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grt-package General Recognition Theory

description

Functions to generate and analyze data for psychology experiments based on the General Recognition Theory.

details

This package is written based mostly on the GRT Toolbox for MATLAB by Alfonso-Reese (2006), although many functions have been renamed and modified from the original in order to make them more general and “R-like.”

The functions grtmnorm and grtMeans are used for design categorization experiments and generating stimuli. The functions glc, gcjc, gqc, and grg are used for fitting the general linear classifier, the general conjunctive classifier, the general quadratic classifier, and the general random guessing model, respectively. The glc, gcjc, and gqc have plot methods (plot.glc, plot.gcjc, plot.gqc. plot3d.glc, plot3d.gqc).

For a complete list of functions, use library(help = "catlearn").
\textit{coef.glc}  

\textbf{Author(s)}  
Kazunaga Matsuki  
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\textbf{References}  

---  

\textit{coef.glc} \hspace{1cm} \textit{Extract 'glc' or 'gcjc' coefficients}  

\textbf{Description}  
Extracts the coefficients from the model object \texttt{glc}, \texttt{glcStruct}, or \texttt{gcjc}.  

\textbf{Usage}  
\begin{verbatim}  
## S3 method for class 'glc'
coef(object, ...)
## S3 method for class 'glcStruct'
coef(object, ...)
## S3 method for class 'gcjc'
coef(object, ...)
\end{verbatim}  

\textbf{Arguments}  
\begin{itemize}  
\item \texttt{object} \hspace{1cm} object of class \texttt{glc} or \texttt{glcStruct}
\item \texttt{...} \hspace{1cm} further arguments
\end{itemize}  

\textbf{Details}  
Both the object \texttt{glc} and \texttt{glcStruct} contain the parameters for the decision boundary in the form:  
\[ a_1x_1 + a_2x_2 \ldots a_nx_n + b = 0 \]  
This function transforms and returns the coefficients of the function solved with respect the \textit{x}_n.  
For the object \texttt{gcjc}, a list of two coefficients (Intercepts) are returned.
Examples

data(subjdemo_2d)
fit.2dl <- glc(response ~ x + y, data=subjdemo_2d,  
category=subjdemo_2d$category, zlimit=7)
plot(fit.2dl, fitdb=FALSE)
abline(coef(fit.2dl), col = "red")
abline(coef(fit.2dl$initpar))

fit.1dx <- update(fit.2dl, . ~ . - y)
abline(v=coef(fit.1dx), col="green")

fit.1dy <- update(fit.2dl, . ~ . - x)
abline(h=coef(fit.1dy), col="blue")

dprime

Calculate d’ (d-prime)

Description

Obtain the standardized distance between the two probability distributions, known as d’ or sensitivity index.

Usage

dprime(x,  
category,  
response,  
par = list(),  
zlimit = Inf,  
type = c("SampleIdeal", "Observer"))
dprimef(means, covs, noise=NULL)

Arguments

x a data frame or matrix containing samples from two multivariate normal distributions.
category a vector or factor of labels of populations to which the samples belong
response a vector or factor specifying the participant’s classification responses for each samples
par object of class glcStruct or a named list containing a set of parameters that specify a general linear decision bound. The list should contain noise, coeffs, bias.
zlimit numeric. The z-scores (or discriminant scores) beyond the specified value will be truncated and replaced with that value. Default to Inf
type a character string specifying the type of d' to be returned. If SampleIdeal, d' is calculated based on ideal (or true) category membership as specified in category. If Observer, d' is calculated using the response vector as a grouping factor.

means a list of numeric vectors containing the means of two distributions

covs a matrix or a list of matrices containing the variance-covariance matrix of the two distributions

noise numeric, perceptual and criterial noise expressed as standard deviation. Default to NULL

Details

The function dprime estimates d' from sample data sets, whereas the function dprimef calculates it from population parameters.

In dprime, if any parts of the argument par are missing, the function will estimate an optimal linear decision bound from supplied x and category. The argument response is not used if type is SampleIdeal.

Author(s)

Author of the original Matlab routines: Leola Alfonso-Reese

Author of R adaptation: Kazunaga Matsuki

References


Examples

data(subjdemo_2d)
d2 <- subjdemo_2d

db <- glcStruct(noise=10, coeff=c(0.514,-0.857),bias=-0.000154)
dprime(d2[,2:3], d2$category, d2$response, par = db, zlimit=7, type='SampleIdeal')

mc <- mcovs(category ~ x + y, data=d2)
dprimef(mc$means, mc$covs)

extractAIC

extractAIC method for class 'gle', 'gqe', 'gejc', and 'grg'

Description

Extract Akaike’s An Information Criteria from a General Linear, Quadratic, or Conjunctive Classifier, or a General Random Guessing model
Usage

```r
## S3 method for class 'glc'
extractAIC(fit, scale, k = 2, ...)

## S3 method for class 'gqc'
extractAIC(fit, scale, k = 2, ...)

## S3 method for class 'gcjc'
extractAIC(fit, scale, k = 2, ...)

## S3 method for class 'grg'
extractAIC(fit, scale, k = 2, ...)
```

Arguments

- `fit` object of class `glc`, `gqc`, `gcjc`, or `grg`
- `scale` unused argument
- `k` numeric specifying the penalty per parameter to be used in calculating AIC. Default to 2.
- `...` further arguments (currently not used).

Details

As with the default method, the criterion used is

\[
AIC = -2 \log L + k \times df,
\]

where \( L \) is the likelihood and \( df \) is the degrees of freedom (i.e., the number of free parameters) of `fit`.

Value

A numeric vector of length 2 including:

- `df` the degrees of freedom for the fitted model `fit`.
- `aic` the Akaike's Information Criterion for `fit`.

Examples

```r
data(subjdemo_2d)
# fit a 2d suboptimal model
fit.2d1 <- glc(response ~ x + y, data=subjdemo_2d,
               category=subjdemo_2d$category, zlimit=7)
extractAIC(fit.2d1)
```
gaborPatch

**gaborPatch**  
*Draw a gray-scale Gabor Patch*

**Description**

Draw a gray-scale Gabor Patch

**Usage**

```r
gaborPatch(sf,
theta = 0,
rad = (theta * pi)/180,
pc = 1,
sigma = 1/6,
 psi = 0,
grating = c("cosine", "sine"),
npoints = 100,
trim = 0,
trim.col = .5,
...)
```

**Arguments**

- `sf` number of cycles per image.
- `theta` orientation in degree. See ‘Details’
- `rad` orientation in radian
- `pc` a fraction (0 to 1) specifying the peak contrast of the Gabor
- `sigma` the standard deviation of the Gaussian mask. Either a single numeric or a numeric vector of length 2.
- `psi` phase offset in radian
- `grating` type of grating to be used. Default to ‘cosine’.
- `npoints` number of points per line used to draw the patch.
- `trim` Gaussian values smaller than the specified value should be trimmed.
- `trim.col` gray level of the trimmed part of the image, between 0 (‘black’) and 1 (‘white’). Default to .5 (‘gray’) Setting it to any other value or NA makes the trimmed part transparent.
- `...` additional parameters for *image* may be passed as arguments to this function.

**Details**

The arguments `theta` and `rad` is the same thing but in different units. If both are supplied, `rad` takes the precedence.
Value

invisibly returns the matrix of the plotted values.

Note

This function is written just for fun; it is not optimized for speed or for performance.

References


Examples

# An imitation of Fredericksen et al.'s (1997) Fig 1.
# that demonstrate the relation between peak contrast
# and perceived size of the Gabor

op <- par(mfcol = c(3, 3), pty = "m", mai = c(0,0,0,0))
for(i in c(.85, .21, .06)){
  for(j in c(1/6, 1/7, 1/8)){
    gaborPatch(20, pc = i, sigma = j)
  }
}
par(op)

## Not run:
# a typical plot of the stimuli and category structure
# often seen in artificial category-learning literatures.
m <- list(c(268, 157), c(332, 93))
covs <- matrix(c(4538, 4351, 4351, 4538), ncol = 2)
II <- grtrnorm(n = 40, np = 2, means = m, covs = covs,
    clip.sd = 4, seed = 1234)
II$sf <- .25*II$x1/50
II$theta <- 11$x2*(18/50)

plot(II[,2:3], xlim = c(-100,600), ylim = c(-200,500),
    pch = 21, bg = c("white","gray") II$category)
abline(a = -175, b = 1)

library(Hmisc)
idx <- c(20, 31, 45, 49, 62)
xpos <- c(0, 100, 300, 420, 550)
ypos <- c(50, 300, 420, -120, 50)
for(i in 1:5){
  j = idx[i]
  segments(x0=II[j,"x1"], y0=II[i,"x2"], x1=xpos[i], y1=ypos[i])
  subplot(gaborPatch(sf=II[j,"sf"], theta=II[j,"theta"]), x=xpos[i], y=ypos[i])
gcjc

General Conjunctive Classifier

Description

Fit a general conjunctive classifier.

Usage

gcjc(formula, data, category, par, config = 1, zlimit = Inf,
   fixed = list(), equal.noise = TRUE, opt = c("nlminb", "optim"),
   lower=Inf, upper=Inf, control=list())

Arguments

  formula  A formula of the form response ~ x1 + x2 + ..., where the response
           specifies the grouping factor (generally a participant’s response) and
           the right hand side specifies the relevant dimensions or features
           of the stimuli.
  data     A data frame from which variables specified in formula are taken.
  category (Optional.) A factor specifying the true category membership
           of the stimuli.
  par      object of class gcjcStruct or a named list containing a set of
           initial parameters - that is, noise and bias (intercepts).
  config   A numeric value specifying the location of the conjunctive category
           in relation to the category bounds. The value 1 indicates the category
           is on the top right (set as default), 2 indicates the top left, 3
           indicates bottom left, and 4 indicates the bottom right.
  zlimit   numeric. The z-scores (or discriminant scores) beyond the specified
           value will be truncated. Default to Inf.
  fixed    A named list of logical vectors specifying whether each of noise
           and bias parameters should be fixed to the initial value. Default to
           list(noise=c(FALSE, TRUE), bias=FALSE). A fatal error will be
           returned if set to all TRUE.
  equal.noise logical. If set to TRUE (default), two bounds will have the
                   same noise parameter.
  opt      A character string specifying the optimizer to be used: either
           nlminb (the default) or optim. If “optim”, “L-BFGS-B” method is
           used (see ‘Details’ of optim).
  lower, upper Bounds on the parameters. see ‘Details’ for default values.
  control  A list of control parameters passed to the internal optimization
           function. See ‘Details’ of nlminb or optim.
Details

If par is not fully specified in the argument, the function attempts to calculate the initial parameter values based on means by category or by response.

The default lower and upper values are selected based on the range of the data input so that the decision bound is found within the range of the data and convergence can be reached.

Value

object of the class gcjc, i.e., a list containing the following components:

- terms: the terms object used.
- call: the matched call.
- model: the design matrix used to fit the model.
- category: the category vector as specified in the input.
- initpar: the initial parameter used to fit the model.
- par: the fitted parameter.
- logLik: the log-likelihood at convergence.

References


See Also
glc, logLik.gcjc, coef.gcjc, plot.gcjc

Examples

data(subjdemo_cj)

m.cj <- gcjc(response ~ x1 + x2, data=subjdemo_cj, config=2, category=subjdemo_cj$category, zlimit=7)
Arguments

- **noise**: a positive non-zero numeric.
- **bias**: numeric vector corresponding to the intercepts of the bounds.
- **config**: A numeric value specifying the location of the conjunctive category in relation to the category bounds. The value 1 indicates the category is on the top right (set as default), 2 indicates the top left, 3 indicates bottom left, and 4 indicates the bottom right.

Value

object of class `gcjcStruct`, which is a list of a named list containing `noise`, `coeffs`, and `bias`.

See Also

`gcjc`, `coef.glcStruct`, `logLik.glcStruct`

Examples

```r
cparams <- gcjcStruct(noise=10, bias=c(100, 200), config=1)
```

---

### Description

Fit a general linear classifier (a.k.a. linear decision-bound model).

### Usage

```r
glc(formula, data, category, par = list(), zlimit = Inf, covstruct=c("unstructured", "scaledIdentity", "diagonal", "identity"), fixed = list(), opt = c("nlminb", "optim"), lower=Inf, upper=Inf, control=list())
```

### Arguments

- **formula**: A formula of the form `response ~ x1 + x2 + ...`, where the response specifies the grouping factor (generally a participant’s response) and the right hand side specifies the relevant dimensions or features of the stimuli.
- **data**: A data frame from which variables specified in `formula` are taken.
- **category**: (Optional.) A factor specifying the true category membership of the stimuli.
- **par**: object of class `glcStruct` or named list containing a set of initial parameters (i.e., `noise`, `coeffs`, `bias`) used to fit the data.
- **zlimit**: numeric. The z-scores (or discriminant scores) beyond the specified value will be truncated. Default to `Inf`.
covstruct  An optional character string. Only used when the initial parameters are not fully specified. See `ldb`.

fixed  A named list of logical vectors specifying whether each of noise, coeffs, and bias parameters should be fixed to the initial value. Default to `list(noise=FALSE, coeffs=FALSE, bias=FALSE)`. A fatal error will be returned if set to all `TRUE`.

opt  A character string specifying the optimizer to be used: either `nlminb` (the default) or `optim`. If “optim”, “L-BFGS-B” method is used (see ‘Details’ of `optim`).

lower, upper  Bounds on the parameters. See ‘Details’ for default values.

control  A list of control parameters passed to the internal optimization function. See ‘Details’ of `nlminb` or `optim`.

Details

If `par` is not fully specified in the argument, the function attempts to calculate the initial parameter values by internally calling the functions `mcovs` and `ldb`. If category is also not specified, the response specified in the `formula` is used as the grouping factor in `mcovs`.

The default lower and upper values vary depending on the dimension of the model (i.e., the number of variables in the right hand side of `formula`). In all cases, default lower and upper values for the `noise` parameter is .001 and 500 respectively. In cases when an one-dimensional model is fitted, lower and upper bounds for the `bias` parameters are selected based on the range of the data input so that the decision bound is found within the reasonable range of the data and convergence can be reached. In all other cases, `coeffs` and `bias` has no limits.

When an one-dimensional model is being fit, `fixed$coeffs` always becomes `TRUE`.

Value

object of the class `glc`, i.e., a list containing the following components:

terms  the `terms` object used.
call  the matched call.
model  the design matrix used to fit the model.
category  the category vector as specified in the input.
initpar  the initial parameter used to fit the model.
par  the fitted parameter.
logLik  the log-likelihood at convergence.

References


glcStruct

General Linear Classifier structure

Description
A named list of model parameters that specify a linear decision bound, containing noise, coeffs, and bias.

Usage

```r
glcStruct(noise, coeffs, bias)
```

Arguments

- **noise**: a positive non-zero numeric.
- **coeffs**: vector. the length of the coeffs should correspond to the number of the model’s dimension.
- **bias**: numeric.

Value

object of class glcStruct, i.e., a named list containing noise, coeffs, and bias. Returned values are normalized, such that each value are divided by the euclidean norm of the coeffs vector, and the sum of coeffs^2 is 1.

See Also

- `gqc`, `ldb`, `logLik.glc`, `coef.glc`, `predict.glc`, `scale.glc`, `plot.glc`, `plot3d.glc`
Examples

```r
gqc <- glcStruct(noise=10, coeffs=c(1, -1), bias=0)
```

---

**gqc**

### General Quadratic Classifier

**Description**

Fit a general quadratic classifier (a.k.a. quadratic decision-bound model).

**Usage**

```r
gqc(formula, data, category, par = list(), zlimit = Inf, fixed = list(), opt = c("nlminb", "optim"), lower=Inf, upper=Inf, control=list())
```

**Arguments**

- **formula**: A formula of the form `response ~ x1 + x2 + ...` where the response specifies the grouping factor (generally a participant’s response) and the right hand side specifies the feature values of the classified stimuli.
- **data**: A data frame from which variables specified in `formula` are taken.
- **category**: (Optional.) A factor specifying the true category membership of the stimuli.
- **par**: object of class `gqcStruct` or named list containing a set of initial parameters used to fit the data.
- **zlimit**: numeric. The z-scores (or discriminant scores) beyond the specified value will be truncated. Default to Inf
- **fixed**: A named list of logical vectors specifying whether each of `pnoise`, `cnoise`, `coeffs`, and `bias` parameters should be fixed to the initial value. Default to all FALSE. A fatal error will result if set to all TRUE.
- **opt**: A character string specifying the optimizer to be used: either `nlminb` (the default) or `optim`. If "optim", "L-BFGS-B" method is used (see ‘Details’ of `optim`)
- **lower, upper**: Bounds on the parameters. Default values of lower and upper are `c(.1, .1, rep(-Inf, length(unlist(par))), and `c(5000, 5000, rep( Inf, length(unlist(par)))-2))`, respectively.
- **control**: A list of control parameters passed to the optimizer. See ‘Details’ of `nlminb` or `optim`
Details

If `par` is not fully specified in the argument, the function attempts to calculate the initial parameter values by internally calling the functions `mcovs` and `qdb`. The response specified in the formula is used as the grouping factor in `mcovs`.

Value

object of class `gqc`, i.e., a list containing the following components:

- `terms` the `terms` object used.
- `call` the matched call.
- `model` the design matrix used to fit the model.
- `category` the category vector as specified in the input.
- `initpar` the initial parameter used to fit the model.
- `par` the fitted parameter.
- `logLik` the log-likelihood at convergence.

References


See Also

`glc`, `qdb`, `logLik.gqc`, `logLik.gqcStruct`, `plot.gqc`, `plot3d.gqc`

Examples

data(subjdemo_2d)
fit.2dq <- gqc(response ~ x + y, data=subjdemo_2d, category=subjdemo_2d$category, zlimit=7)
**gqcStruct**

*General Quadratic Classifier structure.*

**Description**

A named list of model parameters that specify a quadratic decision bound, containing `pnoise`, `cnoise`, `coeffs`, and `bias`.

**Usage**

```r
gqcStruct(pnoise, cnoise, coeffs, bias)
```

**Arguments**

- `pnoise` a positive non-zero numeric.
- `cnoise` a positive non-zero numeric.
- `coeffs` a vector. The length(coefs) should be equal to `sum(1:(dim+1)) - 1` where `dim` is the number of the model's dimension
- `bias` numeric.

**Value**

object of class `gqcStruct`, i.e., a named list containing `pnoise`, `cnoise`, `coeffs`, and `bias`.

**See Also**

- `gqc`, `logLik.gqcStruct`

**Examples**

```r
params <- gqcStruct(pnoise=10, cnoise=100, coeffs=c(1,2,3,4,5), bias=6)
```

---

**grg**

*General Random Guessing model*

**Description**

General Random Guessing model

**Usage**

```r
grg(response, fixed = FALSE, k = 2)
```
Arguments

- **response**: A vector containing participant’s classification responses.
- **fixed**: logical. If TRUE, Fixed Random Guessing model is fitted. If FALSE, General Random Guessing model is fitted. see ‘Details’
- **k**: numeric. the penalty per parameter to be used in calculating AIC. Default to 2.

Details

The function assumes that there are two categories (e.g, ‘A’ and ‘B’) to which each stimulus belongs.

Fixed Random Guessing model assumes that participant responded randomly without response bias; for each stimulus, probability of responding ‘A’ and ‘B’ is .5. There are no free parameters in this model (i.e., df = 0).

General Random Guessing model assumes that participants responded randomly but is biased toward one response. The model estimates the response bias (df = 1).

Value

object of class `grg`, which is a list object containing:

- **par**: the fixed or estimated response bias
- **logLik**: the log-likelihood of the model
- **AIC**: Akaike’s An Information Criterion for the fitted model

References


See Also

- `glc`, `gqc`, `extractAIC.grg`

Examples

```r
data(subjdemo_2d)
fit.grand <- grg(subjdemo_2d$response, fixed=FALSE)

fit.frand <- grg(subjdemo_2d$response, fixed=TRUE)
```
grtMeans

Obtain means of two multivariate normal populations satisfying certain criteria

Description

Obtain means of two multivariate normal populations having the specified covariance structure and centroid, and with which classification based on the optimal decision boundary satisfies the supplied probability of correct classification.

Usage

grtMeans(covs, centroid, optldb, p.correct, initd = 5, stepsize = 1)

Arguments

covs a matrix or a list of matrices specifying the covariance matrices of the variables. Each matrix should be positive-definite and symmetric.

centroid a vector specifying the center of the two population means

optldb object of class glcStruct or a vector of coefficients for the optimal linear decision bound.

p.correct a numeric value between 0 to 1 that specifies the optimal classification performance in terms of probability of correct classification given the decision boundary optbnd.

initd numeric. An initial distance between the means of two populations. Default is 5.

stepsize a positive numeric specifying step size to be taken when searching for the means. Default is 1.

Value

means a list of two vectors specifying the means of two populations.

covs a matrix of (averaged) covariance.

p.correct the obtained probability of correct classification.

Author(s)

Author of the original Matlab routine ‘Design2dGRTexp’: Leola Alfonso-Reese

Author of R adaptation: Kazunaga Matsuki

References

See Also

```
ldb.p.correct
```

Examples

```
foo <- grtMeans(diag(c(625,625)), centroid=c(200, 200*.6),
               optldb=c(.6,-1,0), p.correct=.85)
```

---

**grtrnorm**  
*Sample from multiple multivariate normal distributions*

Description

Generate one or more samples from the two or more specified multivariate normal distributions.

Usage

```
grtrnorm(n, 
           np = 2, 
           means = list(rep(0,np), rep(0,np)), 
           covs = diag(rep(1,np)), 
           clip.sd = Inf, 
           tol = 1e-6, 
           empirical = TRUE, 
           seed = NULL, 
           response.acc = NULL)
```

Arguments

- **n** - the number of samples per population required
- **np** - the number of populations to be sampled from
- **means** - a list of vectors specifying the means of the variable for each populations
- **covs** - a matrix or a list of matrices specifying the covariance matrices of the variables. Each matrix should be positive-definite and symmetric.
- **clip.sd** - an integer specifying the cutoff value of standard score. The standard score of a generated sample exceeding this value should be truncated. Default to Inf (no truncation).
- **tol** - tolerance (relative to largest variance) for numerical lack of positive-definiteness in covs.
- **empirical** - logical. If true, means and covs specify the empirical rather than population means and covariance matrices.
- **seed** - an integer internally supplied as seed argument to the function `set.seed`. If NULL, `.Random.seed` is used.
- **response.acc** - an optional numeric value between 0 and 1, specifying the classification accuracy of a hypothetical observer. See ‘Details’. Default to NULL.
Details

This function is essentially a wrapper to the `mvrnorm` function in MASS package.

If the optional `response.acc` argument is supplied, hypothetical random classification responses with specified accuracy will be generated.

Value

a data frame containing a column of numeric category labels and column(s) of sampled values for each variable, and optionally, a column of hypothetical responses.

Author(s)

Author of the original Matlab routines: Leola Alfonso-Reese

Author of R adaptation: Kazunaga Matsuki

References


Examples

```r
m <- list(c(268,157), c(332, 93))
covs <- matrix(c(4538, 4351, 4351, 4538), ncol=2)
ll <- grtrnorm(n=80, np=2, means=m, covs=covs)

m <- list(c(283,98),c(317,98),c(283,152),c(317,152))
covs <- diag(75, ncol=2, nrow=2)
cj <- grtrnorm(n=c(8,16,16,40), np=4, means=m, covs=covs)
cj$category <- c(1,1,1,2)[cj$category]
```

Description

Find coefficients of the ideal linear decision boundary given the means and covariance of two categories.

Usage

```r
ldb(means, covs, 
  covstruct = c("unstructured", "scaledIdentity", "diagonal", "identity"), 
  noise = 10)
```
Arguments

- **means**: a list of vectors containing means of two distributions.
- **covs**: a matrix or a list of matrix containing the covariance matrix common to the two distributions.
- **covstruct**: character. If "unstructured", the supplied covs is used as-is. If "scaledIdentity", a diagonal covariance matrix with one common variance is used; when the supplied covs has different values on its diagonal, the mean of the diagonal is used. If "diagonal", a diagonal covariance matrix with varying diagonal is used. If "identity", an identity matrix is used. Default to "unstructured"
- **noise**: numeric value. See Details. Default to 10.

Details

The order of vectors in the list means matters as the sign of coeffs and bias in the output will be reversed.

The argument noise is only for convenience; the supplied value is simply bypassed to the output for the subsequent use, i.e., as object of class glcStruct.

Value

The object of class glcStruct

Author(s)

Author of the original Matlab routine ‘lindecisbnd’: Leola Alfonso-Reese
Author of R adaptation: Kazunaga Matsuki

References


See Also

mcovs, qdb, glcStruct, glc

Examples

```r
m <- list(c(187, 142), c(213.4, 97.7))
covs <- diag(c(625, 625))
foo <- ldb(means=m, covs=covs)
```
ldb.p.correct

**Probability of correct classification based on the optimal linear decision bound.**

**Description**

Estimates the probability of correct classification under the condition in which the optimal linear decision boundary is used to categorize the samples from two multivariate normal populations with the specified parameters.

**Usage**

\[
\text{ldb.p.correct}(\text{means}, \text{covs}, \text{noise} = 0)
\]

**Arguments**

- **means**: a list of vectors, each specifying the means of a multivariate normal population.
- **covs**: a matrix or a list of matrices specifying the covariance matrix of each multivariate normal population. If a list is given and \(\text{length(covs)} > 2\), an unweighted average of the matrices is used.
- **noise**: an optional numeric value specifying the noise associated with the decision bound. Default to 0.

**Author(s)**

Author of the original Matlab routine ‘linprobcorr’: Leola Alfonso-Reese

Author of R adaptation: Kazunaga Matsuki

**References**


**Examples**

```r
foo <- grtMeans(diag(c(625,625)), centroid=c(200, 200*.6), optldb=c(.6,-1,0), p.correct=.85)
ldb.p.correct(foo$means, foo$covs)
```
Description

Add a quadratic decision boundary line through the current plot.

Usage

```r
## S3 method for class 'gqcStruct'
lines(x,
    xlim = c(0,1), ylim = c(0,1),
    npoints = 100, col = "black",
    ...)  
```

Arguments

- `x`: object of class `gqcStruct`
- `xlim`: the x limits of the plot. Default to `c(0,1)`
- `ylim`: the y limits of the plot. Default to `c(0,1)`
- `npoints`: numeric. number of points per dimension used to plot the decision bound. Default is 100.
- `col`: the color to be used for the line
- `...`: further arguments.

Value

an invisible list of x- and y-coordinates of the line:

- `x`: a vector of x-coordinates of the line
- `y`: a vector of y-coordinates of the line

See Also

`plot.gqc`, `{plot3d.gqc}`

Examples

```r
data(subjdemo_2d)
fit.2dq <- gqc(response ~ x + y, data=subjdemo_2d, 
               category=subjdemo_2d$category, zlimit=7)
plot(fit.2dq, fitdb=FALSE, initdb=FALSE)
lines(fit.2dq$par, xlim=c(0,400), ylim=c(0,400), col="red")
lines(fit.2dq$initpar, xlim=c(0,400), ylim=c(0,400), col="blue")
```
Description

Extract the log-likelihood of the fitted general linear or conjunctive classifier model.

Usage

```r
## S3 method for class 'glc'
logLik(object, ...)

## S3 method for class 'gcjc'
logLik(object, ...)
```

Arguments

- `object`: object of class glc or gcjc
- `...`: further arguments (currently unused)

Value

The log-likelihood for the general linear or conjunctive classifier represented by the estimated parameters in `object`.

Note

This function is intended for indirect internal use by functions such as AIC. To obtain the log-likelihood of the fitted model applied to new dataset, use `logLik.glcStruct` or `logLik.gcjcStruct`.

See Also

- `glc`, `logLik.glcStruct`, `gcjc`, `logLik.gcjcStruct`

Examples

```r
data(subjdemo_2d)
fit <- glc(response ~ x + y, data=subjdemo_2d,
category=subjdemo_2d$category, zlimit=7)
logLik(fit)
```
**logLik.glcStruct**

**Log-Likelihood of a 'glcStruct' or 'gcjcStruct' Object**

**Description**

Calculate the log-likelihood of the general linear or conjunctive classifier model applied to a data set.

**Usage**

```r
## S3 method for class 'glcStruct'
logLik(object, response, x, zlimit = Inf, ...)

## S3 method for class 'gcjcStruct'
logLik(object, response, x, zlimit = Inf, ...)
```

**Arguments**

- `object`: object of class `glcStruct` or `gcjcStruct` containing the parameter values at which the log-likelihood is to be evaluated.
- `response`: a vector of classification responses used to calculate the log-likelihood of the model.
- `x`: a matrix or dataframe containing values for each stimulus dimensions.
- `zlimit`: integer. Used to truncate the z-scores whose absolute values are greater than `zlimit` when calculating the log-likelihood. Default to `Inf`.
- `...`: further arguments (currently unused)

**Value**

The log-likelihood for the general linear or conjunctive classifier described by `object` fitted against the dataset given by `response` and `x`.

**Note**

The value of attributes, `attr(LBdfBI)` (degrees of freedom) is calculated based on the assumption that all the parameters in `object` are free to vary.

**See Also**

`gqc`, `gqcStruct`, `logLik.glc`, `logLik.gcjc`

**Examples**

```r
m <- list(c(187, 142), c(213, 98))
covs <- diag(625, ncol=2, nrow=2)
db <- ldb(means=m, covs=covs, noise=10)
data(subjdemo_2d)
logLik(db, subjdemo_2d$response, x=subjdemo_2d[2:3], zlimit=7)
```
logLik.gqc

**Description**

Extract the log-likelihood of the fitted general quadratic classifier model.

**Usage**

```r
## S3 method for class 'gqc'
logLik(object, ...)
```

**Arguments**

- `object`: object of class `gqc`
- `...`: further arguments (currently unused)

**Value**

The log-likelihood for the general quadratic classifier represented by the estimated parameters in `object`.

**Note**

This function is intended for indirect internal use by functions such as AIC. To obtain the log-likelihood of the fitted model applied to new dataset, use `logLik.gqcStruct`.

**See Also**

- `gqc`, `logLik.gqcStruct`

---

logLik.gqcStruct

**Description**

Calculate the log-likelihood of the general quadratic classifier model applied to a data set.

**Usage**

```r
## S3 method for class 'gqcStruct'
logLik(object, response, x, zlimit = Inf, ...)
```
Arguments

- **object**: object of class `gqcStruct`
- **response**: a vector of classification responses used to calculate the log-likelihood of the `gqc` model.
- **x**: a matrix or dataframe containing values for each stimulus dimensions.
- **zlimit**: integer. Used to truncate the z-scores whose absolute values are greater than `zlimit` when calculating the log-likelihood. Default to Inf
- **...**: further arguments (currently unused)

Value

The log-likelihood for the general quadratic classifier described by `object` fitted against the dataset given by `response` and `x`.

Note

The value of attributes, attr(., "df") (degrees of freedom) is calculated based on the assumption that all the parameters in `object` are free to vary.

See Also

- `gqc`, `gqcStruct`, `logLik.gqc`

Examples

```r
m <- list(c(187, 142), c(213, 98))
covs <- list(diag(625, ncol=2, nrow=2), diag(600, ncol=2, nrow=2))
db <- qdb(means=m, covs=covs)
data(subjdemo_2d)
logLik(db, subjdemo_2d$response, x=subjdemo_2d[2:3], zlimit=7)
```

Description

Calculate sample means and covariance(s) of multivariate data

Usage

```r
## Default S3 method:
mcovs(x, grouping, pooled=TRUE, ...)

## S3 method for class 'formula'
mcovs(formula, data, pooled=TRUE, ...)
```
Arguments

- **formula**: A formula in the form of `grouping ~ x1 + x2 + ...`, where the right hand side specifies the sample variables.
- **data**: Data frame from which variables specified in `formula` are taken.
- **x**: data frame or Matrix containing sample values.
- **grouping**: a factor specifying the population to which the samples in `x` belong.
- **pooled**: logical. If `true`, pooled variance-covariance matrix is calculated. If `false`, a list of variance-covariance matrices for each groups are calculated. Default to `true`.
- **...**: further arguments

Value

A list containing:

- **N**: total number of samples.
- **counts**: number of samples per groups.
- **lev**: levels of the `grouping` factor
- **means**: a named list of vectors specifying the means for each group. Named according to `lev`.
- **covs**: a named list of variance-covariance matrix(es). Named as `pooled` if `pooled=TRUE`, otherwise according to `lev`.

---

new2old_par

Convert 'new' to 'old' glcStruct format

Description

Converts the glcStruct in ‘new’ format to ‘old’ format whereby a vector of angle is converted to `coeffs`.

Usage

```r
new2old_par(x)
angle2cart(angle)
```

Arguments

- **x**: object of class glcStruct.
- **angle**: vector.
**old2new_par**

**Value**

For `new2old_par`, object of class `glcStruct`.

For `angle2cart`, vector.

**Author(s)**

Author of the original Matlab routines: Leola Alfonso-Reese

Author of R adaptation: Kazunaga Matsuki

**References**


**See Also**

`old2new_par` `cart2angle` `glcStruct`

**Examples**

```r
m <- list(c(187, 142), c(213.4, 97.7))
covs <- diag(c(625, 625))
foo <- ldb(means=m, covs=covs)
bar <- old2new_par(foo)
new2old_par(bar)

angle2cart(bar$angle)
```

---

**Description**

Converts `glcStruct` in the ‘old’ to ‘new’ format for more efficient optimization where `coeffs` vectors are converted to a vector of `angle` with length of `(coeffs) - 1`

**Usage**

```r
old2new_par(x)
cart2angle(cart)
```

**Arguments**

- `x` object of class `glcStruct`.
- `cart` vector.
Value

For `old2new_par`, object of class `glcStruct`.
For `cart2angle`, vector.

Author(s)

Author of the original Matlab routines: Leola Alfonso-Reese
Author of R adaptation: Kazunaga Matsuki

References


Examples

```r
m <- list(c(187, 142), c(213.4, 97.7))
covs <- diag(c(625, 625))
foo <- ldb(means=m, covs=covs)
old2new_par(foo)
cart2angle(foo$coeffs)
```

---

**plot.gcjc**

*Plot Method for Class `gcjc`*

**Description**

Plot the fitted data set and decision boundary.

**Usage**

```r
## S3 method for class 'gcjc'
plot(x, fitdb = TRUE, initdb = FALSE, xlim = NULL, ylim = NULL, bg, pch, ...)
```

**Arguments**

- `x` object of class `gcjc`
- `fitdb` logical. If TRUE, the fitted decision bound is plotted. Default to TRUE
- `initdb` logical. If TRUE, the decision bound specified by the initial parameters is plotted. Default to FALSE
- `xlim` the x limits of the plot
- `ylim` the y limits of the plot
- `bg` the background color to be used for points. Default is `c("white","gray")[response]` where response represents the response vector of the model
- `pch` the symbols to be used as points. Default is `c(21,24)[x$category]`
- `...` further arguments.
Details

This function produces a scatter plot of data matrix in the x and (optionally) decision boundary specified within (i.e., x$par and/or x$initpar).

Examples

```r
m <- list(c(100,200),c(100,100),c(200,100),c(200,200))
covs <- diag(30*2, ncol=2, nrow=2)
set.seed(1)
CI <- grtnorm(n=c(50,20,10,20), np=4, means=m, covs=covs)
CI$category <- c(1,2,2,2)[CI$category]
# create random responses with 80% accuracy
CI$response <- CI$category
set.seed(1)
incorrect <- sample(1:100, size=20)
CI$response[incorrect] <- abs(CI$response[incorrect] - 3)

# now fit the model
m.cj <- gcjc(response ~ x1 + x2, data=CI, config=2, category=CI$category, zlimit=7)
plot(m.cj)
```

plot.glc

Plot Method for Class 'gle'

Description

Plot the fitted data set and linear decision boundary.

Usage

```r
## S3 method for class 'gle'
plot(x, fitdb = TRUE, initdb = FALSE, xlim = NULL, ylim = NULL, bg, pch, ...)
```

Arguments

- `x` object of class glc
- `fitdb` logical. If TRUE, the fitted decision bound is plotted. Default to TRUE
- `initdb` logical. If TRUE, the decision bound specified by the initial parameters is plotted. Default to FALSE
- `xlim` the x limits of the plot
- `ylim` the y limits of the plot
- `bg` the background color to be used for points. Default is c("white", "gray")[response] where response represents the response vector of the model
- `pch` the symbols to be used as points. Default is c(21,24)[x$category]
- `...` further arguments.
Details

This function produces a scatter plot of data matrix in the x and (optionally) decision boundary specified within (i.e., x$par and/or x$initpar).

The look of the plot differs depending on the dimension of the model. If the dimension is 1, the model matrix is plotted on the y-axis, and category vector (as in x$category) is plotted on the x axis. If the dimension is 2, scatter plot of the model matrix is plotted. If the dimension is 3, plot3d.glc is called to create a 3D scatter plot. If the dimension is greater than 3, an error message will be returned.

See Also

plot3d.glc

Examples

data(subjdemo_2d)
fit.2dl <- glc(response ~ x + y, data=subjdemo_2d,
    category=subjdemo_2d$category, zlimit=7)
plot(fit.2dl)

#if one wants to plot decision bounds in
# colors different from the defaults
plot(fit.2dl, fitdb=FALSE)
abline(coef=coef(fit.2dl$par), col="orange")
abline(coef=coef(fit.2dl$initpar), col="purple")
plot3d.glc

xlim  the x limits of the plot. If NULL, limits are calculated from the model matrix. Default to NULL.

ylim  the y limits of the plot. If NULL, limits are calculated from the model matrix. Default to NULL.

bg    the background color to be used for points in 2D scatter plot. Default is c("white", "gray")[response] where response represents the response vector of the model

pch   the symbols to be used as points in 2D scatter plot. Default is c(21, 24)[x$category]

npoints number of points per dimension used to plot the decision bound. Default is 100.

... further arguments.

Details

This function produces a scatter plot of data matrix in the x and (optionally) decision boundary (i.e., x$par and/or x$initpar).

The look of the plot differs depending on the dimension of the model. If the dimension is 2, scatter plot of the model matrix is plotted. If the dimension is 3, plot3d.gqc is called to create a 3D scatter plot. In all other cases, an error message will be returned.

See Also

lines.gqcStruct, plot3d.gqc

Examples

data(subjdemo_2d)
fit.2dq <- gqc(response ~ x + y, data=subjdemo_2d, category=subjdemo_2d$category, zlimit=7)
plot(fit.2dq)

plot3d Method for Class ‘glc’

Description

plot the fitted 3D data set and linear decision boundary.

Usage

## S3 method for class 'glc'
plot3d(x, fitdb = TRUE, initdb = FALSE, lims = NULL, alpha = .5, ...)

Arguments

- `x` object of class `glc`
- `fitdb` logical. If TRUE, the fitted decision bound will be plotted. Default to TRUE
- `initdb` logical. If TRUE, the decision bound specified by the initial parameters will be plotted. Default to FALSE
- `lims` column matrix of the x, y, and z limits of the plot
- `alpha` alpha value for the decision bound surface(s) ranging from 0 (fully transparent) to 1 (opaque). Default is .5.
- `...` further arguments.

Details

This function produces a 3D scatter plot of data matrix in the x and (optionally) decision boundary specified within (i.e., `x$par` and/or `x$initpar`), using `points3d` and `quads3d` in the `rgl` package respectively.

References

Daniel Adler, Oleg Nenadic and Walter Zucchini (2003) RGL: A R-library for 3D visualization with OpenGL

See Also

- `plot.glc`
- `plot3d.gqc`

Examples

```r
## Not run:
data(subjdemo_3d)
fit.3d1 <- glc(response ~ x + y + z, data=subjdemo_3d,
               category=subjdemo_3d$category, zlimit=7)
plot3d(fit.3d1)
## End(Not run)
```

---

**Description**

plot the fitted 3D data set and quadratic decision boundaries.
Usage

```r
## S3 method for class 'gqc'
plot3d(x, fitdb = TRUE, initdb = FALSE,
       lims = NULL, npoints = 100, alpha = .5,
       fill = TRUE, smooth = FALSE, ...)
```

Arguments

- `x`: object of class gqc
- `fitdb`: logical. If TRUE, the fitted decision bound will be plotted. Default to TRUE
- `initdb`: logical. If TRUE, the decision bound specified by the initial parameters will be plotted. Default to FALSE
- `lims`: column matrix of the x, y, and z limits of the plot. If NULL, limits are calculated from the model matrix of x. Default to NULL.
- `npoints`: number of points per dimension (i.e., x, y, and z) used to plot the decision bound surface. Default is 100.
- `alpha`: alpha value for the decision bound surface(s) ranging from 0 (fully transparent) to 1 (opaque). Default is .5
- `fill`: logical. If TRUE, decision bounds (if fitdb or initdb is set to TRUE) should be drawn with filled surfaces. If FALSE, a wire frame should be used. Default to TRUE.
- `smooth`: logical. If TRUE, smooth shading should be used. Default to FALSE.
- `...`: further arguments.

Details

This function produces a 3D scatter plot of data matrix of x and (optionally) quadratic decision boundaries specified within (i.e., x$par and/or x$initpar), using `points3d` function in the rgl package and `contour3d` function in the misc3d package respectively.

References

Daniel Adler, Oleg Nenadic and Walter Zucchini (2003) RGL: A R-library for 3D visualization with OpenGL

See Also

`plot.gqc`, `{plot3d.gqc}`

Examples

```r
## Not run:
data(subjdemo_3d)
fit.3dq <- gqc(response ~ x + y + z, data=subjdemo_3d,
               category=subjdemo_3d$category, zlimit=7)
plot3d(fit.3dq)
```
predict.glc

**predict method for General Linear Classifier**

**Description**

Predicted classification based on `glc` model object.

**Usage**

```r
## S3 method for class 'glc'
predict(object, newdata, seed = NULL, ...)
```

**Arguments**

- `object` : object of class `glc`.
- `newdata` : a vector or a matrix containing new samples with which the classification prediction is to be made.
- `seed` : numeric. The ‘seed’ used for the random number generator.
- `...` : further arguments (currently unused).

**Details**

The function `predict` (or ‘simulate’) classification response of an observer whose noise and linear decision bounds are specified in `object`.

The predicted category labels are matched with those used for the fit in `object`.

If `newdata` is missing, the predictions are made on the data used for the fit.

**Value**

a vector of labels of categories to which each sample in `newdata` is predicted to belong, according to the model in `object`.

**Author(s)**

- Author of the original Matlab routines: Leola Alfonso-Reese
- Author of R adaptation: Kazunaga Matsuki

**References**

Examples

```
data(subjdemo_2d)
fit.2d1 <- glc(response ~ x + y, data=subjdemo_2d,
    category=subjdemo_2d$category, zlimit=7)

m <- list(c(187, 142), c(213.4, 97.7))
covs <- diag(c(900, 900))
newd <- grtrnorm(n=20, np=2, means=m, covs=covs, seed=1234)
predict(fit.2d1, newd[,2:3], seed=1234)
```

---

### qdb  

**Quadratic Decision Bound**

#### Description

Find coefficients of the ideal quadratic decision boundary given the means and covariance of two categories.

#### Usage

```r
qdb(means, covs, pnoise = 10, cnoise = 100, sphere = FALSE)
```

#### Arguments

- `means`: a list of vectors containing means of the two distributions.
- `covs`: a list containing the covariance matrices of the two distributions.
- `pnoise`, `cnoise`: numeric. Defaults set to 10, and 100, respectively. see ‘Details’
- `sphere`: logical. If TRUE, the returned decision bound forms a circle or sphere.

#### Details

The order of vectors in the list `means` and `covs` matters as the sign of `coeffs` and `bias` object in the output will be reversed.

The argument `pnoise` and `cnoise` is only for convenience; the supplied value is simply bypassed to the output for the subsequent use, i.e., as object of class `gqcStruct`.

#### Value

Object of class `gqcStruct`.

#### Author(s)

Author of the original Matlab routine ‘quaddecisbnd’: Leola Alfonso-Reese
Author of R adaptation: Kazunaga Matsuki
References


See Also

mcovs, qdb, gqcStruct, gqc

Examples

```r
m <- list(c(187, 142), c(213.4, 97.7))
covs <- list(diag(c(625, 625)), diag(c(625, 625)))
foo <- qdb(means=m, covs=covs)
```

qdb.p.correct the proportion correct of the quadratic decision boundary.

Description

Calculate the proportion correct obtained by categorizing samples from one multivariate normal population using the quadratic decision boundary.

Usage

```r
qdb.p.correct(x, qdb, refpts = colMeans(x))
```

Arguments

- `x` a vector or matrix containing the values of samples from one multivariate normal population.
- `qdb` object of class `gqcStruct` or a vector containing the values for `coeffs` and `bias` of an quadratic decision bound.
- `refpts` a numeric vector used as a reference point to determine the correct side of the `qdb` for classifying `x`. The length(`refpts`) should be equal to ncol(`x`). Default to `colMeans(x)`.

Details

The function assumes that all the points specified in `x` belong to just one category.

Author(s)

Author of the original Matlab routine ‘quadbndpercorr’: Leola Alfonso-Reese
Author of R adaptation: Kazunaga Matsuki
scale

References

Examples
data(subjdemo_2d)
tmp <- split(subjdemo_2d, subjdemo_2d$category)
mc <- mcovs(category ~ x + y, data=subjdemo_2d, pooled=FALSE)
db <- qdb(mc$means, mc$covs)
qdb.p.correct(tmp[[1]][,2:3], db)

data(subjdemo_2d)
fit.2d1 <- glc(response ~ x + y, data=subjdemo_2d,
category=subjdemo_2d$category, zlimit=7)
scale(fit.2d1)

Description
Return the discriminant scores obtained by applying the general linear classifier to the fitted data.

Usage

```r
## S3 method for class 'glc'
scale(x, initdb = FALSE, zlimit = Inf, ...)
## S3 method for class 'gqc'
scale(x, initdb = FALSE, zlimit = Inf, ...)
```

Arguments

- **x**: object of class glc or gqc
- **initdb**: optional logical. If TRUE, the returned vector represents the z-scores with respect to the initial parameters, rather than the fitted parameters. Defaults to FALSE.
- **zlimit**: optional numeric. Used to truncate the scores beyond the specified value. Default to Inf
- **...**: further arguments (currently unused)

Note
The generic function `scale` is redefined to accept arguments other than `x`, `center`, and `scale`.

Examples

```r
data(subjdemo_2d)
fit.2d1 <- glc(response ~ x + y, data=subjdemo_2d,
category=subjdemo_2d$category, zlimit=7)
scale(fit.2d1)
```
fit.2dq <- gqc(response ~ x + y, data=subjdemo_2d, category=subjdemo_2d$category, zlimit=7)
scale(fit.2dq)

## Not run:
# plots using the discriminant scores
require(Hmisc)
options(digits=3)
fit.2dl <- glm(response ~ x + y, data=subjdemo_2d, category=subjdemo_2d$category, zlimit=7)
# z-scores based on the initial decision bound
# split by the true category membership
zinit <- split(scale(fit.2dl, initdb=TRUE), subjdemo_2d$category)
histbackback(zinit)

# z-scores based on the fitted decision bound
# split by the participants' response
zfit1 <- split(scale(fit.2dl, initdb=FALSE), subjdemo_2d$category)
histbackback(zfit1)

# z-scores based on the fitted decision bound
# split by the true category membership
zfit2 <- split(scale(fit.2dl, initdb=FALSE), subjdemo_2d$response)
histbackback(zfit2)

## End(Not run)

---

**subjdemo_1d**

Sample dataset of a categorization experiment with 1D stimuli.

**Description**

A sample one dimensional stimulus set and response data of a hypothetical participant in a two-category classification experiment involving 500 trials.

**Usage**

subjdemo_1d

**Format**

This data frame contains 500 rows and the following columns:

category  label of the category to which each stimulus belongs.
x  value on the dimension 'x'
response  classification response of a participant.
Source


References


---

**subjdemo_2d**

| Subj Demo 2d | Sample dataset of a categorization experiment with 2D stimuli. |

**Description**

A sample two dimensional stimulus set and response data of a hypothetical participant in a two-category classification experiment involving 500 trials.

**Usage**

**subjdemo_2d**

**Format**

This data frame contains 500 rows and the following columns:

- **category**: label of the category to which each stimulus belongs.
- **x**: value on the dimension ‘x’
- **y**: value on the dimension ‘y’
- **response**: classification response of a participant.

**Source**


**References**

Description

A sample one dimensional stimulus set and response data of a hypothetical participant in a two-category classification experiment involving 500 trials.

Usage

subjdemo_3d

Format

This data frame contains 500 rows and the following columns:

category  label of the category to which each stimulus belongs.
x  value on the dimension 'x'
y  value on the dimension 'y'
z  value on the dimension 'z'
response  classification response of a participant.

Source


References


Description

A sample two dimensional stimulus set and response data of a hypothetical participant in a two-category classification experiment involving 100 trials.

Usage

subjdemo_cj
unscale

Un-scale or re-center the scaled or centered Matrix-like object

Description

This function revert a Matrix-like object that is scaled or centered via scale.default to data with the original scale/center.

Usage

unscale(x)

Arguments

x numeric matrix(like object).

Value

a matrix that are re-centered or un-scaled, based on the value of attributes "scaled:center" and "scaled:scale" of x. If neither of those attributes is specified, x is returned.
See Also
   *scale*

Examples

```r
require(stats)
x <- matrix(1:10, ncol=2)
unscale(z <- scale(x))

# maybe useful for truncating
trunc <- 1
z[abs(z) > trunc] <- sign(z[abs(z) > trunc])*trunc
unscale(z)
```
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