tmp)
```

---

seqplot *Time series plot.*

Description

Time series plot.

Usage

```
seqplot(xts, ...)

## Default S3 method:
seqplot(xts,
        pch.seq=letters,
        groups=as.numeric(cycle(xts)),
        a=NULL, b=NULL, h=NULL, v=NULL,
        ylab=deparse(substitute(xts)),
        xlab="Time",
        lwd=1, lty=c(1,3),
        type="b",
        col=trellis.par.get("superpose.symbol")$col,
        col.line="gray60",
        ...)


## S3 method for class 'ts'
seqplot(xts, pch.seq=letters, groups=as.numeric(cycle(xts)),
        x.at=pretty(time(xts)[groups==min(groups)]),
        x.labels,
        ylab=deparse(substitute(xts)),
        ...)
```

Arguments

xts	Time series
pch.seq	sequence of pch characters for use with the time series. The characters repeat over the cycle of the series.
groups	Numeric vector used to choose the plotting characters over cycles.
a, b, h, v	Arguments to panel.abline.
ylab, xlab, lwd, lty, type	standard trellis arguments.
x.at, x.labels	shortcut for scales=list(x=list(at=x.at, labels=x.labels))
col	Color of dots in sequence plot. The default is to make the choose a number of colors to match the frequency of the time series xts.
col.line	Color of connecting lines. The default is "gray60".
...	Additional arguments to xyplot.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

tsacfplots

Examples

```
seqplot(co2)
```

---

seqplotForecast *seqplot with confidence bands for the forecast region.*

Description

seqplot with confidence bands for the forecast region.

Usage

```
seqplotForecast(xts, forecast, multiplier = 1.96,
                series = deparse(substitute(observed)), ylim,
                CI.percent=round((1-2*(1-pnorm(multiplier)))*100,2),
                main = paste(
                series, " with forecast + ",
                CI.percent, "% CI", sep=""),
                xlab=NULL, ylab=NULL,
                ...) ## x.at, xlim
```

Arguments

xts	This is the observed series
forecast	forecast values based on the model
multiplier	Half-width of confidence interval in standard normal units. Defaults to 1.96.
CI.percent	Width of confidence band. Defaults to the standard normal, two-sided value associated with the multiplier (95 percent for the default multiplier=1.96).
series	Name of time series will be used to construct the main title for the plot.
ylim, xlab, ylab, main	standard trellis parameters
...	additional arguments to xyplot.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

seqplot

---

strip.background0 *Turn off the coloring in the trellis strip labels. Color 0 is the background color.*

Description

Turn off the coloring in the trellis strip labels. Color 0 is the background color.

Usage

```
strip.background0()
```

Author(s)

Richard M. Heiberger <rmh@temple.edu>

strip.useOuterStrips.first

Functions based on strip.default for use with the useOuterScales function.

Description

Functions based on `strip.default` for use with the `useOuterScales` function. See `useOuterScales` for more information.

Usage

```
strip.useOuterStrips.first(which.given, which.panel, var.name, ...)
strip.useOuterStrips.last(which.given, which.panel, var.name, ...)
strip.left.useOuterStrips(which.given, which.panel, var.name, ...)
strip.top2(which.given, which.panel, var.name, ...)
strip.top1(which.given, which.panel, var.name, ...)
strip.left2(which.given, which.panel, var.name, ...)
strip.left1(which.given, which.panel, var.name, ...)
```

Arguments

`which.given`, `which.panel`, `var.name`, `...`
: See `strip.default`.

Details

The appropriate function is chosen by specifying arguments to `useOuterScales`.

`strip.useOuterStrips.first` places strip labels at the top of the first row of lattice panels. Used when `as.table==TRUE`.

`strip.useOuterStrips.last` places strip labels at the top of the first row of lattice panels. Used when `as.table==FALSE`.

`strip.left.useOuterStrips` places strip labels at the left of the first column of lattice panels.

`strip.top2` places row strip labels at the top of each panel.

`strip.top1` places column strip labels at the top of each panel.

`strip.left2` places row strip labels at the left of each panel.

`strip.left1` places column strip labels at the left of each panel.

Value

See `strip.default`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

useOuterScales

Examples

```
## See examples in ?useOuterScales
```

`strip.xysplom` *strip function that is able to place the correlation or regression coefficient into the strip label.*

Description

strip function that is able to place the correlation and/or regression coefficient into the strip label.

Usage

```
strip.xysplom(which.given, which.panel, var.name, factor.levels,
 shingle.intervals, par.strip.text = trellis.par.get("add.text"),
 strip.names = c(TRUE, TRUE), style = 1, ...)
```

Arguments

`which.given`, `which.panel`, `var.name`, `factor.levels`, `shingle.intervals`
: arguments to `strip.default`.

`par.strip.text`, `strip.names`, `style`, `...`
: more arguments to `strip.default`.

Details

The function looks for the specific factor names `c("corr","beta","corr.beta")`. If it finds them, it goes up the calling sequence to locate the data for the panel. Then it calculates the correlation and/of regression coefficient and inserts the calculated value(s) as the value for the strip label.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

xysplom

`sufficient` *Calculates the mean, standard deviation, and number of observations in each group of a data.frame that has one continuous variable and two factors.*

Description

Calculates the mean, standard deviation, and number of observations in each group of a data.frame that has one continuous variable and two factors.

Usage

```
sufficient(x,
           yname = dimnames(x)[[2]][[1]],
           factor.names.keep = dimnames(x)[[2]][-c(1, 2)])
```

Arguments

`x`	`data.frame` containing a continuous variable and two factors.
`yname`	Character name of response variable.
`factor.names.keep`	Character vector containing the names of two factors in the `x` data.frame.

Value

Data.frame containing five columns and as many rows as are implied by the crossing of the two factors. Each row contains the mean in a column with the name `yname` and its factor values in columns named with the name in `factor.names.keep`. The standard deviation of the observations in the group are in the column `"sd"` and the number of observations in the group is in the column `"nobs"`.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

`intxplot`

summary.arma.loop *summary and print and subscript methods for tsdiagplot and related objects.*

Description

summary and print and subscript methods for tsdiagplot and related objects.

Usage

```
## S3 method for class 'arma.loop'
summary(object, ...)
## S3 method for class 'arma.loop.list'
summary(object, ...)
## S3 method for class 'arma.loop'
print(x, ...)
## S3 method for class 'arma.loop.list'
print(x, ...)
## S3 method for class 'tsacfplots'
print(x,
               ts.pos=c(.00, .00,  .70, 1.00),
               acf.pos=c(.65, .10, 1.00,  .90),
               ...,
               portrait=FALSE,
               ts.pos.portrait=c(0, .3, 1, 1),
               acf.pos.portrait=c(.1, 0, .9, .35))
## S3 method for class 'arma.loop'
x[..., drop = TRUE]
## S3 method for class 'diag.arma.loop'
x[..., drop = TRUE]
```

Arguments

x, object	object to be summarized or printed or subscripted.
ts.pos, acf.pos, ts.pos.portrait, acf.pos.portrait	Default positions for print.trellis
portrait	logical. If FALSE, arrange the panels for a landscape orientation. If TRUE, arrange the panels for a portrait orientation.
...	additional arguments
a	
drop	See Extract.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

arma.loop, tsacfplots, tsdiagplot

ToBW.likert *Change colors in a likert plot to shades of Black and White.*

Description

Change colors in a likert plot to shades of Black and White. This function is tailored for a likert plot, an example of a "trellis" object. likert is based on panel.bwplot. There are other places in the structure of a more general "trellis" object where colors are stored. The specifics for this plot is (1) that the colors for negative values in the plot are in reverse order and (2) the color for a neutral-position panel appears on both the positive and negative side. The default values are for three items on the negative side, two on the positive side, and no neutral. See the examples for an example with a neutral.

Usage

```
   ToBW.likert(x,
             colLegendOrder=c("gray70", "gray20", "gray60", "gray75", "gray45"),
##                                ^Ask      Refu      ^Imp    | Impt      Essn
##
               colBarchartOrder=colLegendOrder[c(3,2,1,4,5)],
##                                ^Imp      Refu      ^Ask    | Impt      Essn
               columns=5)
## negative colors are in reverse order in the BarchartOrder
```

Arguments

x	"trellis" object, specifically one constructed by the likert function.
colLegendOrder	Revised value of x$legend$bottom$args$rect$col
colBarchartOrder	Revised value of both x$panel.args.common$col x$panel.args.common$border.
columns	Revised value of x$legend$bottom$args$columns

Value

"trellis" object, identical to the input object except for the colors.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

likert

Examples

```
tmp <- array(1:20, c(4, 5),
             list(letters[1:4],
                  c("NotAsked","VeryNegative","Negative","Positive","VeryPositive")))
tmp

Ltmp <- likert(tmp, ReferenceZero=3.5, col=c("gray85", likertColor(4)), as.percent=TRUE)
Ltmp

ToBW.likert(Ltmp)

## with neutral

tmp2 <- array(1:20, c(4, 5),
             list(letters[1:4],
                  c("VeryNegative","Negative","Neutral","Positive","VeryPositive")))
tmp2

Ltmp2 <- likert(tmp2, ReferenceZero=3, col=likertColor(5),
                as.percent=TRUE, main="Neutral")
Ltmp2

ToBW.likert(Ltmp2,
            colLegendOrder=c("gray20", "gray60", "gray85", "gray75", "gray45"),
##                                                Neu|tral
          colBarchartOrder=c("gray85", "gray60", "gray20",  "gray85", "gray75", "gray45")
##                          Neutral left                        Neutral right
)

update(main="Wrong way to handle neutral",
       ToBW.likert(Ltmp2,
                   colLegendOrder=c("gray20", "gray60", "gray85", "gray75", "gray45"))
      )
```

---

toCQxR *Reshape a 3-way array to a 2-way data.frame that can can be used with a trellis conditioning formula to get the three-way behavior. Used with likertWeighted().*

Description

Reshape a 3-way array to a 2-way data.frame that can can be used with a trellis conditioning formula to get the three-way behavior. Used with `likertWeighted()`.

Usage

```
toCQxR(x, C = 1, R = 2, Q = 3)
```

Arguments

x	Three-way array, with dimensions "Classification", "Responses", "Questions" in some order.
C, R, Q	Integers, one each of 1,2,3; positions of the three dimensions.

Value

Data.frame with CQ rows and Q + N columns, where N is either 1 or 2 for the number of condition variables in the formula for likertWeighted.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

likertWeighted

Examples

```
tmp3 <- array(1:40, c(4,5,2), list(LETTERS[1:4], LETTERS[5:9], LETTERS[10:11]))
tmp3

toCQxR(tmp3)
```

---

tsacfplots *Coordinated time series and ACF and PCF plots.*

Description

Coordinated time series and ACF and PCF plots.

Usage

```
tsacfplots(x,
           ylab=deparse(substitute(x)),
           x.name=ylab[[1]],
           main=paste("Series:", x.name),
           lag.at=NULL,
           lag.max=NULL,
           lag.units=NULL,
           lag.0=TRUE,
           ...)

acf.pacf.plot(x,
       ylab=NULL,
       series=deparse(substitute(x)),
```

```
        main=paste("ACF and PACF:", series),
        lag.max,
        lag.units=frequency(x),
        lag.at=pretty(apacf$lag),
        lag.labels=lag.at*lag.units,
               lag.0=TRUE,
               strip=TRUE, strip.left=FALSE,
        ...)
```

Arguments

x	time series
ylab, main	standard trellis arguments.
x.name, series	Character string, name for the time series.
lag.at	Location of ticks for the acf and pacf plots.
lag.labels	Labels for ticks for the acf and pacf plots.
lag.max	Maximum lag used in the acf and pacf plots.
lag.units	Units for time series, defaults to frequency(x)
lag.0	Logical. If TRUE, then plot the correlation (identically 1) at lag=0. If FALSE, do not plot the correlation at lag=0.
strip, strip.left	Standard lattice arguments described in xyplot.
...	Additional arguments to seqplot for tsacfplots. Additional arguments to strip.default for acf.pacf.plot.

Details

The acf and pacf plots are scaled identically.

Value

"tsacfplots" object containing two "trellis" objects.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

See Also

seqplot

Examples

```
tsacfplots(co2)
acf.pacf.plot(co2)
```

tsdiagplot *Times series diagnostic plots for a structured set of ARIMA models.*

Description

Times series diagnostic plots for a structured set of ARIMA models.

Usage

```
tsdiagplot(x,
           p.max=2, q.max=p.max,
           model=c(p.max, 0, q.max), ## S-Plus
           order=c(p.max, 0, q.max), ## R
           lag.max=36, gof.lag=lag.max,
           armas=arma.loop(x, order=order,
               series=deparse(substitute(x)), ...),
           diags=diag.arma.loop(armas, x,
                                lag.max=lag.max,
                                gof.lag=gof.lag),
           ts.diag=rearrange.diag.arma.loop(diags),
           lag.units=ts.diag$tspar["frequency"],
           lag.lim=range(pretty(ts.diag$acf$lag))*lag.units,
           lag.x.at=pretty(ts.diag$acf$lag)*lag.units,
           lag.x.labels={tmp <- lag.x.at
                      tmp[as.integer(tmp)!=tmp] <- ""
                      tmp},
           lag.0=TRUE,
           main, lwd=0,
           ...)

acfplot(rdal, type="acf",
        main=paste("ACF of std.resid:", rdal$series,
                   "   model:",         rdal$model),
        lag.units=rdal$tspar["frequency"],
        lag.lim=range(pretty(rdal[[type]]$lag)*lag.units),
        lag.x.at=pretty(rdal[[type]]$lag)*lag.units,
        lag.x.labels={tmp <- lag.x.at
                      tmp[as.integer(tmp)!=tmp] <- ""
                      tmp},
        lag.0=TRUE,
        xlim=xlim.function(lag.lim/lag.units),
        ...)

aicsigplot(z, z.name=deparse(substitute(z)), series.name="ts",
           model=NULL,
           xlab="", ylab=z.name,
           main=paste(z.name,  series.name, model),
```

```
           layout=c(1,2), between=list(x=1,y=1), ...)

residplot(rdal,
          main=paste("std.resid:", rdal$series,
                     "   model:",  rdal$model),
          ...)

gofplot(rdal,
        main=paste("P-value for gof:", rdal$series,
                   "   model:",         rdal$model),
       lag.units=rdal$tspar["frequency"],
        lag.lim=range(pretty(rdal$gof$lag)*lag.units),
        lag.x.at=pretty(rdal$gof$lag)*lag.units,
        lag.x.labels={tmp <- lag.x.at
                      tmp[as.integer(tmp)!=tmp] <- ""
                      tmp},
        xlim=xlim.function(lag.lim/lag.units),
        pch=16, ...)
```

Arguments

x	Time series vector.
p.max, q.max	Maximum number of AR and MA arguments to use in the series of ARIMA models.
model	A valid S-Plus model for arima.mle.
order	A valid R order for arima. The additional argument seasonal may also be used.
lag.max	Maximum lag for the acf and pacf plots.
gof.lag	Maximum lag for the gof plots.
armas	An arma.loop object.
diags	An diag.arma.loop object.
ts.diag, rdal	A list constructed as a rearranged diag.arma.loop object.
lag.units	Units for time series, defaults to frequency(x)
lag.lim	scaling for xlim in acf and pacf plots.
lag.x.at, lag.x.labels	Location of ticks and labels for the acf and pacf plots.
lag.0	Logical. If TRUE, then plot the correlation (identically 1) at lag=0. If FALSE, do not plot the correlation at lag=0.
type	"acf" or "pacf"
z	A matrix constructed as the aic or sigma2 component of the sumamry of a arma.loop object.
z.name	"aic" or "sigma2"
series.name	Character string describing the time series.

xlab, ylab, layout, between, pch, xlim, main, lwd
: Standard trellis arguments.

...
: Additional arguments. tsdiagplot sends them to arima or arima.mle. acfplot, aicsigplot residplot, and gofplot send them to xyplot.

Value

tsdiagplot returns a "tsdiagplot" object which is a list of "trellis" objects. It is printed with its own print method.

The other functions return "trellis" objects.

Author(s)

Richard M. Heiberger (rmh@temple.edu)

References

"Displays for Direct Comparison of ARIMA Models" The American Statistician, May 2002, Vol. 56, No. 2, pp. 131-138. Richard M. Heiberger, Temple University, and Paulo Teles, Faculdade de Economia do Porto.

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

tsacfplots, arma.loop

Examples

```
data(tser.mystery.X)
X <- tser.mystery.X

X.dataplot <- tsacfplots(X, lwd=1, pch.seq=16, cex=.7)
X.dataplot

X.loop <- if.R(
               s=
               arma.loop(X, model=list(order=c(2,0,2)))
               ,r=
               arma.loop(X, order=c(2,0,2))
               )
X.dal <- diag.arma.loop(X.loop, x=X)
X.diag <- rearrange.diag.arma.loop(X.dal)
X.diagplot <- tsdiagplot(armas=X.loop, ts.diag=X.diag, lwd=1)
X.diagplot

X.loop
X.loop[["1","1"]]
```

useOuterScales *Put scales for axes only on the bottom and left panels of a lattice display, and give fine control over the placement of strips*

Description

Update a multi-panel "trellis" object so that scales for axes are displayed only on the bottom and left boundaries when printed, instead of in every panel as is usual. This function succeeds even when xlim across columns and ylim across rows are not identical. Multiple options are available for strip labels. The default for strip labels is similar to useOuterStrips. Additional options include outerStrips for each panel and interchanged row and column strip locations. This is only meaningful when there are exactly two conditioning variables.

Usage

```
useOuterScales(x,
           axis.xlab.padding=4,
           ylab.axis.padding=3,
           strip,
           strip.left,
           layout.widths.strip.left=.5,
           layout.heights.strip=.5,
           x.ticks=is.numeric(x$x.limits),
           y.ticks= is.numeric(x$y.limits) +
             if (!missing(strip.left) &&   ## FALSE
                 is.logical(strip.left) && ## explicitly stated
                 !strip.left ) 0
             else 2.5,
           inner=FALSE,
           interchangeRC=FALSE)
```

Arguments

x An object of class "trellis"

ylab.axis.padding, axis.xlab.padding, layout.heights.strip, layout.widths.strip.left

These values are passed to the par.settings:

```
layout.widths=list(ylab.axis.padding=ylab.axis.padding,
                   strip.left=layout.widths.strip.left),
layout.heights=list(axis.xlab.padding=axis.xlab.padding,
                    strip=layout.heights.strip)
```

See trellis.par.get, and the par.settings section of xyplot.

strip, strip.left

useOuterScales controls the strip labels by assigning appropriate functions for these two arguments. The functions used by useOuterScales are described in strip.useOuterStrips.first. useOuterScales uses the values of its strip,

strip.left, inner, interchangeRC, and x$as.table arguments to determine which functions to assign. The default values place the columns strip labels at the top of the top row of panels and the row strip labels at the left of the left column of panels. See the Examples section for the full set of possibilities that are provided.

x.ticks, y.ticks
: x.ticks is used as the ticks argument to panel.axis for the "bottom" axis. y.ticks is used as the ticks argument to panel.axis for the "left" axis. y.ticks needs to be larger when the left strip is present because the tick and label are partially overwritten by the left strip. When the left.strip=FALSE, then we need to make the y.ticks smaller.

inner
: Logical with default FALSE, meaning that the strip labels are displayed only on the top row and left column of the array of panels. When TRUE, the strip labels are displayed on the top and left of every panel.

interchangeRC
: Logical with default FALSE. When TRUE, the column labels appear on the left strip of the panels, and the row labels appear on the top of the panels. TRUE is only meaningful when inner=TRUE.

Details

useOuterScales modifies a "trellis" object with length(dim(x)) == 2 so that when plotted, scales appear on only the top and left panels of the array of panels. Strips appear as specified, by default on the top and left boundaries of the panel layout.

If the original "trellis" object x includes non-default strip and strip.left arguments, they will be ignored. To provide customized strip behaviour, specify the custom strip functions directly as arguments to useOuterStrips.

Value

An object of class "trellis"; essentially the same as x, but with certain properties modified.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

See Also

useOuterStrips, strip.default

Examples

```
OuterScalesData <- data.frame(y=1:16,
                              AA=rep(factor(letters[1:8]), 2),
                              BB=rep(factor(LETTERS[12:13]), each=8),
                              CC=rep(factor(rep(LETTERS[9:11], times=c(3,1,4))), 2))
OuterScalesData

BC0 <- barchart(AA ~ y | BB * CC, data=OuterScalesData,
                origin=0,
```

```
                scales=list(x=list(limits=c(0,16.5)),
                            y=list(relation="free")),
                between=list(x=1, y=1),
                main="0. barchart")
## Not run:
BC0

## End(Not run)
BC1 <- update(
  resizePanels(BC0, h=c(3,1,4)),
  main="1. resizePanels")
BC1

BC2 <- update(
  useOuterStrips(BC1),
  main="2. useOuterStrips") ## package:latticeExtra
BC2

BC3 <- update(
  useOuterScales(BC1),
  main="3. useOuterScales")
BC3

## Not run:
BC4 <- update(
  useOuterScales(BC1),
  ylab="ABC",
  main="4. useOuterScales, ylab")
BC4

BC5 <- update(
  useOuterScales(update(BC1, as.table=TRUE)),
  main="5. useOuterScales, as.table")
BC5

try(useOuterScales(BC1, interchangeRC=TRUE)) ## incompatible options

## End(Not run)

BC6 <- update(
  useOuterScales(BC1, inner=TRUE),
  main="6. useOuterScales, inner")
BC6

## Not run:
BC7 <- update(
  useOuterScales(BC1, inner=TRUE, interchangeRC=TRUE),
  main="7. useOuterScales, inner, interchangeRC")
BC7

BC8 <- update(
  useOuterScales(BC1, strip=FALSE),
  xlab.top=c("L","M"),
```

```
  main="8. useOuterScales, strip=FALSE, xlab.top")
BC8

BC9 <- update(
  useOuterScales(BC1, strip=strip.default),
  main="9. useOuterScales, strip=strip.default")
BC9

try(print(useOuterScales(BC1, strip=date))) ## date is not a valid strip function

BC10 <- update(
  useOuterScales(BC1, strip.left=FALSE),
  ylab=c("I","J","K"),
  main="10. useOuterScales, strip.left=FALSE, ylab")
BC10

BC11 <- update(
  useOuterScales(BC1, strip.left=strip.default),
  main="11. useOuterScales, strip.left=strip.default")
BC11

try(print(useOuterScales(BC1, strip.left=date))) ## date is not a valid strip function

BC12 <- update(
  useOuterScales(BC1,
                 inner=TRUE, interchangeRC=TRUE, strip.left=FALSE),
  xlab.top=c("L","M"),
  main=
"12. useOuterScales, inner, \n interchangeRC=TRUE, strip.left=FALSE, \n xlab.top, strip.background",
  par.settings=list(strip.background=list(col="gray98")))
BC12

BC13 <- update(
  useOuterScales(update(BC1, as.table=TRUE),
                 inner=TRUE, interchangeRC=TRUE, strip.left=FALSE),
  xlab.top=c("L","M"),
 main="13. useOuterScales, inner, \n interchangeRC=TRUE, strip.left=FALSE, \n xlab.top, as.table")
BC13

BC14 <- update(
  useOuterScales(BC1,
                 inner=TRUE, strip=FALSE, interchangeRC=TRUE),
  ylab=list(c("I","J","K"), rot=0),
  main="14. useOuterScales, inner, \n strip=FALSE, interchangeRC, \n ylab")
BC14

BC15 <- update(
  useOuterScales(BC1,
                 strip=FALSE, strip.left=FALSE),
  xlab.top=c("L","M"), ylab=list(c("I","J","K"), rot=0),
  main="15. useOuterScales, strip=FALSE, strip.left=FALSE, \n xlab, ylab")
BC15
```

```
## End(Not run)

## Not run:  ## display 16 options for strip labels with outerScales
useOuterScales16 <- tempfile("useOuterScales16", fileext = ".pdf")
pdf(useOuterScales16, height=16, width=21)
print(BC0,  split=c(1,1,4,4), more=TRUE)
print(BC1,  split=c(2,1,4,4), more=TRUE)
print(BC2,  split=c(3,1,4,4), more=TRUE)
print(BC3,  split=c(4,1,4,4), more=TRUE)
print(BC4,  split=c(1,2,4,4), more=TRUE)
print(BC5,  split=c(2,2,4,4), more=TRUE)
print(BC6,  split=c(3,2,4,4), more=TRUE)
print(BC7,  split=c(4,2,4,4), more=TRUE)
print(BC8,  split=c(1,3,4,4), more=TRUE)
print(BC9,  split=c(2,3,4,4), more=TRUE)
print(BC10, split=c(3,3,4,4), more=TRUE)
print(BC11, split=c(4,3,4,4), more=TRUE)
print(BC12, split=c(1,4,4,4), more=TRUE)
print(BC13, split=c(2,4,4,4), more=TRUE)
print(BC14, split=c(3,4,4,4), more=TRUE)
print(BC15, split=c(4,4,4,4), more=FALSE)
dev.off()

## End(Not run)


## Not run:
## Verify y.ticks default value depends on
##  is.numeric(x$y.limits).
##  and on whether strip.left=FALSE

CB0 <- barchart(y ~ AA | CC * BB, data=OuterScalesData,
                origin=0,
                scales=list(y=list(limits=c(0,16.5)),
                            x=list(relation="free")),
                between=list(x=1, y=1),
                main="CB0. barchart")
CB0

CB1 <- update(
  resizePanels(CB0, w=c(3,1,4)),
  main="CB1. resizePanels")
CB1

CB2 <- update(
  useOuterStrips(CB1),
  main="CB2. useOuterStrips") ## package:latticeExtra
CB2

CB3 <- update(
  useOuterScales(CB1),
  main="CB3. useOuterScales, y.limits is numeric")
CB3
```

```
CB4 <- update(
  useOuterScales(CB1, strip.left=FALSE),
  main="CB4. useOuterScales, y.limits is numeric, strip.left=FALSE")
CB4

BC16 <- update(
  useOuterScales(BC1),
  main="BC16. useOuterScales, y.limits is not numeric")
BC16

BC17 <- update(
  useOuterScales(BC1, strip.left=FALSE),
  main="BC17. useOuterScales, y.limits is not numeric, strip.left=FALSE")
BC17


## End(Not run)

## Not run:
## Verify x.ticks default value depends on
##  is.numeric(x$x.limits).

update(BC3, main="BC3. useOuterScales, x.limits is numeric")

update(CB3, main="CB3. useOuterScales, x.limits is not numeric")


## End(Not run)
```

`useOuterStripsT2L1` *Three-factor generalization of latticeExtra::useOuterStrips*

Description

Three-factor generalization of `latticeExtra::useOuterStrips`

Usage

```
useOuterStripsT2L1(x, ..., strip.height=.4, strip.names=c(TRUE, TRUE))
```

Arguments

`x`	A `lattice` object with `dim(x)==3`.
`...`	Additional arguments to be forwarded to the `strip.default` function.
`strip.height`	Height of each the strip for each factor. The number of factors in the top and left strips may not be the same. This argument is multiplied by the number of factors in each location and sent on to the **lattice** `par.settings` argument for the `layout.widths$strip.left` and `layout.heights$strip` components.

strip.names See strip.default.

Value

A trellis object with two factors in the top strip and 1 factor in the strip.left.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

Examples

```
tmp <- data.frame(A=rep(factor(letters[1:2]), each=12),
                  B=rep(factor(letters[3:5]), each=4, times=2),
                  C=rep(factor(letters[6:9]), times=6),
                  x=1:24,
                  y=1:24)

F <- xyplot(y ~ x | B*A*C, data=tmp,
            panel=function(x, y, labels, ...) {
              panel.text(x, y, matrix(1:24, 6, 4, byrow=TRUE)[panel.number()], ...)
            },
            layout=c(6, 4), between=list(x=c(.5, .5, 1.5), y=1))
F

useOuterStripsT2L1(F)
```

---

vif *Calculate the Variance Inflation Factor*

Description

The VIF for predictor i is $1/(1 - R_i^2)$, where R_i^2 is the R^2 from a regression of predictor i against the remaining predictors.

Usage

```
vif(xx, ...)

## Default S3 method:
vif(xx, y.name, na.action = na.exclude, ...) ## xx is a data.frame

## S3 method for class 'formula'
vif(xx, data, na.action = na.exclude, ...)   ## xx is a formula

## S3 method for class 'lm'
vif(xx, na.action = na.exclude, ...)  ## xx is a "lm" object computed with x=TRUE
```

Arguments

xx	data.frame, or formula, or lm object computed with x=TRUE.
na.action	See na.action.
...	additional arguments.
y.name	Name of Y-variable to be excluded from the computations.
data	A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.

Details

A simple diagnostic of collinearity is the *variance inflation factor, VIF* one for each regression coefficient (other than the intercept). Since the condition of collinearity involves the predictors but not the response, this measure is a function of the X's but not of Y. The VIF for predictor i is $1/(1-R_i^2)$, where R_i^2 is the R^2 from a regression of predictor i against the remaining predictors. If R_i^2 is close to 1, this means that predictor i is well explained by a linear function of the remaining predictors, and, therefore, the presence of predictor i in the model is redundant. Values of VIF exceeding 5 are considered evidence of collinearity: The information carried by a predictor having such a VIF is contained in a subset of the remaining predictors. If, however, all of a model's regression coefficients differ significantly from 0 (p-value $< .05$), a somewhat larger VIF may be tolerable.

Value

Vector of VIF values, one for each X-variable.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

lm.

Examples

```
data(usair)

usair$lnSO2 <- log(usair$SO2)
usair$lnmfg <- log(usair$mfgfirms)
usair$lnpopn <- log(usair$popn)

usair.lm <- lm(lnSO2 ~ temp + lnmfg + wind + precip, data=usair, x=TRUE)
```

```
vif(usair.lm)  ## the lm object must be computed with x=TRUE

vif(lnSO2 ~ temp + lnmfg + wind + precip, data=usair)

vif(usair)

vif(usair, y.name="lnSO2")
```

`X.residuals` *Residuals from the regression of each column of a data.frame against all the other columns.*

Description

Calculate the residuals from the regression of each column of a data.frame against all the other columns.

Usage

```
X.residuals(x, ...)

## Default S3 method:
X.residuals(x, y.name, na.action = na.exclude, ...) ## x is a data.frame

## S3 method for class 'formula'
X.residuals(x, data, na.action = na.exclude, ...)   ## x is a formula

## S3 method for class 'lm'
X.residuals(x, na.action = na.exclude, ...) ## x is a "lm" object computed with x=TRUE
```

Arguments

`x`	`data.frame`, or `formula`, or `lm` object computed with `x=TRUE`.
`na.action`	See `na.action`.
`...`	additional arguments.
`y.name`	Name of Y-variable to be excluded from the computations.
`data`	A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.

Value

Data.frame of residuals, one column from each regression.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

lm, vif, case.lm.

Examples

```
data(usair)
usair$lnSO2 <- log(usair$SO2)
usair$lnmfg <- log(usair$mfgfirms)
usair$lnpopn <- log(usair$popn)

usair.lm <- lm(lnSO2 ~ temp + lnmfg + wind + precip, data=usair)

X.residuals(usair.lm)

X.residuals(lnSO2 ~ temp + lnmfg + wind + precip, data=usair)

X.residuals(usair)

X.residuals(usair, y.name="lnSO2")
```

---

xysplom *scatterplot matrix with potentially different sets of variables on the rows and columns.*

Description

scatterplot matrix with potentially different sets of variables on the rows and columns. The slope or regression coefficient for simple least squares regression can be displayed in the strip label for each panel.

Usage

```
xysplom(x, ...)

## S3 method for class 'formula'
xysplom(x, data=NULL, na.action = na.pass, ...)

## Default S3 method:
xysplom(x, y=x, group, relation="free",
        x.relation=relation, y.relation=relation,
        xlim.in=NULL, ylim.in=NULL,
        corr=FALSE, beta=FALSE, abline=corr||beta, digits=3,
```

```
x.between=NULL, y.between=NULL,
between.in=list(x=x.between, y=y.between),
scales.in=list(
  x=list(relation=x.relation, alternating=FALSE),
  y=list(relation=y.relation, alternating=FALSE)),
strip.in=strip.xysplom,
pch=16, cex=.75,
panel.input=panel.xysplom, ...,
cartesian=TRUE,
plot=TRUE)
```

Arguments

x	In the "formula" method, a formula. In the "default" method, a data.frame. Any variables that are used in a formula with + should be numeric. Factors are not rejected, but their levels will be combined strangely.
...	other arguments to xyplot.
z	
data	data.frame
na.action	See na.action. Defaults to na.pass because xyplot does sensible things with missing data.
y	In the "default" method, a data.frame with the same number of rows as the data.frame in x.
group	In the "default" method, a data.frame with the same number of rows as the data.frame in x.
relation, x.relation, y.relation, scales.in	Alternate ways to get to the scales(relation=) arguments to xyplot.
xlim.in, ylim.in	Alternate ways to get to the scales(limits=) arguments to xyplot.
corr, beta	Display the correlation and/or the regression coefficient for lm(y ~ x) for each panel in an additional strip label.
abline	logical. If TRUE, draw the least squares regression line within each panel. By default the abline is FALSE unless at least one of corr or beta is TRUE.
digits	number of significant digits for the correlation coefficient.
x.between, y.between, between.in	Alternate ways to get to the between= argument to xyplot.
strip.in	strip function that knows how to handle the corr and beta displays.
pch, cex	arguments to xyplot
panel.input	panel function used by xyplot within each panel. When abline==FALSE, the default panel function calls panel.xyplot. When abline==TRUE, the default panel function calls panel.xyplot and panel.abline(lm(y~x, na.action=na.exclude)). Note that we use na.action=na.exclude inside lm.

cartesian	When cartesian==TRUE, the cartesian product of the left-hand side number of variables and the right-hand side number of variables defines the number of panels in the display. When cartesian==FALSE, each variable in the left-hand side is paired with the variable in the corresponding position in the right-hand side and only those pairs are plotted. Both sides must have the same number of variables.
plot	Defaults to TRUE. See details.

Details

The argument plot=TRUE is the normal setting and then the function returns a "trellis" object. When the argument plot=FALSE, the function returns the argument list that would otherwise be sent to xyplot. This list is interesting when the function xysplom was designed because the function works by restructuring the input data and running xyplot on the restructured data.

Value

When plot=TRUE (the normal setting), the "trellis" object containing the graph.
When plot=FALSE, the restructured data that must be sent to the xyplot function.

Author(s)

Richard M. Heiberger <rmh@temple.edu>

References

Heiberger, Richard M. and Holland, Burt (2015). *Statistical Analysis and Data Display: An Intermediate Course with Examples in R*. Second Edition. Springer-Verlag, New York. https://link.springer.com/book/10.1007/978-1-4939-2122-5

See Also

xyplot in R.

Examples

```
## xysplom syntax options

tmp <- data.frame(y=rnorm(12), x=rnorm(12), z=rnorm(12), w=rnorm(12),
                  g=factor(rep(1:2,c(6,6))))
tmp2 <- tmp[,1:4]

xysplom(y + w ~ x , data=tmp, corr=TRUE, beta=TRUE, cartesian=FALSE, layout=c(1,2))

xysplom(y + x ~ z | g, data=tmp, layout=c(2,2))
xysplom(y + x ~ z | g, data=tmp, cartesian=FALSE)

xysplom(w + y ~ x + z, data=tmp)
xysplom(w + y ~ x + z | g, data=tmp, layout=c(2,4))
xysplom(w + y ~ x + z | g, data=tmp, cartesian=FALSE)
```

```
## Not run:
## xyplot in R has many similar capabilities with xysplom
if.R(r=
       xyplot(w + z ~ x + y, data=tmp, outer=TRUE)
     ,s=
       {}
    )

## End(Not run)
```

`z.test` *Z test for known population standard deviation*

Description

Compute the test of hypothesis and compute confidence interval on the mean of a population when the standard deviation of the population is known.

Usage

```
z.test(x, mu = 0, stdev, alternative = c("two.sided", "less", "greater"),
  sd = stdev, n=length(x), conf.level = 0.95, ...)
```

Arguments

`x`	Vector of data values or the mean of the data.
`mu`	Hypothesized mean of the population.
`stdev`	Known standard deviation of the population.
`alternative`	Direction of the alternative hypothesis.
`sd`	Alternative to `stdev`
`n`	The sample size if `x` is the sample mean.
`conf.level`	Confidence level for the interval computation.
`...`	Additional arguments are silently ignored.

Details

Many introductory statistical texts introduce inference by using the Z test and Z based confidence intervals based on knowing the population standard deviation. Most statistical packages do not include functions to do Z tests since the T test is usually more appropriate for real world situations. This function is meant to be used during that short period of learning when the student is learning about inference using Z procedures, but has not learned the T based procedures yet. Once the student has learned about the T distribution the `t.test` function should be used instead of this one (but the syntax is very similar, so this function should be an appropriate introductory step to learning `t.test`).

Value

An object of class `htest` containing the results

Note

This function should be used for learning only, real data should generally use `t.test`. These files `z.test.R` and `z.test.Rd` are from the recently orphaned package TeachingDemos_2.12.1

Author(s)

Greg Snow <538280@gmail.com>

See Also

`t.test`, `print.htest`

Examples

```
x <- rnorm(25, 100, 5)
z.test(x, 99, 5)
```

Index