

Package ‘MultiGroupO’

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Type Package

Title MultiGroup Method and Simulation Data Analysis

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Description Two method new of multigroup and simulation of data.

The first technique called multigroup PCA (mgPCA) this multivariate exploration approach that has the idea of considering the structure of groups and / or different types of variables. On the other hand, the second multivariate technique called Multigroup Dimensionality

Reduction (MDR) it is another multivariate exploration method that is based on projections. In addition, a method called Single Dimension Exploration (SDE) was incorporated for to analyze the exploration of the data. It could help us in a better way to observe the behavior of the multigroup data with certain variables of interest.

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Encoding UTF-8

Imports mvtnorm, rlist, expm, stats, ggplot2, gridExtra, cowplot, plsgenomics, gplots, ggrepel, qgraph, mgm

Suggests knitr, rmarkdown

ByteCompile yes

VignetteBuilder knitr

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NeedsCompilation no

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BIplot

biplot methods

Description

biplot methods

Usage

```
BIplot(
  variates,
  loadings,
  prop_expl_var,
  comp = c(1, 2),
  group = NULL,
  rownamevar = T,
  rownameload = T
)
```

Arguments

variates	is the size of groups
loadings	is a vector of classes
prop_expl_var	data set
comp	component numeric
group	is a vector of groups
rownamevar	is a logical vector where TRUE is the label of the observations, if is FALSE, is index.
rownameload	is a logical vector where TRUE is the label of the vectors of loadings, if is FALSE, is index.

Value

return an graphics .

Examples

```
library(datasets)
obj<-pca(datos=iris[,-5],grupos=iris[,5],Plot=FALSE,center=TRUE,scale=TRUE)
BIplot(variates=obj$variates,loadings=obj$loadings,
prop_expl_var=obj$prop_expl_var,comp=c(1,2),
group=factor(as.numeric(iris[,5])),rownamevar=FALSE,rownameLoad=FALSE)
```

fun.sim	<i>Simulation function of quantitative multigroup data under a multivariate normal distribution</i>
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Description

Simulation function of quantitative multigroup data under a multivariate normal distribution

Usage

```
fun.sim(g, mean1, d, n.var, sds2, corr)
```

Arguments

g	An vector of the size of each group
mean1	An vector of the population means structure
d	distance d for the structure of population means
n.var	2x1 dimension vector whose first component is the number of random variables to simulate and the second component number of noise variables to simulate
sds2	An vector of the variances to simulate for each group noise variables
corr	An vector of the correlation to simulate for each group and noise variables

Value

return an graphics

Examples

```
fun.sim(g=c(20,20),mean1=2,d=0,sds2=c(1,1,1),corr=c(0.5,0.5,0),n.var=c(50,1))
```

mdr	<i>Performs a Multigroup Dimensionality Reduction (MDR) analysis in the given multigroup data matrix. Show MDR graphical output.</i>
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Description

Performs a Multigroup Dimensionality Reduction (MDR) analysis in the given multigroup data matrix. Show MDR graphical output.

Usage

```
mdr(g, grp, data.x, c, Plot = T)
```

Arguments

g	is the size of groups
grp	is a vector of classes
data.x	quantitative data set
c	component numeric
Plot	grafics output of MDR

Value

return an grafics .

Examples

```
sim.list<-fun.sim(g=c(50,50,50),mean1=2,d=0,sds2=c(1,1,1),
corr=c(0.5,0.5,0.5,0),n.var=c(30,30))
```

```
mdr(g=c(50,50,50),grp=as.factor(sim.list$grp),
data.x=sim.list$`lisx`,c=2)
```

mgpca	<i>Performs a Multigroup PCA analysis in the given multigroup data matrix. Show mgpca graphical output.</i>
-------	---

Description

Performs a Multigroup PCA analysis in the given multigroup data matrix. Show mgpca graphical output.

Usage

```
mgpca(
  mat.to.diag,
  mat.x,
  cls,
  Plot = TRUE,
  ncomp = 2,
  center = TRUE,
  scale = TRUE
)
```

Arguments

mat.to.diag	is a matrix with the data
mat.x	is a vector of classes
cls	group
Plot	graphics output of mgpca
ncomp	number of component
center	is a logical vector where TRUE is center (whether the variables should be shifted to be zero centered), if is FALSE, is original data.
scale	is a logical vector where TRUE is scale (indicating whether the variables should be scaled), if is FALSE, is original data.

Value

If **simplify == TRUE** class values. If **simplify == FALSE**, the result is a list of length `nsim` `data.tables`.

Examples

```
library(plsgenomics)
data(SRBCT)
mydata<-SRBCT$X
mydata<-mydata[1:50,1:5]
groups<-as.factor(SRBCT$Y)[1:50]
mat.to.diag1<-new.cov(x=mydata,cls=groups,A=diag(ncol(mydata)))
mgpca(mat.to.diag=mat.to.diag1,mat.x=as.matrix(mydata),
  cls=groups,Plot=TRUE,ncomp=2,center = TRUE,scale = TRUE)
```

 new.cov

Function for the new covariance matrix in the multigroup PCA method

Description

Generates covariance matrix...

Usage

```
new.cov(x, cls, A)
```

Arguments

x is a matrix with the data
 cls is a vector of classes
 A is a symmetric and positive definite matrix associated to inner product respect to the base of its vectorial space.

Value

return an graphics.

Examples

```
library(plsgenomics)
data(SRBCT)
mydata<-SRBCT$X
mydata<-mydata[1:50,1:20]
groups<-as.factor(SRBCT$Y)[1:50]
new.cov(x=mydata,cls=groups,A=diag(ncol(mydata)))
```

pca	<i>Performs a principal components analysis in the given data matrix. Show PCA graphical output.</i>
-----	--

Description

Performs a principal components analysis in the given data matrix. Show PCA graphical output.

Usage

```
pca(datos, grupos, Plot = TRUE, center = TRUE, scale = FALSE)
```

Arguments

datos is a matrix with the data
 grupos is a vector of classes
 Plot vector logic for grafic
 center data set center by columns
 scale data set scaled by columns

Value

return an graphics.

Examples

```
library(plsgenomics)
data(SRBCT)
mydata<-SRBCT$X
mydata<-mydata[1:30,1:20]
groups<-as.factor(SRBCT$Y)[1:30]
pca(datos=mydata, grupos=groups, Plot=TRUE, center=TRUE, scale=FALSE)
```

sde.method	<i>Performs a Single Dimension Exploration (SDE) analysis in the given multigroup data matrix. Show SDE graphical output.</i>
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Description

Performs a Single Dimension Exploration (SDE) analysis in the given multigroup data matrix. Show SDE graphical output.

Usage

```
sde.method(mydata, groups, plt = FALSE)
```

Arguments

mydata	data set
groups	is a vector of classes
plt	grafics

Value

return an grafics .

Examples

```
sim.list2<-fun.sim(g=c(20,50,10),mean1=0.5,d=0,sds2=c(1,1,1),corr=c(0.1,0.5,0.5,0),
n.var=c(20,20))
datos2 <- as.data.frame(sim.list2$x)
datos2<-subset(datos2,select=-grp)
grupos <- sim.list2$grp
grupos<-factor(grupos,labels=c(1,2,3))
sde.method(mydata=datos2,grupos=grupos,plt=FALSE)
```

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