Package 'heplots'

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Type Package

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BugReports https://github.com/friendly/heplots/issues

Description Provides HE plot and other functions for visualizing hypothesis tests in multivariate linear models. HE plots represent sums-of-squares-and-products matrices for linear hypotheses and for error using ellipses (in two dimensions) and ellipsoids (in three dimensions). The related 'candisc' package provides visualizations in a reduced-rank canonical discriminant space when there are more than a few response variables.

License GPL (>= 2)

URL http://friendly.github.io/heplots/

RoxygenNote 5.0.1

VignetteBuilder knitr

NeedsCompilation no

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R **topics documented:**

heplots-package   *Visualizing Hypothesis Tests in Multivariate Linear Models*

Description

The heplots package provides functions for visualizing hypothesis tests in multivariate linear models (MANOVA, multivariate multiple regression, MANCOVA, and repeated measures designs). HE plots represent sums-of-squares-and-products matrices for linear hypotheses and for error using ellipses (in two dimensions), ellipsoids (in three dimensions), or by line segments in one dimension. See Fox, Friendly and Monette (2007) for a brief introduction and Friendly, Monette and Fox (2013) for a general discussion of the role of elliptical geometry in statistical understanding.

Other topics now addressed here include robust MLMs, tests for equality of covariance matrices in MLMs, and chi square Q-Q plots for MLMs.

The package also provides a collection of data sets illustrating a variety of multivariate linear models of the types listed above, together with graphical displays.

Several tutorial vignettes are also included. See vignette(package="heplots").

Details

Package:	heplots
Type:	Package
Version:	1.4-2
Date:	2022-10-09
License:	GPL (>= 2), GPL version 2 or newer

The graphical functions contained here all display multivariate model effects in variable (data) space, for one or more response variables (or contrasts among response variables in repeated measures designs).

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.

heplot1d constructs 1-dimensional analogs of HE plots for model terms and linear hypotheses for single response variables.

For repeated measure designs, between-subject effects and within-subject effects must be plotted separately, because the error terms (E matrices) differ. For terms involving within-subject effects, these functions carry out a linear transformation of the matrix **Y** of responses to a matrix **Y M**, where **M** is the model matrix for a term in the intra-subject design and produce plots of the H and E matrices in this transformed space. The vignette repeated describes these graphical methods for repeated measures designs.

The related **car** package calculates Type II and Type III tests of multivariate linear hypotheses using the Anova and linearHypothesis functions.

The candisc-package package provides functions for visualizing effects for MLM model terms in a low-dimensional canonical space that shows the largest hypothesis relative to error variation. The **candisc** package now also includes related methods for canonical correlation analysis.

The heplots package also contains a large number of multivariate data sets with examples of analyses and graphic displays. Use data(package="heplots") to see the current list.

Author(s)

John Fox, Michael Friendly, and Georges Monette

Maintainer: Michael Friendly, <friendly@yorku.ca>, http://datavis.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.

doi: 10.18637/jss.v017.i06

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, 16(2) 421-444. http://datavis.ca/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*. https://socialsciences.mcmaster.ca/jfox/heplots-dsc-paper.pdf

Friendly, M. (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40.

doi: 10.18637/jss.v037.i04

Fox, J., Friendly, M. & Weisberg, S. (2013). Hypothesis Tests for Multivariate Linear Models Using the car Package. *The R Journal*, **5**(1), https://journal.r-project.org/archive/2013-1/fox-friendly-weisberg.pdf.

Friendly, M., Monette, G. & Fox, J. (2013). Elliptical Insights: Understanding Statistical Methods Through Elliptical Geometry. *Statistical Science*, 2013, **28** (1), 1-39, http://datavis.ca/papers/ellipses.pdf.

Friendly, M. & Sigal, M. (2014). Recent Advances in Visualizing Multivariate Linear Models. *Revista Colombiana de Estadistica*, **37**, 261-283

Friendly, M. & Sigal, M. (2016). Graphical Methods for Multivariate Linear Models in Psychological Research: An R Tutorial. Submitted for publication.

See Also

Anova, linearHypothesis for Anova.mlm computations and tests

candisc-package for reduced-rank views in canonical space

manova for a different approach to testing effects in MANOVA designs

---

AddHealth   *Adolescent Health Data*

Description

This data was taken from the National Longitudinal Study of Adolescent Health. It is a cross-sectional sample of participants from grades 7–12, described and analyzed by Warne (2014).

Usage

```
data("AddHealth")
```

Format

A data frame with 4344 observations on the following 3 variables.

grade an ordered factor with levels 7 < 8 < 9 < 10 < 11 < 12

depression a numeric vector

anxiety a numeric vector

Details

depression is the response to the question "In the last month, how often did you feel depressed or blue?"

anxiety is the response to the question "In the last month, how often did you have trouble relaxing?"

The responses for depression and anxiety were recorded on a 5-point Likert scale, with categories 0="Never", 1="Rarely", 2="Occasionally", 3="Often", 4="Every day"

Source

Warne, R. T. (2014). A primer on Multivariate Analysis of Variance (MANOVA) for Behavioral Scientists. *Practical Assessment, Research & Evaluation*, 19 (1). https://scholarworks.umass.edu/pare/vol19/iss1/17/

Examples

```
data(AddHealth)
# fit mlm
AH.mod <- lm(cbind(depression, anxiety) ~ grade, data=AddHealth)

Anova(AH.mod)
summary(Anova(AH.mod))

heplot(AH.mod, hypotheses="grade.L", fill=c(TRUE, FALSE))
```

Adopted   *Adopted Children*

Description

Data are a subset from an observational, longitudinal, study on adopted children. Is child's intelligence related to intelligence of the biological mother and the intelligence of the adoptive mother?

The child's intelligence was measured at age 2, 4, 8, and 13 for this sample. How does intelligence change over time, and how are these changes related to intelligence of the birth and adoptive mother?

Usage

```
Adopted
```

Format

A data frame with 62 observations on the following 6 variables.

AMED adoptive mother's years of education (proxy for her IQ)

BMIQ biological mother's score on IQ test

Age2IQ IQ of child at age 2

Age4IQ IQ of child at age 4

Age8IQ IQ of child at age 8

Age13IQ IQ of child at age 13

Source

Ramsey, F.L. and Schafer, D.W. (2002). *The Statistical Sleuth: A Course in Methods of Data Analysis (2nd ed)*, Duxbury.

This data set is identical to ex1605 in the Sleuth2 package.

References

Friendly, M. (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40. doi: 10.18637/jss.v037.i04.

Skodak, M. and Skeels, H.M. (1949). A Final Follow-up Study of One Hundred Adopted Children, *Journal of Genetic Psychology* **75**: 85–125.

See Also

ex1605

Examples

```
# Treat as multivariate regression problem
Adopted.mod <- lm(cbind(Age2IQ, Age4IQ, Age8IQ, Age13IQ) ~ AMED + BMIQ,
                   data=Adopted)
Adopted.mod


require(car)
# test overall multivariate regression
print(linearHypothesis(Adopted.mod, c("AMED","BMIQ")), SSP=FALSE)

# show separate linear regressions
op <- par(mfcol=c(2,4), mar=c(4,4,1,1)+.1)
for (i in 3:6) {
dataEllipse(as.matrix(Adopted[,c(1,i)]),
            col="black", levels=0.68, ylim=c(70,140))
abline(lm(Adopted[,i] ~ Adopted[,1]), col="red", lwd=2)

dataEllipse(as.matrix(Adopted[,c(2,i)]),
            col="black", levels=0.68, ylim=c(70,140))
abline(lm(Adopted[,i] ~ Adopted[,2]), col="red", lwd=2)
abline(a=0,b=1, lty=1, col="blue")
}
par(op)

# between-S (MMReg) plots
heplot(Adopted.mod, hypotheses=list("Reg"=c("AMED", "BMIQ")),
main="IQ scores of adopted children: MMReg")

pairs(Adopted.mod, hypotheses=list("Reg"=c("AMED", "BMIQ")))

if(requireNamespace("rgl")){
heplot3d(Adopted.mod, hypotheses=list("Reg"=c("AMED", "BMIQ")),
col = c("red", "blue", "black", "gray"), wire=FALSE)
}

# Treat IQ at different ages as a repeated measure factor
# within-S models & plots
Age <- data.frame(Age=ordered(c(2,4,8,13)))
Anova(Adopted.mod, idata=Age, idesign=~Age, test="Roy")
```

```
# within-S plots
heplot(Adopted.mod, idata=Age, idesign=~Age, iterm="Age",
cex=1.25, cex.lab=1.4, fill=c(FALSE, TRUE),
hypotheses=list("Reg"=c("AMED", "BMIQ"))
)
```

---

arrow3d   *Draw a 3D Arrow in an RGL Scene*

Description

Draws a 3D arrow in an rgl scene with barbs at the arrow head

Usage

```
arrow3d(p0 = c(0, 0, 0), p1 = c(1, 1, 1), barblen, s = 0.05, theta = pi/6, n = 3, ...)
```

Arguments

p0	Initial point (tail of arrow)
p1	Ending point (head of arrow)
barblen	Length of each barb, in data units
s	length of barb as fraction of line length (unless barblen is specified)
theta	opening angle of barbs
n	number of barbs
...	args passed to lines3d for line styling, e.g., color, lwd, etc. See material3d.

Value

Returns (invisibly): integer ID of the line added to the scene

Author(s)

Barry Rowlingson, posted to R-help, 1/10/2010

See Also

lines3d, segments3d,

Examples

```
arrow3d(c(0,0,0), c(2,2,2), barblen=.2, lwd=3, col="black")
arrow3d(c(0,0,0), c(-2,2,2), barblen=.2, lwd=3, col="red")
```

---

bartlettTests   *Bartlett Tests of Homogeneity of Variances*

Description

This function extends `bartlett.test` to a multivariate response setting. It performs the Bartlett test of homogeneity of variances for each of a set of response variables, and prints a compact summary.

Usage

```
bartlettTests(y, group, ...)
```

Arguments

y	A data frame or matrix of numeric response variables in a multivariate linear model.
group	a vector or factor object giving the group for the corresponding elements of the rows of y
...	other arguments, passed to `bartlett.test`

Details

Bartlett's test is the univariate version of Box's M test for equality of covariance matrices. This function provides a univariate follow-up test to Box's M test to give one simple assessment of which response variables contribute to significant differences in variances among groups.

Value

An object of classes "anova" and "data.frame", with one observation for each response variable in y.

Author(s)

Michael Friendly

References

Bartlett, M. S. (1937). Properties of sufficiency and statistical tests. *Proceedings of the Royal Society of London Series A*, **160**, 268-282.

See Also

`boxM` for Box's M test for all responses.

Examples

```
bartlettTests(iris[,1:4], iris$Species)

data(Skulls, package="heplots")
bartlettTests(Skulls[,-1], Skulls$epoch)
```

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 (`Iz`) and ovarian reabsorption (`Iy`), 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)
require(car)

# 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, size="effect",
    xlab="Iz: Ovarian development",
    ylab="Iz: Ovarian reabsorption",
    main="Bees: ~caste*treat*time",
    )

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

# HE plots for this model, with both significance and effect size scaling

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)
}
```

---

boxM   *Box's M-test*

Description

boxM performs the Box's (1949) M-test for homogeneity of covariance matrices obtained from multivariate normal data according to one or more classification factors. The test compares the product of the log determinants of the separate covariance matrices to the log determinant of the pooled covariance matrix, analogous to a likelihood ratio test. The test statistic uses a chi-square approximation.

Usage

```
boxM(Y, ...)

## S3 method for class 'formula'
boxM(Y, data, ...)

## S3 method for class 'lm'
boxM(Y, ...)

## Default S3 method:
boxM(Y, group, ...)

## S3 method for class 'boxM'
summary(object,
    digits = getOption("digits"),
    cov=FALSE, quiet=FALSE, ...)
```

Arguments

Y	The response variable matrix for the default method, or a "mlm" or "formula" object for a multivariate linear model. If Y is a linear-model object or a formula, the variables on the right-hand-side of the model must all be factors and must be completely crossed, e.g., A:B
data	a numeric data.frame or matrix containing n observations of p variables; it is expected that $n > p$.
group	a factor defining groups, or a vector of length n doing the same.

object	a "boxM" object for the summary method
digits	number of digits to print for the summary method
cov	logical; if TRUE the covariance matrices are printed.
quiet	logical; if TRUE printing from the summary is suppressed
...	Arguments passed down to methods.

Details

As an object of class "htest", the statistical test is printed normally by default. As an object of class "boxM", a few methods are available.

There is no general provision as yet for handling missing data. Missing data are simply removed, with a warning.

As well, the computation assumes that the covariance matrix for each group is non-singular, so that $logdet(S_i)$ can be calculated for each group. At the minimum, this requires that $n > p$ for each group.

Box's M test for a multivariate linear model highly sensitive to departures from multivariate normality, just as the analogous univariate test. It is also affected adversely by unbalanced designs. Some people recommend to ignore the result unless it is very highly significant, e.g., p < .0001 or worse.

The summary method prints a variety of additional statistics based on the eigenvalues of the covariance matrices. These are returned invisibly, as a list containing the following components:

- logDet - log determinants
- eigs - eigenvalues of the covariance matrices
- eigstats - statistics computed on the eigenvalues for each covariance matrix:
  product: the product of eigenvalues, $\prod \lambda_i$;
  sum: the sum of eigenvalues, $\sum \lambda_i$;
  precision: the average precision of eigenvalues, $1/\sum(1/\lambda_i)$;
  max: the maximum eigenvalue, λ_1

Value

A list with class c("htest", "boxM") containing the following components:

statistic	an approximated value of the chi-square distribution.
parameter	the degrees of freedom related of the test statistic in this case that it follows a Chi-square distribution.
p.value	the p-value of the test.
cov	a list containing the within covariance matrix for each level of grouping.
pooled	the pooled covariance matrix.
logDet	a vector containing the natural logarithm of each matrix in cov, followed by the value for the pooled covariance matrix
means	a matrix of the means for all groups, followed by the grand means
df	a vector of the degrees of freedom for all groups, followed by that for the pooled covariance matrix

| data.name | a character string giving the names of the data. |
| method | the character string "Box's M-test for Homogeneity of Covariance Matrices". |

Author(s)

The default method was taken from the **biotools** package, Anderson Rodrigo da Silva <anderson.agro@hotmail.com>

Generalized by Michael Friendly and John Fox

References

Box, G. E. P. (1949). A general distribution theory for a class of likelihood criteria. *Biometrika*, 36, 317-346.

Morrison, D.F. (1976) *Multivariate Statistical Methods*.

See Also

leveneTest carries out homogeneity of variance tests for univariate models with better statistical properties.

plot.boxM, a simple plot of the log determinants

covEllipses plots covariance ellipses in variable space for several groups.

Examples

```
data(iris)

# default method
res <- boxM(iris[, 1:4], iris[, "Species"])
res

summary(res)

# visualize (what is done in the plot method)
dets <- res$logDet
ng <- length(res$logDet)-1
dotchart(dets, xlab = "log determinant")
points(dets , 1:4,
cex=c(rep(1.5, ng), 2.5),
pch=c(rep(16, ng), 15),
col= c(rep("blue", ng), "red"))

# formula method
boxM( cbind(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width) ~ Species, data=iris)

### Skulls dat
data(Skulls)
# lm method
skulls.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)
boxM(skulls.mod)
```

---

coefplot   *Coefficient plots for Multivariate Linear Models*

Description

Displays confidence ellipses for all parameters in an multivariate linear model, for a given pair of variables. As such, it is a generalization of `confidenceEllipse`.

Usage

```
coefplot(object, ...)

## S3 method for class 'mlm'
coefplot(object, variables = 1:2, parm = NULL,
df = NULL, level = 0.95, intercept = FALSE,
Scheffe = FALSE, bars = TRUE,
fill = FALSE, fill.alpha = 0.2,
labels = !add, label.pos = NULL,
xlab, ylab,
xlim = NULL, ylim = NULL,
axes = TRUE, main = "", add = FALSE,
lwd = 1, lty = 1, pch = 19, col = palette(),
cex = 2, cex.label = 1.5,
lty.zero = 3, col.zero = 1, pch.zero = '+',
verbose = FALSE, ...)
```

Arguments

`object`	A multivariate linear model, such as fit by `lm(cbind(y1, y2, ...) ~ ...)`
`...`	Other parameters passed to methods
`variables`	Response variables to plot, given as their indices or names
`parm`	Parameters to plot, given as their indices or names
`df`	Degrees of freedom for hypothesis tests
`level`	Confidence level for the confidence ellipses
`intercept`	logical. Include the intercept?
`Scheffe`	If `TRUE`, confidence intervals for all parameters have Scheffe coverage, otherwise, individual coverage.
`bars`	Draw univariate confidence intervals for each of the variables?
`fill`	a logical value or vector. `TRUE` means the confidence ellipses will be filled.
`fill.alpha`	Opacity of the confidence ellipses
`labels`	Labels for the confidence ellipses
`label.pos`	Positions of the labels for each ellipse. See `label.ellipse`

xlab, ylab	x, y axis labels
xlim, ylim	Axis limits
axes	Draw axes?
main	Plot title
add	logical. Add to an existing plot?
lwd	Line widths
lty	Line types
pch	Point symbols for the parameter estimates
col	Colors for the confidence ellipses, points, lines
cex	Character size for points showing parameter estimates
cex.label	Character size for ellipse labels
lty.zero, col.zero, pch.zero	
	Line type, color and point symbol for horizontal and vertical lines at 0, 0.
verbose	logical. Print parameter estimates and variance-covariance for each parameter?

Value

Returns invisibly a list of the coordinates of the ellipses drawn

Author(s)

Michael Friendly

See Also

[confidenceEllipse](#), ~~~

Examples

```
rohwer.mlm <- lm(cbind(SAT,PPVT,Raven)~n+s+ns, data=Rohwer)

coefplot(rohwer.mlm, lwd=2, main="Bivariate coefficient plot for SAT and PPVT", fill=TRUE)
coefplot(rohwer.mlm, add=TRUE, Scheffe=TRUE, fill=TRUE)

coefplot(rohwer.mlm, var=c(1,3))

mod1 <- lm(cbind(SAT,PPVT,Raven)~n+s+ns+na+ss, data=Rohwer)
coefplot(mod1, lwd=2, fill=TRUE, parm=(1:5),
main="Bivariate 68% coefficient plot for SAT and PPVT", level=0.68)
```

---

colDevs   *Calculate column deviations from central values*

Description

`colDevs` calculates the column deviations of data values from a central value (mean, median, etc.), possibly stratified by a grouping variable.

Conceptually, the function is similar to a column-wise [sweep](#), by group, allowing an arbitrary `center` function.

Usage

```
colDevs(x, group, center = mean, ...)
```

Arguments

x	A numeric data frame or matrix.
group	A factor (or variable that can be coerced to a factor) indicating the membership of each observation in x in one or more groups. If missing, all the data is treated as a single group.
center	A function used to center the values (for each group if group is specified. The function must take a vector argument and return a scalar result.
...	Arguments passed down

Details

Non-numeric columns of x are removed, with a warning.

Value

A numeric matrix containing the deviations from the centering function.

Author(s)

Michael Friendly

See Also

[colMeans](#) for column means,

[sweep](#)

Examples

```
data(iris)

Species <- iris$Species
irisdev <- colDevs(iris[,1:4], Species, mean)
irisdev <- colDevs(iris[,1:4], Species, median)
# trimmed mean, using an anonymous function
irisdev <- colDevs(iris[,1:4], Species, function(x) mean(x, trim=0.25))

# no grouping variable: deviations from column grand means
# include all variables (but suppress warning for this doc)
irisdev <- suppressWarnings( colDevs(iris) )
```

---

covEllipses   *Draw classical and robust covariance ellipses for one or more groups*

Description

The function draws covariance ellipses for one or more groups and optionally for the pooled total sample. It uses either the classical product-moment covariance estimate, or a robust alternative, as provided by cov.rob. Provisions are provided to do this for more than two variables, in a scatterplot matrix format.

Usage

```
covEllipses(x, ...)

## S3 method for class 'boxM'
covEllipses(x, ...)

## S3 method for class 'data.frame'
covEllipses(x, group, pooled = TRUE, method = c("classical", "mve", "mcd"), ...)

## S3 method for class 'matrix'
covEllipses(x, group, pooled = TRUE, method = c("classical", "mve", "mcd"), ...)

## Default S3 method:
covEllipses(x, means, df,
        labels = NULL, variables = 1:2, level = 0.68,
        segments = 60,
        center = FALSE, center.pch = "+", center.cex = 2,
        col = getOption("heplot.colors", c("red", "blue", "black", "darkgreen",
                        "darkcyan", "brown", "magenta", "darkgray")),
        lty = 1, lwd = 2,
        fill = FALSE, fill.alpha = 0.3,
        label.pos = 0,
```

```
        xlab, ylab,
        vlabels, var.cex=2,
        main = "",
        xlim, ylim, axes = TRUE,
        offset.axes, add = FALSE,  ...)
```

Arguments

x	The generic argument. For the default method, this is a list of covariance matrices. For the `data.frame` and `matrix` methods, this is a numeric matrix of two or more columns supplying the variables to be analyzed.
group	a factor defining groups, or a vector of length n=nrow(x) doing the same. If missing, a single covariance ellipse is drawn.
pooled	Logical; if `TRUE`, the pooled covariance matrix for the total sample is also computed and plotted
method	the covariance method to be used: classical product-moment (`"classical"`), or minimum volume ellipsoid (`"mve"`), or minimum covariance determinant (`"mcd"`).
means	For the default method, a matrix of the means for all groups (followed by the grand means, if `pooled=TRUE`). Rows are the groups, and columns are the variables. It is assumed that the means have column names corresponding to the variables in the covariance matrices.
df	For the default method, a vector of the degrees of freedom for the covariance matrices
labels	Either a character vector of labels for the groups, or `TRUE`, indicating that group labels are taken as the names of the covariance matrices. Use `labels=""` to suppress group labels, e.g., when add=TRUE
variables	indices or names of the response variables to be plotted; defaults to `1:2`. If more than two variables are supplied, the function plots all pairwise covariance ellipses in a scatterplot matrix format.
level	equivalent coverage of a data ellipse for normally-distributed errors, defaults to `0.68`.
segments	number of line segments composing each ellipse; defaults to `40`.
center	If `TRUE`, the covariance ellipses are centered at the centroid.
center.pch	character to use in plotting the centroid of the data; defaults to `"+"`.
center.cex	size of character to use in plotting the centroid of the data; defaults to `2`.
col	a color or vector of colors to use in plotting ellipses — recycled as necessary A single color can be given, in which case it is used for all ellipses. For convenience, the default colors for all plots produced in a given session can be changed by assigning a color vector via `options(heplot.colors =c(...)`. Otherwise, the default colors are `c("red", "blue", "black", "darkgreen", "darkcyan", "magenta", "brown", "darkgray")`.
lty	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`.

lwd	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.
fill	A logical vector indicating whether each ellipse should be filled or not. The first value is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single fill value can be given. Defaults to FALSE for backward compatibility. See Details below.
fill.alpha	Alpha transparency for filled ellipses, a numeric scalar or vector of values within [0,1], where 0 means fully transparent and 1 means fully opaque. Defaults to 0.3.
label.pos	Label position, a vector of integers (in 0:4) or character strings (in c("center", "bottom", "left", "top", "right")) use in labeling ellipses, recycled as necessary. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the max/min coordinates of the ellipse; the value 0 specifies the centroid of the ellipse object. The default, label.pos=NULL uses the correlation of the ellipse to determine "top" (r>=0) or "bottom" (r<0).
xlab	x-axis label; defaults to name of the x variable.
ylab	y-axis label; defaults to name of the y variable.
vlabels	Labels for the variables can also be supplied through this argument, which is more convenient when length(variables) > 2.
var.cex	character size for variable labels in the pairs plot
main	main plot label; defaults to "", and presently has no effect.
xlim	x-axis limits; if absent, will be computed from the data.
ylim	y-axis limits; if absent, will be computed from the data.
axes	Whether to draw the x, y axes; defaults to TRUE
offset.axes	proportion to extend the axes in each direction if computed from the data; optional.
add	if TRUE, add to the current plot; the default is FALSE. This argument is has no effect when more than two variables are plotted.
...	Other arguments passed to the default method for plot, text, and points

Details

These plot methods provide one way to visualize possible heterogeneity of within-group covariance matrices in a one-way MANOVA design. When covariance matrices are nearly equal, their covariance ellipses should all have the same shape. When centered at a common mean, they should also all overlap.

The can also be used to visualize the difference between classical and robust covariance matrices.

Value

Nothing is returned. The function is used for its side-effect of producing a plot.

Author(s)

Michael Friendly

See Also

heplot, boxM,

cov.rob

Examples

```
data(iris)

# compare classical and robust covariance estimates
covEllipses(iris[,1:4], iris$Species)
covEllipses(iris[,1:4], iris$Species, fill=TRUE, method="mve", add=TRUE, labels="")

# method for a boxM object
x <- boxM(iris[, 1:4], iris[, "Species"])
x
covEllipses(x, fill=c(rep(FALSE,3), TRUE) )
covEllipses(x, fill=c(rep(FALSE,3), TRUE), center=TRUE, label.pos=1:4 )

# method for a list of covariance matrices
cov <- c(x$cov, pooled=list(x$pooled))
df <- c(table(iris$Species)-1, nrow(iris)-3)
covEllipses(cov, x$means, df, label.pos=3, fill=c(rep(FALSE,3), TRUE))

covEllipses(cov, x$means, df, label.pos=3, fill=c(rep(FALSE,3), TRUE), center=TRUE)

# scatterplot matrix version
covEllipses(iris[,1:4], iris$Species,
fill=c(rep(FALSE,3), TRUE), variables=1:4,
fill.alpha=.1)
```

---

cqplot   *Chi Square Quantile-Quantile plots*

Description

A chi square quantile-quantile plots show the relationship between data-based values which should be distributed as χ^2 and corresponding quantiles from the χ^2 distribution. In multivariate analyses, this is often used both to assess multivariate normality and check for outliers, using the Mahalanobis squared distances (D^2) of observations from the centroid.

cqplot is a more general version of similar functions in other packages that produce chi square QQ plots. It allows for classical Mahalanobis squared distances as well as robust estimates based on the MVE and MCD; it provides an approximate confidence (concentration) envelope around the line of unit slope, a detrended version, where the reference line is horizontal, the ability to identify or label unusual points, and other graphical features.

The method for "mlm" objects applies this to the residuals from the model.

Usage

```
cqplot(x, ...)

## S3 method for class 'mlm'
cqplot(x, ...)

## Default S3 method:
cqplot(x, method = c("classical", "mcd", "mve"),
detrend = FALSE, pch = 19, col = palette()[1], cex = par("cex"),
ref.col = "red", ref.lwd = 2,
conf = 0.95, env.col = "gray", env.lwd = 2, env.lty = 1,
env.fill = TRUE, fill.alpha = 0.2,
fill.color = trans.colors(ref.col, fill.alpha),
labels = if (!is.null(rownames(x))) rownames(x) else 1:nrow(x),
id.n, id.method = "y", id.cex = 1, id.col = palette()[1],
xlab, ylab, main, what=deparse(substitute(x)), ylim, ...)
```

Arguments

x	either a numeric data frame or matrix for the default method, or an object of class "mlm" representing a multivariate linear model. In the latter case, residuals from the model are plotted.
...	Other arguments passed to methods
method	estimation method used for center and covariance, one of: "classical" (product-moment), "mcd" (minimum covariance determinant), or "mve" (minimum volume ellipsoid).
detrend	logical; if FALSE, the plot shows values of D^2 vs. χ^2. if TRUE, the ordinate shows values of $D^2 - \chi^2$
pch	plot symbol for points Can be a vector of length equal to the number of rows in x.
col	color for points; the default is the *first* entry in the current color palette (see palette and par.
cex	character symbol size for points. Can be a vector of length equal to the number of rows in x.
ref.col	Color for the reference line
ref.lwd	Line width for the reference line
conf	confidence coverage for the approximate confidence envelope
env.col	line color for the boundary of the confidence envelope
env.lwd	line width for the confidence envelope
env.lty	line type for the confidence envelope
env.fill	logical; should the confidence envelope be filled?
fill.alpha	transparency value for fill.color

fill.color	color used to fill the confidence envelope
labels	vector of text strings to be used to identify points, defaults to rownames(x) or observation numbers if rownames(x) is NULL
id.n	number of points labeled. If id.n=0, the default, no point identification occurs.
id.method	point identification method. The default id.method="y" will identify the id.n points with the largest value of abs(y-mean(y)). See showLabels for other options.
id.cex	size of text for point labels
id.col	color for point labels
xlab	label for horizontal (theoretical quantiles) axis
ylab	label for vertical (empirical quantiles) axis
main	plot title
what	the name of the object plotted; used in the construction of main when that is not specified.
ylim	limits for vertical axis. If not specified, the range of the confidence envelope is used.

Details

The calculation of the confidence envelope follows that used in the SAS program, http://www.datavis.ca/sasmac/cqplot.html which comes from Chambers et al. (1983), Section 6.8.

The essential formula is

$$SE(z_{(i)}) = \frac{\hat{\delta}}{g(q_i)) \times \sqrt{fracp_i(1 - p_i n}}$$

where $z_{(i)}$ is the i-th order value of D^2, $\hat{\delta}$ is an estimate of the slope of the reference line obtained from the corresponding quartiles and $g(q_i)$ is the density of the chi square distribution at the quantile q_i.

Note that this confidence envelope applies only to the D^2 computed using the classical estimates of location and scatter. The car::qqPlot() function provides for simulated envelopes, but only for a univariate measure. Oldford (2016) provides a general theory and methods for QQ plots.

Value

Returns invisibly the vector of squared Mahalanobis distances corresponding to the rows of x or the residuals of the model.

Author(s)

Michael Friendly

References

J. Chambers, W. S. Cleveland, B. Kleiner, P. A. Tukey (1983). *Graphical methods for data analysis*, Wadsworth.

R. W. Oldford (2016), "Self calibrating quantile-quantile plots", *The American Statistician*, 70, 74-90.

See Also

[Mahalanobis](#) for calculation of Mahalanobis squared distance;

[qqplot](#); [qqPlot](#) can give a similar result for Mahalanobis squared distances of data or residuals;
[qqtest](#) has many features for all types of QQ plots.

Examples

```
cqplot(iris[, 1:4])

iris.mod <- lm(as.matrix(iris[,1:4]) ~ Species, data=iris)
cqplot(iris.mod, id.n=3)

# compare with car::qqPlot
car::qqPlot(Mahalanobis(iris[, 1:4]), dist="chisq", df=4)


# Adopted data
Adopted.mod <- lm(cbind(Age2IQ, Age4IQ, Age8IQ, Age13IQ) ~ AMED + BMIQ,
                  data=Adopted)
cqplot(Adopted.mod, id.n=3)
cqplot(Adopted.mod, id.n=3, method="mve")


# Sake data
Sake.mod <- lm(cbind(taste, smell) ~ ., data=Sake)
cqplot(Sake.mod)
cqplot(Sake.mod, method="mve", id.n=2)

# SocialCog data -- one extreme outlier
data(SocialCog)
SC.mlm <-  lm(cbind(MgeEmotions,ToM, ExtBias, PersBias) ~ Dx,
              data=SocialCog)
cqplot(SC.mlm, id.n=1)

# data frame example: stackloss data
data(stackloss)
cqplot(stackloss[, 1:3], id.n=4)                   # very strange
cqplot(stackloss[, 1:3], id.n=4, detrend=TRUE)
cqplot(stackloss[, 1:3], id.n=4, method="mve")
cqplot(stackloss[, 1:3], id.n=4, method="mcd")
```

---

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

centre   A scalar or vector of length 3, giving the centre of the 3D cross

scale   A scalar or vector of length 3, giving the lengths of the arms of the 3D cross

...   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

Diabetes   *Diabetes Dataset*

Description

Reaven and Miller (1979) examined the relationship among blood chemistry measures of glucose tolerance and insulin in 145 nonobese adults. They used the PRIM9 system at the Stanford Linear Accelerator Center to visualize the data in 3D, and discovered a peculiar pattern that looked like a large blob with two wings in different directions.

After further analysis, the subjects were classified as subclinical (chemical) diabetics, overt diabetics and normals. This study was influential in defining the stages of development of Type 2 diabetes. Overt diabetes is the most advanced stage, characterized by elevated fasting blood glucose concentration and classical symptoms. Preceding overt diabetes is the latent or chemical diabetic stage, with no symptoms of diabetes but demonstrable abnormality of oral or intravenous glucose tolerance.

Usage

```
data("Diabetes")
```

Format

A data frame with 145 observations on the following 6 variables.

relwt relative weight, expressed as the ratio of actual weight to expected weight, given the person's height, a numeric vector

glufast fasting plasma glucose level, a numeric vector

glutest test plasma glucose level, a measure of glucose intolerance, a numeric vector

instest plasma insulin during test, a measure of insulin response to oral glucose, a numeric vector

sspg steady state plasma glucose, a measure of insulin resistance, a numeric vector

group diagnostic group, a factor with levels Normal Chemical_Diabetic Overt_Diabetic

Details

glutest was defined as the "area under the plasma glucose curve for the three hour oral glucose tolerance test." Reaven & Miller refer to this variable as "Glucose area".

instest was defined as the "area under the plasma insulin curve", and is referred to in the paper as "Insulin area".

This study was influential in defining the stages of development of Type 2 diabetes. Overt diabetes is the most advanced stage, characterized by elevated fasting blood glucose concentration and classical symptoms. Preceding overt diabetes is the latent or chemical diabetic stage, with no symptoms of diabetes but demonstrable abnormality of oral or intravenous glucose tolerance.

Source

Andrews, D. F. & Herzberg, A. M. (1985). *Data: A Collection of Problems from Many Fields for the Student and Research Worker*, Springer-Verlag, Ch. 36.

Friendly, M. (1991). *SAS System for Statistical Graphics*, Cary, NC: SAS Institute.

References

Reaven, G. M. and Miller, R. G. (1979). An attempt to define the nature of chemical diabetes using a multidimensional analysis. *Diabetologia*, 16, 17-24.

Examples

```
data(Diabetes)
col <- c("blue", "red", "darkgreen")[Diabetes$group]
pch <- c(16,15,17)[Diabetes$group]

# a perplexing plot, similar to Fig 2, but with a loess smooth
plot(instest ~ glutest, data=Diabetes, pch=16,
cex.lab=1.25,
xlab="Glucose area (glutest)",
ylab="Insulin area (instest)")
lines( loess.smooth(Diabetes$glutest, Diabetes$instest), col="blue", lwd=2)

# scatterplot matrix, colored by group
plot(Diabetes[,1:5], col=col, pch=pch)
```

```
# covariance ellipses
covEllipses(Diabetes[,2:5], Diabetes$group, fill=TRUE, pooled=FALSE,
col=col)

covEllipses(Diabetes[,2:5], Diabetes$group, fill=TRUE, pooled=FALSE,
col=col, variables=1:4)

# Box's M test
diab.boxm <- boxM(Diabetes[,2:5], Diabetes$group)
diab.boxm
plot(diab.boxm)

# heplots
diab.mlm <- lm(cbind(glufast, glutest, instest, sspg) ~ group, data=Diabetes)

heplot(diab.mlm)
pairs(diab.mlm, fill=TRUE, fill.alpha=0.1)
```

---

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 c(1, 1, 1), 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: c(2,4,6).
...	Other arguments passed to segments3d and text3d.

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 <- colMeans(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, color="gray", lwd=2)
```

---

etasq   *Measures of Partial Association (Eta-squared) for Linear Models*

Description

Calculates partial eta-squared for linear models or multivariate analogs of eta-squared (or R^2), indicating the partial association for each term in a multivariate linear model. There is a different analog for each of the four standard multivariate test statistics: Pillai's trace, Hotelling-Lawley trace, Wilks' Lambda and Roy's maximum root test.

Usage

```
etasq(x, ...)

## S3 method for class 'lm'
etasq(x, anova = FALSE, partial = TRUE,  ...)

## S3 method for class 'mlm'
etasq(x, ...)

## S3 method for class 'Anova.mlm'
etasq(x, anova = FALSE, ...)
```

Arguments

x	A `lm`, `mlm` or `Anova.mlm` object
anova	A logical, indicating whether the result should also contain the test statistics produced by `Anova()`.
partial	A logical, indicating whether to calculate partial or classical eta^2.
...	Other arguments passed down to [Anova]().

Details

For univariate linear models, classical η^2 = SSH / SST and partial η^2 = SSH / (SSH + SSE). These are identical in one-way designs.

Partial eta-squared describes the proportion of total variation attributable to a given factor, partialing out (excluding) other factors from the total nonerror variation. These are commonly used as measures of effect size or measures of (non-linear) strength of association in ANOVA models.

All multivariate tests are based on the $s = min(p, df_h)$ latent roots of HE^{-1}. The analogous multivariate partial η^2 measures are calculated as:

Pillai's trace (V) $\eta^2 = V/s$

Hotelling-Lawley trace (T) $\eta^2 = T/(T + s)$

Wilks' Lambda (L) $\eta^2 = L^{1/s}$

Roy's maximum root (R) $\eta^2 = R/(R + 1)$

Value

When `anova=FALSE`, a one-column data frame containing the eta-squared values for each term in the model.

When `anova=TRUE`, a 5-column (lm) or 7-column (mlm) data frame containing the eta-squared values and the test statistics produced by `print.Anova()` for each term in the model.

Author(s)

Michael Friendly

References

Muller, K. E. and Peterson, B. L. (1984). Practical methods for computing power in testing the Multivariate General Linear Hypothesis *Computational Statistics and Data Analysis*, 2, 143-158.

Muller, K. E. and LaVange, L. M. and Ramey, S. L. and Ramey, C. T. (1992). Power Calculations for General Linear Multivariate Models Including Repeated Measures Applications. *Journal of the American Statistical Association*, 87, 1209-1226.

See Also

[Anova](#)

Examples

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

etasq(soils.mod, test="Wilks")
etasq(soils.mod, test="Hotelling")
```

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)
require(car)

# 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 for width and circumference", fill=TRUE,
col=c("red", "blue"))

# 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
if(requireNamespace("rgl")){
heplot3d(foot.mod, variables=c(1,2,6),
hypotheses=list("group.1"="group1","group.2"="group2"),
col=c("red", "blue", "green3", "green3" ), wire=FALSE)
}
```

---

glance.mlm   *Glance at an mlm object*

Description

This function takes an "mlm" object, fit by `lm` with a multivariate response. The goal is to return something analogous to `glance.lm` for a univariate response linear model.

In the multivariate case, it returns a `tibble` with one row for each response variable, containing goodness of fit measures, F-tests and p-values.

Usage

```
## S3 method for class 'mlm'
glance(x, ...)
```

Arguments

x	An `mlm` object created by `lm`, i.e., with a multivariate response.
...	Additional arguments. Not used.

Value

A `tibble` with one row for each response variable and the columns:

r.squared R squared statistic, or the percent of variation explained by the model.

adj.r.squared Adjusted R squared statistic, which is like the R squared statistic except taking degrees of freedom into account.

sigma Estimated standard error of the residuals

fstatitic Overall F statistic for the model

numdf Numerator degrees of freedom for the overall test

dendf Denominator degrees of freedom for the overall test

p.value P-value corresponding to the F statistic

nobs Number of observations used

Author(s)

Michael Friendly

See Also

`glance`, `glance.lm`

Examples

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

| gsorth | *Orthogonalize successive columns of a data frame or matrix* |

Description

gsorth uses sequential, orthogonal projections, as in the Gram-Schmidt method, to transform a matrix or numeric columns of a data frame into an uncorrelated set, possibly retaining the same column means and standard deviations as the original.

In statistical applications, interpretation depends on the order of the variables orthogonalized. In multivariate linear models, orthogonalizing the response, Y variables provides the equivalent of step-down tests, where Y1 is tested alone, and then Y2.1, Y3.12, etc. can be tested to determine their additional contributions over the previous response variables.

Similarly, orthogonalizing the model X variables provides the equivalent of Type I tests, such as provided by anova.

Usage

```
gsorth(y, order, recenter = TRUE, rescale = TRUE, adjnames = TRUE)
```

Arguments

y	A numeric data frame or matrix
order	An integer vector specifying the order of and/or a subset of the columns of y to be orthogonalized. If missing, order=1:p where p=ncol(y).
recenter	If TRUE, the result has same column means as original; else means = 0 for cols 2:p.
rescale	If TRUE, the result has same column standard deviations as original; else sd = residual variance for cols 2:p
adjnames	If TRUE, the column names of the result are adjusted to the form Y1, Y2.1, Y3.12, by adding the suffixes '.1', '.12', etc. to the original column names.

Details

The method is equivalent to setting each of columns 2:p to the residuals from a linear regression of that column on all prior columns, i.e.,

```
z[,j] <- resid( lm( z[,j] ~ as.matrix(z[,1:(j-1)]), data=z) )
```

However, for accuracy and speed the transformation is carried out using the QR decomposition.

Value

Returns a matrix or data frame with uncorrelated columns. Row and column names are copied to the result.

Author(s)

Michael Friendly

See Also

qr,

Examples

```
GSiris <- gsorth(iris[,1:4])
GSiris <- gsorth(iris, order=1:4)   # same, using order
str(GSiris)
zapsmall(cor(GSiris))
colMeans(GSiris)
# sd(GSiris) -- sd(<matrix>) now deprecated
apply(GSiris, 2, sd)

# orthogonalize Y side
GSiris <- data.frame(gsorth(iris[,1:4]), Species=iris$Species)
iris.mod1 <- lm(as.matrix(GSiris[,1:4]) ~ Species, data=GSiris)
Anova(iris.mod1)

# orthogonalize X side
rohwer.mod <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss, data=Rohwer)
Anova(rohwer.mod)

# type I tests for Rohwer data
Rohwer.orth <- cbind(Rohwer[,1:5], gsorth(Rohwer[, c("n", "s", "ns", "na", "ss")], adjnames=FALSE))

rohwer.mod1 <- lm(cbind(SAT, PPVT, Raven) ~ n + s + ns + na + ss, data=Rohwer.orth)
Anova(rohwer.mod1)
# compare with anova()
anova(rohwer.mod1)

# compare heplots for original Xs and orthogonalized, Type I
heplot(rohwer.mod)
heplot(rohwer.mod1)
```

Headache   *Treatment of Headache Sufferers for Sensitivity to Noise*

Description

A study was conducted investigating the effectiveness of different kinds of psychological treatment on the sensitivity of headache sufferers to noise, described in Hand and Taylor (1987), Study E.

In a pre-post design, 98 patients were first assessed for the volume of noise which they found uncomfortable (U) and definitely uncomfortable (DU). They were then given relaxation training, where they listened to the noise at the DU level and given instruction breathing techniques and the use of visual imagery to distract them from discomfort. One of four treatments was then applied, and all patients were reassessed for the noise volume they considered uncomfortable (U) and definitely uncomfortable (DU).

Usage

```
data(Headache)
```

Format

A data frame with 98 observations on the following 6 variables.

type Type of headache, a factor with levels `Migrane Tension`

treatment Treatment group, a factor with levels `T1 T2 T3 Control`. See Details

u1 Noise level rated as Uncomfortable, initial measure

du1 Noise level rated as Definitely Uncomfortable, initial measure

u2 Noise level rated as Uncomfortable, final measure

du2 Noise level rated as Definitely Uncomfortable, final measure

Details

The treatments are described as follows:

T1 Listened again to the tone at their initial DU level, for the same amount of time they were able to tolerate it before.

T2 Same as T1, with one additional minute exposure

T3 Same as T2, but were explicitly instructed to use the relaxation techniques

Control These subject experienced no further exposure to the noise tone until the final sensitivity measures were taken

Hand and Taylor described several substantive hypotheses related to the differences among treatments. In the `Headache` data frame, these have been included as `contrasts(Headache$treatment)`

Source

D. J. Hand and C. C. Taylor (1987). *Multivariate analysis of variance and repeated measures: a practical approach for behavioural scientists* London: Chapman and Hall. ISBN: 0412258005. Table E.1.

Examples

```
data(Headache)
str(Headache)

# basic MLM, specifying between-S effects
headache.mod <- lm(cbind(u1, du1, u2, du2) ~ type * treatment, data=Headache)

##############################
## between-S tests
##############################
Anova(headache.mod, test="Roy")

# test each contrast separately
```

```
print(linearHypothesis(headache.mod, hypothesis="treatment1", test="Roy"), SSP=FALSE)
print(linearHypothesis(headache.mod, hypothesis="treatment2", test="Roy"), SSP=FALSE)
print(linearHypothesis(headache.mod, hypothesis="treatment3", test="Roy"), SSP=FALSE)


heplot(headache.mod, variables=c(1,3),
hypotheses=paste("treatment", 1:3, sep=""),
hyp.labels=c("extra.exp", "no.inst", "explicit.inst"),
xlab="u1: Initial sensitivity", ylab="u2: Final sensitivity",
main="Headache data: Unpleasant levels")
abline(0, 1, lty=5, col="gray")

heplot(headache.mod, variables=c(2,4),
hypotheses=paste("treatment", 1:3, sep=""),
xlab="du1: Initial sensitivity", ylab="du2: Final sensitivity",
main="Headache data: Definitely Unpleasant levels")
abline(0, 1, lty=5, col="gray")

pairs(headache.mod)

##############################
# between-S and within-S tests
##############################
idata = expand.grid(level=factor(c("U", "DU")), phase=factor(1:2))
Anova(headache.mod, idata=idata, idesign=~level*phase)
```

---

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. These include MANOVA models (all explanatory variables are factors), multivariate regression (all quantitative predictors), MANCOVA models, homogeneity of regression, as well as repeated measures designs treated from a multivariate perspective.

Usage

```
heplot(mod, ...)

## S3 method for class 'mlm'
heplot(mod, terms, hypotheses, term.labels = TRUE,
    hyp.labels = TRUE, err.label="Error", label.pos=NULL,
    variables = 1:2, error.ellipse = !add,
    factor.means = !add, grand.mean = !add, remove.intercept = TRUE,
    type = c("II", "III", "2", "3"), idata=NULL, idesign=NULL,
icontrasts=c("contr.sum", "contr.poly"),
```

```
imatrix=NULL, iterm=NULL, markH0=!is.null(iterm),
    manova, size = c("evidence", "effect.size"),
    level = 0.68, alpha = 0.05, segments = 60,
    center.pch = "+", center.cex=2,
    col = getOption("heplot.colors",
              c("red", "blue", "black", "darkgreen",
                "darkcyan","magenta", "brown","darkgray")),
    lty = 2:1, lwd = 1:2,
    fill=FALSE, fill.alpha=0.3,
    xlab, ylab, main = "", xlim, ylim, axes=TRUE, offset.axes,
    add = FALSE, verbose = FALSE, warn.rank = 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.
hypotheses	optional list of linear hypotheses for which to plot hypothesis matrices; hypotheses are specified as for the [linearHypothesis](#) function in the car package; the list elements can be named, in which case the names are used.
term.labels	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.
hyp.labels	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.
err.label	Label for the error ellipse
label.pos	Label position, a vector of integers (in 0:4) or character strings (in c("center", "bottom", "left", "top", "right"), or in c("C", "S", "W", "N", "E") use in labeling ellipses, recycled as necessary. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the max/min co-ordinates of the ellipse; the value 0 specifies the centroid of the ellipse object. The default, label.pos=NULL uses the correlation of the ellipse to determine "top" (r>=0) or "bottom" (r<0). Even more flexible options are described in [label.ellipse](#)
variables	indices or names of the two response variables to be plotted; defaults to 1:2.
error.ellipse	if TRUE, plot the error ellipse; defaults to TRUE, if the argument add is FALSE (see below).
factor.means	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 add is FALSE (see below).
grand.mean	if TRUE, plot the centroid for all of the data; defaults to TRUE, if the argument add is FALSE (see below).
remove.intercept	if TRUE (the default), do not plot the ellipse for the intercept even if it is in the MANOVA table.

type	"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).
idata	an optional data frame giving a factor or factors defining the intra-subject model for multivariate repeated-measures data. See Friendly (2010) and Details of [Anova](#) for an explanation of the intra-subject design and for further explanation of the other arguments relating to intra-subject factors.
idesign	a one-sided model formula using the "data" in idata and specifying the intra-subject design for repeated measure models.
icontrasts	names of contrast-generating functions to be applied by default to factors and ordered factors, respectively, in the within-subject "data"; the contrasts must produce an intra-subject model matrix in which different terms are orthogonal. The default is c("contr.sum", "contr.poly").
imatrix	In lieu of `idata` and `idesign`, you can specify the intra-subject design matrix directly via `imatrix`, in the form of list of named elements. Each element gives the columns of the within-subject model matrix for an intra-subject term to be tested, and must have as many rows as there are responses; the columns of the within-subject model matrix for *different* terms must be mutually orthogonal. *This functionality requires* car *version 2.0 or later.*
iterm	For repeated measures designs, you must specify one intra-subject term (a character string) to select the SSPE (E) matrix used in the HE plot. Hypothesis terms plotted include the `iterm` effect as well as all interactions of `iterm` with `terms`.
markH0	A logical value (or else a list of arguments to [mark.H0](#)) used to draw cross-hairs and a point indicating the value of a point null hypothesis. The default is TRUE if `iterm` is non-NULL.
manova	optional Anova.mlm object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
size	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 at level alpha extends outside of the error ellipse; if `"effect.size"`, the hypothesis ellipse is on the same scale as the error ellipse.
level	equivalent coverage of ellipse for normally-distributed errors, defaults to `0.68`, giving a standard 1 SD bivariate ellipse.
alpha	significance level for Roy's greatest-root test statistic; if size="evidence", then the hypothesis ellipse is scaled so that it just touches the error ellipse at the specified alpha level; a larger hypothesis ellipse *somewhere* in the space of the response variables therefore indicates statistical significance; defaults to `0.05`.
segments	number of line segments composing each ellipse; defaults to `60`.
center.pch	character to use in plotting the centroid of the data; defaults to `"+"`.
center.cex	size of character to use in plotting the centroid of the data; defaults to `2`.
col	a color or vector of colors to use in plotting ellipses; the first color is used for the error ellipse; the remaining colors — recycled as necessary — are used for the hypothesis ellipses. A single color can be given, in which case it is used for all ellipses. For convenience, the default colors for all heplots produced in a given session can be changed by assigning a color vector via options(heplot.colors =c(...). Otherwise, the default colors are c("red", "blue", "black", "darkgreen", "darkcyan", "magenta", "brown", "darkgray").

lty	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.
lwd	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.
fill	A logical vector indicating whether each ellipse should be filled or not. The first value is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single fill value can be given. Defaults to FALSE for backward compatibility. See Details below.
fill.alpha	Alpha transparency for filled ellipses, a numeric scalar or vector of values within [0,1], where 0 means fully transparent and 1 means fully opaque.
xlab	x-axis label; defaults to name of the x variable.
ylab	y-axis label; defaults to name of the y variable.
main	main plot label; defaults to "".
xlim	x-axis limits; if absent, will be computed from the data.
ylim	y-axis limits; if absent, will be computed from the data.
axes	Whether to draw the x, y axes; defaults to TRUE
offset.axes	proportion to extend the axes in each direction if computed from the data; optional.
add	if TRUE, add to the current plot; the default is FALSE. If TRUE, the error ellipse is not plotted.
verbose	if TRUE, print the MANOVA table and details of hypothesis tests; the default is FALSE.
warn.rank	if TRUE, do not suppress warnings about the rank of the hypothesis matrix when the ellipse collapses to a line; the default is FALSE.
...	arguments to pass down to plot, text, and points.

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 degenerate 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 linearHypothesis for details.

For repeated measure designs, where the response variables correspond to one or more variates observed under a within-subject design, between-subject effects and within-subject effects must be plotted separately, because the error terms (E matrices) differ. When you specify an intra-subject term (iterm), the analysis and HE plots amount to analysis of the matrix **Y** of responses post-multiplied by a matrix **M** determined by the intra-subject design for that term. See Friendly (2010) or the vignette("repeated") in this package for an extended discussion and examples.

The related candisc package provides functions for visualizing a multivariate linear model in a low-dimensional view via a generalized canonical discriminant analyses. heplot.candisc and heplot3d.candisc provide a low-rank 2D (or 3D) view of the effects for a given term in the space of maximum discrimination.

When an element of fill is TRUE, the ellipse outline is drawn using the corresponding color in col, and the interior is filled with a transparent version of this color specified in fill.alpha. To produce filled (non-degenerate) ellipses without the bounding outline, use a value of lty=0 in the corresponding position.

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
radius	the radius for the unit circles used to generate the ellipses

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.

doi: 10.18637/jss.v017.i06

Friendly, M. (2007). HE plots for Multivariate General Linear Models. *Journal of Computational and Graphical Statistics*, **16**(2) 421–444. http://datavis.ca/papers/jcgs-heplots.pdf

Friendly, Michael (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40.

doi: 10.18637/jss.v037.i04

Fox, J., Friendly, M. & Weisberg, S. (2013). Hypothesis Tests for Multivariate Linear Models Using the car Package. *The R Journal*, **5**(1), https://journal.r-project.org/archive/2013-1/fox-friendly-weisberg.pdf.

Friendly, M. & Sigal, M. (2014) Recent Advances in Visualizing Multivariate Linear Models. *Revista Colombiana de Estadistica*, **37**, 261-283.

See Also

Anova, linearHypothesis for details on testing MLMs.

heplot1d, heplot3d, pairs.mlm, mark.H0 for other HE plot functions. coefplot.mlm for plotting confidence ellipses for parameters in MLMs.

trans.colors for calculation of transparent colors. label.ellipse for labeling positions in plotting H and E ellipses.

candisc, heplot.candisc for reduced-rank views of mlms in canonical space.

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)

# try filled ellipses
heplot(iris.mod, hypotheses=hyp, fill=TRUE, fill.alpha=0.2, col=c("red", "blue"))
heplot(iris.mod, hypotheses=hyp, fill=TRUE, col=c("red", "blue"), lty=c(0,0,1,1))
# vary label position and fill.alpha
heplot(iris.mod, hypotheses=hyp, fill=TRUE, fill.alpha=c(0.3,0.1), col=c("red", "blue"),
       lty=c(0,0,1,1), label.pos=0:3)


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 car 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)
col <- c("red", "black", "blue", "cyan", "magenta", "brown", "gray")
heplot(rohwer.mod, col=col)
```

```
# Add ellipse to test all 5 regressors
heplot(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")), col=col, fill=TRUE)
# View all pairs
pairs(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")))
# or 3D plot
if(requireNamespace("rgl")){
col <- c("pink", "black", "blue", "cyan", "magenta", "brown", "gray")
heplot3d(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")), col=col)
}
```

---

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"),
idata=NULL, idesign=NULL, icontrasts=c("contr.sum", "contr.poly"),
imatrix=NULL, iterm=NULL, manova,
size = c("evidence", "effect.size"), level = 0.68, alpha = 0.05,
center.pch = "|",
    col = getOption("heplot.colors",
                    c("red", "blue", "black", "darkgreen",
                      "darkcyan","magenta", "brown","darkgray")),
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.

hypotheses	optional list of linear hypotheses for which to plot hypothesis matrices; hypotheses are specified as for the [linearHypothesis](#) function in the car package; the list elements can be named, in which case the names are used.
term.labels	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.
hyp.labels	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.
variables	indices or names of the two response variables to be plotted; defaults to 1:2.
error.ellipse	if TRUE, plot the error ellipse; defaults to TRUE, if the argument add is FALSE (see below).
factor.means	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 add is FALSE (see below).
grand.mean	if TRUE, plot the centroid for all of the data; defaults to TRUE, if the argument add is FALSE (see below).
remove.intercept	
	if TRUE (the default), do not plot the ellipse for the intercept even if it is in the MANOVA table.
type	"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).
idata	an optional data frame giving a factor or factors defining the intra-subject model for multivariate repeated-measures data. See Details of [Anova](#) for an explanation of the intra-subject design and for further explanation of the other arguments relating to intra-subject factors.
idesign	a one-sided model formula using the "data" in idata and specifying the intra-subject design for repeated measure models.
icontrasts	names of contrast-generating functions to be applied by default to factors and ordered factors, respectively, in the within-subject "data"; the contrasts must produce an intra-subject model matrix in which different terms are orthogonal. The default is c("contr.sum", "contr.poly").
imatrix	In lieu of idata and idesign, you can specify the intra-subject design matrix directly via imatrix, in the form of list of named elements. Each element gives the columns of the within-subject model matrix for an intra-subject term to be tested, and must have as many rows as there are responses; the columns of the within-subject model matrix for *different* terms must be mutually orthogonal. *This functionality requires* car *version 2.0 or later.*
iterm	For repeated measures designs, you must specify one intra-subject term (a character string) to select the SSPE (E) matrix used in the HE plot. Hypothesis terms plotted include the iterm effect as well as all interactions of iterm with terms.
manova	optional Anova.mlm object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
size	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.
level	equivalent coverage of ellipse for normally-distributed errors, defaults to 0.68.
alpha	significance level for Roy's greatest-root test statistic; if size="evidence", 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.
center.pch	character to use in plotting the centroid of the data; defaults to "|".
col	a color or vector of colors to use in plotting ellipses; the first color is used for the error ellipse; the remaining colors — recycled as necessary — are used for the hypothesis ellipses. A single color can be given, in which case it is used for all ellipses. For convenience, the default colors for all heplots produced in a given session can be changed by assigning a color vector via options(heplot.colors =c(...). Otherwise, the default colors are c("red", "blue", "black", "darkgreen", "darkcyan", "magenta", "brown", "darkgray").
lty	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.
lwd	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.
xlab	x-axis label; defaults to name of the x variable.
main	main plot label; defaults to "".
xlim	x-axis limits; if absent, will be computed from the data.
axes	Whether to draw the x, y axes; defaults to TRUE
offset.axes	proportion to extend the axes in each direction if computed from the data; optional.
add	if TRUE, add to the current plot; the default is FALSE. If TRUE, the error ellipse is not plotted.
verbose	if TRUE, print the MANOVA table and details of hypothesis tests; the default is FALSE.
...	arguments to pass down to plot, text, and points.

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:

H	ranges for the hypothesis terms
E	range for E
xlim	x-axis limits

Author(s)

Michael Friendly

See Also

Anova, linearHypothesis 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)
```

---

heplot3d   *Three-Dimensional HE Plots*

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, err.label="Error", variables = 1:3, error.ellipsoid = !add,
    factor.means = !add, grand.mean = !add, remove.intercept = TRUE,
    type = c("II", "III", "2", "3"), idata=NULL, idesign=NULL,
  icontrasts=c("contr.sum", "contr.poly"), imatrix=NULL, iterm=NULL,
    manova, size = c("evidence", "effect.size"),
    level = 0.68, alpha = 0.05,  segments = 40,
  col=getOption("heplot3d.colors",
              c("red", "blue", "black", "darkgreen",
                "darkcyan","magenta", "brown","darkgray")),
    lwd=c(1, 4),
    shade=TRUE, shade.alpha=0.2, 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,
cex.label = 1.5,
add = FALSE, verbose = FALSE,
warn.rank = 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.
hypotheses	optional list of linear hypotheses for which to plot hypothesis matrices; hypotheses are specified as for the [linearHypothesis](#) function in the `car` package; the list elements can be named, in which case the names are used.
term.labels	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.
hyp.labels	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.
err.label	Label for the error ellipse
variables	indices or names of the three response variables to be plotted; defaults to `1:3`.
error.ellipsoid	if `TRUE`, plot the error ellipsoid; defaults to `TRUE`, if the argument add is `FALSE` (see below).
factor.means	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 add is `FALSE` (see below).
grand.mean	if `TRUE`, plot the centroid for all of the data; defaults to `TRUE`, if the argument add is `FALSE` (see below).
remove.intercept	if `TRUE` (the default), do not plot the ellipsoid for the intercept even if it is in the MANOVA table.
type	"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).
idata	an optional data frame giving a factor or factors defining the intra-subject model for multivariate repeated-measures data. See Details of [Anova](#) for an explanation of the intra-subject design and for further explanation of the other arguments relating to intra-subject factors.
idesign	a one-sided model formula using the "data" in idata and specifying the intra-subject design for repeated measure models.

icontrasts	names of contrast-generating functions to be applied by default to factors and ordered factors, respectively, in the within-subject "data"; the contrasts must produce an intra-subject model matrix in which different terms are orthogonal. The default is c("contr.sum", "contr.poly").
imatrix	In lieu of idata and idesign, you can specify the intra-subject design matrix directly via imatrix, in the form of list of named elements. Each element gives the columns of the within-subject model matrix for an intra-subject term to be tested, and must have as many rows as there are responses; the columns of the within-subject model matrix for *different* terms must be mutually orthogonal. *This functionality requires* car *version 2.0 or later.*
iterm	For repeated measures designs, you must specify one intra-subject term (a character string) to select the SSPE (E) matrix used in the HE plot. Hypothesis terms plotted include the iterm effect as well as all interactions of iterm with terms.
manova	optional Anova.mlm object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
size	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.
level	equivalent coverage of ellipsoid for normally-distributed errors, defaults to 0.68.
alpha	significance level for Roy's greatest-root test statistic; if size="evidence", 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.
segments	number of segments composing each ellipsoid; defaults to 40.
col	a color or vector of colors to use in plotting ellipsoids; the first color is used for the error ellipsoid; the remaining colors — recycled as necessary — are used for the hypothesis ellipsoid. A single color can be given, in which case it is used for all ellipsoid. For convenience, the default colors for all heplots produced in a given session can be changed by assigning a color vector via options(heplot3d.colors =c(...). Otherwise, the default colors are c("pink", "blue", "black", "darkgreen", "darkcyan", "magenta", "brown", "darkgray").
lwd	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 c(1, 4).
shade	a logical scalar or vector, indicating whether the ellipsoids should be rendered with [shade3d](). Works like col, except that FALSE is used for any 1 df degenerate ellipsoid.
shade.alpha	a numeric value in the range [0,1], or a vector of such values, giving the alpha transparency for ellipsoids rendered with shade=TRUE.
wire	a logical scalar or vector, indicating whether the ellipsoids should be rendered with [wire3d](). Works like col, except that TRUE is used for any 1 df degenerate ellipsoid.
bg.col	background colour, "white" or "black", defaulting to "white".

fogtype	type of "fog" to use for depth-cueing; the default is "none". See bg.
fov	field of view angle; controls perspective. See viewpoint.
offset	proportion of axes to off set labels; defaults to 0.01.
xlab	x-axis label; defaults to name of the x variable.
ylab	y-axis label; defaults to name of the y variable.
zlab	z-axis label; defaults to name of the z variable.
xlim	x-axis limits; if absent, will be computed from the data.
ylim	y-axis limits; if absent, will be computed from the data.
zlim	z-axis limits; if absent, will be computed from the data.
cex.label	text size for ellipse labels
add	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.
verbose	if TRUE, print the MANOVA table and details of hypothesis tests; the default is FALSE.
warn.rank	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.
...	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. https://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://datavis.ca/papers/jcgs-heplots.pdf

See Also

Anova, linearHypothesis, for details on MANOVA tests and linear hypotheses

heplot, pairs.mlm, for other plotting methods for mlm objects

rgl-package, for details about 3D plots with rgl

heplot3d.candisc for 3D HE plots in canonical space.

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"), wire=FALSE)

# Plastic data
plastic.mod <- lm(cbind(tear, gloss, opacity) ~ rate*additive, data=Plastic)
## Not run:
heplot3d(plastic.mod, col=c("red", "blue", "brown", "green3"), wire=FALSE)

## End(Not run)
```

Hernior	*Recovery from Elective Herniorrhaphy*

Description

A data set on measures of post-operative recovery of 32 patients undergoing an elective herniorrhaphy operation, in relation to pre-operative measures.

Usage

```
data(Hernior)
```

Format

A data frame with 32 observations on the following 9 variables.

age patient age

sex patient sex, a factor with levels f m

pstat physical status (ignoring that associated with the operation). A 1-5 scale, with 1=perfect health, 5=very poor health.

build body build, a 1-5 scale, with 1=emaciated, 2=thin, 3=average, 4=fat, 5=obese.

cardiac preoperative complications with heart, 1-4 scale, with 1=none, 2=mild, 3=moderate, 4=severe.

resp preoperative complications with respiration, 1-4 scale, with 1=none, 2=mild, 3=moderate, 4=severe.

leave condition upon leaving the recovery room, a 1-4 scale, with 1=routine recovery, 2=intensive care for observation overnight, 3=intensive care, with moderate care required, 4=intensive care, with moderate care required.

los length of stay in hospital after operation (days)

nurse level of nursing required one week after operation, a 1-5 scale, with 1=intense, 2=heavy, 3=moderate, 4=light, 5=none (?); see Details

Details

leave, nurse and los are outcome measures; the remaining variables are potential predictors of recovery status.

The variable nurse is recorded as 1-4, with remaining (20) entries entered as "-" in both sources. It is not clear whether this means "none" or NA. The former interpretation was used in constructing the R data frame, so nurse==5 for these observations. Using Hernior$nurse[Hernior$nurse==5] <- NA would change to the other interpretation, but render nurse useless in a multivariate analysis.

The ordinal predictors could instead be treated as factors, and there are also potential interactions to be explored.

Source

Mosteller, F. and Tukey, J. W. (1977), *Data analysis and regression*, Reading, MA: Addison-Wesley. Data Exhibit 8, 567-568. Their source: A study by B. McPeek and J. P. Gilbert of the Harvard Anesthesia Center.

References

Hand, D. J., Daly, F., Lunn, A. D., McConway, K. J. and Ostrowski, E. (1994), *A Handbook of Small Data Sets*, Number 484, 390-391.

Examples

```
str(Hernior)
Hern.mod <- lm(cbind(leave, nurse, los) ~
               age + sex +  pstat +  build + cardiac + resp, data=Hernior)
Anova(Hern.mod, test="Roy") # actually, all tests are identical

# test overall regression
print(linearHypothesis(Hern.mod, c("age", "sexm", "pstat", "build", "cardiac", "resp")), SSP=FALSE)

# joint test of age, sex & caridac
print(linearHypothesis(Hern.mod, c("age", "sexm", "cardiac")), SSP=FALSE)

# HE plots
clr <- c("red", "darkgray", "blue", "darkgreen", "magenta", "brown", "black")
heplot(Hern.mod, col=clr)
pairs(Hern.mod, col=clr)
```

```
## Enhancing the pairs plot ...
# create better variable labels
vlab <- c("LeaveCondition\n(leave)",
          "NursingCare\n(nurse)",
          "LengthOfStay\n(los)")
# Add ellipse to test all 5 regressors simultaneously
hyp <- list("Regr" = c("age", "sexm", "pstat", "build", "cardiac", "resp"))
pairs(Hern.mod, hypotheses=hyp, col=clr, var.labels=vlab)

## Views in canonical space for the various predictors
if (require(candisc)) {
Hern.canL <- candiscList(Hern.mod)
plot(Hern.canL, term="age")
plot(Hern.canL, term="sex")
plot(Hern.canL, term="pstat")  # physical status
}
```

---

interpPlot   *Plot an Interpolation Between Two Related Data Sets*

Description

Plot an interpolation between two related data sets, typically transformations of each other. This function is designed to be used in animations.

Points are plotted via the linear interpolation,

$$XY = XY1 + \alpha(XY2 - XY1)$$

The function allows plotting of the data ellipse, the linear regression line, and line segments showing the movement of points.

Usage

```
interpPlot(xy1, xy2, alpha,
xlim, ylim, points=TRUE, add=FALSE, col=palette()[1],
ellipse = FALSE, ellipse.args = NULL,
abline=FALSE, col.lines = palette()[2], lwd=2,
id.method = "mahal", labels=rownames(xy1),
id.n = 0, id.cex = 1, id.col = palette()[1],
segments=FALSE, segment.col="darkgray",
 ...)
```

Arguments

xy1	First data set, a 2-column matrix or data.frame
xy2	Second data set, a 2-column matrix or data.frame

alpha	The value of the interpolation fraction, typically (but not necessarily) `0 <= alpha` `<= 1`).
xlim, ylim	x, y limits for the plot. If not specified, the function uses the ranges of `rbind(xy1,` `xy2)`.
points	Logical. Whether to plot the points in the current interpolation?
col	Color for plotted points.
add	Logical. Whether to add to an existing plot?
ellipse	logical. TRUE to plot a `dataEllipse`
ellipse.args	other arguments passed to `dataEllipse`
abline	logical. TRUE to plot the linear regression line for XY
col.lines	line color
lwd	line width
id.method	How points are to be identified. See [showLabels](#).
labels	observation labels
id.n	Number of points to be identified. If set to zero, no points are identified.
id.cex	Controls the size of the plotted labels. The default is 1
id.col	Controls the color of the plotted labels.
segments	logical. TRUE to draw lines segments from xy1 to xy
segment.col	line color for segments
...	other arguments passed to `plot()`

Details

Interpolations other than linear can be obtained by using a non-linear series of `alpha` values. For example `alpha=sin(seq(0,1,.1)/sin(1)` will give a sinusoid interpolation.

Value

Returns invisibly the interpolated XY points.

Note

The examples here just use on-screen animations to the console graphics window. The [animation](#) package provides facilities to save these in various formats.

Author(s)

Michael Friendly

See Also

[dataEllipse](#), [showLabels](#), [animation](#)

Examples

```
###################################################
# animate an AV plot from marginal to conditional
###################################################
data(Duncan, package="car")
duncmod <- lm(prestige ~ income + education, data=Duncan)
mod.mat <- model.matrix(duncmod)

# function to do an animation for one variable
dunc.anim <- function(variable, other, alpha=seq(0, 1, .1)) {
  var <- which(variable==colnames(mod.mat))
  duncdev <- scale(Duncan[,c(variable, "prestige")], scale=FALSE)
  duncav <- lsfit(mod.mat[, -var], cbind(mod.mat[, var], Duncan$prestige),
          intercept = FALSE)$residuals
  colnames(duncav) <- c(variable, "prestige")

  lims <- apply(rbind(duncdev, duncav),2,range)

  for (alp in alpha) {
    main <- if(alp==0) paste("Marginal plot:", variable)
      else paste(round(100*alp), "% Added-variable plot:", variable)
    interpPlot(duncdev, duncav, alp, xlim=lims[,1], ylim=lims[,2], pch=16,
      main = main,
      xlab = paste(variable, "| ", alp, other),
      ylab = paste("prestige | ", alp, other),
      ellipse=TRUE, ellipse.args=(list(levels=0.68, fill=TRUE, fill.alpha=alp/2)),
      abline=TRUE, id.n=3, id.cex=1.2, cex.lab=1.25)
    Sys.sleep(1)
  }
}

# show these in the R console
if(interactive()) {
dunc.anim("income", "education")

dunc.anim("education", "income")
}

###########################################
# correlated bivariate data with 2 outliers
# show rotation from data space to PCA space
###########################################

set.seed(123345)
x <- c(rnorm(100), 2, -2)
y <- c(x[1:100] + rnorm(100), -2, 2)
XY <- cbind(x=x, y=y)
rownames(XY) <- seq_along(x)
XY <- scale(XY, center=TRUE, scale=FALSE)

# start, end plots
```

```
dataEllipse(XY, pch=16, levels=0.68, id.n=2)
mod <- lm(y~x, data=as.data.frame(XY))
abline(mod, col="red", lwd=2)

pca <- princomp(XY, cor=TRUE)
scores <- pca$scores
dataEllipse(scores, pch=16, levels=0.68, id.n=2)
abline(lm(Comp.2 ~ Comp.1, data=as.data.frame(scores)), lwd=2, col="red")

# show interpolation

# functions for labels, as a function of alpha
main <- function(alpha) {if(alpha==0) "Original data"
  else if(alpha==1) "PCA scores"
  else paste(round(100*alpha,1), "% interpolation")}
xlab <- function(alpha) {if(alpha==0) "X"
  else if(alpha==1) "PCA.1"
  else paste("X +", alpha, "(X - PCA.1)")}
ylab <- function(alpha) {if(alpha==0) "Y"
  else if(alpha==1) "PCA.2"
  else paste("Y +", alpha, "(Y - PCA.2)")}

interpPCA <- function(XY, alpha = seq(0,1,.1)) {
  XY <- scale(XY, center=TRUE, scale=FALSE)
  if (is.null(rownames(XY))) rownames(XY) <- 1:nrow(XY)
  pca <- princomp(XY, cor=TRUE)
  scores <- pca$scores

  for (alp in alpha) {
    interpPlot(XY, scores, alp,
      pch=16,
      main = main(alp),
      xlab = xlab(alp),
      ylab = ylab(alp),
      ellipse=TRUE, ellipse.args=(list(levels=0.68, fill=TRUE, fill.alpha=(1-alp)/2)),
      abline=TRUE, id.n=2, id.cex=1.2, cex.lab=1.25, segments=TRUE)
    Sys.sleep(1)
  }
}

# show in R console
if(interactive()) {
interpPCA(XY)
}

## Not run:
library(animation)
saveGIF({
  interpPCA(XY, alpha <- seq(0,1,.1))},
  movie.name="outlier-demo.gif", ani.width=480, ani.height=480, interval=1.5)


## End(Not run)
```

`Iwasaki_Big_Five`   *Personality Traits of Cultural Groups*

Description

This dataset, from Grice & Iwasaki (2007), gives scores on the five personality scales of the NEO PI-r (Costa & McCrae, 1992), called the "Big Five" personality traits: Neuroticism, Extraversion, Openness-to-Experience, Agreeableness, and Conscientiousness.

Usage

```
data("Iwasaki_Big_Five")
```

Format

A data frame with 203 observations on the following 7 variables.

ID ID number

Group a factor with levels `Eur Asian_Amer Asian_Intl`

N Neuroticism score

E Extraversion score

O Openness score

A Agreeableness score

C Conscientiousness score

Details

The groups are:

Eur European Americans (Caucasians living in the United States their entire lives)

Asian_Amer Asian Americans (Asians living in the United States since before the age of 6 years)

Asian_Intl Asian Internationals (Asians who moved to the United States after their 6th birthday)

The factor `Group` is set up to compare E vs. Asian and the two Asian groups

Source

Grice, J., & Iwasaki, M. (2007). A truly multivariate approach to MANOVA. *Applied Multivariate Research*, **12**, 199-226. https://doi.org/10.22329/amr.v12i3.660.

References

Costa Jr, P. T., & McCrae, R. R. (1992). *Revised NEO Personality Inventory (NEO PI-R) and NEO Five-Factor Inventory (NEOFFI) professional manual*. Psychological Assessment Resources.

Examples

```
data(Iwasaki_Big_Five)
str(Iwasaki_Big_Five)

mod <- lm(cbind(N, E, O, A, C) ~ Group, data=Iwasaki_Big_Five)

Anova(mod)

# heplots
labs <- c("Neuroticism", "Extraversion", "Openness", "Agreeableness", "Consientiousness" )

heplot(mod,
        fill = TRUE, fill.alpha = 0.2,
        cex.lab = 1.5,
        xlab = labs[1], ylab = labs[2])

heplot(mod, variables = c(2,5),
        fill = TRUE, fill.alpha = 0.2,
        cex.lab = 1.5,
        xlab = labs[2], ylab = labs[5])

pairs(mod,
      fill = TRUE, fill.alpha = 0.2, var.labels = labs)
```

---

label.ellipse   *Label an ellipse*

Description

`label.ellipse` is used to a draw text label on an ellipse at its center or somewhere around the periphery in a very flexible way.

Usage

```
label.ellipse(ellipse, label, col = "black", label.pos = NULL, xpd = TRUE,
  tweak = 0.5 * c(strwidth("M"), strheight("M")), ...)
```

Arguments

ellipse	A two-column matrix of coordinates for the ellipse boundary
label	Character string to be used as the ellipse label
col	Label color
label.pos	Label position relative to the ellipse. See details
xpd	Should the label be allowed to extend beyond the plot limits?
tweak	A vector of two lengths used to tweak label positions
...	Other parameters passed to text, e.g., cex, ...

Details

If `label.pos=NULL`, the function uses the sign of the correlation represented by the ellipse to determine a position at the top ($r >= 0$) or bottom ($r < 0$) of the ellipse. Integer values of 0, 1, 2, 3 and 4, respectively indicate positions at the center, below, to the left of, above and to the right of the max/min coordinates of the ellipse. Label positions can also be specified as the corresponding character strings c("center", "bottom", "left", "top", "right"), or compass directions, c("C", "S", "W", "N", "E"), or Other integer `label.pos` values, 5:nrow(ellipse) are taken as indices of the row coordinates to be used for the ellipse label. Equivalently, `label.pos` can also be a *fraction* in (0,1), interpreted as the fraction of the way around the unit circle, counterclockwise from the point (1,0).

Author(s)

Michael Friendly

See Also

[heplot](#)

Examples

```
circle <- function(center=c(0,0), radius=1, segments=60) {
   angles <- (0:segments)*2*pi/segments
   circle <- radius * cbind( cos(angles), sin(angles))
   t( c(center) + t( circle ))
}

label_demo <- function(ell) {
  plot(-2:2, -2:2, type="n", asp=1, main="label.pos values and points (0:60)")
  lines(ell, col="gray")
  points(0, 0, pch="+", cex=2)

  labs <- c("center", "bot", "left", "top", "right")
  for (i in 0:4) {
    label.ellipse(ell, label=paste(i, ":", labs[i+1]), label.pos = i)
  }
  for( i in 5*c(1,2, 4,5, 7,8, 10,11)) {
    points(ell[i,1], ell[i,2], pch=16)
    label.ellipse(ell, label=i, label.pos=i)
  }
}

circ <- circle(radius=1.8)
label_demo(circ)

ell <-circ %*% chol(matrix( c(1, .5, .5, 1), 2, 2))
label_demo(ell)
```

---

leveneTests | *Levene Tests of Homogeneity of Variances*

Description

This function extends leveneTest to a multivariate response setting. It performs the Levene test of homogeneity of variances for each of a set of response variables, and prints a compact summary.

Usage

```
leveneTests(y, group, center = median, ...)
```

Arguments

y	A data frame or matrix of numeric response variables in a multivariate linear model.
group	a vector or factor object giving the group for the corresponding elements of the rows of y
center	The name of a function to compute the center of each group; mean gives the original Levene's (1960) test; the default, median, provides a more robust test suggested by Brown and Forsythe (1974).
...	other arguments, passed to leveneTest

Value

An object of classes "anova" and "data.frame", with one observation for each response variable in y.

Author(s)

Michael Friendly

References

Levene, H. (1960). Robust Tests for Equality of Variances. In Olkin, I. *et al.* (Eds.), *Contributions to Probability and Statistics: Essays in Honor of Harold Hotelling*, Stanford University Press, 278-292.

Brown, M. B. & Forsythe, A. B. (1974). Robust Tests For Equality Of Variances *Journal of the American Statistical Association*, **69**, 364-367.

See Also

leveneTest, bartlettTests

Examples

```
leveneTests(iris[,1:4], iris$Species)

# handle a 1-column response?
leveneTests(iris[,1, drop=FALSE], iris$Species)

data(Skulls, package="heplots")
leveneTests(Skulls[,-1], Skulls$epoch)
```

---

logdetCI	*Calculate confidence interval for log determinant of covariance matrices*

Description

This function uses asymptotic results described by Cai et. al (2016), Theorem 1, to calculate approximate, normal theory confidence intervals (CIs) for the log determinant of one or more sample covariance matrices.

Their results are translated into a CI via the approximation

$$\log det(\widehat{\Sigma}) - bias \pm z_{1-\alpha/2} \times SE$$

where $\widehat{\Sigma}$ is the sample estimate of a population covariance matrix, $bias$ is a bias correction constant and SE is a width factor for the confidence interval. Both $bias$ and SE are functions ofS the sample size, n and number of variables, p.

This function is included here only to provide an approximation to *graphical accuracy* for use with Box's M test for equality of covariance matrices, boxM and its associated plot.boxM method.

Usage

```
logdetCI(cov, n, conf = 0.95, method = 1, bias.adj = TRUE)
```

Arguments

cov	a covariance matrix or a (named) list of covariance matrices, all the same size
n	sample size, or vector of sample sizes, one for each covariance matrix
conf	confidence level
method	Three methods are provided, based on Cai et. al Theorem 1 (method=1), Corollary 1 (method=2) and Corollary 2 (method=3), each with different bias and SE values.
bias.adj	logical; set FALSE to exclude the bias correction term.

Details

Cai et. al (2015) claim that their Theorem 1 holds with either p fixed or $p(n)$ growing with n, as long as $p(n) \leq n$. Their Corollary 1 (method=2) is the special case when p is fixed. Their Corollary 2 (method=3) is the special case when $0 \leq p/n < 1$ is fixed.

The properties of this CI estimator are unknown in small to moderate sample sizes, but it seems to be the only one available. It is therefore experimental in this version of the package and is subject to change in the future.

The $bias$ term offsets the confidence interval from the sample estimate of $\log det(\widehat{\Sigma})$. When p is large relative to n, the confidence interval may not overlap the sample estimate.

Strictly speaking, this estimator applies to the MLE of the covariance matrix $\widehat{\Sigma}$, i.e., using n rather than $n-1$ in as the divisor. The factor $(n-1/n)$ has not yet been taken into account here.

Value

A data frame with one row for each covariance matrix. `lower` and `upper` are the boundaries of the confidence intervals. Other columns are `logdet`, `bias`, `se`.

Author(s)

Michael Friendly

References

Cai, T. T.; Liang, T. & Zhou, H. H. (2015) Law of log determinant of sample covariance matrix and optimal estimation of differential entropy for high-dimensional Gaussian distributions. *Journal of Multivariate Analysis*, 137, 161-172. doi: 10.1016/j.jmva.2015.02.003

See Also

boxM, plot.boxM

Examples

```
data(iris)
iris.mod <- lm(as.matrix(iris[,1:4]) ~ iris$Species)
iris.boxm <- boxM(iris.mod)
cov <- c(iris.boxm$cov, list(pooled=iris.boxm$pooled))
n <- c(rep(50, 3), 150)

CI <- logdetCI( cov, n=n, conf=.95, method=1)
CI
plot(iris.boxm, xlim=c(-14, -8), main="Iris data, Box's M test", gplabel="Species")
arrows(CI$lower, 1:4, CI$upper, 1:4, lwd=3, angle=90, len=.1, code=3)

CI <- logdetCI( cov, n=n, conf=.95, method=1, bias.adj=FALSE)
CI
plot(iris.boxm, xlim=c(-14, -8), main="Iris data, Box's M test", gplabel="Species")
arrows(CI$lower, 1:4, CI$upper, 1:4, lwd=3, angle=90, len=.1, code=3)
```

Mahalanobis   *Classical and Robust Mahalanobis Distances*

Description

This function is a convenience wrapper to [mahalanobis](#) offering also the possibility to calculate robust Mahalanobis squared distances using MCD and MVE estimators of center and covariance (from [cov.rob](#))

Usage

```
Mahalanobis(x, center, cov, method = c("classical", "mcd", "mve"), nsamp = "best", ...)
```

Arguments

x	a numeric matrix or data frame with, say, p columns
center	mean vector of the data; if this and cov are *both* supplied, the function simply calls [mahalanobis](#) to calculate the result, ignoring the method argument.
cov	covariance matrix (pxp) of the data
method	estimation method used for center and covariance, one of: "classical" (product-moment), "mcd" (minimum covariance determinant), or "mve" (minimum volume ellipsoid).
nsamp	passed to [cov.rob](#), just to make this argument explicit
...	other arguments passed to [cov.rob](#)

Details

Any missing data in a row of x causes NA to be returned for that row.

Value

A numeric vector of squared Mahalanobis distances corresponding to the rows of x.

Author(s)

Michael Friendly

See Also

[mahalanobis](#), [cov.rob](#)

Examples

```
summary(Mahalanobis(iris[, 1:4]))
summary(Mahalanobis(iris[, 1:4], method="mve"))
summary(Mahalanobis(iris[, 1:4], method="mcd"))
```

---

mark.H0   *Mark a point null hypothesis in an HE plot*

Description

A utility function to draw and label a point in a 2D (or 3D) HE plot corresponding to a point null hypothesis being tested. This is most useful for repeated measure designs where null hypotheses for within-S effects often correspond to (0,0).

Usage

```
mark.H0(x = 0, y = 0, z=NULL, label, cex = 2, pch = 19, col = "green3", lty = 2, pos = 2)
```

Arguments

x	Horizontal coordinate for H0
y	Vertical coordinate for H0
z	z coordinate for H0. If not NULL, the function assumes that a heplot3d plot has been drawn.
label	Text used to label the point. Defaults to expression(H[0]) in 2D plots.
cex	Point and text size. For 3D plots, the function uses size=5*cex in a call to [points3d]().
pch	Plot character. Ignored for 3D plots.
col	Color for text, character and lines
lty	Line type for vertical and horizontal reference lines. Not drawn if lty=0.
pos	Position of text. Ignored for 3D plots

Value

None. Used for side effect of drawing on the current plot.

Author(s)

Michael Friendly

See Also

[cross3d](), ~~~

Examples

```
Vocab.mod <- lm(cbind(grade8,grade9,grade10,grade11) ~ 1, data=VocabGrowth)
idata <-data.frame(grade=ordered(8:11))

heplot(Vocab.mod, type="III", idata=idata, idesign=~grade, iterm="grade",
main="HE plot for Grade effect")
mark.H0()
```

---

mathscore   *Math scores for basic math and word problems*

Description

Scores for two groups of school children taught by different math teachers and tested for both basic math (BM) problems and solving word problems (WP).

Usage

```
data("mathscore")
```

Format

A data frame with 12 observations on the following 3 variables.

group a factor with levels 1 2

BM Basic Math score, a numeric vector

WP Word Problems score, a numeric vector

Source

Fictitious data

Examples

```
data(mathscore)
str(mathscore)

math.mod <- lm(cbind(BM, WP) ~ group, data=mathscore)
car::Anova(math.mod)

# scatterplot with data ellipses
car::scatterplot(WP ~ BM | group, data=mathscore,
ellipse=list(levels=0.68), smooth=FALSE, pch=c(15,16),
legend=list(coords = "topright"))

# HE plot
heplot(math.mod, fill=TRUE,
  cex=2, cex.lab=1.8,
xlab="Basic math", ylab="Word problems")
```

MockJury   *Effects Of Physical Attractiveness Upon Mock Jury Decisions*

Description

Male participants were shown a picture of one of three young women. Pilot work had indicated that the one woman was beautiful, another of average physical attractiveness, and the third unattractive. Participants rated the woman they saw on each of twelve attributes. These measures were used to check on the manipulation by the photo.

Then the participants were told that the person in the photo had committed a Crime, and asked to rate the seriousness of the crime and recommend a prison sentence, in Years.

Does attractiveness of the "defendant" influence the sentence or perceived seriousness of the crime? Does attractiveness interact with the nature of the crime?

Usage

```
data(MockJury)
```

Format

A data frame with 114 observations on the following 17 variables.

Attr Attractiveness of the photo, a factor with levels `Beautiful Average Unattractive`

Crime Type of crime, a factor with levels `Burglary` (theft of items from victim's room) `Swindle` (conned a male victim)

Years length of sentence given the defendant by the mock juror subject

Serious a rating of how serious the subject thought the defendant's crime was

exciting rating of the photo for 'exciting'

calm rating of the photo for 'calm'

independent rating of the photo for 'independent'

sincere rating of the photo for 'sincere'

warm rating of the photo for 'warm'

phyattr rating of the photo for 'physical attractiveness'

sociable rating of the photo for 'exciting'

kind rating of the photo for 'kind'

intelligent rating of the photo for 'intelligent'

strong rating of the photo for 'strong'

sophisticated rating of the photo for 'sophisticated'

happy rating of the photo for 'happy'

ownPA self-rating of the subject for 'physical attractiveness'

Source

From Dr. Wuensch's StatData Page, http://core.ecu.edu/psyc/wuenschk/StatData/PLASTER.dat

References

Data from the thesis by Plaster, M. E. (1989). *Inmates as mock jurors: The effects of physical attractiveness upon juridic decisions.* M.A. thesis, Greenville, NC: East Carolina University.

Examples

```
# manipulation check:  test ratings of the photos classified by Attractiveness
jury.mod1 <- lm( cbind(phyattr, happy, independent, sophisticated) ~ Attr, data=MockJury)
Anova(jury.mod1, test="Roy")
##
## Type II MANOVA Tests: Roy test statistic
##       Df test stat approx F num Df den Df    Pr(>F)
## Attr  2    1.7672   48.156      4    109 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

heplot(jury.mod1, main="HE plot for manipulation check")
pairs(jury.mod1)

if (require(candisc)) {
jury.can <- candisc(jury.mod1)
jury.can
heplot(jury.can, main="Canonical HE plot")
}

# influence of Attr of photo and nature of crime on Serious and Years
jury.mod2 <- lm( cbind(Serious, Years) ~ Attr * Crime, data=MockJury)
Anova(jury.mod2, test="Roy")
heplot(jury.mod2)

# stepdown test (ANCOVA), controlling for Serious
jury.mod3 <- lm( Years ~ Serious + Attr * Crime, data=MockJury)
Anova(jury.mod3)

# need to consider heterogeneous slopes?
jury.mod4 <- lm( Years ~ Serious * Attr * Crime, data=MockJury)
anova(jury.mod3, jury.mod4)
```

NeuroCog *Neurocognitive Measures in Psychiatric Groups*

Description

The primary purpose of the study (Hartman, 2016, Heinrichs et al. (2015)) was to evaluate patterns and levels of performance on neurocognitive measures among individuals with schizophrenia and schizoaffective disorder using a well-validated, comprehensive neurocognitive battery specifically designed for individuals with psychosis (Heinrichs et al. (2008))

The main interest was in determining how well these measures distinguished among all groups and whether there were variables that distinguished between the schizophrenia and schizoaffective groups.

Usage

```
data("NeuroCog")
```

Format

A data frame with 242 observations on the following 10 variables.

Dx Diagnostic group, a factor with levels `Schizophrenia Schizoaffective Control`

Speed Speed of processing domain T score, a numeric vector

Attention Attention/Vigilance Domain T score, a numeric vector

Memory Working memory a numeric vector

Verbal Verbal Learning Domain T score, a numeric vector

Visual Visual Learning Domain T score, a numeric vector

ProbSolv Reasoning/Problem Solving Domain T score, a numeric vector

SocialCog Social Cognition Domain T score, a numeric vector

Age Subject age, a numeric vector

Sex Subject gender, a factor with levels `Female Male`

Details

Neurocognitive function was assessed using the MATRICS Consensus Cognitive Battery (MCCB; Nuechterlein et al., 2008). The MCCB consists of 10 individually administered tests that measure cognitive performance in seven domains: speed of processing, attention/vigilance, working memory, verbal learning, visual learning, reasoning and problem solving, and social cognition.

The clinical sample comprised 116 male and female patients who met the following criteria: 1) a diagnosis of schizophrenia (n = 70) or schizoaffective disorder (n = 46) confirmed by the Structured Clinical Interview for DSM-IV-TR Axis I Disorders; 2) outpatient status; 3) a history free of developmental or learning disability; 4) age 18-65; 5) a history free of neurological or endocrine disorder; and 6) no concurrent DSM-IV-TR diagnosis of substance use disorder.

Non-psychiatric control participants (n = 146) were screened for medical and psychiatric illness and history of substance abuse. Patients were recruited from three outpatient clinics in Hamilton, Ontario, Canada. Control participants were recruited through local newspaper and online classified advertisements for paid research participation.

Source

Hartman, L. I. (2016). Schizophrenia and Schizoaffective Disorder: One Condition or Two? Unpublished PhD dissertation, York University.

Heinrichs, R.W., Pinnock, F., Muharib, E., Hartman, L.I., Goldberg, J.O., & McDermid Vaz, S. (2015). Neurocognitive normality in schizophrenia revisited. *Schizophrenia Research: Cognition*, **2** (4), 227-232. doi: 10.1016/j.scog.2015.09.001

References

Heinrichs, R. W., Ammari, N., McDermid Vaz, S. & Miles, A. (2008). Are schizophrenia and schizoaffective disorder neuropsychologically distinguishable? *Schizophrenia Research*, **99**, 149-154.

Nuechterlein K.H., Green M.F., Kern R.S., Baade L.E., Barch D., Cohen J., Essock S., Fenton W.S., Frese F.J., Gold J.M., Goldberg T., Heaton R., Keefe R.S.E., Kraemer H., Mesholam-Gately R., Seidman L.J., Stover E., Weinberger D.R., Young A.S., Zalcman S., Marder S.R. (2008) The MATRICS Consensus Cognitive Battery, Part 1: Test selection, reliability, and validity. *American Journal of Psychiatry*, **165** (2), 203-213. https://pubmed.ncbi.nlm.nih.gov/18172019/.

Examples

```
data(NeuroCog)
NC.mlm <- lm(cbind( Speed, Attention, Memory, Verbal, Visual, ProbSolv) ~ Dx,
             data=NeuroCog)
Anova(NC.mlm)

# test contrasts
contrasts(NeuroCog$Dx)
print(linearHypothesis(NC.mlm, "Dx1"), SSP=FALSE)
print(linearHypothesis(NC.mlm, "Dx2"), SSP=FALSE)

# pairwise HE plots
pairs(NC.mlm, var.cex=1.5)

# canonical discriminant analysis
if (require(candisc)) {
  NC.can <- candisc(NC.mlm)
  NC.can

  plot(NC.can, ellipse=TRUE, rev.axes=c(TRUE,FALSE), pch=c(7,9,10))
}
```

NLSY *National Longitudinal Survey of Youth Data*

Description

The dataset come from a small random sample of the U.S. National Longitudinal Survey of Youth.

Usage

```
data(NLSY)
```

Format

A data frame with 243 observations on the following 6 variables.

math Math achievement test score

read Reading achievement test score

antisoc score on a measure of child's antisocial behavior, `0:6`

hyperact score on a measure of child's hyperactive behavior, `0:5`

income yearly income of child's father

educ years of education of child's father

Details

In this dataset, `math` and `read` scores are taken at the outcome variables. Among the remaining predictors, `income` and `educ` might be considered as background variables necessary to control for. Interest might then be focused on whether the behavioural variables `antisoc` and `hyperact` contribute beyond that.

Source

This dataset was derived from a larger one used by Patrick Curran at the 1997 meeting of the Society for Research on Child Development (SRCD). A description now only exists on the WayBack Machine, http://web.archive.org/web/20050404145001/http://www.unc.edu/~curran/example.html.

More details are available at http://web.archive.org/web/20060830061414/http://www.unc.edu/~curran/srcd-docs/srcdmeth.pdf.

Examples

```
data(NLSY)

#examine the data
scatterplotMatrix(NLSY, smooth=FALSE)

# test control variables by themselves
# -----------------------------------
mod1 <- lm(cbind(read,math) ~ income+educ, data=NLSY)
Anova(mod1)
heplot(mod1, fill=TRUE)

# test of overall regression
coefs <- rownames(coef(mod1))[-1]
linearHypothesis(mod1, coefs)
heplot(mod1, fill=TRUE, hypotheses=list("Overall"=coefs))
```

```
# additional contribution of antisoc + hyperact over income + educ
# ---------------------------------------------------------------
mod2 <- lm(cbind(read,math) ~ antisoc + hyperact + income + educ, data=NLSY)
Anova(mod2)

coefs <- rownames(coef(mod2))[-1]
heplot(mod2, fill=TRUE, hypotheses=list("Overall"=coefs, "mod2|mod1"=coefs[1:2]))
linearHypothesis(mod2, coefs[1:2])

heplot(mod2, fill=TRUE, hypotheses=list("mod2|mod1"=coefs[1:2]))
```

Oslo   *Oslo Transect Subset Data*

Description

The Oslo data set contains chemical concentrations of 332 samples of different plant species collected along a 120 km transect running through the city of Oslo, Norway. It is a subset of the OsloTransect data provided by the rrcov package.

Usage

```
data(Oslo)
```

Format

A data frame with 332 observations on the following 14 variables.

site transect site ID, a factor with levels 102 103 104 105 106 107 108 109 111 112 113 114 115
    116 117 118 119 121 122 123 124 125 126 127 128 129 131 132 133 134 135 136 138 139
    141 142 143 144

XC X coordinate, a numeric vector

YC Y coordinate, a numeric vector

forest forest type, a factor with levels birspr mixdec pine sprbir sprpin spruce

weather weather type, a factor with levels cloud moist nice rain

litho lithological type, a factor with levels camsed (Cambro-Silurian sedimentary), gneis_o (Precambrian gneisses - Oslo), gneis_r (- Randsfjord), magm (Magmatic rocks)

altitude altitude, a numeric vector

Cu Copper, a numeric vector

Fe Iron, a numeric vector

K Potassium, a numeric vector

Mg Magnesium, a numeric vector

Mn Manganese, a numeric vector

P Lead, a numeric vector

Zn Zinc, a numeric vector

Details

The `OsloTransect` contains 360 observations, with 9 observations per site. Only 7 chemical elements were retained from the 25 contained in the `OsloTransect` data, and these were all log-transformed, following Todorov and Filzmoser (2009).

Only complete cases on these variables were retained, and two lithological types of low frequency were removed, leaving 332 observations.

Source

Reimann, C., Arnoldussen, A., Boyd, R., Finne, T.E., Koller, F., Nordgulen, Oe., And Englmaier, P. (2007) Element contents in leaves of four plant species (birch, mountain ash, fern and spruce) along anthropogenic and geogenic concentration gradients, *The Science of the Total Environment*, 377, 416-433.

References

Todorov V. and Filzmoser P. (2009) Robust statistic for the one-way MANOVA, submitted to the *Journal of Environmetrics*.

Examples

```
data(Oslo)
table(Oslo$litho)

Oslo.mod <- lm(cbind(Cu, K, Mg, Mn, P, Zn) ~ litho, data=Oslo)
Anova(Oslo.mod)

heplot(Oslo.mod, var=c("Cu", "Mn"))
pairs(Oslo.mod)

## Not run:
if(require(candisc)) {
  Oslo.can <- candisc(Oslo.mod)
  Oslo.can
  heplot(Oslo.can)
  if(requireNamespace("rgl")){
    heplot3d(Oslo.can, shade=TRUE, wire=FALSE, alpha=0.5, var.col="red")
  }
}

## End(Not run)
```

---

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, var.labels, var.cex=2,
  type = c("II", "III", "2", "3"),
idata=NULL, idesign=NULL, icontrasts=NULL, imatrix=NULL, iterm=NULL, manova,
 offset.axes = 0.05, digits = getOption("digits") - 1, fill=FALSE, fill.alpha=0.3, ...)
```

Arguments

x	an object of class mlm.
variables	indices or names of the three of more response variables to be plotted; defaults to all of the responses.
var.labels	labels for the variables plotted in the diagonal panels; defaults to names of the response variables.
var.cex	character expansion for the variable labels.
type	"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).
idata	an optional data frame giving a factor or factors defining the intra-subject model for multivariate repeated-measures data. See Details of [Anova](#) for an explanation of the intra-subject design and for further explanation of the other arguments relating to intra-subject factors.
idesign	a one-sided model formula using the "data" in idata and specifying the intra-subject design for repeated measure models.
icontrasts	names of contrast-generating functions to be applied by default to factors and ordered factors, respectively, in the within-subject "data"; the contrasts must produce an intra-subject model matrix in which different terms are orthogonal. The default is c("contr.sum", "contr.poly").
imatrix	In lieu of idata and idesign, you can specify the intra-subject design matrix directly via imatrix, in the form of list of named elements. Each element gives the columns of the within-subject model matrix for an intra-subject term to be tested, and must have as many rows as there are responses; the columns of the within-subject model matrix for *different* terms must be mutually orthogonal. *This functionality requires* car *version 2.0 or later.*
iterm	For repeated measures designs, you must specify one intra-subject term (a character string) to select the SSPE (E) matrix used in the HE plot. Hypothesis terms plotted include the iterm effect as well as all interactions of iterm with terms.
manova	optional Anova.mlm object for the model; if absent a MANOVA is computed. Specifying the argument can therefore save computation in repeated calls.
offset.axes	proportion to extend the axes in each direction; defaults to 0.05.
digits	number of significant digits in axis end-labels; taken from the "digits" option.

fill	A logical vector indicating whether each ellipse should be filled or not. The first value is used for the error ellipse, the rest — possibly recycled — for the hypothesis ellipses; a single fill value can be given. Defaults to FALSE for backward compatibility. See Details of `heplot`
fill.alpha	Alpha transparency for filled ellipses, a numeric scalar or vector of values within `[0,1]`, where 0 means fully transparent and 1 means fully opaque. Defaults to 0.3.
...	arguments to pass down to `heplot`, which is used to draw each panel of the display.

Author(s)

Michael Friendly

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. `https://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://datavis.ca/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")))
```

Parenting	*Father Parenting Competence*

Description

The data, from an exercise given by Meyers et al. (2006) relates to 60 fathers assessed on three subscales of a Perceived Parenting Competence Scale. The fathers were selected from three groups: (a) fathers of a child with no disabilities; (b) fathers with a physically disabled child; (c) fathers with a mentally disabled child.

Usage

```
data("Parenting")
```

Format

A data frame with 60 observations on the following 4 variables.

group a factor with levels `Normal Physical Disability Mental Disability`

caring caretaking responsibilities, a numeric vector

emotion emotional support provided to the child, a numeric vector

play recreational time spent with the child, a numeric vector

Details

The scores on the response variables are discrete.

Source

Meyers, L. S., Gamst, G, & Guarino, A. J. (2006). *Applied Multivariate Research: Design and Interpretation*, Thousand Oaks, CA: Sage Publications, <https://studysites.sagepub.com/amrStudy/>, Exercises 10B.

Examples

```
data(Parenting)
require(car)

# fit the MLM
parenting.mod <- lm(cbind(caring, emotion, play) ~ group, data=Parenting)
Anova(parenting.mod)

# Box's M test
boxM(parenting.mod)
plot(boxM(parenting.mod))

parenting.mod <- lm(cbind(caring, emotion, play) ~ group, data=Parenting)
Anova(parenting.mod)
# test contrasts
print(linearHypothesis(parenting.mod, "group1"), SSP=FALSE)
print(linearHypothesis(parenting.mod, "group2"), SSP=FALSE)


heplot(parenting.mod)
# display tests of contrasts
hyp <- list("N:MP" = "group1", "M:P" = "group2")
heplot(parenting.mod, hypotheses=hyp)

# make a prettier plot
heplot(parenting.mod, hypotheses=hyp, asp=1,
       fill=TRUE, fill.alpha=c(0.3,0.1),
       col=c("red", "blue"),
       lty=c(0,0,1,1), label.pos=c(1,1,3,2),
       cex=1.4, cex.lab=1.4, lwd=3)

pairs(parenting.mod, fill=TRUE, fill.alpha=c(0.3, 0.1))
```

```
## Not run:
heplot3d(parenting.mod, wire=FALSE)

## End(Not run)
```

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)
```

| plot.boxM | *Plot for Box's M test and generalizations* |

Description

This function creates a simple dot chart showing the contributions (log determinants) of the various groups to Box's M test for equality of covariance matrices.

Because Box's M test is based on a specific function (log determinant) of the covariance matrices in the groups compared to the pooled covariance matrix, this function also also allow plots of other measures based on the eigenvalues of these covariance matrices.

Usage

```
## S3 method for class 'boxM'
plot(x,
            gplabel = NULL,
            which = c("logDet", "product", "sum", "precision", "max"),
            log = which=="product",
            pch = c(16, 15),
            cex = c(2, 2.5),
            col = c("blue", "red"),
            rev = FALSE,
            xlim,
            conf=0.95, method=1, bias.adj=TRUE, lwd=2,
            ...)
```

Arguments

x	A "boxM" object resulting from [boxM](#)
gplabel	character string used to label the group factor.
which	Measure to be plotted. The default, "logDet", is the standard plot. Other values are: "product", "sum", "precision" and "max"
log	logical; if TRUE, the log of the measure is plotted. The default, which=="product", produces a plot equivalent to the plot of "logDet".
pch	a vector of two point symbols to use for the individual groups and the pooled data, respectively
cex	character size of point symbols, a vector of length two for groups and pooled data, respectively
col	colors for point symbols, a vector of length two for the groups and the pooled data
rev	logical; if TRUE, the order of the groups is reversed on the vertical axis.
xlim	x limits for the plot
conf	coverage for approximate confidence intervals, 0 <= conf < 1 ; use conf=0 to suppress these

method	confidence interval method; see [logdetCI](#)
bias.adj	confidence interval bias adjustment; see [logdetCI](#)
lwd	line width for confidence interval
...	Arguments passed down to [dotchart](#).

Details

Confidence intervals are only available for the default Box M test, using `which="logDet"`.

Author(s)

Michael Friendly

See Also

[boxM](#), [logdetCI](#)

[dotchart](#)

Examples

```
# Iris data
res <- boxM(iris[, 1:4], iris[, "Species"])
plot(res, gplabel="Species")

# Skulls data
skulls.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)
skulls.boxm <- boxM(skulls.mod)
plot(skulls.boxm, gplabel="Epoch")
plot(skulls.boxm, gplabel="Epoch", bias.adj=FALSE)

# other measures
 plot(skulls.boxm, which="product", gplabel="Epoch", xlim=c(10,14))
 plot(skulls.boxm, which="sum", gplabel="Epoch")
 plot(skulls.boxm, which="precision", gplabel="Epoch")
 plot(skulls.boxm, which="max", gplabel="Epoch")
```

---

plot.robmlm   *Plot observation weights from a robust multivariate linear models*

Description

Creates an index plot of the observation weights assigned in the last iteration of [robmlm](#). Observations with low weights have large residual squared distances and are potential multivariate outliers with respect to the fitted model.

Usage

```
## S3 method for class 'robmlm'
plot(x, labels,
     id.weight = 0.7, id.pos = 4,
     pch = 19,
     col = palette()[1], cex = par("cex"),
     segments = FALSE,
     xlab = "Case index", ylab = "Weight in robust MANOVA", ...)
```

Arguments

x	A "robmlm" object
labels	Observation labels; if not specified, uses rownames from the original data
id.weight	Threshold for identifying observations with small weights
id.pos	Position of observation label relative to the point
pch	Point symbol(s); can be a vector of length equal to the number of observations in the data frame
col	Point color(s)
cex	Point character size(s)
segments	logical; if TRUE, draw line segments from 1.o down to the point
xlab	x axis label
ylab	y axis label
...	other arguments passed to plot

Value

Returns invisibly the weights for the observations labeled in the plot

Author(s)

Michael Friendly

See Also

robmlm

Examples

```
data(Skulls)
sk.rmod <- robmlm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)
plot(sk.rmod, col=Skulls$epoch)
axis(side=3, at=15+seq(0,120,30), labels=levels(Skulls$epoch), cex.axis=1)

# Pottery data

pottery.rmod <- robmlm(cbind(Al,Fe,Mg,Ca,Na)~Site, data=Pottery)
plot(pottery.rmod, col=Pottery$Site, segments=TRUE)
```

```
# SocialCog data

data(SocialCog)
SC.rmod <- robmlm(cbind( MgeEmotions, ToM, ExtBias, PersBias) ~ Dx,
                  data=SocialCog)
plot(SC.rmod, col=SocialCog$Dx, segments=TRUE)
```

Pottery2   *Chemical Analysis of Romano-British Pottery*

Description

Results of chemical analyses of 48 specimens of Romano-British pottery published by Tubb et al. (1980). The numbers are the percentage of various metal oxides found in each sample for elements of concentrations greater than 0.01%. This is the original data set from Tubb et al. (1980), in contrast to `Pottery`.

Usage

```
data(Pottery2)
```

Format

A data frame with 48 observations on the following 12 variables.

Region a factor with levels Gl NF Wales

Site a factor with levels AshleyRails Caldicot Gloucester IsleThorns Llanedryn

Kiln a factor with levels 1 2 3 4 5

Al amount of aluminum oxide, Al_2O_3

Fe amount of iron oxide, Fe_2O_3

Mg amount of magnesium oxide, MgO

Ca amount of calcium oxide, CaO

Na amount of sodium oxide, Na_2O

K amount of potassium oxide, K_2O

Ti amount of titanium oxide, TiO_2

Mn amount of manganese oxide, MnO

Ba amount of BaO

Details

The specimens are identified by their rownames in the data frame. Kiln indicates at which kiln site the pottery was found; Site gives the location names of those sites. The kiln sites come from three Regions, ("Gl"=1, "Wales"=(2, 3), "NF"=(4, 5)), where the full names are "Gloucester", "Wales", and "New Forrest".

The variable Kiln comes pre-supplied with contrasts to test interesting hypotheses related to Site and Region.

Source

Originally slightly modified from files by David Carlson, now at [RBPottery](#).

References

Baxter, M. J. 2003. *Statistics in Archaeology.* Arnold, London.

Carlson, David L. 2017. *Quantitative Methods in Archaeology Using R.* Cambridge University Press, pp 247-255, 335-342.

Tubb, A., A. J. Parker, and G. Nickless. 1980. The Analysis of Romano-British Pottery by Atomic Absorption Spectrophotometry. *Archaeometry*, **22**, 153-171.

See Also

[Pottery](#) for the related (subset) data set; [RBPottery](#) for a newer version with more variables.

Examples

```
data(Pottery2)
# contrasts for Kiln correspond to between Region [,1:2] and within Region [,3:4]
contrasts(Pottery2$Kiln)

pmod <-lm(cbind(Al,Fe,Mg,Ca,Na,K,Ti,Mn,Ba)~Kiln, data=Pottery2)
Anova(pmod)

# extract coefficient names for linearHypotheses
coefs <- rownames(coef(pmod))[-1]

# test differences among regions
linearHypothesis(pmod, coefs[1:2])
# test differences within regions B, C
linearHypothesis(pmod, coefs[3:4])

heplot(pmod, fill=c(TRUE,FALSE), hypotheses=list("Region" =coefs[1:2], "WithinBC"=coefs[3:4]))

# all pairwise views;  note that Ba shows no effect
pairs(pmod, fill=c(TRUE,FALSE))

# canonical view, via candisc::heplot

if (require(candisc)) {
```

```
# canonical analysis: how many dimensions?
(pcan <- candisc(pmod))

heplot(pcan, scale=18, fill=c(TRUE,FALSE), var.col="darkgreen", var.lwd=2, var.cex=1.5)

## Not run:
heplot3d(pcan, scale=8)

## End(Not run)
}
```

Probe   *Response Speed in a Probe Experiment*

Description

Data from a probe experiment testing whether immediate memory for sentences is influenced by the phrase structure of the sentence. The data sets come from Timm (1975), Ex. 3.14 and Ex. 3.16 (p.244)

Procedure: Subjects listened to tape-recorded sentences. Each sentence was followed by a "probe word" from one of 5 positions within the sentence. The subject had to respond with the word which immediately followed the probe word in the sentence. The dependent measure is response speed = k(1/reaction time).

Sample sentence:

```
*       The tall man met the young girl who got the new hat.
Pos'ns:     1   2           3   4    5
Function:  ADJ1 SUBJ      ADJ2  OBJ  REL.PN
```

In Probe2, there are two groups of subjects, pre-selected on a test of short term memory.

Usage

```
data(Probe1)
  data(Probe2)
```

Format

Probe1: A data frame with 11 observations on the following 5 variables.

p1 speed at position 1

p2 speed at position 2

p3 speed at position 3

p4 speed at position 4

p5 speed at position 5

Probe2: A data frame with 20 observations on the following 6 variables.

stm Short term memory capacity: a factor with levels High Low

p1 speed at position 1

p2 speed at position 2

p3 speed at position 3

p4 speed at position 4

p5 speed at position 5

Details

These data sets (fictitious) are used as examples of single-sample and two-sample profile analysis or simple repeated measure designs with structured contrasts.

Source

Timm, N. (1975) *Multivariate analysis, with applications in education and psychology* Brooks/Cole.

Examples

```
data(Probe1)
boxplot(Probe1)

pmod1 <- lm(cbind(p1,p2,p3,p4,p5) ~ 1, data=Probe1)
idata <- data.frame(position=factor(1:5))

library(car)
(pmod1.aov <- Anova(pmod1, idata=idata, idesign=~position))

# using default contrasts (p5 as reference level)
heplot(pmod1, manova=pmod1.aov,
      iterm="position",
      type="III",
      idata=idata, idesign=~position)
pairs(pmod1, manova=pmod1.aov,
      iterm="position",
      type="III",
      idata=idata, idesign=~position)

# contrasts for substantative hypotheses regarding
# sentence position effects
C <- matrix(c(
1, 1, -1, -1, 0,
1, -1, 1, -1, 0,
1, -1, -1, 1, 0,
1, 1, 1, 1, -4), 5, 4)
rownames(C) <- paste("p", 1:5, sep="")
colnames(C) <- c("SubPred", "AdjNoun", "SPxAN", "RelPN")

contrasts(idata$position)<- C
(pmod1.aov <- Anova(pmod1, idata=idata, idesign=~position))
```

```
heplot(pmod1, manova=pmod1.aov, iterm="position", type="III", idata=idata, idesign=~position)
pairs(pmod1, manova=pmod1.aov, iterm="position", type="III", idata=idata, idesign=~position)
```

RatWeight   *Weight Gain in Rats Exposed to Thiouracil and Thyroxin*

Description

The data are from a study of weight gain, where investigators randomly assigned 30 rats to three treatment groups: treatment 1 was a control (no additive); treatments 2 and 3 consisted of two different additives (thiouracil and thyroxin respectively) to the rats drinking water. Weight was measured at baseline (week 0) and at weeks 1, 2, 3, and 4. Due to an accident at the beginning of the study, data on 3 rats from the thyroxin group are unavailable.

Usage

```
data(RatWeight)
```

Format

A data frame with 27 observations on the following 6 variables.

trt a factor with levels `Control Thiouracil Thyroxin`

wt0 Weight at Week 0 (baseline weight)

wt1 Weight at Week 1

wt2 Weight at Week 2

wt3 Weight at Week 3

wt4 Weight at Week 4

Details

The `trt` factor comes supplied with contrasts comparing `Control` to each of `Thiouracil` and `Thyroxin`.

Source

Originally from Box (1950), Table D (page 389), where the values for weeks 1-4 were recorded as the gain in weight for that week.

Fitzmaurice, G. M. and Laird, N. M. and Ware, J. H (2004). *Applied Longitudinal Analysis*, New York, NY: Wiley-Interscience. https://rdrr.io/rforge/ALA/.

References

Box, G.E.P. (1950). Problems in the analysis of growth and wear curves. *Biometrics*, 6, 362-389.

Friendly, Michael (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40.

doi: 10.18637/jss.v037.i04.

Examples

```
data(RatWeight)
contrasts(RatWeight$trt)

rat.mod <- lm(cbind(wt0, wt1, wt2, wt3, wt4) ~ trt, data=RatWeight)
rat.mod

idata <- data.frame(week = ordered(0:4))
Anova(rat.mod, idata=idata, idesign=~week, test="Roy")

# quick look at between group effects
pairs(rat.mod)

# between-S, baseline & week 4
heplot(rat.mod, col=c("red", "blue", "green3", "green3"),
variables=c(1,5),
hypotheses=c("trt1", "trt2"),
main="Rat weight data, Between-S effects")

# within-S
heplot(rat.mod, idata=idata, idesign=~week, iterm="week",
col=c("red", "blue", "green3"),
# hypotheses=c("trt1", "trt2"),
main="Rat weight data, Within-S effects")
```

ReactTime   *Reaction Time Data*

Description

Data from Maxwell and Delaney (1990, p. 497) representing the reaction times of 10 subjects in some task where visual stimuli are tilted at 0, 4, and 8 degrees; with noise absent or present. Each subject responded to 3 tilt x 2 noise = 6 conditions. The data thus comprise a repeated measure design with two within-S factors.

Usage

```
data(ReactTime)
```

Format

A data frame with 10 observations giving the reaction time for the 6 conditions.

deg0NA a numeric vector
deg4NA a numeric vector
deg8NA a numeric vector
deg0NP a numeric vector
deg4NP a numeric vector
deg8NP a numeric vector

Source

Baron, J. and Li, Y. (2003). *Notes on the use of R for psychology experiments and questionnaires*, https://cran.r-project.org/doc/contrib/Baron-rpsych.pdf

References

Michael Friendly (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40.

doi: 10.18637/jss.v037.i04.

Maxwell, S. E. & Delaney, H. D. (1990). *Designing Experiments and Analyzing Data: A model comparison perspective*. Pacific Grove, CA: Brooks/Cole.

Examples

```
data(ReactTime)
(RT.mod <- lm(as.matrix(ReactTime)~1))

# within-S factors
within <- expand.grid(tilt=ordered(c(0,4,8)), noise=c("NA", "NP"))
Anova(RT.mod, idata=within, idesign=~tilt * noise)

heplot(RT.mod, idata=within, idesign=~tilt * noise, iterm="tilt")

# plotting means and std errors directly

levels <- expand.grid(Tilt=c(0,4,8), noise=c("NA", "NP"))
(means.df <- data.frame(levels, mean=colMeans(ReactTime), se=sqrt(diag(var(ReactTime)))/9))

with(means.df, {
plot(Tilt, mean, type="n", main="Reaction Time data", xlab="Tilt", ylab="Reaction time")
colors <- rep(c("red", "blue"), each=3)
pts <- rep(c(15, 16), each=3)

lines(Tilt[1:3], mean[1:3], col="red", lwd=2)
lines(Tilt[4:6], mean[4:6], col="blue", lwd=2)
points(Tilt, mean, pch=pts, col=colors, cex=1.2)
arrows(Tilt, mean-se, Tilt, mean+se, angle=90, code=3,
col=colors, len=.05, lwd=2)
# labels at last point, in lieu of legend
text(Tilt[3], mean[3]-10, labels="NA", col="red", pos=1)
text(Tilt[6], mean[6]-10, labels="NP", col="blue", pos=1)
}
)
```

---

robmlm   *Robust Fitting of Multivariate Linear Models*

Description

Fit a multivariate linear model by robust regression using a simple M estimator.

These S3 methods are designed to provide a specification of a class of robust methods which extend `mlms`, and are therefore compatible with other `mlm` extensions, including [Anova](#) and [heplot](#).

Usage

```
robmlm(X, ...)

## S3 method for class 'formula'
robmlm(formula, data, subset, weights, na.action,
model = TRUE, contrasts = NULL, ...)

## Default S3 method:
robmlm(X, Y, w,
P = 2 * pnorm(4.685, lower.tail = FALSE), tune, max.iter = 100,
psi = psi.bisquare, tol = 1e-06, initialize, verbose = FALSE, ...)


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

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

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

Arguments

formula	a formula of the form cbind(y1, y2, ...) ~ x1 + x2 + ...
data	a data frame from which variables specified in `formula` are preferentially to be taken.
subset	An index vector specifying the cases to be used in fitting.
weights	a vector of prior weights for each case.
na.action	A function to specify the action to be taken if NAs are found. The 'factory-fresh' default action in R is [na.omit](#), and can be changed by [options](#)(na.action=).
model	should the model frame be returned in the object?
contrasts	optional contrast specifications; see [lm](#) for details.
...	other arguments, passed down. In particular relevant control arguments can be passed to the to the robmlm.default method.
X	for the default method, a model matrix, including the constant (if present)

Y	for the default method, a response matrix
w	prior weights
P	two-tail probability, to find cutoff quantile for chisq (tuning constant); default is set for bisquare weight function
tune	tuning constant (if given directly)
max.iter	maximum number of iterations
psi	robustness weight function; `psi.bisquare` is the default
tol	convergence tolerance, maximum relative change in coefficients
initialize	modeling function to find start values for coefficients, equation-by-equation; if absent WLS (`lm.wfit`) is used
verbose	show iteration history? (TRUE or FALSE)
x	a `robmlm` object
object	a `robmlm` object

Details

Fitting is done by iterated re-weighted least squares (IWLS), using weights based on the Mahalanobis squared distances of the current residuals from the origin, and a scaling (covariance) matrix calculated by `cov.trob`. The design of these methods were loosely modeled on `rlm`.

An internal `vcov.mlm` function is an extension of the standard `vcov` method providing for observation weights.

Value

An object of class `"robmlm"` inheriting from `c("mlm", "lm")`.

This means that the returned `"robmlm"` contains all the components of `"mlm"` objects described for `lm`, plus the following:

weights	final observation weights
iterations	number of iterations
converged	logical: did the IWLS process converge?

The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` extract various useful features of the value returned by `robmlm`.

Author(s)

John Fox; packaged by Michael Friendly

References

A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics*. Wadsworth & Brooks/Cole.

See Also

rlm, cov.trob

Examples

```
##############
# Skulls data

# make shorter labels for epochs and nicer variable labels in heplots
Skulls$epoch <- factor(Skulls$epoch, labels=sub("c","",levels(Skulls$epoch)))
# variable labels
vlab <- c("maxBreadth", "basibHeight", "basialLength", "nasalHeight")

# fit manova model, classically and robustly
sk.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)
sk.rmod <- robmlm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)

# standard mlm methods apply here
coefficients(sk.rmod)

# index plot of weights
plot(sk.rmod$weights, type="h", xlab="Case Index", ylab="Robust mlm weight", col="gray")
points(sk.rmod$weights, pch=16, col=Skulls$epoch)
axis(side=1, at=15+seq(0,120,30), labels=levels(Skulls$epoch), tick=FALSE, cex.axis=1)

# heplots to see effect of robmlm vs. mlm
heplot(sk.mod, hypotheses=list(Lin="epoch.L", Quad="epoch.Q"),
    xlab=vlab[1], ylab=vlab[2], cex=1.25, lty=1)
heplot(sk.rmod, hypotheses=list(Lin="epoch.L", Quad="epoch.Q"),
    add=TRUE, error.ellipse=TRUE, lwd=c(2,2), lty=c(2,2),
    term.labels=FALSE, hyp.labels=FALSE, err.label="")


##############
# Pottery data

pottery.mod <- lm(cbind(Al,Fe,Mg,Ca,Na)~Site, data=Pottery)
pottery.rmod <- robmlm(cbind(Al,Fe,Mg,Ca,Na)~Site, data=Pottery)
Anova(pottery.mod)
Anova(pottery.rmod)

# index plot of weights
plot(pottery.rmod$weights, type="h")
points(pottery.rmod$weights, pch=16, col=Pottery$Site)

# heplots to see effect of robmlm vs. mlm
heplot(pottery.mod, cex=1.3, lty=1)
heplot(pottery.rmod, add=TRUE, error.ellipse=TRUE, lwd=c(2,2), lty=c(2,2),
    term.labels=FALSE, err.label="")


##############
# Prestige data
```

```
# treat women and prestige as response variables for this example
prestige.mod <- lm(cbind(women, prestige) ~ income + education + type, data=Prestige)
prestige.rmod <- robmlm(cbind(women, prestige) ~ income + education + type, data=Prestige)

coef(prestige.mod)
coef(prestige.rmod)
# how much do coefficients change?
round(coef(prestige.mod) - coef(prestige.rmod),3)

# pretty plot of case weights
plot(prestige.rmod$weights, type="h", xlab="Case Index", ylab="Robust mlm weight", col="gray")
points(prestige.rmod$weights, pch=16, col=Prestige$type)
legend(0, 0.7, levels(Prestige$type), pch=16, col=palette()[1:3], bg="white")

heplot(prestige.mod, cex=1.4, lty=1)
heplot(prestige.rmod, add=TRUE, error.ellipse=TRUE, lwd=c(2,2), lty=c(2,2),
    term.labels=FALSE, err.label="")
```

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**(2) 421–444. http://datavis.ca/papers/jcgs-heplots.pdf

Examples

```
str(Rohwer)

## 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
## Not run:
col <- c("red", "green3", "blue", "cyan", "magenta", "brown", "gray")
heplot3d(rohwer.mod, hypotheses=list("Regr" = c("n", "s", "ns", "na", "ss")),
                     col=col, wire=FALSE)

## End(Not run)

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

# overlay the separate HE plots
heplot(rohwer.ses1, ylim=c(40,110),col=c("red", "black"))
heplot(rohwer.ses2, add=TRUE, col=c("blue", "black"), grand.mean=TRUE, error.ellipse=TRUE)
```

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 root-stocks 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)

# test two orthogonal contrasts among the rootstocks
hyp <- matrix(c(2,-1,-1,-1,-1,2,  1, 0,0,0,0,-1), 2, 6, byrow=TRUE)
linearHypothesis(root.mod, hyp)
```

```
heplot(root.mod, hypotheses=list(Contrasts=hyp, C1=hyp[1,], C2=hyp[2,]))

heplot1d(root.mod, hypotheses=list(Contrasts=hyp, C1=hyp[1,], C2=hyp[2,]))
```

Sake   *Taste Ratings of Japanese Rice Wine (Sake)*

Description

Siotani et al. (1985) describe a study of Japanese rice wine (sake) used to investigate the relationship between two subjective ratings (taste and smell) and a number of physical measurements on 30 brands of sake.

These data provide one example of a case where a multivariate regression doesn't benefit from having multiple outcome measures, using the standard tests. Barrett (2003) uses this data to illustrate influence measures for multivariate regression models.

Usage

```
data(Sake)
```

Format

A data frame with 30 observations on the following 10 variables.

taste mean taste rating

smell mean smell rating

pH pH measurement

acidity1 one measure of acidity

acidity2 another measure of acidity

sake Sake-meter score

rsugar direct reducing sugar content

tsugar total sugar content

alcohol alcohol content

nitrogen formol-nitrogen content

Details

The taste and smell values are the mean ratings of 10 experts on some unknown scale.

Source

Siotani, M. Hayakawa, T. & Fujikoshi, Y. (1985). *Modern Multivariate Statistical Analysis: A Graduate Course and Handbook.* American Sciences Press, p. 217.

References

Barrett, B. E. (2003). Understanding Influence in Multivariate Regression. *Communications in Statistics - Theory and Methods* 32 (3), 667-680.

Examples

```
data(Sake)
# quick look at the data
boxplot(scale(Sake))

Sake.mod <- lm(cbind(taste,smell) ~ ., data=Sake)

library(car)
Anova(Sake.mod)

predictors <- colnames(Sake)[-(1:2)]
# overall multivariate regression test
linearHypothesis(Sake.mod, predictors)

heplot(Sake.mod, hypotheses=list("Regr" = predictors))
```

---

schooldata   *School Data*

Description

School Data, from Charnes et al. (1981). The aim is to explain scores on 3 different tests, `reading`, `mathematics` and `selfesteem` from 70 school sites by means of 5 explanatory variables related to parents and teachers.

Usage

```
data(schooldata)
```

Format

A data frame with 70 observations on the following 8 variables.

education Education level of mother as measured in terms of percentage of high school graduates among female parents

occupation Highest occupation of a family member according to a pre-arranged rating scale

visit Parental visits index representing the number of visits to the school site

counseling Parent counseling index calculated from data on time spent with child on school-related topics such as reading together, etc.

teacher Number of teachers at a given site

reading Reading score as measured by the Metropolitan Achievement Test

mathematics Mathematics score as measured by the Metropolitan Achievement Test

selfesteem Coopersmith Self-Esteem Inventory, intended as a measure of self-esteem

Details

This dataset was shamelessly borrowed from the FRB package.

The relationships among these variables are unusual, a fact only revealed by plotting.

Source

A. Charnes, W.W. Cooper and E. Rhodes (1981). Evaluating Program and Managerial Efficiency: An Application of Data Envelopment Analysis to Program Follow Through. *Management Science*, **27**, 668-697.

Examples

```
data(schooldata)
# initial screening
plot(schooldata)

# better plot
library(corrgram)
corrgram(schooldata,
         lower.panel=panel.ellipse,
         upper.panel=panel.pts)

#fit the MMreg model
school.mod <- lm(cbind(reading, mathematics, selfesteem) ~
              education + occupation + visit + counseling + teacher, data=schooldata)

# shorthand: fit all others
school.mod <- lm(cbind(reading, mathematics, selfesteem) ~ ., data=schooldata)
car::Anova(school.mod)

# HE plots
heplot(school.mod, fill=TRUE, fill.alpha=0.1)
pairs(school.mod, fill=TRUE, fill.alpha=0.1)

# robust model, using robmlm()
school.rmod <- robmlm(cbind(reading, mathematics, selfesteem) ~ ., data=schooldata)
# note that counseling is now significant
car::Anova(school.rmod)

# Index plot of the weights
wts <- school.rmod$weights
notable <- which(wts < 0.8)
plot(wts, type = "h", col="gray", ylab = "Observation weight")
points(1:length(wts), wts,
       pch=16,
       col = ifelse(wts < 0.8, "red", "black"))

text(notable, wts[notable],
     labels = notable,
     pos = 3,
     col = "red")
```

```
# Index plot of the weights
wts <- school.rmod$weights
notable <- which(wts < 0.8)
plot(wts, type = "h", col="gray", ylab = "Observation weight")
points(1:length(wts), wts,
        pch=16,
        col = ifelse(wts < 0.8, "red", "black"))

text(notable, wts[notable],
     labels = notable,
     pos = 3,
     col = "red")


# compare classical HE plot with that based on the robust model
heplot(school.mod, cex=1.4, lty=1, fill=TRUE, fill.alpha=0.1)
heplot(school.rmod,
       add=TRUE,
       error.ellipse=TRUE,
       lwd=c(2,2), lty=c(2,2),
     term.labels=FALSE, err.label="",
       fill=TRUE)
```

Skulls   *Egyptian Skulls*

Description

Measurements made on Egyptian skulls from five epochs.

Usage

```
data("Skulls")
```

Format

A data frame with 150 observations on the following 5 variables.

epoch the epoch the skull as assigned to, an ordered factor with levels c4000BC c3300BC, c1850BC, c200BC, and cAD150, where the years are only given approximately, of course.

mb maximal breadth of the skull.

bh basibregmatic height of the skull.

bl basialiveolar length of the skull.

nh nasal height of the skull.

Details

The epochs correspond to the following periods of Egyptian history:

1. the early predynastic period (circa 4000 BC);
2. the late predynastic period (circa 3300 BC);
3. the 12th and 13th dynasties (circa 1850 BC);
4. the Ptolemiac period (circa 200 BC);
5. the Roman period (circa 150 AD).

The question is whether the measurements change over time. Non-constant measurements of the skulls over time would indicate interbreeding with immigrant populations.

Note that using polynomial contrasts for epoch essentially treats the time points as equally spaced.

Source

D. J. Hand, F. Daly, A. D. Lunn, K. J. McConway and E. Ostrowski (1994). *A Handbook of Small Datasets*, Chapman and Hall/CRC, London.

References

Thomson, A. and Randall-Maciver, R. (1905) *Ancient Races of the Thebaid*, Oxford: Oxford University Press.

Hand, D. J., F. Daly, A. D. Lunn, K. J. McConway and E. Ostrowski (1994). *A Handbook of Small Datasets*, Chapman and Hall/CRC, London.

Examples

```
data(Skulls)
library(car)    # for Anova

# make shorter labels for epochs
Skulls$epoch <- factor(Skulls$epoch, labels=sub("c","",levels(Skulls$epoch)))

# longer variable labels
vlab <- c("maxBreadth", "basibHeight", "basialLength", "nasalHeight")

# fit manova model
sk.mod <- lm(cbind(mb, bh, bl, nh) ~ epoch, data=Skulls)

Anova(sk.mod)
summary(Anova(sk.mod))

# test trends over epochs
print(linearHypothesis(sk.mod, "epoch.L"), SSP=FALSE) # linear component
print(linearHypothesis(sk.mod, "epoch.Q"), SSP=FALSE) # quadratic component

# typical scatterplots are not very informative
scatterplot(mb ~ bh|epoch, data=Skulls,
            ellipse = list(levels=0.68),
```

```
            smooth=FALSE,
            legend = list(coords="topright"),
            xlab=vlab[2], ylab=vlab[1])

scatterplot(mb ~ bl|epoch, data=Skulls,
            ellipse = list(levels=0.68),
            smooth=FALSE,
            legend = list(coords="topright"),
            xlab=vlab[3], ylab=vlab[1])

# HE plots

heplot(sk.mod,
       hypotheses=list(Lin="epoch.L", Quad="epoch.Q"),
       xlab=vlab[1], ylab=vlab[2])

pairs(sk.mod,
      hypotheses=list(Lin="epoch.L", Quad="epoch.Q"),
      var.labels=vlab)

# 3D plot shows that nearly all of hypothesis variation is linear!
## Not run:
heplot3d(sk.mod, hypotheses=list(Lin="epoch.L", Quad="epoch.Q"), col=c("pink", "blue"))

# view in canonical space
if (require(candisc)) {
sk.can <- candisc(sk.mod)
sk.can
heplot(sk.can)
heplot3d(sk.can)
}

## End(Not run)
```

SocGrades   *Grades in a Sociology Course*

Description

The data set SocGrades contains four outcome measures on student performance in an introductory
sociology course together with six potential predictors. These data were used by Marascuilo and
Levin (1983) for an example of canonical correlation analysis, but are also suitable as examples
of multivariate multiple regression, MANOVA, MANCOVA and step-down analysis in multivariate
linear models.

Usage

```
data(SocGrades)
```

Format

A data frame with 40 observations on the following 10 variables.

class Social class, an ordered factor with levels 1 > 2 > 3

sex sex, a factor with levels F M

gpa grade point average

boards College Board test scores

hssoc previous high school unit in sociology, a factor with 2 no, yes

pretest score on course pretest

midterm1 score on first midterm exam

midterm2 score on second midterm exam

final score on final exam

eval course evaluation

Details

midterm1, midterm2, final, and possibly eval are the response variables. All other variables are potential predictors.

The factors class, sex, and hssoc can be used with as.numeric in correlational analyses.

Source

Marascuilo, L. A. and Levin, J. R. (1983). *Multivariate Statistics in the Social Sciences* Monterey, CA: Brooks/Cole, Table 5-1, p. 192.

Examples

```
data(SocGrades)
# basic MLM
grades.mod <- lm(cbind(midterm1, midterm2, final, eval) ~
class + sex + gpa + boards + hssoc + pretest, data=SocGrades)

Anova(grades.mod, test="Roy")

clr <- c("red", "blue", "darkgreen", "magenta", "brown", "black", "darkgray")
heplot(grades.mod, col=clr)
pairs(grades.mod, col=clr)

## Not run:
heplot3d(grades.mod, col=clr, wire=FALSE)

## End(Not run)

if (require(candisc)) {
# calculate canonical results for all terms
grades.can <- candiscList(grades.mod)
# extract canonical R^2s
unlist(lapply(grades.can, function(x) x$canrsq))
```

```
# plot class effect in canonical space
heplot(grades.can, term="class", scale=4)

# 1 df terms: show canonical scores and weights for responses
plot(grades.can, term="sex")
plot(grades.can, term="gpa")
plot(grades.can, term="boards")
}
```

SocialCog   *Social Cognitive Measures in Psychiatric Groups*

Description

The general purpose of the study (Hartman, 2016, Heinrichs et al. (2015)) was to evaluate patterns
and levels of performance on neurocognitive measures among individuals with schizophrenia and
schizoaffective disorder using a well-validated, comprehensive neurocognitive battery specifically
designed for individuals with psychosis (Heinrichs et al. (2008))

The data here are for a subset of the observations in NeuroCog for which measures on various scales
of social cognition were also available. Interest here is on whether the schizophrenia group can be
distinguished from the schizoaffective group on these measures.

The Social Cognitive measures were designed to tap various aspects of the perception and cognitive
procession of emotions of others. Emotion perception was assessed using a Managing Emotions
(MgeEmotions) score from the MCCB. A "theory of mind" (ToM) score assessed ability to read
the emotions of others from photographs of the eye region of male and female faces. Two other
measures, externalizing bias (ExtBias) and personalizing bias (PersBias) were calculated from
a scale measuring the degree to which individuals attribute internal, personal or situational causal
attributions to positive and negative social events.

Usage

```
data("SocialCog")
```

Format

A data frame with 139 observations on the following 5 variables.

Dx Diagnostic group, a factor with levels Schizophrenia, Schizoaffective, Control

MgeEmotions Score on the Managing emotions test, a numeric vector

ToM Score on the The Reading the Mind in the Eyes test (theory of mind), a numeric vector

ExtBias Externalizing Bias score, a numeric vector

PersBias Personal Bias score, a numeric vector

Details

See [NeuroCog](#) for a description of the sample. Only those with complete data on all the social cognitive measures are included in this data set.

There is one extreme outlier in the schizophrenia group and other possible outliers in the control group, left in here for tutorial purposes.

Source

Hartman, L. I. (2016). Schizophrenia and Schizoaffective Disorder: One Condition or Two? Unpublished PhD dissertation, York University.

Heinrichs, R.W., Pinnock, F., Muharib, E., Hartman, L.I., Goldberg, J.O., & McDermid Vaz, S. (2015). Neurocognitive normality in schizophrenia revisited. *Schizophrenia Research: Cognition*, **2** (4), 227-232. doi: 10.1016/j.scog.2015.09.001

Examples

```
data(SocialCog)
SC.mod <- lm(cbind(MgeEmotions, ToM, ExtBias, PersBias) ~ Dx, data=SocialCog)
SC.mod
Anova(SC.mod)

# test hypotheses of interest in terms of contrasts
print(linearHypothesis(SC.mod, "Dx1"), SSP=FALSE)
print(linearHypothesis(SC.mod, "Dx2"), SSP=FALSE)

#' ## HE plots

heplot(SC.mod, hypotheses=list("Dx1"="Dx1", "Dx2"="Dx2"),
fill=TRUE, fill.alpha=.1)

pairs(SC.mod, fill=c(TRUE,FALSE), fill.alpha=.1)
```

---

statList   *Calculate statistics for levels of factors*

Description

`statList` provides a general method for calculating univariate or multivariate statistics for a matrix or data.frame stratified by one or more factors.

Usage

```
statList(X, factors, FUN, drop = FALSE, ...)

colMeansList(X, factors, drop = FALSE, ...)

covList(X, factors, drop = FALSE, ...)
```

Arguments

X	A matrix or data frame containing the variables to be summarized
factors	A vector, matrix or data frame containing the factors for which X is to be summarized. If factors is not specified, the result is calculated for all of the data in X.
FUN	A function to be applied to the pieces of X, as split by factors.
drop	Logical, indicating whether empty levels of factors are to be dropped from the result.
...	Other arguments, passed to FUN.

Details

statList is the general function. X is first split by factors, and FUN is applied to the result.

colMeansList and covList are just calls to statList with the appropriate FUN.

Value

Returns a list of items corresponding to the unique elements in factors, or the interaction of factors. Each item is the result of applying FUN to that collection of rows of X. The items are named according to the levels in factors.

Author(s)

Michael Friendly

See Also

[colMeans](), [termMeans]()

Examples

```
# grand means
statList(iris[,1:4], FUN=colMeans)
# species means
statList(iris[,1:4], iris$Species, FUN=colMeans)
# same
colMeansList(iris[,1:4], iris$Species)

# var-cov matrices, by species
covList(iris[,1:4], iris$Species)

# multiple factors
iris$Dummy <- sample(c("Hi","Lo"),150, replace=TRUE)
colMeansList(iris[,1:4], iris[,5:6])
```

---

termMeans	*Calculate Means for a Term in a Multivariate Linear Model*

Description

termMeans is a utility function designed to calculate means for the levels of factor(s) for any term in a multivariate linear model.

Usage

```
termMeans(mod, term, label.factors=FALSE, abbrev.levels=FALSE)
```

Arguments

mod	An mlm model object
term	A character string indicating a given term in the model. All factors in the term must be included in the model, even if they are in the model data frame.
label.factors	If true, the rownames for each row in the result include the name(s) of the factor(s) involved, followed by the level values. Otherwise, the rownames include only the levels of the factor(s), with multiple factors separated by ':'
abbrev.levels	Either a logical or an integer, specifying whether the levels values of the factors in the term are to be abbreviated in constructing the rownames. An integer specifies the minimum length of the abbreviation for each factor in the term.

Value

Returns a matrix whose columns correspond to the response variables in the model and whose rows correspond to the levels of the factor(s) in the term.

Author(s)

Michael Friendly

See Also

[aggregate](), [colMeans]()

[statList](), [colMeansList]()

Examples

```
factors <- expand.grid(A=factor(1:3),B=factor(1:2),C=factor(1:2))
n <- nrow(factors)
responses <-data.frame(Y1=10+round(10*rnorm(n)),Y2=10+round(10*rnorm(n)))
test <- data.frame(factors, responses)
mod <- lm(cbind(Y1,Y2) ~ A*B, data=test)

termMeans(mod, "A")
```

```
termMeans(mod, "A:B")
termMeans(mod, "A:B", label.factors=TRUE)
## Not run:
termMeans(mod, "A:B:C")     # generates an error

## End(Not run)

plastic.mod <- lm(cbind(tear, gloss, opacity) ~ rate*additive, data=Plastic)
colors = c("red", "darkblue", "darkgreen", "brown")
heplot(plastic.mod, col=colors, cex=1.25)
# add means for interaction term
intMeans <- termMeans(plastic.mod, 'rate:additive', abbrev=2)
points(intMeans[,1], intMeans[,2], pch=18, cex=1.2, col="brown")
text(intMeans[,1], intMeans[,2], rownames(intMeans), adj=c(0.5,1), col="brown")
```

TIPI   *Data on the Ten Item Personality Inventory*

Description

The Ten Item Personality Inventory (Gosling et al. 2003) is a brief inventory of the Big Five personality domains (Extraversion, Neuroticism, Conscientiousness, Agreeableness, and Openness to experience). This dataset, originally from the Open Source Psychometrics Project (https://openpsychometrics.org/), was used by Jones et al. (2020), from which we obtained this version.

In addition to scores on the Big Five scales, the dataset contains 11 demographic variables on the participants, potentially useful in multivariate analyses.

Usage

```
data("TIPI")
```

Format

A data frame with 1799 observations on the following 16 variables.

Extraversion a numeric vector

Neuroticism a numeric vector

Conscientiousness a numeric vector

Agreeableness a numeric vector

Openness a numeric vector

education an ordered factor with levels <HS < HS < Univ < Grad

urban an ordered factor with levels Rural < Suburban < Urban

gender a factor with levels M F

engnat a factor with levels Native Non-native

age a numeric vector

religion a factor with levels Agnostic Atheist Buddhist Christian (Catholic) Christian
      (Mormon) Christian (Protestant) Christian (Other) Hindu Jewish Muslim Sikh Other

orientation a factor with levels Heterosexual Bisexual Homosexual Asexual Other

race a factor with levels Asian Arab Black Indig-White Other

voted a factor with levels Yes No

married a factor with levels Never married Currently married Previously married

familysize a numeric vector

Details

Scores on each personality domain were calculated by averaging items assigned to each domain
(after reverse scoring specific items). In this version, total scores for each scale were calculated by
averaging the positively and negatively coded items, for example, TIPI$Extraversion <- (TIPI$E
+ (8-TIPI$E_r))/2.

Then, for the present purposes, some tidying was done:

- 100 cases with 'gender=="Other" were deleted;
- codes for levels of 'education', 'engnat' and 'race' were abbreviated for ease of use in graph-
  ics.

Source

Jones, P.J., Mair, P., Simon, T. et al. (2020). Network Trees: A Method for Recursively Partitioning
Covariance Structures. *Psychometrika*, **85**, 926?945. https://doi.org/10.1007/s11336-020-09731-4

References

Gosling, S. D., Rentfrow, P. J., & Swann, W. B, Jr. (2003). A very brief measure of the Big-Five
personality domains. *Journal of Research in Personality*, **37**, 504?528.

Examples

```
data(TIPI)
# fit an mlm
tipi.mlm <- lm(cbind(Extraversion, Neuroticism, Conscientiousness, Agreeableness, Openness)
               ~ engnat + gender + education, data = TIPI )
Anova(tipi.mlm)

heplot(tipi.mlm, fill=TRUE, fill.alpha=0.1)

pairs(tipi.mlm, fill=TRUE, fill.alpha=0.1)

# candisc works best for factors with >2 levels
library(candisc)
tipi.can <- candisc(tipi.mlm, term="education")
tipi.can

heplot(tipi.can, fill=TRUE, fill.alpha=0.1,
       var.col = "darkred", var.cex = 1.5, var.lwd = 3)
```

---

trans.colors   *Make Colors Transparent*

Description

Takes a vector of colors (as color names or rgb hex values) and adds a specified alpha transparency to each.

Usage

```
trans.colors(col, alpha = 0.5, names = NULL)
```

Arguments

col	A character vector of colors, either as color names or rgb hex values
alpha	alpha transparency value(s) to apply to each color (0 means fully transparent and 1 means opaque)
names	optional character vector of names for the colors

Details

Colors (col) and alpha need not be of the same length. The shorter one is replicated to make them of the same length.

Value

A vector of color values of the form "#rrggbbaa"

Author(s)

Michael Friendly

See Also

col2rgb, rgb, adjustcolor,

Examples

```
trans.colors(palette(), alpha=0.5)

# alpha can be vectorized
trans.colors(palette(), alpha=seq(0, 1, length=length(palette())))

# lengths need not match: shorter one is repeated as necessary
trans.colors(palette(), alpha=c(.1, .2))

trans.colors(colors()[1:20])
```

```
# single color, with various alphas
trans.colors("red", alpha=seq(0,1, length=5))
# assign names
trans.colors("red", alpha=seq(0,1, length=5), names=paste("red", 1:5, sep=""))
```

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

Friendly, Michael (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40.

doi: 10.18637/jss.v037.i04.

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, type="III")

##Type III Repeated Measures MANOVA Tests: Pillai test statistic
##             Df test stat approx F num Df den Df    Pr(>F)
##(Intercept)  1     0.653  118.498       1     63 4.115e-16 ***
##grade        1     0.826   96.376       3     61 < 2.2e-16 ***


heplot(Vocab.mod, type="III", idata=idata, idesign=~grade, iterm="grade",
main="HE plot for Grade effect")

### doing this 'manually' by explicitly transforming Y -> Y M
# 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")
mark.H0()
```

WeightLoss	*Weight Loss Data*

Description

Contrived data on weight loss and self esteem over three months, for three groups of individuals: Control, Diet and Diet + Exercise. The data constitute a double-multivariate design.

Usage

```
data(WeightLoss)
```

Format

A data frame with 34 observations on the following 7 variables.

group a factor with levels Control Diet DietEx.

wl1 Weight loss at 1 month

wl2 Weight loss at 2 months

wl3 Weight loss at 3 months

se1 Self esteem at 1 month

se2 Self esteem at 2 months

se3 Self esteem at 3 months

Details

Helmert contrasts are assigned to group, comparing Control vs. (Diet DietEx) and Diet vs. DietEx.

Source

Originally taken from http://www.csun.edu/~ata20315/psy524/main.htm, but modified slightly

References

Friendly, Michael (2010). HE Plots for Repeated Measures Designs. *Journal of Statistical Software*, 37(4), 1-40.

doi: 10.18637/jss.v037.i04.

Examples

```
data(WeightLoss)
str(WeightLoss)
table(WeightLoss$group)

contrasts(WeightLoss$group) <- matrix(c(-2,1,1, 0, -1, 1),ncol=2)
(wl.mod<-lm(cbind(wl1,wl2,wl3,se1,se2,se3)~group, data=WeightLoss))

heplot(wl.mod, hypotheses=c("group1", "group2"))
pairs(wl.mod, variables=1:3)
pairs(wl.mod, variables=4:6)

# within-S variables
within <- data.frame(measure=rep(c("Weight loss", "Self esteem"),each=3), month=rep(ordered(1:3),2))

# doubly-multivariate analysis: requires car 2.0+
## Not run:
if (packageDescription("car")[["Version"]] >= 2) {
imatrix <- matrix(c(
1,0,-1, 1, 0, 0,
1,0, 0,-2, 0, 0,
1,0, 1, 1, 0, 0,
0,1, 0, 0,-1, 1,
0,1, 0, 0, 0,-2,
0,1, 0, 0, 1, 1), 6, 6, byrow=TRUE)

# NB: for heplots the columns of imatrix should have names
colnames(imatrix) <- c("WL", "SE", "WL.L", "WL.Q", "SE.L", "SE.Q")
```

```
rownames(imatrix) <- colnames(WeightLoss)[-1]
(imatrix <- list(measure=imatrix[,1:2], month=imatrix[,3:6]))
contrasts(WeightLoss$group) <- matrix(c(-2,1,1,
                                         0,-1,1), ncol=2)

(wl.mod<-lm(cbind(wl1, wl2, wl3, se1, se2, se3)~group, data=WeightLoss))
(wl.aov <- Anova(wl.mod, imatrix=imatrix, test="Roy"))

heplot(wl.mod, imatrix=imatrix, iterm="group:measure")
}

## End(Not run)

# do the correct analysis 'manually'
unit <- function(n, prefix="") {
J <-matrix(rep(1, n), ncol=1)
rownames(J) <- paste(prefix, 1:n, sep="")
J
}

measure <- kronecker(diag(2), unit(3, 'M')/3, make.dimnames=TRUE)
colnames(measure)<- c('WL', 'SE')

between <- as.matrix(WeightLoss[,-1])

between.mod <- lm(between ~ group, data=WeightLoss)
Anova(between.mod)

heplot(between.mod, hypotheses=c("group1", "group2"),
xlab="Weight Loss", ylab="Self Esteem",
col=c("red", "blue", "brown"),
main="Weight Loss & Self Esteem: Group Effect")

month <- kronecker(diag(2), poly(1:3), make.dimnames=TRUE)
colnames(month)<- c('WL', 'SE')
trends <- as.matrix(WeightLoss[,-1])
within.mod <- lm(trends ~ group, data=WeightLoss)
Anova(within.mod)

heplot(within.mod)
heplot(within.mod, hypotheses=c("group1", "group2"),
xlab="Weight Loss", ylab="Self Esteem",
type="III", remove.intercept=FALSE,
term.labels=c("month", "group:month"),
main="Weight Loss & Self Esteem: Within-S Effects")
mark.H0()
```

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