Package ‘kimod’

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Type Package

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

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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

## 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 , ...)
Biplot

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()[57],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=Col1, Type="SQRT", xlim=c(-2,2), ylim=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="CMP")`

`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 y-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
See Also

CompPlot, TrajPlot.

Examples

Z2<-DiStatis(NCI60Selec, Scale=TRUE, Center=TRUE)
M<-Bootstrap(Z2)
if (interactive()) {
  BootPlot(M)
}
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))
BootPlot(M, Points = FALSE, cex.lab = 0.7, cex.axis = 0.7,
         las = 1, xlim = c(-0.003, 0.002), ylim = c(-0.005, 0.007),
         legend = FALSE, col = Colores2)
legend("topleft", unique(Colores1), col = unique(Colores2),
       bty = "n", pch = 16, cex = 1)

---

**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)

### S4 method for signature 'DiStatis'

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

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

```r
{  
  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.
• QRO.Boot(x), QRO.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

diplay("showClass("Bootstrap")"

CompPlot

Plot a CompPlot of a DiStatis object

Description

Plot a CompPlot of a DiStatis object

Usage

```R
# 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()[100],9),rep(colors()[461],7),rep(colors()[450],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)
}
```
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

DiStatis(Data = NULL, Distance = c(), Center = TRUE, Scale = TRUE, CorrelVector = 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, pearsong, 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.

CorrelVector

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.Cords: 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

Accesors

- 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.Cords(x), Compromise.Cords(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

showClass("DiStatis")

---

### GroupProj

**GroupProj of SelectVar object**

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"), ...)
```

## S4 method for signature 'SelectVar'

```r
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.
The methods implemented are "average" ([unweighted pair-] group arithmetic average method, aka "single" (single linkage), "complete" (complete linkage), "ward" (Ward's method), "weighted" (weighted average linkage, aka a generalization "flexible" which uses a constant version of) the Lance-Williams formula and the par.method argument. Also, a generalization "average" aka a using the Lance-Williams formula and par.method. (See `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

```r
{
  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.

Fields

- SortList list the clustering variables
- ProyGroups coords (beta) for Groups representant.
- Groups list of clusters.
Accesors

- SortList(x), SortList(x) <- value: list the clustering variables
- ProyGroups(x), ProyGroups(x) <- value: coords (beta) for Groups representant.
- Groups(x), Groups(x) <- 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**

**NCI60Selec_ESet**

**Examples**

```r
data(NCI60Selec)
```

<table>
<thead>
<tr>
<th>NCI60Selec_ESet</th>
<th>Microarray gene expression profiles of the NCI 60 cell lines from 4 different platforms.</th>
</tr>
</thead>
</table>

**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**

```r
data(NCI60Selec_ESet)
```

**Format**

NCI60Selec_ESet This data is an list of length 4.

**Value**

NCI60Select_ESet: list of ExpressionSet from four microarrays studies.

**Source**


**References**


**Examples**

```r
data(NCI60Selec_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

\texttt{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

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

print(A)
}
\end{verbatim}

Description

\texttt{print.DiStatis} a \texttt{DiStatis} object Generic Print/Summary method for \texttt{DiStatis} class output visualization.

Usage

\begin{verbatim}
## S4 method for signature 'DiStatis'
print(x)
\end{verbatim}

Arguments

\begin{itemize}
\item \texttt{x} \hspace{1cm} \texttt{DiStatis} class object.
\end{itemize}

Value

according to the call

\texttt{print} console output text with increasing detail of \texttt{DiStatis} object.

Author(s)

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

See Also

\texttt{DiStatis}
print.GP

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

print.GP
print.GP
print.GP

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

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

```r
## 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

```r
(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
```r
## 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
```r
Z2<-DiStatis(NCI60Selec, Scale=TRUE, Center=TRUE)
RVPlot(Z2)
```
**SelectVar**

**Function SelectVar of DiStatis object**

**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**

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

```
## 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")`. Criterious 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 obtain 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. object,ord=FALSE.

**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(NCI60Select)
  Z1<-DiStatis(NCI60Select)
  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)
summary.Bootstrap

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

showClass("SelectVar")

summary.Bootstrap  print.Bootstrap or summary.Bootstrap a Bootstrap object

Description

Generic Print/Summary method for Bootstrap class output visualization.

Usage

## S4 method for signature 'Bootstrap'
summary(object)

Arguments

object  Bootstrap class object.
Value
according to the call
summary console output text with increasing detail of Bootstrap object.

Author(s)
M L Zingaretti, J A Demey, J L Vicente-Villardon, J R Demey

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

summary(A)
}

summary.DiStatis summary.DiStatis a DiStatis object

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-Zambrano, J L Vicente-Villardon, J R Demey

See Also
DiStatis
**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
{
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  summary(fit)
}
```
summary.SV  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
{
  data(NCI60Selec)
  fit<-DiStatis(NCI60Selec,Scale=TRUE,Center=TRUE)
  A<-SelectVar(fit,Crit="p-val(Bonf)",perc=0.95)

  summary(A)
}
```

---

**TrajPlot**  

Plot a TrajPlot of a DiStatis object

### Description

Plot a TrajPlot of a DiStatis object
## S4 method for signature 'DiStatis'

```r
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

```r
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

data(winesassesors)
Index

*Topic datasets
DiStatis, 9
NCI60Select, 14
NCI60Select, ESet, 15

*Topic winesassesors
 winesassesors, 28

agnes, 13

Biplot, 2, 2, 12, 23
Biplot, SelectVar-method (Biplot), 2
Bootstrap, 4
Bootstrap, Bootstrap-method (Bootstrap), 4
Bootstrap-class, 6
Bootstrap-methods (Bootstrap), 5

class: DiStatis (DiStatis-class), 10
Comparisions.Boot (Bootstrap-class), 6
Comparisions.Boot, Bootstrap-method (Bootstrap-class), 6
Comparisions.Boot<-, Bootstrap-method (Bootstrap-class), 6
CompPlot, 5, 7, 12
CompPlot, DiStatis-method (CompPlot), 7
Compromise.Coods (DiStatis-class), 10
Compromise.Coods, DiStatis-method (DiStatis-class), 10
Compromise.Coods<-, DiStatis-method (DiStatis-class), 10
Compromise.Matrix (DiStatis-class), 10
Compromise.Matrix, DiStatis-method (DiStatis-class), 10
Compromise.Matrix<-, DiStatis-method (DiStatis-class), 10
Coord.Select (SelectVar-class), 22
Coord.Select, SelectVar-method (SelectVar-class), 22
Coord.Select<-, SelectVar-method (SelectVar-class), 22

DiStatis, 9, 12, 17, 24
DiStatis-class, 10, 10

DiStatis-methods (DiStatis), 9

EigValues.Boot (Bootstrap-class), 6
EigValues.Boot, Bootstrap-method (Bootstrap-class), 6
EigValues.Boot<-, Bootstrap-method (Bootstrap-class), 6
Elipses.Boot (Bootstrap-class), 6
Elipses.Boot, Bootstrap-method (Bootstrap-class), 6
Elipses.Boot<-, Bootstrap-method (Bootstrap-class), 6
Euclid.Img (DiStatis-class), 10
Euclid.Img, DiStatis-method (DiStatis-class), 10
Euclid.Img<-, DiStatis-method (DiStatis-class), 10

GroupProj, 3, 12, 18, 25
GroupProj, SelectVar-method (GroupProj), 12
GroupProj-class, 13
GroupProj-SelectVar-methods (GroupProj), 12
Groups (GroupProj-class), 13
Groups, GroupProj-method (GroupProj-class), 13
Groups<-, GroupProj-method (GroupProj-class), 13

Inertia.Boot (Bootstrap-class), 6
Inertia.Boot, Bootstrap-method (Bootstrap-class), 6
Inertia.Boot<-, Bootstrap-method (Bootstrap-class), 6
Inertia.comp (DiStatis-class), 10
Inertia.comp, DiStatis-method (DiStatis-class), 10
Inertia.comp<-, DiStatis-method (DiStatis-class), 10
Inertia.RV (DiStatis-class), 10
Inertia.RV, DiStatis-method (DiStatis-class), 10
Inertia.RV<-,DiStatis-method
(DiStatis-class), 10

List.Selec.Est (SelectVar-class), 22
List.Selec.Est,SelectVar-method
(SelectVar-class), 22
List.Selec.Est<-,SelectVar-method
(SelectVar-class), 22
List.Selec.Var (SelectVar-class), 22
List.Selec.Var,SelectVar-method
(SelectVar-class), 22
List.Selec.Var<-,SelectVar-method
(SelectVar-class), 22

NCI60Selec, 14
NCI60Selec_ESet, 15

PanelPlot, 16
PanelPlot,DiStatis-method (PanelPlot), 16
print, 16
print,Bootstrap-method
(print.Bootstrap), 16
print,DiStatis-method (print.DiStatis), 17
print,GroupProj-method (print.GP), 18
print,SelectVar-method (print.SV), 19
print.Bootstrap, 16, 23
print.DiStatis, 17, 17
print.GP, 18, 18
print.SV, 19, 19
ProyGroups (GroupProj-class), 13
ProyGroups,GroupProj-method
(GroupProj-class), 13
ProyGroups<-,GroupProj-method
(GroupProj-class), 13

QRO.Boot (Bootstrap-class), 6
QRO.Boot,Bootstrap-method
(Bootstrap-class), 6
QRO.Boot<-,Bootstrap-method
(Bootstrap-class), 6

Ratios.Boot (Bootstrap-class), 6
Ratios.Boot,Bootstrap-method
(Bootstrap-class), 6
Ratios.Boot<-,Bootstrap-method
(Bootstrap-class), 6
RQQ (DiStatis-class), 10
RQQ,DiStatis-method (DiStatis-class), 10
RQQ<-,DiStatis-method (DiStatis-class), 10
RV (DiStatis-class), 10
RV,DiStatis-method (DiStatis-class), 10
RV<-,DiStatis-method (DiStatis-class), 10
RVPlot, 20
RVPlot,DiStatis-method (RVPlot), 20
SelectVar, 19, 21, 26
SelectVar,DiStatis-method (SelectVar), 21
SelectVar-class, 22
SelectVar-methods (SelectVar), 21
SortList (GroupProj-class), 13
SortList,GroupProj-method
(GroupProj-class), 13
SortList<-,GroupProj-method
(GroupProj-class), 13
Stability.Boot (Bootstrap-class), 6
Stability.Boot,Bootstrap-method
(Bootstrap-class), 6
Stability.Boot<-,Bootstrap-method
(Bootstrap-class), 6
summary, 16, 26
summary,Bootstrap-method
(summary.Bootstrap), 23
summary,DiStatis-method
(summary.DiStatis), 24
summary,GroupProj-method
(summary.GP), 25
summary,SelectVar-method
(summary.SV), 26
summary.Bootstrap, 23, 23
summary.DiStatis, 24, 24
summary.GP, 25, 25
summary.SV, 26

Table.Select (SelectVar-class), 22
Table.Select,SelectVar-method
(SelectVar-class), 22
Table.Select<-,SelectVar-method
(SelectVar-class), 22
Trajectories (DiStatis-class), 10
Trajectories,DiStatis-method
(DiStatis-class), 10
Trajectories<-,DiStatis-method
(DiStatis-class), 10
TrajPlot, 5, 26
TrajPlot,DiStatis-method (TrajPlot), 26

winesassessors, 28