

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

Collate 'ReadData.R' 'DiStatis-Class.R' 'Bootstrap-Class.R'
'SelectVar-Class.R' 'GroupProj-Class.R' 'Auxiliares.R'
'CalculateDist.R' 'ComputeDistances.R' 'cbinPad.R'
'DiStatis-DiStatis.R' 'DiStatis-CompPlot.R' 'DiStatis-RVPlot.R'
'DiStatis-PanelPlot.R' 'DiStatis-TrajPlot.R' 'DiStatis-print.R'
'DiStatis-Bootstrap.R' 'Bootstrap-BootPlot.R'

'Bootstrap-print.R' 'DiStatis-SelectVar.R' 'SelectVar-print.R'
 'SelectVar-Biplot.R' 'GroupProj.R' 'GroupProj-print.R'

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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 ,...)
```

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

```
{
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,xlim=c(-3,3),ylim=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,xlim=c(-3,3),
      ylim=c(-3,3),Groups=TRUE,NGroups=6)
legend("topright",unique(Colores1),col=unique(Colores2),
      bty="n",pch=16,cex=0.6)
data(winesassessors)
Z3<-DiStatis(winesassessors)
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",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

```

## S4 method for signature 'Bootstrap'
BootPlot(x,xlabProj=NULL,ylabProj=
  NULL,mainProj=NULL,legend=TRUE,colour=NULL,
  xlim=NULL,ylim=NULL,Points=TRUE,...)

```

Arguments

<code>x</code>	object of Bootstrap-Class
<code>xlabProj</code>	character for the x-label title for plot
<code>ylabProj</code>	character for the x-label title for plot
<code>mainProj</code>	main to proj plot
<code>legend</code>	Logical. It indicates whether the legend prints
<code>colour</code>	colours for ellipsis
<code>xlim</code>	bounds of x-axis
<code>ylim</code>	bounds of y-axis
<code>Points</code>	logical if is true, the points are plotted
<code>...</code>	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

Funtion Bootstrap of a DiStatis object

Description

This function is use 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

1. Efron, B., Tibshirani, R.J. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.
2. Ringrose, T.J. (1992). Bootstrapping and Correspondence Analysis in Archaeology. Journal of Archaeological. Science.19:615-629.

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)
- Comparisons.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(

Accessors

- `Ratios.Boot(x)`, `Ratios.Boot(x) <-value`: Ratios (with Bonferroni Correction for all observations in compromise from all dimensions)
- `Comparisons.Boot(x)`, `Comparisons.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.
- `Stability.Boot(x)`, `Stability.Boot(x) <-value`: Bootstrap Stability.
- `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

1. Efron, B., Tibshirani, RJ. (1993). An introduction to the bootstrap. New York: Chapman and Hall. 436p.
2. Ringrose, T.J. (1992). Bootstrapping and Correspondence Analysis in Archaeology. Journal of Archaeological. Science.19:615-629.

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

```
{
## 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()[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)
}
```

DiStatis	<i>DiStatis of a DiStatis object High level constructor of DiStatis class object</i>
----------	--

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, pearsonabs, 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

1. Abdi, H., Williams, L.J., Valentin, D., & Bennani-Dosse, M. (2012). STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. *WIREs Comput Stat*, 4, 124-167.
2. Escoufier, Y. (1976). Operateur associe a un tableau de donnees. *Annales de laInsee*, 22-23, 165-178.
3. Escoufier, Y. (1987). The duality diagram: a means for better practical applications. En P. Legendre & L. Legendre (Eds.), *Developments in Numerical Ecology*, pp. 139-156, NATO Advanced Institute, Serie G. Berlin: Springer.
4. L'Hermier des Plantes, H. (1976). Structuration des Tableaux a Trois Indices de la Statistique. [These de Troisieme Cycle]. University of Montpellier, France.

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.

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

1. Abdi, H., Williams, L.J., Valentin, D., & Bennani-Dosse, M. (2012). STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. *WIREs Comput Stat*, 4, 124-167.
2. Escoufier, Y. (1976). Operateur associe a un tableau de donnees. *Annales de laInsee*, 22-23, 165-178.
3. Escoufier, Y. (1987). The duality diagram: a means for better practical applications. En P. Legendre & L. Legendre (Eds.), *Developments in Numerical Ecology*, pp. 139-156, NATO Advanced Institute, Serie G. Berlin: Springer.
4. L'Hermier des Plantes, H. (1976). *Structuration des Tableaux a Trois Indices de la Statistique*. [These de Troisieme Cycle]. University of Montpellier, France.

See Also

[CompPlot](#), [Biplot DiStatis](#), and additional related DiStatis class functions.

Examples

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

GroupProj

GroupProj of *SelectVar* object

Description

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

Usage

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

```
## 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 <i>SelectVar</i> 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 b "single" (single linkage), "complete" (complete linkage), "ward" (Ward's method), "weighted" (weighted average linkage, aka b its generalization "flexible" which uses (a constant version of) the Lance-Williams formula and the par.method argument, and "gaverage" a generalized "average" aka b 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)
}
```

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

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
- ProjGroups coords (beta) for Groups representant.
- Groups list of clusters.

Accessors

- `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

Cell Miner <http://discover.nci.nih.gov/cellminer/>.

References

Reinhold WC, Sunshine M, Liu H, Varma S, Kohn KW, Morris J, Doroshow J, Pommier Y CellMiner: A Web-Based Suite of Genomic and Pharmacologic Tools to Explore Transcript and Drug Patterns in the NCI-60 Cell Line Set. *Cancer Research*. 2012 Jul, 15;72(14):3499-511

Examples

```
data(NCI60Selec)
```

NCI60Selec_ESet	<i>Microarray gene expression profiles of the NCI 60 cell lines from 4 different platforms.</i>
-----------------	---

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_ESet)
```

Format

NCI60Selec_ESet This data is an list of length 4.

Value

NCI60Select_ESet: list of ExpressionSet from four microarrays studies.

Source

Cell Miner <http://discover.nci.nih.gov/cellminer/>.

References

Reinhold WC, Sunshine M, Liu H, Varma S, Kohn KW, Morris J, Doroshow J, Pommier Y CellMiner: A Web-Based Suite of Genomic and Pharmacologic Tools to Explore Transcript and Drug Patterns in the NCI-60 Cell Line Set. *Cancer Research*. 2012 Jul, 15;72(14):3499-511

Examples

```
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

print console output text with increasing detail of Bootstrap object.

Author(s)

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

Examples

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

  print(A)

}
```

print.DiStatis [print.DiStatis](#) a DiStatis object Generic Print/Summary method for DiStatis class output visualization.

Description

[print.DiStatis](#) a DiStatis object Generic Print/Summary method for DiStatis class output visualization.

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-Villardón, J R Demey

See Also

[DiStatis](#)

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-Villardón, 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 <i>SelectVar</i> object Generic Print/Summary method for <i>SelectVar</i> 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-Villardón, 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 *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").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. 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

1. Demey, J., Vicente-Villardón, J. L., Galindo, M.P. & Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. *Bioinformatics*, 24(24), 2832-2838.
2. Gabriel, K. (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika* 58(3), 453–467.

3. Gower, J. & Hand, D. (1996). Biplots, Monographs on statistics and applied probability. 54. London: Chapman and Hall., 277 pp.

Examples

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

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.
3. Plotting Biplot-Group.

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.

Accessors

- 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

1. Demey, J., Vicente-Villardón, J. L., Galindo, M.P. & Zambrano, A. (2008) Identifying Molecular Markers Associated With Classification Of Genotypes Using External Logistic Biplots. *Bioinformatics*, 24(24), 2832-2838.
2. Gabriel, K. (1971). The biplot graphic display of matrices with application to principal component analysis. *Biometrika* 58(3), 453–467.
3. Gower, J. & Hand, D. (1996). *Biplots, Monographs on statistics and applied probability*. 54. London: Chapman and Hall., 277 pp.

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-Villardón, 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-Villardón, J R Demey

See Also

[DiStatis](#)

Examples

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

  summary(fit)
}
```

summary.GP

[summary.GP](#) a *GroupProj* object

Description

[summary.GP](#) a *GroupProj* object

Usage

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

Arguments

object *GroupProj* class object.

Value

according to the call

summary console output text with increasing detail of *GroupProj* object.

Author(s)

M L Zingaretti, J A Demey-Zambrano, J L Vicente-Villardón, 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")

  summary(M3)
}
```

summary.SV	summary a <i>SelectVar</i> object Generic Print/Summary method for <i>SelectVar</i> class output visualization.
------------	---

Description

[summary](#) a *SelectVar* object Generic Print/Summary method for *SelectVar* class output visualization.

Usage

```
## 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-Villardón, 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)

  summary(A)
}
```

TrajPlot	<i>Plot a TrajPlot of a DiStatis object</i>
----------	---

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)
}
```

winesassessors

Description of a set of wines by a group of expert assessors.

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(winesassessors)
```

Format

winesassessors 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 differents variables types.

Source

Abdi, H., Williams, L.J., Valentin, D., & Bennani-Dosse, M. (2012). STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat, 4, 124-167.

References

Abdi, H., Williams, L.J., Valentin, D., & Bennani-Dosse, M. (2012). STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat, 4, 124-167.

Examples

```
data(winesassessors)
```

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