Package ‘kimod’

November 20, 2016

Type Package

Title A k-tables approach to integrate multiple Omics-Data

Version 1.2.0

Date 2015-12-7

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Description
This package allows to work with mixed omics data (transcriptomics, proteomics, microarray-chips, rna-seq data), introducing the following improvements: distance options (for numeric and/or categorical variables) for each of the tables, bootstrap resampling techniques on the residuals matrices for all methods, that enable perform confidence ellipses for the projection of individuals, variables and biplot methodology to project variables (gene expression) on the compromise. Since the main purpose of the package is to use these techniques to omic data analysis, it includes an example data from four different microarray platforms (i.e.,Agilent, Affymetrix HGU 95, Affymetrix HGU 133 and Affymetrix HGU 133plus 2.0) on the NCI-60 cell lines. NCI60_4arrays is a list containing the NCI-60 microarray data with only few hundreds of genes randomly selected in each platform to keep the size of the package small. The data are the same that the package omicade4 used to implement the co-inertia analysis. The references in packages follow the style of the APA-6th norm.

License GPL (=2)

LazyData TRUE

biocViews Microarray, Visualization, GeneExpression, ExperimentData, Proteomics

Depends R(>= 3.3),methods

Imports cluster, graphics, Biobase

Biplot

Plot a Biplot of a SelectVar class object

Description

Plot a Biplot of a SelectVar class object

Usage

```r
## S4 method for signature 'SelectVar'
Biplot(x, xlab=NULL, ylab=NULL, mainP=NULL,
      xlimi=NULL, ylimi=NULL, labelObs=TRUE, labelVars=TRUE,
      colVar="black", colObs="black",
      pchPoints=15, Type=c("RMP","CMP","SQRT","HJ"),
      Groups=FALSE, NGroups=2, ...)
```
**Arguments**

- `x` DiStatis class object.
- `xlab` character for the x-label title for plot.
- `ylab` character for the x-label title for plot.
- `mainP` the main Biplot.
- `xlimi` (vector) Bounds to x-axis.
- `ylimi` (vector) Bounds to y-axis.
- `labelObs` Logical. indicates whether the labels of observations are prints. Default is TRUE.
- `labelVars` Logical. indicates whether the labels of variables are prints. Default is TRUE.
- `colVar` character col for colours of the variables in the plot. Default is black.
- `colObs` character col for colours of the observations in the plot. Default is black.
- `pchPoints` Either an integer specifying a symbol or a single character to be used as the default in plotting points.
- `Type` type of Biplot. Options are CMP RMP SQRT or HJ.
- `Groups` Logical. If is TRUE, the variables are grouped. See `GroupProj`.
- `NGroups` Only if the Groups are TRUE. Indicate the number the groups of variables.
- `...` additional parameters for plot.

**Value**

plotted Biplot/s of the component/s of the given SelectVar object.

**Author(s)**

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

**Examples**

```r
\{
  data(NCI60Selec)
  Z1<-DiStatis(NCI60Selec)
  M1<-SelectVar(Z1,Crit="R2-Adj")
  Colores1<-c(rep("Breast",5),rep("CNS",6),rep("Colon",7),
  rep("Leukemia",6),rep("Melanoma",10),rep("Lung",9),
  rep("Ovarian",7),rep("Prostate",2),rep("Renal",8))
  Colores2<-c(rep(colors()[657],5),rep(colors()[637],6),
  rep(colors()[537],7),rep(colors()[552],6),rep(colors()[571],10),
  rep(colors()[300],9),rep(colors()[461],7),rep(colors()[450],2),
  rep(colors()[432],8))
  Biplot(M1,labelObs = FALSE,labelVars=FALSE,
  colObs=Colores2,Type="SQRT",las=1,cex.axis=0.8,
  cex.lab=0.8,xlimi=c(-3,3),ylimi=c(-3,3))
  legend("topright",unique(Colores1),col=unique(Colores2),
  bty="n",pch=16,cex=0.6)
  Biplot(M1,labelObs = FALSE,labelVars=TRUE,colObs=Colores2,
  Type="SQRT",las=1,cex.axis=0.8,cex.lab=0.8,xlimi=c(-3,3),
  ylimi=c(-3,3),Groups=TRUE,NGroups=6)
  legend("topright",unique(Colores1),col=unique(Colores2),
  bty="n",pch=16,cex=0.6)
  data(winesassesors)
\}```
Z3<-DiStatis(winesassesors)
M3<-SelectVar(Z3,Crit="R2-Adj")
Col1<-c(rep("NZ",4),rep("FR",4),rep("CA",4))
Col2<-c(rep(2,4),rep(3,4),rep(4,4))
Biplot(M3,labelObs=FALSE,labelVars=TRUE,colObs=Col2,
Type="SQRT",xlimi=c(-2,2),ylimi=c(-2,2),las=1,cex.axis=0.8,
cex.lab=0.8)
legend("topright",unique(Col1),col=unique(Col2),bty="n",pch=16,cex=0.8)
Biplot(M1,labelObs = FALSE,labelVars=FALSE,colObs=Colores2,
Type="OMP")
legend("topright",unique(Colores1),
col=unique(Colores2),bty="n",pch=16,cex=1)
}

---

**BootPlot**

*Plot a BootPlot of a Bootstrap object*

**Description**

Plot a BootPlot of a Bootstrap object

**Usage**

```r
## S4 method for signature 'Bootstrap'
BootPlot(x,xlabProj=NULL, ylabProj=NULL,mainProj=NULL,legend=TRUE,colour=NULL,
xlimi=NULL,ylimi=NULL,Points=TRUE,...)
```

**Arguments**

- `x` object of Bootstrap-Class
- `xlabProj` character for the x-label title for plot
- `ylabProj` character for the x-label title for plot
- `mainProj` main to proj plot
- `legend` Logical. It indicates whether the legend prints
- `colour` colours for ellipsis
- `xlimi` bounds of x-axis
- `ylimi` bounds of y-axis
- `Points` logical if is true, the points are plotted
- `...` additional parameters for plot (generics)

**Value**

plotted Bootplot/s of the component/s of the given Bootstrap object.

**Author(s)**

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey
### Bootstrap

**Function**: Bootstrap of a DiStatis object

### Description

This function is used to make Bootstrap from DiStatis object. Bootstrap resampling techniques are applied on the residuals matrices obtained from SVD of the Compromise and the RV matrix to do multiple comparisons between studies and confidence ellipses for the projections of observations in the compromise.

### Usage

```
Bootstrap(object, NRep = 100, Dims = 2)
```

### Arguments

- **object**: It is the object of DiStatis Class.
- **NRep**: Number of repetitions to do the bootstrapping. Default is 100.
- **Dims**: Number of dimensions used to do the bootstrapping. Default is 2.

### Value

Bootstrap class object with the corresponding completed slots according to the given model

### Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey
References


Examples

{  
data(NCI60Selec)
Z1<-DiStatis(NCI60Selec)
B<-Bootstrap(Z1)
Z2<-DiStatis(NCI60Selec,Center=FALSE,Scale=FALSE)
B2<-Bootstrap(Z2,NRep=200)
}

---

Bootstrap-class

Class Bootstrap: Bootstrap S4 class (kimod: k-tables approach to integrate multiple Omics-Data Multiple dataset)

Description

Bootstrap to DiStatis object.

Features

1. Bootstrap Implementation
2. Confidence Intervals from Bootstrap implementation
3. Plotting Bootstrap

Fields

- Ratios.Boot Ratios (with Bonferroni Correction for all observations in compromise from all dimensions)
- Comparisions.Boot Comparision (difference between observations) from all dimensions
- Elipses.Boot List of all projections from the elipses plot.
- Stability.Boot Bootstrap Stability
- QRO.Boot Rpresentation Quality of observations (Bootstrap)
- EigValues.Boot confidence interval for eigenvalues (from SVD Compromise)
- Inertia.Boot confidence interval for inertia(}
Accesors

- Ratios.Boot(x), Ratios.Boot(x) <- value: Ratios (with Bonferroni Correction for all observations in compromise from all dimensions)
- Comparisions.Boot(x), Comparisions.Boot(x) <- value: Comparison (difference between observations) from all dimensions.
- Elipses.Boot(x), Elipses.Boot(x) <- value: List of all projections from the elipses plot.
- QR0.Boot(x), QR0.Boot(x) <- value: Representation Quality of observations (Bootstrap)
- EigValues.Boot(x), EigValues.Boot(x) <- value: confidence interval for eigenvalues (from SVD Compromise)
- Inertia.Boot(x), Inertia.Boot(x) <- value: confidence interval for inertia(%) of all dimensions (from SVD Compromise).

Bootstrap-general-functions

- print Basic output for Bootstrap class
- summary Basic statistics for Bootstrap class
- Bootstrap Getters for their respective slots.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

References


Examples

showClass("Bootstrap")

CompPlot

Plot a CompPlot of a DiStatis object

Description

Plot a CompPlot of a DiStatis object

Usage

## S4 method for signature 'DiStatis'
CompPlot(x,xlabProj=NULL, ylabProj=NULL, xlabBar="Inertia(%)",ylabBar="Values",mainBar=NULL,mainProj=NULL, pchPoints=15,legend=TRUE ,colBar="red",colObs="black",barPlot=TRUE,...)
Arguments

- **x**: DiStatis class object.
- **xlabProj**: character for the x-label title for plot
- **ylabProj**: character for the x-label title for plot
- **xlabBar**: character for the x-label title for barPlot
- **ylabBar**: character for the y-label title for barPlot
- **mainBar**: main to histogram plot
- **mainProj**: main to proj plot
- **pchPoints**: pch for points in plot.
- **legend**: Logical. indicates whether the legend prints
- **colBar**: character col for bars in the BarPlot
- **colObs**: character col for observations in the plot
- **barPlot**: logical indicates whether the barPlot is prints

... additional parameters for plot

Value

plotted CompPlot/s of the component/s of the given DiStatis object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

Examples

```r
# Not run:
data(NCI60Selec)
Z2<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
Colores2<-c(rep(colors()[657],5),rep(colors()[637],6),
            rep(colors()[537],7),rep(colors()[552],6),rep(colors()[57],10),
            rep(colors()[300],9),rep(colors()[461],7),rep(colors()[1450],2),
            rep(colors()[432],8))
Colores1<-c(rep("Breast",5),rep("CNS",6),rep("Colon",7),
            rep("Leukemia",6),rep("Melanoma",10),rep("Lung",9),rep("Ovarian",7),
            rep("Prostate",2),rep("Renal",8))
CompPlot(Z2,xlabBar="",colObs=Colores2,pch=15,las=1,
cex=2,legend=FALSE,barPlot=FALSE,cex.main=0.6,cex.lab=0.6,
cex.axis=0.6,las=1)
legend("topleft",unique(Colores1),col=unique(Colores2),
bty="n",pch=16,cex=1)
```

## End(Not run)
```
**DiStatis**

**DiStatis of a DiStatis object**

**High level constructor of DiStatis class object**

**Description**

This is the function that makes DiStatis Methodology: Statis is part of the PCA family and therefore the main analytical tool for STATIS is the singular value decomposition (SVD) and the generalized singular value decomposition (GSVD) of a matrix. The goal of Statis is to analyze several data sets of variables that were collected on the same set of observations. Originally, the comparisons were drawn from the compute of the scalar product between the different tables. In this approach, the condition is made more flexible, allowing the incorporation of different distance measurements (including the scalar product) to compare the tables.

Function to do Statis (K-tables methodology) with distance options

**Usage**

```r
DiStatis(Data = NULL, Distance = c(), Center = TRUE, Scale = TRUE,
Corre1Vector = TRUE, Frec = FALSE, Traj = TRUE)
```

**Arguments**

**Data**

The data frame or of k-tables type. The Observations should be in rows (common elements in DAnisostatis), the variables and Studies must be in columns. After the name of the variable an underscore (_) must be written to indicate the Study (eg. Var1_Est1, eg. Var1_EstK, for more information see the data object). The name of a variable can include any symbol except an underscore (_). REMEMBER the underscore (_) should be reserved to indicate the study. Also, the Data can be a list of k components. Each element of the list is one of the tables with observations in rows and variables in columns. The elements of list must be data.frame or ExpressionSet data.

**Distance**

Vector is the length equal to the number of studies that indicates the kind of distance (or scalar product) that is calculated in each study. If not specify (or is wrong specify) the scalar product is used. The options can be ScalarProduct, euclidean, manhattan, canberra, pearson, pearsanabs, spearman, spearmanabs, mahalanobis. In the binary data the distance can be: jaccard, simple matching, sokal&sneath, Roger&Tanimoto, Dice, Hamman, Ochiai, Sokal&Sneath, Phi-Pearson, Gower&Legendre.

**Center**

A logical value. If TRUE, the data frame is centered by the mean. By default is TRUE.

**Scale**

A logical value indicating whether the column vectors (of the data.frame) should be standardized by the rows weight, by default is TRUE.

**Corre1Vector**

A logical value. If TRUE (default), Vectorial correlation coefficient is computed for the RV matrix. If FALSE the Hilbert-Smith distance is used in the RV matrix.

**Frec**

Logical. Should the data be treated data as frequencies? By default is FALSE.

**Traj**

Logical. Should the trajectories analysis be done? By default is TRUE.

**Format**

An object of class NULL of length 0.
Details

STATIS methods: to more information, see references.

Value

DiStatis

DiStatis class object with the corresponding completed slots according to the given model

Note

use DiStatis-class high level constructor for the creation of the class instead of directly calling its constructor by new means.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

References


Examples

{
  data(NCI60Selec_ESet)
  Z1<-DiStatis(NCI60Selec_ESet)
  data(winesassesors)
  Z3<-DiStatis(winesassesors)
}

DiStatis-class

Class DiStatis DiStatis S4 class (kimod: k-tables approach to integrate multiple Omics-Data Multiple dataset)

Description

Statis with Distance options implementation.
DiStatis-class

Features

1. DiStatis (Statis with Distance options)
2. Bootstrap Implementation
3. Biplot Implementation with variable selection
4. Clustering of variables
5. Plotting compromise, bootstrap, trajectories, Biplot.

Fields

- distances.methods: The character indicating the metrics used.
- Inertia.RV: Inertia (%) explained for all tables.
- RV: Vectorial Correlation Matrix between studies.
- Euclid.Im: Euclidean Image of all studies.
- Inertia.Comp: Inertia (%) explained for all dimensions of compromise matrix.
- Compromise.Coords: Projection of all observations in compromise (Coords).
- Compromise.Matrix: Compromise Matrix from statis methodology.
- RQO: Representation Quality of observations in compromise matrix.
- Trajectories: List of trajectories from Statis methodology

Accessors

- Inertia.RV(x), Inertia.RV(x) <- value: Inertia (%) explained for all tables.
- RV(x), RV(x) <- value: Vectorial Correlation Matrix between studies.
- Euclid.Im(x), Euclid.Im(x) <- value: Euclidean Image of all studies.
- Inertia.Comp(x), Inertia.Comp(x) <- value: Inertia (%) explained for all dimensions of compromise matrix.
- Compromise.Coords(x), Compromise.Coords(x) <- value: Projection of all observations in compromise (Coords).
- Compromise.Matrix(x), Compromise.Matrix(x) <- value: Compromise Matrix from statis methodology.
- RQO(x), RQO(x) <- value: Representation Quality of observations in compromise matrix.
- Trajectories(x), Trajectories(x) <- value: List of trajectories from Statis methodology.

DiStatis-general-functions

- print Basic output for DiStatis class
- summary Basic statistics for DiStatis class
- DiStatis Getters for their respective slots.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey
References


See Also

CompPlot, Biplot DiStatis, and additional related DiStatis class functions.

Examples

```r
showClass("DiStatis")
```

---

**GroupProj**  
GroupProj of SelectVar object

**Description**

This function calculates the relashionship between genes and samples from SelectVar method. Also, computes agglomerative hierarchical clustering of the dataset.

**Usage**

```r
GroupProj(object, NGroups = 2, metric = c("euclidean", "manhattan"),
          method = c("ward", "single", "complete", "weighted", "flexible"), ...)
```

```r
# S4 method for signature 'SelectVar'
GroupProj(object, NGroups = 2, metric = c("euclidean",
                                         "manhattan"), method = c("ward", "single", "complete", "weighted",
                                         "flexible"), ...)```

**Arguments**

- **object**  
  it is an object of SelectVar Class.

- **NGroups**  
  An integer scalar or vector with the desired number of clusters.

- **metric**  
  The character string specifying the metric to be used to calculate dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences.
method  character string defining the clustering method. The methods implemented are "average" (unweighted pair group arithmetic average method, aka single linkage), "complete" (complete linkage), "ward" (Ward’s method), "weighted" (weighted average linkage, aka "flexible" which uses a constant version of the Lance-Williams formula and the par.method argument, and "gaverage" a generalized "average" aka also using the Lance-Williams formula and par.method. (See agnes).

... Additional parameters for agnes.

Value

GroupProj  GroupProj with the corresponding completed slots

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

Examples

{  
data(NCI60Selec)  
Z1<-DiStatis(NCI60Selec)  
M1<-SelectVar(Z1,Crit="R2-Adj")  
A1<-GroupProj(M1,method="ward",metric="euclidean",NGroups=6)  
data(winesassesors)  
Z2<-DiStatis(winesassesors)  
M2<-SelectVar(Z2,Crit="R2-Adj")  
A2<-GroupProj(M2,method="ward",metric="euclidean",NGroups=6)  
}

Description

Class GroupProj GroupProj S4 class (kimod: k-tables approach to integrate multiple Omics-Data of Multiple dataset) GroupProj to SelectVar object.

Features

1. It cluster variables for SelectVar from all tables (Studies) in STATIS Methodology.

Fields

• SortList list the clustering variables
• ProyGroups coords (beta) for Groups representant.
• Groups list of clusters.
**Accessors**

- `SortList(x)` \(\rightarrow\) value: list the clustering variables
- `ProyGroups(x)` \(\rightarrow\) value: coords (beta) for Groups representant.
- `Groups(x)` \(\rightarrow\) value: Groups list of clusters.

**GroupProj-general-functions**

- `print` Generates the basic output for Bootstrap class
- `summary` Generates the basic statistics for Bootstrap class
- `GroupProj` Getters for their respective slots.

**Author(s)**

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

**Examples**

```
showClass("GroupProj")
```

| NCI60Selec | Microarray gene expression profiles of the NCI 60 cell lines from 4 different platforms. |

**Description**

The 60 human tumour cell lines are derived from patients with leukaemia, melanoma, lung, colon, central nervous system, ovarian, renal, breast and prostate cancers. The cell line panel is widely used in anti-cancer drug screen. In this dataset, a subset of microarray gene expression of the NCI 60 cell lines from four different platforms are combined in a list.

**Usage**

```
data(NCI60Selec)
```

**Format**

NCI60Selec This data is an list of length 4.

**Value**

NCI60Select list of data.frame.

**Source**


**References**

NCI60Seq_ESet

Examples

data(NCI60Seq)

NCI60Seq_ESet  Microarray gene expression profiles of the NCI 60 cell lines from 4 different platforms.

Description

The 60 human tumour cell lines are derived from patients with leukaemia, melanoma, lung, colon, central nervous system, ovarian, renal, breast and prostate cancers. The cell line panel is widely used in anti-cancer drug screen. In this dataset, a subset of microarray gene expression of the NCI 60 cell lines from four different platforms are combined in a list.

Usage

data(NCI60Seq_ESet)

Format

NCI60Seq_ESet This data is an list of length 4.

Value

NCI60Select_ESet: list of ExpressionSet from four microarrays studies.

Source


References


Examples

data(NCI60Seq_ESet)
PanelPlot

Plot a PanelPlot of a DiStatis object

Description

Plot a PanelPlot of a DiStatis object

Usage

## S4 method for signature 'DiStatis'
PanelPlot(x)

Arguments

x     DiStatis class object.

Value

Panel plot of the given DiStatis object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

Examples

{
  data(NCI60Selec)
  Z2<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  PanelPlot(Z2)
  data(winesassesors)
  Z3<-DiStatis(winesassesors)
  PanelPlot(Z3)
}

print.Bootstrap

print or summary a Bootstrap object

Description

Generic Print/Summary method for Bootstrap class output visualization.

Usage

## S4 method for signature 'Bootstrap'
print(x)

Arguments

x     Bootstrap class object.
Value

according to the call

print console output text with increasing detail of Bootstrap object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardon, J R Demey

Examples

{
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  A<-Bootstrap(fit)

  print(A)

}

print.DiStatis


Description


Usage

## S4 method for signature 'DiStatis'
print(x)

Arguments

x DiStatis class object.

Value

according to the call

print console output text with increasing detail of DiStatis object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardon, J R Demey

See Also

DiStatis
print.GP

Examples
{
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  print(fit)
}

print.GP

print.GP a GroupProj object Generic print.GP method for GroupProj class output visualization.

Description

print.GP a GroupProj object Generic print.GP method for GroupProj class output visualization.

Usage

## S4 method for signature 'GroupProj'
print(x)

Arguments

x GroupProj class object.

Value

according to the call

print console generates output text with increasing detail of GroupProj object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardon, J R Demey

See Also

GroupProj

Examples
{
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  A<-SelectVar(fit,Crit="p-val(Bonf)",perc=0.95)
  M3<-GroupProj(A,NGroups=4,method="ward",metric="euclidean")
  print(M3)
  summary(M3)
}
print.SV

print.SV a SelectVar object Generic Print/Summary method for SelectVar class output visualization.

Description

print.SV a SelectVar object Generic Print/Summary method for SelectVar class output visualization.

Usage

```
## S4 method for signature 'SelectVar'
print(x)
```

Arguments

x SelectVar class object.

Value

according to the call

print the console output the text with increasing detail of SelectVar object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardon, J R Demey

See Also

SelectVar

Examples

```
{
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  A<-SelectVar(fit,Crit="p-val(Bonf)",perc=0.95)
  print(A)
  summary(A)
}
```
RVPlot

Plot a RVPlot of a DiStatis object

Description

Plot a RVPlot of a DiStatis object

Usage

## S4 method for signature 'DiStatis'
RVPlot(x,xlabProj="Dim 1", ylabProj="Dim 2", 
  xlabBar="Inertia(%)",ylabBar="Values" ,mainBar=NULL,mainProj=NULL, 
  colArrows="black",legend=TRUE ,colBar="red",barPlot=TRUE,...)

Arguments

x             DiStatis class object.
xlabProj      character for the x-label title for plot
ylabProj      character for the y-label title for plot
xlabBar       character for the x-label title for barPlot
ylabBar       character for the y-label title for barPlot
mainBar       the main histogram plot
mainProj      the main proj plot
colArrows     character col for arrows in ProjPlot
legend        Logical. indicates whether the legend prints
colBar        character col for bars in the BarPlot
barPlot       logical indicates whether the barPlot is prints
...            additional parameters for plot

Value

plotted RVplot/s of the component/s of the given DiStatis object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

Examples

{
  Z2<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  RVPlot(Z2)
}
**SelectVar**

### Description

This function calculates the biplot method through the compromise matrix to select genes `SelectVar` from DiStatis Class Object. High level constructor of `SelectVar` class object.

### Usage

```r
SelectVar(object, ord = FALSE, Crit = c("R2-Adj", "p-val(Bonf)", "AIC", "BIC"), perc = 0.9, Dims = 2)
```

```r
## S4 method for signature 'DiStatis'
SelectVar(object, ord = FALSE, Crit = c("R2-Adj", "p-val(Bonf)", "AIC", "BIC"), perc = 0.9, Dims = 2)
```

### Arguments

- **object**: Object is an object of DiStatis Class.
- **ord**: Logical. If TRUE, the models with intercept are computed, else the intercept is zero.
- **Crit**: c("R2-Adj", "p-val(Bonf)", "AIC", "BIC"). Criteria of selection. "R2-Adj", "p-val (Bonf)", "AIC", "BIC". Choose "R2-Adj" or "p-val (Bonf)" (Bonferroni correction), "AIC" or "BIC".
- **perc**: The value of percentil that indicate how much data than are selected.
- **Dims**: Numeric that indicates the number of dimensions to use for do the model. Default is 2.

### Details

This function allows to build the biplot for continuous response, using an external procedure to obtained the regresors in the linear model (the response being an continuous variable). This function allows the selection of genes using the goodness of fit of the Models Biplot.

### Value

- **SelectVar**: SelectVar class object with the corresponding completed slots according to the given model.

### Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

### References


**Examples**

```r
{
  data(NCI60Selec)
  Z1<-DiStatis(NCI60Selec)
  M1<-SelectVar(Z1,Crit="R2-Adj",perc=0.95)
  M2<-SelectVar(Z1,Crit="p-val(Bonf)",perc=0.95)
}
```

---

**SelectVar-class**

Class `SelectVar` S4 class (kimod: k-tables approach to integrate multiple Omics-Data Multiple dataset) `SelectVar` to DiStatis object.

**Description**

Class `SelectVar` S4 class (kimod: k-tables approach to integrate multiple Omics-Data Multiple dataset) `SelectVar` to DiStatis object.

**Features**

1. SelectVar (Generate a biplot making linear model of all variables over the Compromise Matrix)
2. Plotting Biplot.

**Fields**

- Coord.Select matrix are coordenates (Betas) of selected variables.
- Table.Select return to the data frame with all variables selected (from all studies or tables)
- List.Selec.Var return to the character with the names of all variables selected.
- List.Selec.Est list of all variables selected (with its respective table)
- Compromise.Coords Coords of projected observations in compromise matrix.

**Accesors**

- `Coord.Select(x), Coord.Select(x) <- value`: matrix are coordenates (Betas) of selected variables.
- `Table.Select(x), Table.Select(x) <- value`: return to the data frame with all variables selected (from all studies or tables)
- `List.Selec.Var(x), List.Selec.Var(x) <- value`: return to the character with the names of all variables selected.
- `List.Selec.Est(x), List.Selec.Est(x) <- value`: return to the character with the names of all variables selected. list of all variables selected (with its respective table)
SelectVar-general-functions

**print**  Generated basic output for SelectVar class  
**summary**  Generated basic statistics for SelectVar class  
**SelectVar**  Getters for their respective slots.

SelectVar-general-functions

**print**  Basic output for SelectVar class  
**summary**  Basic statistics for SelectVar class

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

References


See Also

**Biplot**, and additional related SelectVar class functions.

Examples

```r
showClass("SelectVar")
```
## summary.DiStatis

**Description**

`summary.DiStatis` a DiStatis object

**Usage**

```
## S4 method for signature 'DiStatis'
summary(object)
```

**Arguments**

- `object` DiStatis class object.

**Value**

- `summary` console output text with increasing detail of DiStatis object.

**Author(s)**

M L Zingaretti, J A Demey, J L Vicente-Villardon, J R Demey

**See Also**

`DiStatis`
Example

```r
\begin{verbatim}
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)

  summary(fit)
\end{verbatim}
```

Description

**summary.GP** a GroupProj object

Usage

```r
## S4 method for signature 'GroupProj'
summary(object)
```

Arguments

- `object` GroupProj class object.

Value

- `summary` console output text with increasing detail of GroupProj object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardon, J R Demey

See Also

- `GroupProj`

Examples

```r
\begin{verbatim}
  \{ 
    data(NCI60Selec)
    fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)

    A<-SelectVar(fit,Crit="p-val(Bonf)",perc=0.95)
    M3<-GroupProj(A,NGroups=4,method="ward",metric="euclidean")

    summary(M3)
  \}
\end{verbatim}
```
**TrajPlot**

---

**summary**

*a SelectVar object Generic Print/Summary method for SelectVar class output visualization.*

---

### Description

*summary* a SelectVar object Generic Print/Summary method for SelectVar class output visualization.

### Usage

```r
## S4 method for signature 'SelectVar'
summary(object)
```

### Arguments

- `object` SelectVar class object.

### Value

- `summary` console output text with increasing detail of SelectVar object.

### Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardon, J R Demey

### See Also

- `SelectVar`

### Examples

```r
example <- function(){
  data(NCI60Selec)
  fit <- DiStatis(NCI60Selec, Scale=TRUE, Center=TRUE)
  A <- SelectVar(fit, Crit="p-val(Bonf)", perc=0.95)
  summary(A)
}
```

---

**TrajPlot**

---

### Description

Plot a TrajPlot of a DiStatis object

---
Usage

## S4 method for signature 'DiStatis'
TrajPlot(x,xlabT="Dim 1", ylabT="Dim 2",
mainTraj=NULL,legend=TRUE ,xlimi=NULL,ylimi=NULL,panel=TRUE,
colours=NULL,...)

Arguments

x             DiStatis class object.

xlabT         character for the x-label title for plot

ylabT         character for the y-label title for plot

mainTraj      the main proj plot

legend        Logical. Indicates whether the legend prints

xlimi         vector bounds to x-axes.

ylimi         vector bounds to y-axes.

panel         logical if is true, the trajectories are plotted in panel-plot

colours       for plot

...            additional parameters for plot

Value

plotted Trajectories Plot of the given DiStatis object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente Villardon, J R Demey

Examples

{
  Z2<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  Colores2<-c(rep(colors()[657],5),rep(colors()[637],6),
    rep(colors()[537],7),rep(colors()[552],6),rep(colors()[57],10),
    rep(colors()[300],8),rep(colors()[461],7),rep(colors()[450],2),
    rep(colors()[432],7))
  Colores1<-c(rep("Breast",5),rep("CNS",6),rep("Colon",7),
    rep("Leukemia",6),rep("Melanoma",10),rep("Lung",8),rep("Ovarian",7),
    rep("Prostate",2),rep("Renal",7))
  TrajPlot(Z2,xlabT = "",ylabT="",colours=Colores2,legend=FALSE)
  legend("topleft",unique(Colores1),col=unique(Colores2),bty="n",pch=16,cex=1)
}

Description

Were selected twelve wines made from Sauvignon Blanc grapes coming from three wine regions (four wines from each region): New Zealand, France, and Canada and then were interviewed 10 expert assessors to evaluate these wines.

Usage

data(winesassesors)

Format

winesassesors This data frame contains an list of length 10 with 12 rows each. There are 10 studies, the assessors.

Value

List with 10 items (all data.frame) with 12 rows each (common elements in Statis Methods) and different variables types.

Source


References


Examples

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