

Package ‘heplots’

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Type Package

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Author John Fox, Michael Friendly, and Georges Monette

Maintainer Michael Friendly <friendly@yorku.ca>

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Description Represents sums-of-squares-and-products matrices for linear hypotheses and for error using ellipses (in two dimensions) and ellipsoids (in three dimensions).

License GPL (>= 2)

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heplots-package	<i>Visualizing Tests in Multivariate Linear Models</i>
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Description

The `heplots` package provides functions for visualizing hypothesis tests in multivariate linear models. They represent sums-of-squares-and-products matrices for linear hypotheses and for error using ellipses (in two dimensions) and ellipsoids (in three dimensions). See Fox, Friendly and Monette (2007) for a brief introduction.

Details

Package: heplots
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 License: GPL version 2 or newer

The graphical functions contained here all display multivariate model effects in variable space:

`heplot` constructs two-dimensional HE plots for model terms and linear hypotheses for pairs of response variables in multivariate linear models.

`heplot3d` constructs analogous 3D plots for triples of response variables.

`pairs.mlm` constructs a “matrix” of pairwise HE plots.

The related `car-package` package calculates tests of multivariate linear hypotheses. The `candisc-package` package provides functions for visualizing effects for model terms in a low-dimensional canonical space that shows the largest hypothesis relative to error variation.

Author(s)

John Fox, Michael Friendly, and Georges Monette

Maintainer: Michael Friendly <friendly@yorku.ca>

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, 17(6), 1-42. <http://www.>

jstatsoft.org/v17/i06/

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16(2) 421-444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

Fox, J., Friendly, M. & Monette, G. (2007). Visual hypothesis tests in multivariate linear models: The heplots package for R. *DSC 2007: Directions in Statistical Computing*. <http://socserv.socsci.mcmaster.ca/jfox/heplots-dsc-paper.pdf>

See Also

[Anova](#), [linear.hypothesis](#)

Bees

Captive and maltreated bees

Description

Pabalan, Davey and Packe (2000) studied the effects of captivity and maltreatment on reproductive capabilities of queen and worker bees in a complex factorial design.

Bees were placed in a small tube and either held captive (CAP) or shaken periodically (MAL) for one of 5, 7.5, 10, 12.5 or 15 minutes, after which they were sacrificed and two measures: ovarian development (I_z) and ovarian reabsorption (I_y), were taken. A single control group was measured with no such treatment, i.e., at time 0; there are $n=10$ per group.

The design is thus nearly a three-way factorial, with factors `caste` (Queen, Worker), `treat` (CAP, MAL) and `time`, except that there are only 11 combinations of Treatment and Time; we call these `trtime` below.

Usage

```
data(Bees)
```

Format

A data frame with 246 observations on the following 6 variables.

caste a factor with levels Queen Worker

treat a factor with levels " " CAP MAL

time an ordered factor: time of treatment

Iz an index of ovarian development

Iy an index of ovarian reabsorption

trtime a factor with levels 0 CAP05 CAP07 CAP10 CAP12 CAP15 MAL05 MAL07 MAL10 MAL12 MAL15

Details

Models for the three-way factorial design, using the formula `cbind(Iz, Iy) ~ caste*treat*time` ignore the control condition at `time==0`, where `treat==NA`.

To handle the additional control group at `time==0`, while separating the effects of Treatment and Time, 10 contrasts can be defined for the `trtime` factor in the model `cbind(Iz, Iy) ~ caste*trtime`. See `demo(bees.contrasts)` for details.

In the `heplot` examples below, the default `size="evidence"` displays are too crowded to interpret, because some effects are so highly significant. The alternative effect-size scaling, `size="effect"`, makes the relations clearer.

Source

Pabalan, N., Davey, K. G. & Packe, L. (2000). Escalation of Aggressive Interactions During Staged Encounters in *Halictus ligatus* Say (Hymenoptera: Halictidae), with a Comparison of Circle Tube Behaviors with Other Halictine Species *Journal of Insect Behavior*, **13**, 627-650.

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, **17**, 1-42.

Examples

```
data(Bees)

# 3-way factorial, ignoring 0 group
bees.mod <- lm(cbind(Iz, Iy) ~ caste*treat*time, data=Bees)
Anova(bees.mod)

op<-palette(c(palette()[1:4], "brown", "magenta", "olivedrab", "darkgray"))
heplot(bees.mod, xlab="Iz: Ovarian development", ylab="Iz: Ovarian reabsorption",
       main="Bees: ~caste*treat*time")
heplot(bees.mod, xlab="Iz: Ovarian development", ylab="Iz: Ovarian reabsorption",
       main="Bees: ~caste*treat*time", size="effect")

# two-way design, using trtime
bees.mod1 <- lm(cbind(Iz, Iy) ~ caste*trtime, data=Bees)
Anova(bees.mod1)

heplot(bees.mod1, xlab="Iz: Ovarian development", ylab="Iz: Ovarian reabsorption",
       main="Bees: ~caste*trtime")
heplot(bees.mod1, xlab="Iz: Ovarian development", ylab="Iz: Ovarian reabsorption",
       main="Bees: ~caste*trtime", size="effect")
palette(op)

# effect plots for separate responses
if(require(effects)) {
  bees.lm1 <-lm(Iy ~ treat*caste*time, data=Bees)
  bees.lm2 <-lm(Iz ~ treat*caste*time, data=Bees)
}
```

```
bees.eff1 <- allEffects(bees.lm1)
plot(bees.eff1, multiline=TRUE, ask=FALSE)

bees.eff2 <- allEffects(bees.lm2)
plot(bees.eff2, multiline=TRUE, ask=FALSE)
}
```

`cross3d`*Draw a 3D cross in an rgl scene*

Description

Draws a 3D cross or axis vectors in an rgl scene.

Usage

```
cross3d(centre = rep(0, 3), scale = rep(1, 3), ...)
```

Arguments

<code>centre</code>	A scalar or vector of length 3, giving the centre of the 3D cross
<code>scale</code>	A scalar or vector of length 3, giving the lengths of the arms of the 3D cross
<code>...</code>	Other arguments, passed on to segments3d

Value

Used for its side-effect, but returns (invisibly) a 6 by 3 matrix containing the end-points of three axes, in pairs.

Author(s)

Michael Friendly

See Also

[segments3d](#)

ellipse3d.axes *Draw axes of a 3D ellipsoid*

Description

A function to draw the major axes of a 3D ellipsoid from a correlation, covariance or sums of squares and cross products matrix.

Usage

```
ellipse3d.axes(x, centre = c(0, 0, 0), scale = c(1, 1, 1),
              level = 0.95, t = sqrt(qchisq(level, 3)), which = 1:3,
              labels = TRUE, label.ends=c(2,4,6), ...)
```

Arguments

x	A square positive definite matrix at least 3x3 in size. It will be treated as the correlation or covariance of a multivariate normal distribution.
centre	The center of the ellipse
scale	If x is a correlation matrix, then the standard deviations of each parameter can be given in the scale parameter. This defaults to <code>c(1, 1, 1)</code> , so no rescaling will be done.
level	The confidence level of a simultaneous confidence region. The default is 0.95, for a 95% region. This is used to control the size of the ellipsoid.
t	The size of the ellipsoid may also be controlled by specifying the value of a t-statistic on its boundary.
which	This parameter selects which variables from the object will be plotted. The default is the first 3.
labels	Either a logical value, a character string, or a character vector of length 3. If TRUE, the default, the axes are labeled PC1, PC2, PC3. If a single character string, the digits 1, 2, 3 are pasted on the end.
label.ends	A vector of length 3 indicating which ends of the axes should be labeled, corresponding to a selection of rows of the 6 x 3 matrix of axes end points. Default: <code>c(2, 4, 6)</code> .
...	Other arguments passed to <code>segments3d</code> and <code>text3d</code> .

Value

Returns a 6 x 3 matrix containing the end points of the three axis lines in pairs by rows.

Author(s)

Michael Friendly

See Also

[segments3d](#), [text3d](#), [ellipse3d](#)

Examples

```
data(iris)
iris3 <- iris[,1:3]
cov <- cov(iris3)
mu <- mean(iris3)
col <- c("blue", "green", "red")[iris$Species]

library(rgl)
plot3d(iris3, type="s", size=0.4, col=col, cex=2, box=FALSE, aspect="iso")
plot3d(ellipse3d(cov, centre=mu, level=0.68), col="gray", alpha=0.2, add = TRUE)

axes <- ellipse3d.axes(cov, centre=mu, level=0.68)
```

FootHead

Head measurements of football players

Description

Data collected as part of a preliminary study examining the relation between football helmet design and neck injuries. There are 30 subjects in each of three groups: High school football players, college players and non-football players.

Usage

```
data(FootHead)
```

Format

A data frame with 90 observations on the following 7 variables.

group a factor with levels High school College Non-football

width a numeric vector: head width at widest dimension

circum a numeric vector: head circumference

front.back a numeric vector: front to back distance at eye level

eye.top a numeric vector: eye to top of head

ear.top a numeric vector: ear to top of head

jaw a numeric vector: jaw width

Source

Rencher, A. C. (1995), *Methods of Multivariate Analysis*, New York: Wiley, Table 8.3.

Examples

```

data(FootHead)
str(FootHead)

# use Helmert contrasts for group
contrasts(FootHead$group) <- contr.helmert
contrasts(FootHead$group)

foot.mod <- lm(cbind(width, circum, front.back, eye.top, ear.top, jaw)~group, data=FootHead)
Manova(foot.mod)

# show the HE plot for the first two variables
heplot(foot.mod, main="HE plot")

# show it with tests of Helmert contrasts
heplot(foot.mod, hypotheses=list("group.1"="group1", "group.2"="group2"),
       col=c("red", "blue", "green3", "green3"),
       main="HE plot with orthogonal Helmert contrasts")

# show all pairwise HE plots
pairs(foot.mod)

# ... with tests of Helmert contrasts
pairs(foot.mod, hypotheses=list("group.1"="group1", "group.2"="group2"),
      col=c("red", "blue", "green3", "green3"), hyp.labels=FALSE)

# see that the hypothesis for groups really is 2D
heplot3d(foot.mod, variables=c(1,2,6),
         hypotheses=list("group.1"="group1", "group.2"="group2"),
         col=c("red", "blue", "green3", "green3"), wire=FALSE)

```

heplot

Two-Dimensional HE Plots

Description

This function plots ellipses representing the hypothesis and error sums-of-squares-and-products matrices for terms and linear hypotheses in a multivariate linear model.

Usage

```

heplot(mod, ...)

## S3 method for class 'mlm':
heplot(mod, terms, hypotheses, term.labels = TRUE,
       hyp.labels = TRUE, variables = 1:2, error.ellipse = !add,
       factor.means = !add, grand.mean = !add, remove.intercept = TRUE,
       type = c("II", "III", "2", "3"), manova, size = c("evidence", "effect.size"),

```

```

level = 0.68, alpha = 0.05, segments = 40, center.pch = "+", col = palette()[-1]
lty = 2:1, lwd = 1:2, xlab, ylab, main = "", xlim, ylim, axes=TRUE, offset.axes
add = FALSE, verbose = FALSE, warn.rank = FALSE, ...)

```

Arguments

<code>mod</code>	a model object of class "mlm".
<code>terms</code>	a logical value or character vector of terms in the model for which to plot hypothesis matrices; if missing or TRUE, defaults to all terms; if FALSE, no terms are plotted.
<code>hypotheses</code>	optional list of linear hypotheses for which to plot hypothesis matrices; hypotheses are specified as for the <code>linear.hypothesis</code> function in the <code>car</code> package; the list elements can be named, in which case the names are used.
<code>term.labels</code>	logical value or character vector of names for the terms to be plotted. If TRUE (the default) the names of the terms are used; if FALSE, term labels are not plotted.
<code>hyp.labels</code>	logical value or character vector of names for the hypotheses to be plotted. If TRUE (the default) the names of components of the list of hypotheses are used; if FALSE, hypothesis labels are not plotted.
<code>variables</code>	indices or names of the two response variables to be plotted; defaults to 1:2.
<code>error.ellipse</code>	if TRUE, plot the error ellipse; defaults to TRUE, if the argument <code>add</code> is FALSE (see below).
<code>factor.means</code>	logical value or character vector of names of factors for which the means are to be plotted, or TRUE or FALSE; defaults to TRUE, if the argument <code>add</code> is FALSE (see below).
<code>grand.mean</code>	if TRUE, plot the centroid for all of the data; defaults to TRUE, if the argument <code>add</code> is FALSE (see below).
<code>remove.intercept</code>	if TRUE (the default), do not plot the ellipse for the intercept even if it is in the MANOVA table.
<code>type</code>	"type" of sum-of-squares-and-products matrices to compute; one of "II", "III", "2", or "3", where "II" is the default (and "2" is a synonym).
<code>manova</code>	optional <code>Anova.mlm</code> object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
<code>size</code>	how to scale the hypothesis ellipse relative to the error ellipse; if "evidence", the default, the scaling is done so that a "significant" hypothesis ellipse extends outside of the error ellipse; if "effect.size", the hypothesis ellipse is on the same scale as the error ellipse.
<code>level</code>	equivalent coverage of ellipse for normally-distributed errors, defaults to 0.68.
<code>alpha</code>	significance level for Roy's greatest-root test statistic; if <code>size="evidence"</code> , then the hypothesis ellipse is scaled so that it just touches the error ellipse at the specified alpha level; a larger hypothesis ellipse therefore indicates statistical significance; defaults to 0.05.

<code>segments</code>	number of line segments composing each ellipse; defaults to 40.
<code>center.pch</code>	character to use in plotting the centroid of the data; defaults to "+".
<code>col</code>	a colour or vector of colours to use in plotting ellipses; the first colour is used for the error ellipse; the remaining colours — recycled as necessary — are used for the hypothesis ellipses; a single colour can be given, in which case it is used for all ellipses. Defaults to the current colour palette, less its first element.
<code>lty</code>	vector of line types to use for plotting the ellipses; the first is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single line type can be given. Defaults to 2 : 1.
<code>lwd</code>	vector of line widths to use for plotting the ellipses; the first is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single line width can be given. Defaults to 1 : 2.
<code>xlab</code>	x-axis label; defaults to name of the x variable.
<code>ylab</code>	y-axis label; defaults to name of the y variable.
<code>main</code>	main plot label; defaults to "".
<code>xlim</code>	x-axis limits; if absent, will be computed from the data.
<code>ylim</code>	y-axis limits; if absent, will be computed from the data.
<code>axes</code>	Whether to draw the x, y axes; defaults to TRUE
<code>offset.axes</code>	proportion to extend the axes in each direction if computed from the data; optional.
<code>add</code>	if TRUE, add to the current plot; the default is FALSE. If TRUE, the error ellipse is not plotted.
<code>verbose</code>	if TRUE, print the MANOVA table and details of hypothesis tests; the default is FALSE.
<code>warn.rank</code>	if TRUE, do not suppress warnings about the rank of the hypothesis matrix when the ellipse collapses to a line; the default is FALSE.
<code>...</code>	arguments to pass down to <code>plot</code> , <code>text</code> , and <code>points</code> .

Details

The `heplot` function plots a representation of the covariance ellipses for hypothesized model terms and linear hypotheses (H) and the corresponding error (E) matrices for two response variables in a multivariate linear model (mlm).

The plot helps to visualize the nature and dimensionality response variation on the two variables jointly in relation to error variation that is summarized in the various multivariate test statistics (Wilks' Lambda, Pillai trace, Hotelling-Lawley trace, Roy maximum root). Roy's maximum root test has a particularly simple visual interpretation, exploited in the `size="evidence"` version of the plot. See the description of argument `alpha`.

For a 1 df hypothesis term (a quantitative regressor, a single contrast or parameter test), the H matrix has rank 1 (one non-zero latent root of HE^{-1}) and the H ellipse collapses to a line.

Typically, you fit a mlm with `mymlm <- lm(cbind(y1, y2, y3, ...) ~ modelterms)`, and plot some or all of the `modelterms` with `heplot(mymlm, ...)`. Arbitrary linear hypotheses related to the terms in the model (e.g., contrasts of an effect) can be included in the plot using the `hypotheses` argument. See [linear.hypothesis](#) for details.

Value

The function invisibly returns an object of class "heplot", with coordinates for the various hypothesis ellipses and the error ellipse, and the limits of the horizontal and vertical axes. These may be useful for adding additional annotations to the plot, using standard plotting functions. (No methods for manipulating these objects are currently available.)

The components are:

H	a list containing the coordinates of each ellipse for the hypothesis terms
E	a matrix containing the coordinates for the error ellipse
center	x,y coordinates of the centroid
xlim	x-axis limits
ylim	y-axis limits

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, **17**(6), 1–42. <http://www.jstatsoft.org/v17/i06/>

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, **16**(2) 421–444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

See Also

[Anova](#), [linear.hypothesis](#), [heplot3d](#), [pairs.mlm](#).

Examples

```
## iris data
contrasts(iris$Species)<-matrix(c(0,-1,1, 2, -1, -1), 3,2)
contrasts(iris$Species)

iris.mod <- lm(cbind(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width) ~
Species, data=iris)

hyp <- list("V:V"="Species1", "S:VV"="Species2")
heplot(iris.mod, hypotheses=hyp)
# compare with effect-size scaling
heplot(iris.mod, hypotheses=hyp, size="effect", add=TRUE)

hep <-heplot(iris.mod, variables=c(1,3), hypotheses=hyp)
str(hep)

# all pairs
pairs(iris.mod, hypotheses=hyp, hyp.labels=FALSE)

## Pottery data, from cars package
data(Pottery)
pottery.mod <- lm(cbind(Al, Fe, Mg, Ca, Na) ~ Site, data=Pottery)
```

```

heplot(pottery.mod)
heplot(pottery.mod, terms=FALSE, add=TRUE, col="blue",
       hypotheses=list(c("SiteCaldicot = 0", "SiteIsleThorns=0")),
       hyp.labels="Sites Caldicot and Isle Thorns")

## Rohwer data, multivariate multiple regression/ANCOVA
##-- ANCOVA, assuming equal slopes
rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ SES + n + s + ns + na + ss, data=Rohwer)
Anova(rohwer.mod)
heplot(rohwer.mod)
# Add ellipse to test all 5 regressors
heplot(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
# View all pairs
pairs(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
# or 3D plot
heplot3d(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))

```

heplot1d

One-Dimensional HE Plots

Description

This function plots a 1-dimensional representation of the hypothesis (H) and error (E) sums-of-squares-and-products matrices for terms and linear hypotheses in a multivariate linear model.

In particular, for a given response, the 1-D representations of H and E matrices correspond to line segments. The E “ellipse” is shown as a filled rectangle whose width equals the mean squared error for that response. The H “ellipse” for each model term is shown as a line segment whose length represents either the size of the effect or the evidence for that effect.

This version is an initial sketch. Details of the implementation are subject to change.

Usage

```
heplot1d(mod, ...)
```

```
## S3 method for class 'mlm':
```

```

heplot1d(mod, terms, hypotheses, term.labels = TRUE, hyp.labels = TRUE,
         variables = 1, error.ellipse = !add, factor.means = !add, grand.mean = !add,
         remove.intercept = TRUE, type = c("II", "III", "2", "3"), manova,
         size = c("evidence", "effect.size"), level = 0.68, alpha = 0.05, segments =
         center.pch = "|", col = palette()[-1], lty = 2:1, lwd = 1:2, xlab, main =
         xlim, axes = TRUE, offset.axes, add = FALSE, verbose = FALSE, ...)

```

Arguments

mod	a model object of class "mlm".
terms	a logical value or character vector of terms in the model for which to plot hypothesis matrices; if missing or TRUE, defaults to all terms; if FALSE, no terms are plotted.

<code>hypotheses</code>	optional list of linear hypotheses for which to plot hypothesis matrices; hypotheses are specified as for the <code>linear.hypothesis</code> function in the <code>car</code> package; the list elements can be named, in which case the names are used.
<code>term.labels</code>	logical value or character vector of names for the terms to be plotted. If <code>TRUE</code> (the default) the names of the terms are used; if <code>FALSE</code> , term labels are not plotted.
<code>hyp.labels</code>	logical value or character vector of names for the hypotheses to be plotted. If <code>TRUE</code> (the default) the names of components of the list of hypotheses are used; if <code>FALSE</code> , hypothesis labels are not plotted.
<code>variables</code>	indices or names of the two response variables to be plotted; defaults to <code>1:2</code> .
<code>error.ellipse</code>	if <code>TRUE</code> , plot the error ellipse; defaults to <code>TRUE</code> , if the argument <code>add</code> is <code>FALSE</code> (see below).
<code>factor.means</code>	logical value or character vector of names of factors for which the means are to be plotted, or <code>TRUE</code> or <code>FALSE</code> ; defaults to <code>TRUE</code> , if the argument <code>add</code> is <code>FALSE</code> (see below).
<code>grand.mean</code>	if <code>TRUE</code> , plot the centroid for all of the data; defaults to <code>TRUE</code> , if the argument <code>add</code> is <code>FALSE</code> (see below).
<code>remove.intercept</code>	if <code>TRUE</code> (the default), do not plot the ellipse for the intercept even if it is in the MANOVA table.
<code>type</code>	“type” of sum-of-squares-and-products matrices to compute; one of <code>"II"</code> , <code>"III"</code> , <code>"2"</code> , or <code>"3"</code> , where <code>"II"</code> is the default (and <code>"2"</code> is a synonym).
<code>manova</code>	optional <code>Anova.mlm</code> object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
<code>size</code>	how to scale the hypothesis ellipse relative to the error ellipse; if <code>"evidence"</code> , the default, the scaling is done so that a “significant” hypothesis ellipse extends outside of the error ellipse; if <code>"effect.size"</code> , the hypothesis ellipse is on the same scale as the error ellipse.
<code>level</code>	equivalent coverage of ellipse for normally-distributed errors, defaults to <code>0.68</code> .
<code>alpha</code>	significance level for Roy’s greatest-root test statistic; if <code>size="evidence"</code> , then the hypothesis ellipse is scaled so that it just touches the error ellipse at the specified alpha level; a larger hypothesis ellipse therefore indicates statistical significance; defaults to <code>0.05</code> .
<code>segments</code>	number of line segments composing each ellipse; defaults to <code>40</code> .
<code>center.pch</code>	character to use in plotting the centroid of the data; defaults to <code>" "</code> .
<code>col</code>	a colour or vector of colours to use in plotting ellipses; the first colour is used for the error ellipse; the remaining colours — recycled as necessary — are used for the hypothesis ellipses; a single colour can be given, in which case it is used for all ellipses. Defaults to the current colour palette, less its first element.
<code>lty</code>	vector of line types to use for plotting the ellipses; the first is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single line type can be given. Defaults to <code>2:1</code> .

<code>lwd</code>	vector of line widths to use for plotting the ellipses; the first is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single line width can be given. Defaults to <code>1:2</code> .
<code>xlab</code>	x-axis label; defaults to name of the x variable.
<code>main</code>	main plot label; defaults to <code>" "</code> .
<code>xlim</code>	x-axis limits; if absent, will be computed from the data.
<code>axes</code>	Whether to draw the x, y axes; defaults to <code>TRUE</code>
<code>offset.axes</code>	proportion to extend the axes in each direction if computed from the data; optional.
<code>add</code>	if <code>TRUE</code> , add to the current plot; the default is <code>FALSE</code> . If <code>TRUE</code> , the error ellipse is not plotted.
<code>verbose</code>	if <code>TRUE</code> , print the MANOVA table and details of hypothesis tests; the default is <code>FALSE</code> .
<code>...</code>	arguments to pass down to <code>plot</code> , <code>text</code> , and <code>points</code> .

Value

The function invisibly returns an object of class `"heplot1d"`, with coordinates for the various hypothesis ellipses and the error ellipse, and the limits of the horizontal and vertical axes. (No methods for manipulating these objects are currently available.)

The components are:

<code>H</code>	ranges for the hypothesis terms
<code>E</code>	range for E
<code>xlim</code>	x-axis limits

Author(s)

Michael Friendly

See Also

[Anova](#), [linear.hypothesis](#) for hypothesis tests in `mlms`
[heplot](#), [heplot3d](#), [pairs.mlm](#) for other HE plot methods

Examples

```
## Plastics data
plastic.mod <- lm(cbind(tear, gloss, opacity) ~ rate*additive, data=Plastic)
heplot1d(plastic.mod, col=c("pink", "blue"))
heplot1d(plastic.mod, col=c("pink", "blue"), variables=2)
heplot1d(plastic.mod, col=c("pink", "blue"), variables=3)

## Bees data
bees.mod <- lm(cbind(Iz, Iy) ~ caste*treat*time, data=Bees)
heplot1d(bees.mod)
heplot1d(bees.mod, variables=2)
```

Description

This function plots ellipsoids in 3D representing the hypothesis and error sums-of-squares-and-products matrices for terms and linear hypotheses in a multivariate linear model.

Usage

```
heplot3d(mod, ...)

## S3 method for class 'mlm':
heplot3d(mod, terms, hypotheses, term.labels = TRUE,
  hyp.labels = TRUE, variables = 1:3, error.ellipsoid = !add,
  factor.means = !add, grand.mean = !add, remove.intercept = TRUE,
  type = c("II", "III", "2", "3"), manova, size = c("evidence", "effect.size"),
  level = 0.68, alpha = 0.05, segments = 40, col = palette()[-1], lwd=c(1, 4),
  shade=TRUE, shade.alpha=0.1, wire=c(TRUE,FALSE),
  bg.col = c("white", "black"), fogtype = c("none", "exp2", "linear", "exp"),
  fov = 30, offset = 0.01, xlab, ylab, zlab, xlim, ylim, zlim, add = FALSE, verbo
  warn.rank = FALSE, ...)
```

Arguments

<code>mod</code>	a model object of class "mlm".
<code>terms</code>	a logical value or character vector of terms in the model for which to plot hypothesis matrices; if missing or TRUE, defaults to all terms; if FALSE, no terms are plotted.
<code>hypotheses</code>	optional list of linear hypotheses for which to plot hypothesis matrices; hypotheses are specified as for the linear.hypothesis function in the <code>car</code> package; the list elements can be named, in which case the names are used.
<code>term.labels</code>	logical value or character vector of names for the terms to be plotted. If TRUE (the default) the names of the terms are used; if FALSE, term labels are not plotted.
<code>hyp.labels</code>	logical value or character vector of names for the hypotheses to be plotted. If TRUE (the default) the names of components of the list of hypotheses are used; if FALSE, hypothesis labels are not plotted.
<code>variables</code>	indices or names of the three response variables to be plotted; defaults to 1:3.
<code>error.ellipsoid</code>	if TRUE, plot the error ellipsoid; defaults to TRUE, if the argument <code>add</code> is FALSE (see below).
<code>factor.means</code>	logical value or character vector of names of factors for which the means are to be plotted, or TRUE or FALSE; defaults to TRUE, if the argument <code>add</code> is FALSE (see below).

<code>grand.mean</code>	if TRUE, plot the centroid for all of the data; defaults to TRUE, if the argument <code>add</code> is FALSE (see below).
<code>remove.intercept</code>	if TRUE (the default), do not plot the ellipsoid for the intercept even if it is in the MANOVA table.
<code>type</code>	“type” of sum-of-squares-and-products matrices to compute; one of "II", "III", "2", or "3", where "II" is the default (and "2" is a synonym).
<code>manova</code>	optional <code>Anova.mlm</code> object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
<code>size</code>	how to scale the hypothesis ellipsoid relative to the error ellipsoid; if "evidence", the default, the scaling is done so that a “significant” hypothesis ellipsoid extends outside of the error ellipsoid; if "effect.size", the hypothesis ellipsoid is on the same scale as the error ellipsoid.
<code>level.alpha</code>	equivalent coverage of ellipsoid for normally-distributed errors, defaults to 0.68. significance level for Roy’s greatest-root test statistic; if <code>size="evidence"</code> , then the hypothesis ellipsoid is scaled so that it just touches the error ellipsoid at the specified alpha level; a larger hypothesis ellipsoid therefore indicates statistical significance; defaults to 0.05.
<code>segments</code>	number of segments composing each ellipsoid; defaults to 40.
<code>col</code>	a colour or vector of colours to use in plotting ellipsoids; the first colour is used for the error ellipsoid; the remaining colours — recycled as necessary — are used for the hypothesis ellipsoids; a single colour can be given, in which case it is used for all ellipsoids. Defaults to the current colour palette, less its first element.
<code>lwd</code>	a two-element vector giving the line width for drawing ellipsoids (including those that degenerate to an ellipse) and for drawing ellipsoids that degenerate to a line segment. The default is <code>c(1, 4)</code> .
<code>shade</code>	a logical scalar or vector, indicating whether the ellipsoids should be rendered with <code>shade3d</code> . Works like <code>col</code> , except that FALSE is used for any 1 df degenerate ellipsoid.
<code>shade.alpha</code>	a numeric value in the range [0,1], or a vector of such values, giving the alpha transparency for ellipsoids rendered with <code>shade=TRUE</code> .
<code>wire</code>	a logical scalar or vector, indicating whether the ellipsoids should be rendered with <code>wire3d</code> . Works like <code>col</code> , except that TRUE is used for any 1 df degenerate ellipsoid.
<code>bg.col</code>	background colour, "white" or "black", defaulting to "white".
<code>fogtype</code>	type of “fog” to use for depth-cueing; the default is "none". See <code>bg</code> .
<code>fov</code>	field of view angle; controls perspective. See <code>viewpoint</code> .
<code>offset</code>	proportion of axes to off set labels; defaults to 0.01.
<code>xlab</code>	x-axis label; defaults to name of the x variable.
<code>ylab</code>	y-axis label; defaults to name of the y variable.
<code>zlab</code>	z-axis label; defaults to name of the z variable.
<code>xlim</code>	x-axis limits; if absent, will be computed from the data.

<code>ylim</code>	y-axis limits; if absent, will be computed from the data.
<code>zlim</code>	z-axis limits; if absent, will be computed from the data.
<code>add</code>	if TRUE, add to the current plot; the default is FALSE. If TRUE, the error ellipsoid is neither plotted nor returned in the output object.
<code>verbose</code>	if TRUE, print the MANOVA table and details of hypothesis tests; the default is FALSE.
<code>warn.rank</code>	if TRUE, do not suppress warnings about the rank of the hypothesis matrix when the ellipsoid collapses to an ellipse or line; the default is FALSE.
<code>...</code>	arguments passed from generic.

Details

When the H matrix for a term has rank < 3, the ellipsoid collapses to an ellipse (rank(H)=2) or a line (rank(H)=1).

Rotating the plot can be particularly revealing, showing views in which H variation is particularly large or small in relation to E variation. See [play3d](#) and [movie3d](#) for details on creating animations.

The arguments `xlim`, `ylim`, and `zlim` can be used to expand the bounding box of the axes, but cannot decrease it.

Value

`heplot3d` invisibly returns a list containing the bounding boxes of the error (E) ellipsoid and for each term or linear hypothesis specified in the call. Each of these is a 2 x 3 matrix with rownames "min" and "max" and colnames corresponding to the variables plotted. An additional component, `center`, contains the coordinates of the centroid in the plot.

The function also leaves an object named `.frame` in the global environment, containing the rgl object IDs for the axes, axis labels, and bounding box; these are deleted and the axes, etc. redrawn if the plot is added to.

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, 17(6), 1-42. <http://www.jstatsoft.org/v17/i06/>

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16(2) 421-444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

See Also

[Anova](#), [linear.hypothesis](#), for details on MANOVA tests and linear hypotheses

[heplot](#), [pairs.mlm](#), for other plotting methods for `mlm` objects

[rgl-package](#),

[heplot3d.candisc](#).

Examples

```
# Soils data, from car package
soils.mod <- lm(cbind(pH,N,Dens,P,Ca,Mg,K,Na,Conduc) ~ Block + Contour*Depth, data=Soils)
Anova(soils.mod)

heplot(soils.mod, variables=c("Ca", "Mg"))
pairs(soils.mod, terms="Depth", variables=c("pH", "N", "P", "Ca", "Mg"))

heplot3d(soils.mod, variables=c("Mg", "Ca", "Na"))

# Plastic data
plastic.mod <- lm(cbind(tear, gloss, opacity) ~ rate*additive, data=Plastic)
heplot3d(plastic.mod)
```

pairs.mlm

Pairwise HE Plots

Description

The function (in the form of an `mlm` method for the generic `pairs` function) constructs a “matrix” of pairwise HE plots (see [heplot](#)) for a multivariate linear model.

Usage

```
## S3 method for class 'mlm':
pairs(x, variables, type = c("II", "III", "2", "3"),
      offset.axes = 0.05, digits = getOption("digits") - 1, ...)
```

Arguments

<code>x</code>	an object of class <code>mlm</code> .
<code>variables</code>	indices or names of the three or more response variables to be plotted; defaults to all of the responses.
<code>type</code>	“type” of sum-of-squares-and-products matrices to compute; one of <code>"II"</code> , <code>"III"</code> , <code>"2"</code> , or <code>"3"</code> , where <code>"II"</code> is the default (and <code>"2"</code> is a synonym).
<code>offset.axes</code>	proportion to extend the axes in each direction; defaults to 0.05.
<code>digits</code>	number of significant digits in axis end-labels; taken from the <code>"digits"</code> option.
<code>...</code>	arguments to pass down to <code>heplot</code> , which is used to draw each panel of the display.

References

Friendly, M. (2006). Data Ellipses, HE Plots and Reduced-Rank Displays for Multivariate Linear Models: SAS Software and Examples *Journal of Statistical Software*, 17(6), 1-42. <http://www.jstatsoft.org/v17/i06/>

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16(2) 421-444. <http://www.math.yorku.ca/SCS/Papers/jcgs-heplots.pdf>

See Also

[heplot](#), [heplot3d](#)

Examples

```
# ANCOVA, assuming equal slopes
rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ SES + n + s + ns + na + ss, data=Rohwer)

# View all pairs, with ellipse for all 5 regressors
pairs(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
```

Plastic

Plastic Film Data

Description

An experiment was conducted to determine the optimum conditions for extruding plastic film. Three responses were measured in relation to two factors, rate of extrusion and amount of an additive.

Usage

```
data(Plastic)
```

Format

A data frame with 20 observations on the following 5 variables.

tear a numeric vector: tear resistance

gloss a numeric vector: film gloss

opacity a numeric vector: film opacity

rate a factor representing change in the rate of extrusion with levels Low (-10%), High (10%)

additive a factor with levels Low (1.0%), High (1.5%)

Source

Johnson, R.A. & Wichern, D.W. (1992). *Applied Multivariate Statistical Analysis*, 3rd ed., Prentice-Hall. Example 6.12 (p. 266).

References

Krzanowski, W. J. (1988). *Principles of Multivariate Analysis. A User's Perspective*. Oxford. (p. 381)

Examples

```
str(Plastic)
plastic.mod <- lm(cbind(tear, gloss, opacity) ~ rate*additive, data=Plastic)
Anova(plastic.mod)

pairs(plastic.mod)
```

Rohwer

Rohwer Data Set

Description

Data from an experiment by William D. Rohwer on kindergarten children designed to examine how well performance on a set of paired-associate (PA) tasks can predict performance on some measures of aptitude and achievement.

Usage

```
data(Rohwer)
```

Format

A data frame with 69 observations on the following 10 variables.

group a numeric vector, corresponding to SES
SES Socioeconomic status, a factor with levels Hi Lo
SAT a numeric vector: score on a Student Achievement Test
PPVT a numeric vector: score on the Peabody Picture Vocabulary Test
Raven a numeric vector: score on the Raven Progressive Matrices Test
n a numeric vector: performance on a 'named' PA task
s a numeric vector: performance on a 'still' PA task
ns a numeric vector: performance on a 'named still' PA task
na a numeric vector: performance on a 'named action' PA task
ss a numeric vector: performance on a 'sentence still' PA task

Details

The variables SAT, PPVT and Raven are responses to be potentially explained by performance on the paired-associate (PA) learning taskn, s, ns, na, and ss.

Source

Timm, N.H. 1975). *Multivariate Analysis with Applications in Education and Psychology*. Wadsworth (Brooks/Cole), Examples 4.3 (p. 281), 4.7 (p. 313), 4.13 (p. 344).

References

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16, in press. <http://www.math.yorku.ca/SCS/Papers/heplots.pdf>

Examples

```
str(Rohwer)

# fit separate models for Lo/Hi SES
rohwer.ses1 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss, data=Rohwer, subset=SES=="Lo")
rohwer.ses2 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss, data=Rohwer, subset=SES=="Hi")

# ANCOVA, assuming equal slopes
rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ SES + n + s + ns + na + ss, data=Rohwer)
Anova(rohwer.mod)

# Visualize the ANCOVA model
heplot(rohwer.mod)
# Add ellipse to test all 5 regressors
heplot(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
# View all pairs
pairs(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
# or 3D plot
heplot3d(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
```

 RootStock

Growth of Apple Trees from Different Root Stocks

Description

In a classic experiment carried out from 1918 to 1934, growth of apple trees of six different rootstocks were compared on four measures of size.

Usage

```
data(RootStock)
```

Format

A data frame with 48 observations on the following 5 variables.

rootstock a factor with levels 1 2 3 4 5 6

girth4 a numeric vector: trunk girth at 4 years (mm x 100)

ext4 a numeric vector: extension growth at 4 years (m)

girth15 a numeric vector: trunk girth at 15 years (mm x 100)

weight15 a numeric vector: weight of tree above ground at 15 years (lb x 1000)

Details

This is a balanced, one-way MANOVA design, with n=8 trees for each rootstock.

Source

Andrews, D. and Herzberg, A. (1985). *Data: A Collection of Problems from Many Fields for the Student and Research Worker* Springer-Verlag, pp. 357–360.

References

Rencher, A. C. (1995). *Methods of Multivariate Analysis*. New York: Wiley, Table 6.2

Examples

```
data(RootStock)
## maybe str(RootStock) ; plot(RootStock) ...
root.mod <- lm(cbind(girth4, ext4, girth15, weight15) ~ rootstock, data=RootStock)
Anova(root.mod)

pairs(root.mod)
```

VocabGrowth

Vocabulary growth data

Description

Data from the Laboratory School of the University of Chicago. They consist of scores from a cohort of pupils in grades 8-11 on the vocabulary section of the Cooperative Reading Test. The scores are scaled to a common, but arbitrary origin and unit of measurement, so as to be comparable over the four grades.

Usage

```
data(VocabGrowth)
```

Format

A data frame with 64 observations on the following 4 variables.

grade8 Grade 8 vocabulary score

grade9 Grade 9 vocabulary score

grade10 Grade 10 vocabulary score

grade11 Grade 11 vocabulary score

Details

Since these data cover an age range in which physical growth is beginning to decelerate, it is of interest whether a similar effect occurs in the acquisition of new vocabulary.

Source

R.D. Bock, *Multivariate statistical methods in behavioral research*, McGraw-Hill, New York, 1975, pp453.

References

Keesling, J.W., Bock, R.D. et al, "The Laboratory School study of vocabulary growth", University of Chicago, 1975.

Examples

```
data(VocabGrowth)

# Standard Multivariate & Univariate repeated measures analysis
Vocab.mod <- lm(cbind(grade8,grade9,grade10,grade11) ~ 1, data=VocabGrowth)
idata <-data.frame(grade=ordered(8:11))
Anova(Vocab.mod, idata=idata, idesign=~grade)

# calculate Y M, using polynomial contrasts
trends <- as.matrix(VocabGrowth) %**% poly(8:11, degree=3)
colnames(trends)<- c("Linear", "Quad", "Cubic")

# test all trend means = 0 == Grade effect
within.mod <- lm(trends ~ 1)

Manova(within.mod)
heplot(within.mod, terms="(Intercept)", col=c("red", "blue"), type="3",
       term.labels="Grade",
       main="HE plot for Grade effect")
points(0,0, cex=2.5, col="green", pch=19)
text(0,0, expression(H[0]), col="green", pos=2)
abline(h=0, col="green")
abline(v=0, col="green")
```

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