Package ‘groc’

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Imports pls, mgcv, robustbase, MASS

Depends rrcov

Suggests ppls

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corrob

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corrob Robust correlation measure

Description

Compute robust estimates of the correlation between two variables using the Orthogonalized Gnanadesikan-Kettenring pairwise estimator.

Usage

   corrob(t, u)

Arguments

   t a numeric vector containing the data for the first variable.
   u a numeric vector containing the data for the second variable.

Details

   This function uses the covRob function from the robust package.

Value

   Value of the robust correlation.
**Author(s)**

Martin Bilodeau (<bilodeau@dms.umontreal.ca>) and Pierre Lafaye de Micheaux (<lafaye@unsw.edu.au>)

**References**


**See Also**

covrob, dcov

**Examples**

data(stackloss)
corrob(stackloss$Air.Flow, stackloss$Water.Temp)

covrob(data, corr = FALSE, distance = TRUE, na.action = na.fail, estim = "auto", control = covRob.control(estim, ...), ...)
control

a list of control parameters to be used in the numerical algorithms. See covRob.control for the possible control parameters and their default settings. This argument is ignored when estim = "auto".

... control parameters may be passed directly when estim != "auto".

Details

This function was part of the 'robust' package and it has been copied to the current package due to an ORPHANED Maintainer.

The covRob function selects a robust covariance estimator that is likely to provide a good estimate in a reasonable amount of time. Presently this selection is based on the problem size. The Donoho-Stahel estimator is used if there are less than 1000 observations and less than 10 variables or less than 5000 observations and less than 5 variables. If there are less than 50000 observations and less than 20 variables then the MCD is used. For larger problems, the Orthogonalized Quadrant Correlation estimator is used.

The MCD and Reweighted-MCD estimates (estim = "mcd" and estim = "weighted" respectively) are computed using the covMcd function in the robustbase package. By default, covMcd returns the reweighted estimate; the actual MCD estimate is contained in the components of the output list prefixed with raw.

The M estimate (estim = "M") is computed using the covMest function in the rrcov package. For historical reasons the Robust Library uses the MCD to compute the initial estimate.

The Donoho-Stahel (estim = "donostah") estimator is computed using the CovSde function provided in the rrcov package.

The pairwise estimators (estim = "pairwisegk" and estim = "pairwiseqc") are computed using the CovOgk function in the rrcov package.

Value

an object of class "covRob" with components:

call       an image of the call that produced the object with all the arguments named.
cov        a numeric matrix containing the final robust estimate of the covariance/correlation matrix.
center     a numeric vector containing the final robust estimate of the location vector.
dist       a numeric vector containing the squared Mahalanobis distances computed using robust estimates of covariance and location contained in cov and center. If distance = FALSE this element will me missing.
raw.cov    a numeric matrix containing the initial robust estimate of the covariance/correlation matrix. If there is no initial robust estimate then this element is set to NA.
raw.center a numeric vector containing the initial robust estimate of the location vector. If there is no initial robust estimate then this element is set to NA.
raw.dist   a numeric vector containing the squared Mahalanobis distances computed using the initial robust estimates of covariance and location contained in raw.cov and raw.center. If distance = FALSE or if there is no initial robust estimate then this element is set to NA.
covrob

**Description**

Compute robust estimates of the covariance between two variables using the robust tau estimate of univariate scale, as proposed by Maronna and Zamar (2002).

**Usage**

```
covrob(t, u)
```

**Arguments**

- `t`: a numeric vector containing the data for the first variable.
- `u`: a numeric vector containing the data for the second variable.

**Details**

This function uses the `scaleTau2` function from the `robustbase` package.
Value

Value of the robust covariance.

Author(s)

Martin Bilodeau (<bilodeau@dms.umontreal.ca>) and Pierre Lafaye de Micheaux (<lafaye@unsw.edu.au>)

References


See Also

corrob, dcov

Examples

data(stackloss)
covrob(stackloss$Air.Flow, stackloss$Water.Temp)

covRob.control

Control Parameters for Robust Covariance Estimation

Description

This function is used to create a list of control parameters for the underlying robust estimator used in the covRob function.

Usage

covRob.control(estim, ...)

Arguments

estim a character vector of length one giving the name of the estimator to generate the control parameters for.

... control parameters appropriate for the robust estimator specified in estim in the form name = value and separated by commas. Omitted parameters receive their default values.

Details

This function was part of the ‘robust’ package and it has been copied to the current package due to an ORPHANED Maintainer.

The control parameters are estimator specific. Information on the control parameters (and their default values) can be found in the help files of each of the robust covariance estimators.
Value

a list of control parameters appropriate for the robust estimator given in estim. The value of estim occupies the first element of the list.

See Also

This function is a utility function for covRob.<br>
The underlying robust estimators are: CovSde, covMcd and CovOgk. Power-users should consider calling these functions directly.

Examples

mcd.control <- covRob.control("mcd", quan = 0.75, ntrial = 1000)

ds.control <- covRob.control("donostah", prob = 0.95)

qc.control <- covRob.control("pairwiseqc")

dcov

Distance covariance matrix.

Description

Compute the distance covariance measure of Szekely, Rizzo, and Bakirov (2007) between two samples. Warning: Only valid to compute the distance covariance for two random variables X and Y. This means that X and Y cannot be random Vectors. If this is the case, consider the package energy.

Usage

dcov(x, y, Cpp = TRUE)

Arguments

x data of first sample
y data of second sample
Cpp logical. If TRUE (the default), computations are performed using a C version of the code.

Details

See energy.

Value

returns the sample distance covariance.
Author(s)

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References

http://dx.doi.org/10.1214/009053607000000505

See Also

covrob, corrob

Examples

data(stackloss)
dcov(stackloss$Air.Flow, stackloss$Water.Temp)

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### groc

#### groc method

**Description**

Generalized regression on orthogonal components.

**Usage**

```r
## Default S3 method:
groc(formula, ncomp, data, subset, na.action, plsrob =
    FALSE, method = c("lm", "lo", "s", "lts"), D = NULL,
    gamma = 0.75, Nc = 10, Ng = 20, scale = FALSE, Cpp =
    TRUE, model = TRUE, x = FALSE, y = FALSE, sp = NULL, ...)

groc(...)
```

**Arguments**

- **formula**: a model formula. Most of the `lm` formula constructs are supported. See below.
- **ncomp**: the number of components (orthogonal components) to include in the model.
- **data**: an optional data frame with the data to fit the model from.
- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.
- **na.action**: a function which indicates what should happen when the data contain missing values.
- **plsrob**: logical. If TRUE, we use the D=covrob measure of dependence with the least trimmed squares method="lts".
method

character giving the name of the method to use. The user can supply his own function. The methods available are linear models, "lm", local polynomials, "lo", smoothing splines, "s", and least trimmed squares, "lts".

D

function with two arguments, each one being a vector, which measures the dependence between two variables using n observations from them. If NULL, the covariance measure will be used. The user can supply his own function.

gamma

parameter used with the option plsrob=TRUE. It defines the quantile used to compute the "lts" regression. The default gamma=0.75 gives a breakdown of 25% for a good compromise between robustness and efficiency. The value gamma=0.5 gives the maximal breakdown of 50%.

Nc

integer, number of cycles in the grid algorithm.

Ng

integer, number of points for the grid in the grid algorithm.

scale

logical, Should we scale the data.

Cpp

logical, if TRUE this function will use a C++ implementation of the grid algorithm. The FALSE value should not be used, unless to get a better understanding of the grid algorithm or to compare the speed of computation between R and C++ versions of this algorithm.

model

a logical. If TRUE, the model frame is returned.

x

a logical. If TRUE, the model matrix is returned.

y

a logical. If TRUE, the response is returned.

sp

A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. 'length(sp)' should be equal to 'ncomp' and corresponds to the number of underlying smoothing parameters.

... further arguments to be passed to or from methods.

Value

Y

vector or matrix of responses.

fitted.values

an array of fitted values.

residuals

residuals

T

a matrix of orthogonal components (scores). Each column corresponds to a component.

R

a matrix of directions (loadings). Each column is a direction used to obtain the corresponding component (scores).

Gobjects

contain the objects produced by the fit of the responses on the orthogonal components.

Hobjects

contain the objects produced by the "lts" fit of each deflated predictors on the orthogonal components. Hobjects are produced when plsrob=TRUE.

B

matrix of coefficients produced by the "lm" fit of each deflated predictors on the last component. B is produced when plsrob=FALSE.
Xmeans a vector of means of the X variables.
Ymeans a vector of means of the Y variables.
D Dependence measure used.
V a matrix whose columns contain the right singular vectors of the data. Computed in the preprocessing to principal component scores when the number of observations is less than the number of predictors.
dnnames dimnames of ‘fitted.values’
ncomp the number of components used in the modelling.
method the method used.
scale Logical. TRUE if the responses have been scaled.
call the function call.
terms the model terms.
plsrob Logical. If plsrob=TRUE, a robust partial least squares fit.
model if model=TRUE, the model frame.

Author(s)
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References

Examples

```r
## Not run:
library(MASS)

# Codes for Example 1
require("groc")
data("wood")
out <- groc(y ~ x1 + x2 + x3 + x4 + x5, ncomp = 1, data = wood,
D = corrob, method = "lts")
corrob(wood$y, fitted(out))^2
plot(out)

# Codes for Example 2
out <- groc(Volume ~ Height + Girth, ncomp = 1, D = spearman,
method = "s", data = trees)
```
cor(trees$Volume, fitted(out))^2
plot(out$T, trees$Volume, xlab = "First component",
     ylab = "Volume", pch = 20)
lines(sort(out$T), fitted(out)[order(out$T)])
out <- boxcox(Volume ~ Height + Girth, data = trees,
        lambda = seq(-0.5, 0.5, length = 100), plotit = FALSE)
lambda <- out$x[which.max(out$y)]
out <- lm(Volume ^ lambda ~ Height + Girth, data = trees)
cor(trees$Volume, fitted(out)^(1/lambda))^2

# Codes for Example 3#

plsr.out <- pls(y ~ x1 + x2 + x3 + x4 + x5, data = wood)
groc.out <- groc(y ~ x1 + x2 + x3 + x4 + x5, data = wood)
apply(abs((fitted(plsr.out) - fitted(groc.out)) /
             fitted(plsr.out)), 3, max) * 100

# Codes for Example 4#

set.seed(1)
n <- 200
x1 <- runif(n, -1, 1)
x2 <- runif(n, -1, 1)
y <- x1 * x2 + rnorm(n, 0, sqrt(.04))
data <- data.frame(x1 = x1, x2 = x2, y = y)
plsr.out <- pls(y ~ x1 + x2, data = data)
groc.out <- groc(y ~ x1 + x2, D = dcov, method = "s", data = data)
plsr.v <- crossval(plsr.out, segment.type = "consecutive")
groc.v <- grocCrossval(groc.out, segment.type = "consecutive")
groc.v$validation$PRESS
plsr.v$validation$PRESS
gam.data <- data.frame(y = y, t1 = groc.out$T[, 1], t2 = groc.out$T[, 2])
gam.out <- gam(y ~ s(t1) + s(t2), data = gam.data)
par(mfrow = c(1, 2))
plot(gam.out)
par(mfrow = c(1, 1))
PRESS <- 0
for(i in 1:10){
    data.in <- data[-(((i - 1) * 20 + 1) : (i * 20)), ]
    data.out <- data[((i - 1) * 20 + 1) : (i * 20), ]
    ppr.out <- ppr(y ~ x1 + x2, nterms = 2, optlevel = 3, data = data.in)
    PRESS <- PRESS + sum((predict(ppr.out, newdata = data.out)-data.out$y)^2)
}
PRESS

# Codes for Example 5#

data("yarn")
dim(yarn$NIR)
n <- nrow(yarn)
system.time(plsr.out <- plsr(density ~ NIR, ncomp = n - 2, data = yarn))
system.time(groc.out <- groc(density ~ NIR, Nc = 20, ncomp = n - 2, data = yarn))
max(abs((fitted(plsr.out) - fitted(groc.out)) / fitted(plsr.out))) * 100
plsr.v$validation$PRESS
groc.v$<-grocCrossval(groc.out, segments = n, trace = FALSE)
groc.v$validation$PRESS
groc.v$validation$PREMAD

############################
# Codes for Example 6      #
############################
data("prim7")
prim7.out <- groc(X1 ~ ., ncomp = 3, D = dcov, method = "s", data = prim7)
prim7.out$R
pca <- princomp(~ ., data = as.data.frame(prim7[, -1]))
prim7.pca <- data.frame(X1 = prim7$X1, scores = pca$scores)
prim7.pca.out <- groc(X1 ~ ., ncomp = 3, D = dcov, method = "s",
data = prim7.pca)
pca$loadings
groc.v$<-grocCrossval(prim7.out, segment.type = "consecutive")
groc.v$validation$PRESS
plsr.out <- plsr(X1 ~ ., ncomp = 3, data = prim7)
plsr.v$<-crossval(plsr.out, segment.type = "consecutive")
plsr.v$validation$PRESS
PRESS <- 0
for(i in 1 : 10){
data.in <- prim7[(-((i - 1) * 50 + 1) : (i * 50)), ]
data.out <- prim7[((i - 1) * 50 + 1) : (i * 50), ]
ppr.out <- ppr(X1 ~ ., nterms = 3, optlevel = 3, data = data.in)
PRESS <- PRESS + sum((predict(ppr.out, newdata = data.out) - data.out$X1) ^ 2)
}
PRESS

############################
# Codes for Example 7      #
############################
n <- 50 ; B <- 30
mat.cor <- matrix(0, nrow = B, ncol = 3) ; mat.time <- matrix(0, nrow = B, ncol = 3)
for (i in 1:B) {
    X <- matrix(runif(n * 5, -1, 1), ncol = 5)
    A <- matrix(runif(n * 50, -1, 1), nrow = 5)
y <- (X[,1] + X[,2])^2 + (X[,1] + 5 * X[,2])^2 + rnorm(n)
    X <- cbind(X, X)
    D <- data.frame(X = X, y = y)
    mat.time[i,1] <- system.time(out1 <- plsr(y ~ X, , ncomp = 2, data = D))[1]
    mat.time[i,2] <- system.time(out2 <- ppr(y ~ X, , nterms = 2, data = D))[1]
    mat.time[i,3] <- system.time(out3 <- groc(y ~ X, D = dcov, method = "s", ncomp = 2, data = D))[1]
    mat.cor[i,1] <- cor(y, fitted(out1)[,,2], fitted(out2), fitted(out3)[,,2])
}
colMeans(mat.cor)
colMeans(mat.time)
# Codes for Example 8

data("oliveoil")
n <- nrow(oliveoil)
plsr.out <- plsr(sensory ~ chemical, data = oliveoil, method = "simpls")
groc.out <- groc(sensory ~ chemical, data = oliveoil)
max(abs((fitted(plsr.out) - fitted(groc.out)) / fitted(plsr.out))) * 100

groc.v <- grocCrossval(groc.out, segments = n)
groc.v$validation$PRESS

colMeans(groc.v$validation$PRESS)
Y <- oliveoil$sensory
for (j in 1:ncol(Y)) print(cor(Y[, j], fitted(groc.out)[, j, 2]))

# Codes for Example 9

require("ppls")
data("cookie")
X <- as.matrix(log(cookie[1:40, 51:651]))
Y <- as.matrix(cookie[1:40, 701:704])
X <- X[, 2:601] - X[, 1:600]
data <- data.frame(Y = I(Y), X = I(X))
n <- nrow(data)
q <- ncol(Y)
xl <- "Wavelength index"
yl <- "First differences of log(1/reflectance)"
matplot(1:ncol(X), t(X), lty = 1, xlab = xl, ylab = yl, type = "l")
out1 <- plsr(Y ~ X, ncomp = n - 2, data = data)
cv <- crossval(out1, segments = n)
cv.mean <- colMeans(cv$validation$PRESS)
plot(cv.mean, xlab = "h", ylab = "Average PRESS", pch = 20)
h <- 3
for (j in 1:q) print(cor(Y[, j], fitted(out1)[, j, h]))
set.seed(1)
out2 <- groc(Y ~ X, ncomp = h, data = data, plsrob = TRUE)
for (j in 1:q) print(corrob(Y[, j], fitted(out2)[, j, h]))
plot(out2)

# Codes for Example 10

set.seed(2)
n <- 30
t1 <- sort(runif(n, -1, 1))
y <- t1 + rnorm(n, mean = 0, sd = .05)
y[c(14, 15, 16)] <- y[c(14, 15, 16)] + .5
data <- data.frame(x1 = t1, x2 = 2 * t1, x3 = -1.5 * t1, y = y)
out <- groc(y ~ x1 + x2 + x3, ncomp = 1, data = data, plsrob = TRUE)
tau <- scaleTau2(residuals(out), mu.too = TRUE)
std.res <- scale(residuals(out), center = tau[1], scale = tau[2])
index <- which(abs(std.res) > 3)
groc.fit <- read.table("prmresid.txt")
plot(t1, y, pch = 20)
matlines(t1, cbind(t1, fitted(out), y - prm.res), lty = 1 : 3)
legend(.4, -.5, legend = c("true model", "groc", "prm"), lty = 1 : 3)
text(t1[index], y[index], index, cex = .8, pos = 3)

# Codes for Example 11 #

data("pulpfiber")
X <- as.matrix(pulpfiber[, 1:4])
Y <- as.matrix(pulpfiber[, 5:8])
data <- data.frame(X = I(X), Y = I(Y))
set.seed(55481)
out.rob <- groc(Y ~ X, data = data, plsrob = TRUE)
plot(out.rob, cex = .6)
out.simpls <- groc(Y ~ X, data = data)
cv.rob <- grocCrossval(out.rob, segment.type = "consecutive")
PREMAD.rob <- cv.rob$validation$PREMAD[, 4]
PREMAD.rob
PREMAD.simpls <- cv.rob$validation$PREMAD[, 4]
PREMAD.simpls
(PREMAD.rob - PREMAD.simpls) / PREMAD.simpls * 100

## End(Not run)

groc.fit

Fitting a groc model

Description

Fits a groc model with the grid algorithm.

Usage

groc.fit(X, Y, ncomp = min(nrow(X) - 1, ncol(X)), D = NULL, gamma = 0.75, method = NULL, plsrob = FALSE, Nc = 10, Ng = 20, scale = FALSE, Cpp = TRUE, stripped = FALSE, maxiter = 100, sp = NULL, ...)

Arguments

X 
a matrix of predictors. NAs and Infs are not allowed.
Y 
a vector or matrix of responses. NAs and Infs are not allowed.
ncomp 
the number of components to be used in the modelling.
D 
Dependence measure.
**gamma**

Used to set the breakdown value when `method="lts"`.

**method**

the method to be used. Currently only 'lm', 'lo', 'l', and 'lts'.

**plsrob**

Logical. If `TRUE`, the function sets `D=covrov` and `method="lts"` for a robust partial least squares fit.

**Nc**

Integer. Number of cycles in the grid algorithm

**Ng**

Integer. Number of points for the grid in the grid algorithm.

**scale**

Logical. If `TRUE` the responses are scaled.

**Cpp**

Logical. If `TRUE`, computations are performed in a faster way using a C code.

**stripped**

logical. If `TRUE` the calculations are stripped as much as possible for speed; this is meant for use with cross-validation or simulations when only the coefficients are needed. Defaults to `FALSE`.

**maxiter**

Integer. Maximal number of iterations in the grid algorithm. Used only when there are more than one response.

**sp**

A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. `length(sp)` should be equal to `ncomp` and corresponds to the number of underlying smoothing parameters.

... other arguments. Currently ignored.

**Value**

**Y**

data used as response.

**fitted.values**

an array of fitted values. Its element `[i,j,k]` is the fitted value for observation `i`, response `j`, and when `k` components are used.

**residuals**

an array of regression residuals. It has the same dimensions as `fitted.values`.

**T**

a matrix of orthogonal components (scores). Each column corresponds to a component.

**R**

a matrix of directions (loadings). Each column is a direction used to obtain the corresponding component (scores).

**Gobjects**

contain the objects produced by the fit of the responses on the orthogonal components.

**Hobjects**

contain the objects produced by the "lts" fit of each deflated predictors on the orthogonal components. **Hobjects** are produced when `plsrob=TRUE`.

**B**

matrix of coefficients produced by the "lm" fit of each deflated predictors on the last component. **B** is produced when `plsrob=FALSE`.

**Xmeans**

a vector of means of the X variables.

**Ymeans**

a vector of means of the Y variables.

**D**

Dependence measure used.

**V**

a matrix whose columns contain the right singular vectors of the data. Computed in the preprocessing to principal component scores when the number of observations is less than the number of predictors.

**dnnames**

dimnames of `fitted.values`
Author(s)

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References


grocCrossval

Cross-validation of groc models

Description

A “stand alone” cross-validation function for groc objects.

Usage

grocCrossval(object, segments = 10, segment.type = c("random", "consecutive","interleaved"), length.seg, trace = 15, ...)

Arguments

- object: a groc object; the regression to cross-validate.
- segments: the number of segments to use, or a list with segments (see below).
- segment.type: the type of segments to use.
- length.seg: Positive integer. The length of the segments to use.
- trace: if TRUE, tracing is turned on. If numeric, it denotes a time limit (in seconds). If the estimated total time of the cross-validation exceeds this limit, tracing is turned on.
- ...: additional arguments, sent to the underlying fit function.

Details

This function performs cross-validation on a model fit by groc. It can handle models such as groc(Y ~ X,...).

Note that to use grocCrossval, the data must be specified with a data argument when fitting object.

If segments is a list, the arguments segment.type and length.seg are ignored. The elements of the list should be integer vectors specifying the indices of the segments.

Otherwise, segments of type segment.type are generated. How many segments to generate is selected by specifying the number of segments in segments, or giving the segment length in length.seg. If both are specified, segments is ignored.

When tracing is turned on, the segment number is printed for each segment.
Value

The supplied object is returned, with an additional component validation, which is a list with components

- **method**: equals "CV" for cross-validation.
- **pred**: an array with the cross-validated predictions.
- **PRESS**: a matrix of PRESS values for models with 1, \ldots, ncomp components. Each row corresponds to one response variable.
- **PREMAD**: a matrix of PREMAD values for models with 1, \ldots, ncomp components. Each row corresponds to one response variable.
- **RMSEP**: a matrix of sqrt(PRESS/nobj) values for models with 1, \ldots, ncomp components. Each row corresponds to one response variable.
- **segments**: the list of segments used in the cross-validation.
- **ncomp**: the number of components.

Author(s)

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References


Examples

data(yarn, package = "pls")
yarn.groc <- groc(density ~ NIR, 6, data = yarn)
yarn.cv <- grocCrossval(yarn.groc, segments = 10)

yarn.cv$validation$PRESS
yarn.cv$validation$PREMAD

Description

Functions to extract information from groc objects: the model frame, the model matrix.

Usage

```r
## S3 method for class 'groc'
model.frame(object, ...)
## S3 method for class 'groc'
model.matrix(object, ...)
```
plot.groc

Arguments

object, formula

A groc object. The fitted model.

... other arguments sent to underlying functions.

Details

model.frame.groc returns the model frame; i.e., a data frame with all variables necessary to generate the model matrix. See model.frame for details.

model.matrix.groc returns the (possibly coded) matrix used as $X$ in the fitting. See model.matrix for details.

Value

model.frame.groc returns a data frame with all variables necessary to generate the model matrix.

model.matrix.groc returns the $X$ matrix.

Author(s)

Ron Wehrens and Bjørn-Helge Mevik

See Also

coe, fitted, residuals, model.frame

Description

A function to plot groc objects.

Usage

## S3 method for class 'groc'
plot(x, h=x$ncomp, cex=0.8, ...)

Arguments

x A groc object.

h Number of components in the model.

cex Character expansion factor for point labels.

... Further arguments passed to internal plot function.
Details

If plsrob=FALSE, a plot of robust Mahalanobis distances for residuals versus robust Mahalanobis distances for components. Useful for identification of good points, vertical outliers, good and bad leverage points.

If plsrob=TRUE, the previous plot is done with another similar plot of classical Mahalanobis distances to compare the identification of the various type of points obtained by classical or robust partial least squares.

Author(s)

Martin Bilodeau (<bilodeau@dms.umontreal.ca>) and Pierre Lafaye de Micheaux (<lafaye@unsw.edu.au>)

References


Examples

```r
## This example takes some time:
## Not run:
data("pulpfiber", package="robustbase")
X <- as.matrix(pulpfiber[, 1:4])
Y <- as.matrix(pulpfiber[, 5:8])
data <- data.frame(X=I(X), Y=I(Y))
set.seed(55481)
out.rob <- groc(Y ~ X, data=data, plsrob=TRUE)
plot(out.rob, cex=.6)
## End(Not run)
```

---

**predict.groc**

**Predict Method for groc**

Description

Prediction for groc models. New responses or scores are predicted using a fitted model and a new matrix of observations.

Usage

```r
## S3 method for class 'groc'
predict(object, newdata, ncomp = object$ncomp, na.action = na.pass, ...)
```
Arguments

object
newdata
ncomp
na.action
...

Value

A three dimensional array of predicted response values is returned. The dimensions correspond to the observations, the response variables and the model sizes, respectively.

Author(s)

Martin Bilodeau (<bilodeau@dms.umontreal.ca>) and Pierre Lafaye de Micheaux (<lafaye@unsw.edu.au>)

References


See Also

plot.groc

Examples

data("wood", package="robustbase")
out <- groc(y ~ x1+x2+x3*x4+x5, ncomp=1, data=wood, D=corrob, method="lts")
predict(out)

newdata<- data.frame(x1= 0.5, x2=0.1, x3=0.4, x4=0.5, x5=0.8)
predict(out,newdata)

prim7 Dataset

Description

The data prim7 is a particle physics experiment analyzed by projection pursuit regression in Friedman and Stuetzle (1981). It has 7 variables on 500 observations. The data set is described in Friedman and Tukey (1974).
**Format**

This data frame contains the following columns:

- **X1** First variable.
- **X2** Second variable.
- **X3** Third variable.
- **X4** Fourth variable.
- **X5** Fifth variable.
- **X6** Sixth variable.
- **X7** Seventh variable.

**References**


**Examples**

```r
data(prim7)
```

---

**summary.groc**  
*Summary and Print Methods for groc objects*

**Description**

Summary and print methods for groc objects.

**Usage**

```r
## S3 method for class 'groc'
summary(object, what = "validation",
         digits = 4, print.gap = 2, ...)
## S3 method for class 'groc'
print(x, ...)
```

**Arguments**

- **x, object**  
a groc object
- **what**  
character, only "validation" for the moment
- **digits**  
integer. Minimum number of significant digits in the output. Default is 4.
- **print.gap**  
Integer. Gap between columns of the printed tables.
- **...**  
Other arguments sent to underlying methods.
Details

If what is "validation", the cross-validated PRESS, RPEMAD and RMSEPs (if available) are given.

Value

print.groc return the object invisibly.

Author(s)

P. Lafaye de Micheaux

References


See Also

groc, grocCrossval

Examples

data("yarn", package="pls")
yarn.groc <- groc(density ~ NIR, 6, data = yarn)
yarn.cv <- grocCrossval(yarn.groc, segments = 10)
print(yarn.groc)
summary(yarn.cv)
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