Package ‘bclust’

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Type Package

Title Bayesian Hierarchical Clustering Using Spike and Slab Models

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Description Builds a dendrogram using log posterior as a natural distance defined by the model and meanwhile waits the clustering variables. It is also capable to computing equivalent Bayesian discrimination probabilities. The adopted method suites small sample large dimension setting. The model parameter estimation maybe difficult, depending on data structure and the chosen distribution family.

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bclust .................................................. 2
bclustvS ............................................... 4
bdiscrim ............................................. 5
diptplot ............................................. 8
dpplot ................................................. 10
gaelle ................................................. 12
imp ...................................................... 13
**Description**

The function clusters data saved in a matrix using an additive linear model with disappearing random effects. The model has built-in spike-and-slab components which quantifies important variables for clustering and can be extracted using the `imp` function.

**Usage**

```r
bclust(x, rep.id=1:nrow(x), effect.family="gaussian", var.select=TRUE, transformed.par, labels=NULL)
```

**Arguments**

- **x**
  A numeric matrix, with clustering individuals in rows and variables in columns.

- **rep.id**
  A vector consisting of positive integer elements having the same length as the number of rows of `x`. This vector identifies replicates of a clustering type such that the total number of clustering types is `max(rep.id)`. If nothing is declared the function presupposes that the data are unreplicated, that is each row of `x` is a clustering type.

- **effect.family**
  Distribution family of the disappearing random components. The choices are "gaussian" or "alaplace" allowing Gaussian or asymmetric Laplace family, respectively.

- **var.select**
  A logical value, `TRUE` for fitting models that define spike-and-slab distribution in variable level and allows Bayesian variable selection.

- **transformed.par**
  The transformed model parameters in a vector. The length of the vector depends on the chosen model and the availability of variable selection. The log transformation is supposed to be applied for the variance parameters, the identity for the mean, and the logit for the proportions. The function `loglikelihood` can be used to estimate them from the data.

- **labels**
  A vector of strings referring to the labels of clustering types. The length of the vector should match to `max(rep.id)`. The first element corresponds to the label of the type having the smallest integer value in `rep.id`, the second element refers to the label of the type having the second smallest integer in `rep.id`, and so on.
Details

The function calls internal C functions depending on the chosen model. The C-stack of the system may overflow if you have a large dataset. You may need to adjust the stack before running R using your operation system command line. If you use Linux, open a console and type `ulimit -s unlimited` and then run R in the same console. The Microsoft Windows users don’t need to increase the stack size.

We assumed a Bayesian linear model for clustering being

\[ y_{vct} = \mu + \eta_{vct} + \delta_v \gamma_{vc} \theta_{vc} + \epsilon_{vct} \]

where \( y_{vct} \) is the available data on variable \( v \), cluster \( c \), clustering type \( t \), and replicate \( r \); \( \eta_{vct} \) is the between-type error, \( \theta_{vc} \) is the disappearing random component controlled by the Bernoulli variables \( \delta_v \) with success probability \( q \) and \( \gamma_{vc} \) with success probability \( p \); and \( \epsilon_{vct} \) is the between-replicate error. The types inside a cluster share the same \( \theta_{vc} \), but may arise with a different \( \eta_{vct} \). For more details see Vahid Partovi Nia and Anthony C. Davison (2012)

Value

data
repno
merge
height
logposterior
clustNnumber
cut
transformedNpar
labels
effectNfamily
varNselect

References


See Also

loglikelihood, meancss, imp.
Examples

```r
data(gaelle)

# unreplicated clustering
gaelle.bclust<-bclust(x=gaelle, 
transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68))
par(mfrow=c(2,1))
plot(as.dendrogram(gaelle.bclust))
abline(h=gaelle.bclust$cut)
plot(gaelle.bclust$clust.number, gaelle.bclust$logposterior, 
  xlab="Number of clusters",ylab="Log posterior",type="b")
abline(h=max(gaelle.bclust$logposterior))

# replicated clustering
gaelle.id<-rep(1:14,c(3,rep(4,13)))
# first 3 rows replication of ColWT
# 4 replications for the others

gaelle.lab<-c("ColWT","d172","d263","isa2",
  "sex4","dpe2","mex1","sex3","pgm","sex1",
  "WswT","tpt","RLDWT","Ke103")

gaelle.bclust<-bclust(gaelle.id=gaelle.id,labels=gaelle.lab, 
transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68))
plot(as.dendrogram(gaelle.bclust))
abline(h=gaelle.bclust$cut)
plot(gaelle.bclust$clust.number, gaelle.bclust$logposterior, 
  xlab="Number of clusters",ylab="Log posterior",type="b")
abline(h=max(gaelle.bclust$logposterior))
```

bclustvs

---

**bclustvs (Bayesian CLUSTERing with Variable Selection)** is a class

---

**Description**

The `bclustvs` object can be regarded as a Bayesian extension of the `hclust` object that additionally contains information of a Bayesian dendrogram. You can convert any `bclustvs` object to a dendrogram object using `as.dendrogram`.

**Value**

- **data** The data matrix, reordered according to `rep.id`.
- **repno** The number of replicates of the values of `rep.id`.
- **merge** The merge matrix in `hclust` object format.
- **height** A monotone vector referring to the height of the constructed tree.
- **logposterior** The log posterior for each merge.
- **clust.number** The number of clusters in each merge.
The value of the height corresponding to the maximum of the log posterior in agglomerative path.

The transformed values of the model parameters. The log transformation is applied for the variance parameters, the identity for the mean, and the logit for the proportions.

The labels associated to each clustering type.

The distribution assigned to the disappearing random effect.

Availability of variable selection chosen in the function arguments.

**Description**

This function provides a discrimination method equivalent to the **bclust** clustering function.

**Usage**

```r
bdiscrim(training, training.id, 
training.labels = NULL, predict, 
predict.label = rownames(predict)[1], 
effect.family = "gaussian", var.select = TRUE, 
transformed.par, priorprob = rep(1, max(training.id) + 1))
```

**Arguments**

- **training**: A numeric matrix of the training set with observations in rows and variables in columns.
- **training.id**: A vector consisting of positive integer elements having the same length as the number of rows of `training`. This vector identifies observations of a class such that the total number of classes is `max(training.id)`.
- **training.labels**: A vector of strings referring to the labels of each class. The length of the vector should match to `max(training.id)`. The first element corresponds to the label of the type having the smallest integer value in `training.id`, the second element refers to the label of the type having the second smallest integer in `training.id`, and so on.
- **predict**: A single discriminating type to be classified to one of the classes, with replications of the discriminating type in rows and variables in columns. The number of variables should be the same as in `training`. If it is not specified just the variable and variable-class importances will be calculated.
- **predict.label**: A single string, the label of the discriminating type.
**effect.family** Distribution family of the disappearing random components of the model. The choices are "gaussian" or "alaplace" allowing Gaussian or asymmetric Laplace family, respectively.

**var.select** A logical value, TRUE for fitting models that define a spike-and-slab distribution in variable level and allows Bayesian variable selection.

**transformed.par** The transformed model parameters in a vector. The length of the vector depends on the chosen model and the availability of variable selection. The log transformation is supposed to be applied for the variance parameters, the identity for the mean, and the logit for the proportions. The function `loglikelihood` can be used to estimate them from the data.

**priorprob** The prior probabilities for each class in a vector. The length of the vector should be the number of classes \( \max(\text{training.id}) \) plus one (the prior probability that the predict set raises its own class). If nothing is specified a uniform discrete prior is considered.

### Details

The function calls internal C functions depending on the chosen model. The C-stack of the system may overflow if you have a large dataset. You may need to adjust the stack before running R using your operational system command line.

We assumed a Bayesian linear model for classification being

\[
y_{vctr} = \mu + \eta_{vct} + \delta_{vc} \gamma_{vc} \theta_{vc} + \epsilon_{vctr}
\]

where \( y_{vctr} \) is the available data on variable \( v \), cluster \( c \), type \( t \), and replicate \( r \); \( \eta_{vct} \) is the between-type error, \( \theta_{vc} \) is the disappearing random component controlled by the Bernoulli variables \( \delta_{v} \) with success probability \( q \) and \( \gamma_{vc} \) with success probability \( p \); and \( \epsilon_{vctr} \) is the between-replicate error. The function computes the posterior probability that the predict data share the same \( \theta_{vc} \). This function also considers that the predict data may arise its own class. For more details see Vahid Partovi Nia and Anthony C. Davison (2012)

### Value

- **probs** The posterior probabilities in a matrix with one row.
- **var** The variable importances, each being a log Bayes factor.
- **varclass** The variable-class importances, each being a log Bayes factor.

### References


### See Also

`loglikelihood`, `bclust`, `profileplot`. 
Examples

data(gaelle)
gaelle.id<-rep(1:13,rep(4,13)) # all mutants have 4 replicates
gaelle.lab<-c("d172","d263","isa2",
"sex4","dpe2","mex1","sex3","pgm","sex1","WsWT",
"tpt","RLDWT","ke103")

gaelle.bdiscrim<-bdiscrim(gaelle[1:3],
training.id=gaelle.id,training.labels=gaelle.lab,
transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68),
predict=gaelle[1:3], predict.label="ColWT")
# classify ColWT to one of the types

par(mfrow=c(1,1)) # retrieve graphic defaults
par(mar=c(UL TL TL R) + PN1) C leave some space for labels

ColWT.prob<-as.vector(gaelle.bdiscrim$probs)

# plots discrimination probabilities
bp <- barplot(ColWT.prob,ylim=c(0,1)) # plot bars
title("ColWT Discrimination")
text(bp, par("usr")[3]-0.05, srt = 90,adj=1,
labels = colnames(gaelle.bdiscrim$probs),
xpd = TRUE)
# plot variable labels

mtext(1, text = "Mutant", line = 4,cex=1.5)
# add x axis label
mtext(2, text = "Probability", line = 3,cex=1.2)
# add y axis labels
abline(h=1/length(ColWT.prob))
# draw plot a as a reference line prior probabilities line

# plots sorted discrimination probabilities
par(mfrow=c(1,1)) # retrieve graphic defaults
par(mar = c(5, 4, 4, 2) + 0.1) # leave some space for labels
bp <- barplot(sort(ColWT.prob,decreasing=TRUE),ylim=c(0,1),
col=heat.colors(length(ColWT.prob))) # plot bars
text(bp, par("usr")[3]-0.05, srt = 90,adj=1,
labels = colnames(gaelle.bdiscrim$probs)[order(ColWT.prob,decreasing=TRUE)],
        xpd = TRUE) # plot variable labels
mtext(1, text = "Mutant", line = 4,cex=1.5)# add x axis label
mtext(2, text = "Probability", line = 3,cex=1.2)# add y axis labels
abline(h=1/length(ColWT.prob))

varclassimp<-gaelle.bdiscrim$varclass
# use thresholds to define blob colors
ditplot

```
blob<-matrix(0,nrow(varclassimp),ncol(varclassimp))
blob[varclassimp<=0]<-0
blob[varclassimp>0]<-1
blob[varclassimp>1]<-2
blob[varclassimp>3]<-3
blob[varclassimp>5]<-4
#log bayes factor thresholding
varimp<-gaelle.bdismcr$var
varcol<-rep(0,ncol(gaelle))
varcol[varimp>0]<-1

var.order<-order(gaelle.bdismcr$var,decreasing=TRUE)
profileplot(x=gaelle[-(1:3),var.order],rep.id=gaelle.id,
labels=gaelle.lab,scale=1,blob.matrix=blob,ylab.mar=5,
xlab.mar=7)
#plot var class importance on profile plot using blobs
# and sort variables according to variable importance values

viplot(varimp=varimp,xlab=colnames(gaelle)[var.order],
ylab=10,sort=TRUE,col=varcol[var.order])
#plot sorted variable importances
```

ditplot
dendrogram-image-teeth plot

Description

This is a handy function to plot a bclustvs object. The function attaches a coloured horizontal dendrogram to the left side of an image plot with the optimal grouping highlighted by a teethplot on the right.

Usage

```
ditplot(x, xlab = colnames(x$data),
ylab = x$labels, xlab.cex = 1,
ylab.cex = 1, dendrogram.lwd = 1, dendrogram.size = 2,
xlab.mar = 3, ylab.mar = 3, image.col = rainbow(20),
horizbar.plot = FALSE,
horizbar.col = rev(c(heat.colors(5)[-4], "white")),
horizbar.distance = 4,varimp = rep(0, ncol(x$data)),
horizbar.size = 0.5, vertbar = NULL,
vertbar.col = rainbow(max(vertbar)),
teeth.size = 0.25, plot.width = 10)
```
Arguments

x  A bclusfvs object.
xlab  A vector of strings elements. The labels for the clustering types automatically extracted from x.
ylab  A vector of strings. The variable labels automatically extracted from x.
xlab.cex  A positive value, the magnitude of the clustering type labels.
ylab.cex  A positive value, the magnitude of the variable labels.
dendrogram.lwd  A positive value, the thickness of lines used to plot the dendrogram.
dendrogram.size  A positive value, the size of the dendrogram plot.
xlab.mar  A positive value, the margin reserved to write variable labels.
ylab.mar  A positive value, the margin reserved to write type labels.
image.col  Colours used for the image plot.
horizbar.plot  A logical value, if TRUE a horizontal bar is plotted according to categorised varimp.
horizbar.col  Colours used for the horizontal bar.
horizbar.distance  A positive value, the distance between the horizbar and the image plot.
varimp  A numerical vector denoting the importance of variables. We propose to use the imp function to compute these values. If it is specified, the variables will be ordered respect to this vector.
horizbar.size  A positive value, the size of the horizontal bar.
vertbar  A positive integer vector that may be used to draw an additional vertical bar on the right of the teeth plot. This may be helpful to represent another optional grouping on the data.
vertbar.col  The colours used to plot the additional vertical bar.
teeth.size  A positive value, the size of the teeth plot.
plot.width  A positive value, the width of the whole plot. If the plot region is unbalanced in width and height, adjust this value.

Details

The varimp is assumed to be log Bayes factors and therefore categorised according to Kass and Raftery (1995) for a better visualisation.

References


See Also
dptplot, teethplot, profileplot, viplot.
**Examples**

```r
data(gaelle)

gaelle.bclust <- bclust(gaelle, transformed.par = c(-1.84, -0.99, 1.63, 0.08, -0.16, -1.68))
dptplot(gaelle.bclust, varimp = imp(gaelle.bclust)$var, horizbar.plot = TRUE, plot.width = 5, horizbar.size = 0.2, ylab.mar = 4)

# unreplicated clustering

wildtype <- rep(1:55) # initiate a vector
wildtype[c(1:3, 48:51, 40:43)] <- 2 # associate 2 to wildtypes
dptplot(gaelle.bclust, varimp = imp(gaelle.bclust)$var, horizbar.plot = TRUE, plot.width = 5, horizbar.size = 0.2, vertbar = wildtype, vertbar.col = c("white", "violet"), ylab.mar = 4)

# mark wildtype plants using violet

gaelle.id <- rep(1:14, c(3, rep(4, 13)))
# first 3 rows replication of ColWT, 4 for the rest
gaelle.lab <- c("ColWT", "d172", "d263", "isa2", "sex4", "dpe2", "mex1", "sex3", "pgm", "sex1", "W5WT", "tpt", "RLDWT", "ke103")
gaelle.bclust <- bclust(gaelle, rep.id = gaelle.id, labels = gaelle.lab, transformed.par = c(-1.84, -0.99, 1.63, 0.08, -0.16, -1.68))
dptplot(gaelle.bclust, varimp = imp(gaelle.bclust)$var, horizbar.plot = TRUE)

# replicated clustering
```

---

**dptplot**

* dendrogram-profile-teeth plot

**Description**

This is a plot function suitable for visualisation of a bclust vs object when the bclust function is used on replicated data, but can be applied for unreplicated data too. The function attaches a coloured horizontal dendrogram to the left side of a profile plot with the optimal grouping highlighted by a teethplot on the right.

**Usage**

```r
dptplot(x, scale = 1, xlab = colnames(x$data), ylab = x$labels, xlab.cex = 1, ylab.cex = 1, dendrogram.lwd = 1, dendrogram.size = 2, xlab.mar = 3, ylab.mar = 3, horizbar.plot = FALSE, horizbar.col = rev(c(heat.colors(5)[-4], "white")), horizbar.distance = 4, varimp = rep(0, ncol(x$data)), horizbar.size = 0.5, vertbar = NULL, vertbar.col = rainbow(max(vertbar)), teeth.size = 0.25, plot.width = 10)
```
Arguments

- `x`: A `bclustvs` object.
- `scale`: A positive value. If the profile plots are too noisy or too flat, adjust the scaling factor.
- `xlab`: A string vector, the labels for the clustering types.
- `ylab`: A string vector, the variable labels.
- `xlab.cex`: A positive value, the magnitude of the type labels.
- `ylab.cex`: A positive value, the magnitude of the variable labels.
- `dendrogram.lwd`: A positive value, the thickness of lines used to plot the dendrogram.
- `dendrogram.size`: A positive value, the size of the dendrogram plot.
- `xlab.mar`: A positive value, the margin reserved to write variable labels.
- `ylab.mar`: A positive value, the margin reserved to write type labels.
- `horizbar.plot`: A logical value. If `TRUE` a horizontal bar is plotted according to the `varimp`.
- `horizbar.col`: Colours of the horizontal bar.
- `horizbar.distance`: A positive value, the distance between the horizontal bar and the profile plot.
- `varimp`: A numerical vector denoting the importance of variables. We propose to use `imp` function to get the values. If it is specified, the variables will be ordered respect to this vector.
- `horizbar.size`: A positive value, the size of the horizontal bar.
- `vertbar`: A positive integer vector that may be used to draw an additional vertical bar on the right of the `teethplot`. This may be helpful to represent another optional grouping on the data.
- `vertbar.col`: The colours used to plot the additional vertical bar.
- `teeth.size`: A positive integer, the size of the `teethplot`.
- `plot.width`: A positive integer, the width of the whole plot. If the plot region is unbalanced in width and height, adjust this value.

Details

The `varimp` is assumed to be the log Bayes factor and therefore categorised according to Kass and Raftery (1995) for a better visualisation. If `varimp` is not result of the `imp` function, keep `horizbar.plot=FALSE`.

References


See Also

ditplot, profileplot, teethplot, viplot.
**Examples**

```r
data(gaelle)

# first 3 rows replication of ColWT, 4 for the rest

# replicated clustering

gaelle.bclust<bclust(gaelle, labels=gaelle.lab, transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68))
dptplot(gaelle.bclust, scale=5, varimp=imp(gaelle.bclust)$var, horizbar.plot=TRUE)

#unreplicated clustering

wildtype<rep(1,55) #initiate a vector
wildtype[c(1:3,48:51,40:43)]<2 #associate 2 to wildtypes
dptplot(gaelle.bclust, scale=10, varimp=imp(gaelle.bclust)$var, horizbar.plot=TRUE,plot.width=5,horizbar.size=0.2,ylab.mar=4)
```

**Description**

The dataset consists of replicates of 14 mutants to study metabolite pathways of genetically modified samples of *Arabidopsis thaliana*. Values of 43 metabolites are measured for each sample which are supposed to monitor their genetic changes. The data involve two mutants defective in starch biosynthesis, *pgm* and *isa2*; four defective in starch degradation *sex1*, *sex4*, *mex1*, and *dpe2*; a mutant for comparison that accumulates starch as a pleitropic effect, *tpt*; four uncharacterised mutants, *deg172*, *deg263*, *ke103*, and *sex3*; and three wild type plants, *WsWT*, *RLDWT*, and *ColWT*. There are four replicates of all samples except the last for which there are three [http://www.plantphysiol.org/cgi/content/abstract/143/4/1484](http://www.plantphysiol.org/cgi/content/abstract/143/4/1484).

**Usage**

```r
data(gaelle)
```

**Format**

Matrix with 55 observations measured on 43 variables.
References


Examples

data(gaelle)
heatmap(gaelle)

---

**imp**

*calculates variable and variable-cluster importances*

**Description**

The function computes the log Bayes factors for the hypothesis H0: the variable or the variable-cluster combination is useful for clustering against H1: the variable or the variable-cluster combination is useless. The Bayes factors are computed for the optimal allocation found by the bclust function.

**Usage**

```r
imp(x)
```

**Arguments**

- `x` A `bclustvs` object.

**Value**

- `var` A vector being the log Bayes factor of $\delta_v = 1$ against $\delta_v = 0$, see `bclust` for details.
- `varclust` A vector being the log Bayes factor of $\gamma_{vc} = 1$ against $\gamma_{vc} = 0$, see `bclust` for details.
- `repno` The number of replicates producing each row of `varclust`.
- `labels` The vector of variable labels extracted from the `bclustvs` object.
- `order` The order of `var` useful to sort `var`, `varclust`, and `labels`.

**See Also**

- `bclust`.
Examples

data(gaelle)

gaelle.id<-rep(1:14,c(3,rep(4,13)))
# first 3 rows replication of ColWT, 4 for the rest

gaelle.bclust<-bclust(gaelle,rep.id=gaelle.id,
transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68),
var.select=TRUE)

gaelle.imp<-imp(gaelle.bclust)

# plot the variable importances
par(mfrow=c(1,1)) # retrieve graphic defaults

mycolor<-gaelle.imp$var
mycolor<-c()
mycolor[gaelle.imp$var>0]<-"black"
mycolor[gaelle.imp$var<0]<-"white"

viplot(var=gaelle.imp$var,xlab=gaelle.imp$labels,col=mycolor)
# plot important variables with black

viplot(var=gaelle.imp$var,xlab=gaelle.imp$labels,
sort=TRUE,col=heat.colors(length(gaelle.imp$var)),
xlab.mar=10,ylab.mar=10)
mtext(1, text = "Metabolite", line = 7,cex=1.5)# add x axis label
mtext(2, text = "Log Bayes Factor", line = 3,cex=1.2)# add y axis labels
# sort importances and use heat colors add some labels to the x and y axes

loglikelihood

computes the model log likelihood useful for estimation of the transformed.par

Description

The function is useful for deriving the maximum likelihood estimates of the model parameters.

Usage

loglikelihood(x.mean,x.css,repno,transformed.par,
effect.family="gaussian",var.select=TRUE)

Arguments

x.mean The mean matrix of the clustering types from the meancss function.
x.css The corrected sum of squares matrix of the clustering types from the meancss function.
repno

The vector containing the number of replications of each clustering type corresponding to the each row of x.mean and x.css, from the meancss function.

transformed.par

The vector of transformed model parameters that the data likelihood will be evaluated at. The transformation is the log for the variance parameters, the identity for the mean, and the logit for the proportions. The length of the vector depends on the chosen effect.family and var.select.

effect.family

Distribution family of the disappearing random components. Choices are "gaussian" or "alaplace" allowing Gaussian or asymmetric Laplace family, respectively.

var.select

A logical value, TRUE for fitting models that define spike-and-slab in variable level, thus allowing Bayesian variable selection.

Details

Sometimes estimation of the model parameters is difficult, always check the convergence of the optimisation algorithm. The asymmetric Laplace model, effect.family="alaplace", is often more difficult to optimise than effect.family="gaussian".

If data are standardised (having general mean zero and general variance one) the log likelihood function is usually maximised over values between -5 and 5.

The transformed.par is a vector of transformed model parameters having length 5 up to 7 depending on the chosen model.

The transformed.par is (log $\sigma^2$, log $\sigma^2_\eta$, log $\sigma^2_\theta$, $\mu$, logit$p$, logit$q$) a vector of length 6 when using effect.family = "gaussian" and var.select=TRUE,

and is (log $\sigma^2$, log $\sigma^2_\eta$, log $\sigma^2_\theta$, log $\sigma^2_\theta_L$, log $\sigma^2_\theta_R$, $\mu$, logit$p$, logit$q$) a vector of length 7 for effect.family="alaplace" and var.select=TRUE.

When var.select=FALSE the $q$ parameter is dropped, yielding a vector of length 5 for effect.family="gaussian" and a vector of length 6 for effect.family="alaplace".

We assumed a Bayesian linear model being

$$y_{vctr} = \mu + \eta_{vct} + \delta_v \gamma_{vct} \theta_{vc} + \varepsilon_{vctr}$$

where $y_{vctr}$ is the available data on variable $v$, cluster(or class) $c$, type $t$, and replicate $r$; $\eta_{vct}$ is the between-type error, $\theta_{vc}$ is the disappearing random component controlled by the Bernoulli variables $\delta_v$ with success probability $q$ and $\gamma_{vct}$ with success probability $p$; and $\varepsilon_{vctr}$ is the between-replicate error. The types inside a cluster (or class) share the same $\theta_{vc}$, but may arise with a different $\eta_{vct}$.

The model parameters has natural interpretations, $\sigma^2$ is the between replicate error variance; $\sigma^2_\eta$ is the variance of between-type error; $\sigma^2_\theta$ is the variance of the disappearing random component which is decomposed to $\sigma^2_\theta_L$, $\sigma^2_\theta_R$ the left and the right tail variances if the model is asymmetric Laplace; $\mu$ is the general level; $p$ is the proportion of active variable-cluster (or variable-class) combinations, and $q$ is the proportion of the active variables. For more details see Vahid Partovi Nia and Anthony C. Davison (2012)
meancss

computes statistics necessary for the evaluation of the log likelihood

Description

The function is useful for deriving arguments of the loglikelihood function.

Usage

meancss(x, rep.id=1:nrow(x))

Arguments

x
   The data matrix, subjects in rows, variables in columns.

rep.id
   A vector of positive integers referring to replication of the types. The same integer is associated to the the replicates of the same type. Not specifying this vector preproposes that the data are unreplicated.
profileplot

Details

This function facilitates the usage of the loglikelihood function.

Value

- **mean**: The mean of types.
- **css**: The corrected sum of squares of types.
- **repno**: The vector containing the number of replications of types according to rep.id.

See Also

- loglikelihood.

Examples

```r
data(gaelle)
gaelle.id <- rep(1:14, c(3, rep(4, 13)))
# first 3 rows replication of Co1NT, 4 for the rest
mc.gaelle <- mean_css(gaelle, gaelle.id)
loglikelihood(x.mean = mc.gaelle$mean, x.css = mc.gaelle$css,
repno = mc.gaelle$repno, transformed.par = rep(0, 6))
# evaluates likelihood at rep(0,6)
```

profileplot  

*a plot useful to visualise replicated data*

Description

The profile plot is a flexible function creating profiles of replicated data with many useful options. The resulting plot can be attached to other plots like a horizontal dendrogram plot or a teethplot.

Usage

```r
profileplot(x, rep.id, labels = NULL, scale = 1,
col.names = colnames(x), plot.order = 1:max(rep.id),
xlab.mar = 5, ylab.mar = 5, xlab.cex = 0.8,
ylab.cex = 1, profile.col = rep(1, max(rep.id)),
blob.matrix = matrix(0, ncol = ncol(x), nrow = max(rep.id)),
blob.col = rev(heat.colors(max(blob.matrix))), blob.cex = 1.5)
```

Arguments

- **x**: The data matrix with subjects in rows and variables in columns.
- **rep.id**: A positive integer vector referring to replication of a subject such that the total number of subjects is max(rep.id).
labels
The labels of each subject. The first element corresponds to the subject that takes
value 1 in rep.id, the second element is the one that takes value 2 in rep.id
and so on.
scale
A positive value. If the profile plots are noisy or flat, adjust the scaling factor.
col.names
The data column labels (variable labels) in a string vector.
plot.order
A positive integer vector, the order that subjects should be plotted. This is useful
if you like to attach this plot to a dendrogram or a teeth plot.
xlab.mar
A positive value, the margin reserved for the column (variable) labels.
ylab.mar
A positive value, the margin reserved for the subject labels.
xlab.cex
A positive value, the magnitude of the variable labels.
ylab.cex
A positive value, the magnitude of the subject labels.
profile.col
Colours that you may used to plot each profile.
blob.matrix
An integer matrix denoting where to plot a colour blob and which colour should
be used in which location. The number of rows of this matrix should be max(
rep.id ) and the number of columns should be ncol(x). The value 0 plots no
blobs, value 1 refers to plotting a blob with a colour specified in blob.col.
blob.col
The colours that is used for each value of blob.matrix
blob.cex
The magnitude of blobs.

Details
Some of the options may be useless for just a profile plot, but all of them are beneficial for a good
visual representation of data when the plot is attached to a dendrogram or a teethplot.

See Also
toothplot, ditplot, dptplot.

Examples

data(gaelle)
#take a subset of gaelle data
subgaelle<-gaelle[1:11,]

#use thresholds to define blob colors
blob<-matrix(0,nrow(subgaelle),ncol(subgaelle))
blob[abs(subgaelle)<0.74]<-0
blob[abs(subgaelle)>0.74]&<-1
blob[abs(subgaelle)>0.94]<-2
blob[abs(subgaelle)>1.28]<-3
profileplot(subgaelle[1:nrow(subgaelle)],scale=10,blob.matrix=blob)

#make a profile plot with colored blobs
####### attach a profileplot to a teeth plot
subgaelle.bclust<-bclust(subgaelle,
transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68))
# divide plot space into two unequal parts
teethplot  produces teeth plot useful for demonstrating a grouping on clustered subjects

Description
The function alone is useless but can be attached to a horizontal dendrogram, a profile plot, or an image plot to show a specified partitioning.

Usage

```
teethplot(x, teeth.space = 0.25, teeth.lwd = 1)
```

Arguments

- `x` A `bclustvs` object.
- `teeth.space` The space between two teeth, a value between 0 and 0.25.
- `teeth.lwd` The thickness of the lines used to draw the teeth.

Details
The teeth plot for the moment shows the grouping vertically.
viplot

variable importance plot

viplot

variable importance plot

Description

This function plots variable importances using a barplot.

Usage

viplot(varimp, xlab, xlab.mar = 5, ylab.mar = 4, xlab.srt = 90,
       xlab.cex = 1, sort = FALSE, ...)

Arguments

varimp A numeric vector, variable importances.

xlab A vector of strings. Labels to be plotted on x-axis.

xlab.mar A positive value. The margin reserved for x-axis labels.

ylab.mar A positive value, The margin reserved for y-axis labels.

xlab.srt A numeric value, amount of rotation of the x-axis labels.

xlab.cex A positive value, magnitude of x-axis labels.

sort A logical value, TRUE if sorted variables should be plotted.

... The barplot options.
Details

It is not straightforward to rotate x labels of a barplot. This function does it easily.

See Also

imp, dtpplot, ditplot.

Examples

data(gaelle)
gaelle.bclust<-bclust(gaelle, transformed.par=c(-1.84,-0.99,1.63,0.08,-0.16,-1.68))
gaelle.imp<-imp(gaelle.bclust)
viplot(varimp=gaelle.imp$var)
# solid plot

viplot(varimp=gaelle.imp$var,xlab=imp(gaelle.bclust)$labels, sort=TRUE,col=heat.colors(length(gaelle.imp$var)))
# sorted plot with heat colors and labels
Index

bclust, 2, 6, 13, 16
bclustvs, 4
bdiscrim, 5, 16

ditplot, 8, 11, 18, 20, 21
dptplot, 9, 10, 18, 20, 21

gaelle, 12

imp, 3, 13, 21

loglikelihood, 2, 3, 6, 14, 16, 17

meancss, 3, 14–16, 16

profileplot, 6, 9, 11, 17, 20

toothplot, 9, 11, 18, 19

viplot, 9, 11, 20