Package ‘mogsa’

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Type Package

Title Multiple omics data integrative clustering and gene set analysis

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Description This package provides a method for doing gene set analysis based on multiple omics data.

License GPL-2

Depends R (>= 3.2.0)

Imports methods, graphite, genefilter, BiocGenerics, gplots, GSEABase, Biobase, parallel, corpcor, svd, cluster

VignetteBuilder knitr

Suggests BiocStyle, knitr

biocViews GeneExpression, PrincipalComponent, StatisticalMethod, Clustering, Software

NeedsCompilation no

R topics documented:

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Description

Modern "omics" technologies enable quantitative monitoring of the abundance of various biological molecules in a high-throughput manner, accumulating an unprecedented amount of quantitative information on a genomic scale. Gene set analysis is a particularly useful method in high throughput data analysis since it can summarize single gene level information into the biological informative gene set levels. This package provide a method do the gene set analysis based on multiple omics data that describing the same set of observations/samples.

Details

Package: mogsa
Type: Package
Version: 1.3.1
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Depends: methods

The main function in the package is "mogsa", see the function help manu for more details.
annotate.gs

Author(s)
Chen Meng
Maintainer: Chen Meng <chen.meng@tum.de>

References
Chen Meng, Dominic Helm, Martin Frejno, and Bernhard Kuster. moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. Journal of Proteome Research 2016.

Examples
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)

# using a list of data.frame as input
mgsa1 <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)

# using moa as input
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
smoa <- sup.moa(ana, sup=NCI60_4array_supdata, nf=3)
mgsa2 <- mogsa(x = ana, sup=NCI60_4array_supdata, nf=3)
mgsa3 <- mogsa(x = ana, sup=smoa)

---

annotate.gs  Summary annotation information of a gene set

Description
Retrieve variables/features (genes) mapped to the annotated data sets in a gene set. Also returns the information about presence and absence of a feature for a specific data set.

Usage
annotate.gs(mgsa, gs)

Arguments
- mgsa: An object of class mogsa-class or moa.sup-class.
- gs: The name of a geneset

Value
This function returns a data.frame. The first column shows the name of features. The last column is for the count of how many data sets has the corresponding features. Columns in the middle contains logical value indicating whether a feature is presented in a particular data set.

Author(s)
Chen Meng
See Also
see GIS

Examples

```r
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
msa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
             proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
allgs <- colnames(NCI60_4array_supdata[[1]])
annotate.gs(msa, allgs[1])
```

---

**bootMbpca**  
*Bootstrap mbpca to estimate the coherence of different data sets*

Description

Bootstrap mbpca to estimate the coherence of different data sets and estimate the number of components should be included in an analysis.

Usage

```r
bootMbpca(moa, mc.cores = 1, B = 100, replace = TRUE,
          resample = c("sample", "gene", "total"), log = "y", ncomp = NULL, method = NULL,
          maxiter = 1000, svd.solver = c("svd", "fast.svd", "propack"), plot = TRUE)
```

Arguments

- **moa**: An object of `moa` returned by `mbpca`.
- **mc.cores**: Integer; number of cores used in bootstrap. This value is passed to function `mclapply`
- **B**: Integer; number of bootstrap
- **replace**: Logical; sampling with or without replacement
- **resample**: Could be one of "sample", "gene" or "total". "sample" and "gene" means sample-wise and variable-wise resampling, respectively. "total" means total resampling.
- **log**: Could be "x" , "y" or "xy" for plot log axis
- **ncomp**: Passed to function `mbpca`. In most of cases, user do not need to specify this argument because it could be inferred from `moa`.
- **method**: Passed to function `mbpca`. In most of cases, user do not need to specify this argument because it could be inferred from `moa`.
- **maxiter**: Passed to function `mbpca`. In most of cases, user do not need to specify this argument because it could be inferred from `moa`.
- **svd.solver**: Passed to function `mbpca`. In most of cases, user do not need to specify this argument because it could be inferred from `moa`.
- **plot**: Logical; whether the result should be plotted.
Details
update details.

Value
It returns a matrix, columns are eigenvalues for different components. Each rows is a bootstrap sample.

Author(s)
Chen Meng

Examples
# see examples in \code{\link{mbpca}}

bootMbpcaK
An internal function called by bootMbpca.

Description
An internal function called by bootMbpca.

Usage
bootMbpcaK(data, replace, B = 100, mc.cores = 1, resample = c("sample", "total", "gene"), ncomp, method, k, center = FALSE, scale = FALSE, option = "uniform", maxiter = 1000, svd.solver = c("svd", "fast.svd", "propack"))

Arguments
data A list of matrix to bootstrap.
replace A logical variable to indicate sampling with or without replacement
B Integer; number of bootstrap.
mc.cores Integer; number of cores used in bootstrap. This value is passed to function mclapply.
resample Could be one of "sample", "gene" or "total", "sample" and "gene" means sample-wise and variable-wise resampling, respectively. "total" means total resampling.
ncomp passed to mbpca.
method passed to mbpca.
k passed to mbpca.
center passed to mbpca.
scale passed to mbpca.
option passed to mbpca.
maxiter passed to mbpca.
svd.solver passed to mbpca.
Value

A matrix of mbpca eigenvalues resulted from bootstrap samples

Author(s)

Chen Meng

See Also

bootMbpca

box.gs.feature

boxplot of gene set variables across all samples.

Description

boxplot to show the variables (e.g. gene expression) of a gene set across all samples.

Usage

box.gs.feature(x, gs, moa = NULL, col = 1, layout = NULL, plot = TRUE, obs.order = NULL, ...)

Arguments

x
Gene set want to be explored

gs
An object of class mgsa-class or moa.sup-class

moa
An object of class moa. It is required if x is an object of class moa.sup-class

col
The color code for samples

layout
The layout control, see examples.

plot
A logical indicates whether the result should be plotted. If FALSE, a list of expression matrix of the gene set genes is returned. Otherwise nothing returned.

obs.order
Can be used to reorder the matrix, could be used when clustering result is available.

...
The arguments passed to boxplot

Details

This is a convenient function used to explore the expression of a set of features/genes

Value

Do not return anything (plot=TRUE) or return a list of matrix (plot=FALSE) depends on plot argument.

Author(s)

Chen meng
Examples

# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
mgsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
              proc.row = "center_ssq!", w.data = "inertia", statis = TRUE)

allgs <- colnames(NCI60_4array_supdata[[1]])
colcode <- as.factor(sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\."), ",", 1))
a <- box.gs.feature(x=mgsa, gs=allgs[5], type=3, col=colcode, plot=FALSE)
box.gs.feature(x=mgsa, gs=allgs[5], type=3, col=colcode, plot=TRUE, layout=matrix(c(1:4, 2, 2)))

---

**combine-methods**

Combine two objects of class mgsa into one.

## Description

This function could only be used to combine two "mgsa" objects at present; using "Reduce" function to combine more.

## Usage

```r
combine(x, y, ...)
```

## Arguments

- `x` one mgsa object
- `y` another mgsa object
- `...` ignored. Only two mgsa objects could be combined, using "Reduce" to combine more than two sets.

## Value

A combined object of class mgsa will be returned.

## Methods

signature(x = "mgsa", y = "mgsa") To combine two objects of mgsa.

This function could only be used to combine two "mgsa" objects; using "Reduce" function to combine more.

## Examples

```r
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
# split gene set annotation into two sets.
sup1 <- lapply(NCI60_4array_supdata, function(x) x[, 1:10])
sup2 <- lapply(NCI60_4array_supdata, function(x) x[, -(1:10)])
# project two sets of annotation
```
decompose.gs.group <- mogsa(x = NCI60_4arrays, sup=sup1, nf=9, 
proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)

mgsa2 <- mogsa(x = NCI60_4arrays, sup=sup2, nf=9, 
proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)

# combine two independent mgsa sets
mgsa_comb <- combine(mgsa1, mgsa2)
dim(getmgsa(mgsa1, "score"))
dim(getmgsa(mgsa2, "score"))
dim(getmgsa(mgsa_comb, "score"))
decompose.gs.ind

Author(s)

Chen Meng

References

TBA

See Also

See Also `decompose.gs.ind`

Examples

# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)

# using a list of data.frame as input
mgsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
               proc.row = "center_ssq!", w.data = "inertia", statis = TRUE)

colcode <- as.factor(sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\."), ",")
decompose.gs.group(x = mgsa, gs = 2, group = colcode, decomp = "data", plot = TRUE)
decompose.gs.group(x = mgsa, gs = 2, group = colcode, decomp = "pc", nf = 3, plot = TRUE)

.subtitle

Description

Barplot of decomposed gene set scores, either with respect to datasets or axes.

Usage

decompose.gs.ind(x, gs, obs, type = 3, nf = 2, plot=TRUE, col.data = NULL,
col.pc = NULL, legend = TRUE)

Arguments

x

An object of class `mgsa-class` or `moa.sup-class`

gs

The gene set want to exam.

obs

The observations want to exam.

type

Which type of plot. type=1 - the data-pc mode; type=2 - the pc-data mode;
type=3 - both. See detail.

nf

The number of axes/PCs to be calculated and plotted.

plot

A logical indicates if a plot should be drawn

col.data

The bar color of datasets

col.pc

The bar color of PCs

legend

A logical if legend should be shown
Details

type=1 (the data-pc mode), the axes/PCs are represented as the narrow bars with different colors and the background wide bars behind narrow bars are gene set scores for datasets, which is calculated from the sum of all underlying individual axes/PC scores. When type=2 (the pc-data mode) the interpretation of narrow and wide bars are in the other way around. If type=3, both are shown.

This function could only be used to check the decomposition of gene set scores of a single observation. So the function is not efficient when the number of observation is large. Another function `decompose.gs.group`, could be used in this case, particularly when the cluster information of the observation panel is available.

Value

Return nothing or a matrix depends on how argument `plot` is set.

Author(s)

Chen Meng

References

TBA

See Also

See Also as `decompose.gs.group`

Examples

```r
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
mgsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
              proc.row = "center_ssq!", w.data = "inertia", statis = TRUE)
allgs <- colnames(NCI60_4array_supdata[[1]])
# plot
decompose.gs.ind(x=mgsa, gs=allgs[5], obs="BR.MDA_MB_231", type=2, nf=5)
# or
# decompose.gs.ind(x=getmgsa(mgsa, "sup"), gs=allgs[5], obs="BR.MDA_MB_231", type=3, nf=5)
```

deflat
deflat function used by `mbpca`

Description

An internal function called by `mbpca`.

Usage

deflat(x, t, tb, pb, method = "globalScore")
## Arguments

- **x**: A list of matrix want to deflat
- **t**: The global scores returned by `msvd` or `nipalsSoftK`
- **tb**: The block scores returned by `msvd` or `nipalsSoftK`
- **pb**: The block loadings returned by `msvd` or `nipalsSoftK`
- **method**: A character to specify the deflation strategy, could be one of c("globalScore", "blockLoading", "blockScore").

## Value

A list of deflated matrix

## Author(s)

Chen Meng

---

### distMoa

*Calculate the distance matrix from an object of class moa-class.*

### Description

A convenient function to calculate the distance matrix from an object of class *moa-class*.

### Usage

```r
distMoa(x, nf = NA, tol = 1e-05, method = "euclidean", diag = FALSE, upper = FALSE, p = 2)
```

### Arguments

- **x**: An object of class *moa-class*.
- **nf**: Integer; the number of component used to calculate the distance. Default setting (NA) will keep all the axes.
- **tol**: Numerical; the tolerance of component with low variance.
- **method**: passed to function `dist`
- **diag**: passed to function `dist`
- **upper**: passed to function `dist`
- **p**: passed to function `dist`

### Value

An object of class `dist`, see function "dist".

### Author(s)

Chen Meng
Examples

```r
# see examples in \code{\link{mbpca}}

data("NCI60_4arrays")
moa <- mbpca(NCI60_4arrays, ncomp = 10, k = "all", method = "globalScore", option = "lambda1",
          center=TRUE, scale=FALSE)

dst <- distMoa(moa)
```

Description

get values/slot in an object of class "mgsa". The "mgsa" consists of two S4 class objects, \code{moa-class} and \code{moa.sup-class}. This function could extract values in these two components directly.

Usage

```r
getmgsa(mgsa, value)
```

Arguments

- `mgsa` An object of class \code{mgsa-class}.
- `value` The name of the value want to extract from "mgsa". See detail for options.

Details

- if value in c("call", "moa", "sup"), the function equal function \code{slot}.
- if value in c("eig", "tau", "partial.eig", "eig.vec", "loading", "fac.scr", "partial.fs", "ctr.obs", "ctr.var",
              "ctr.tab", "RV"), the function extract corresponding value from \code{moa-class}.
- if value in c("data", "coord.sep", "coord.comb", "score", "score.data", "score.pc", "score.sep", "p.val"),
              the function extract value from \code{moa.sup-class}.

Value

The function return the selected value in "mgsa".

Author(s)

Chen Meng

References

TBA
GIS

Examples

# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)

mgsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
              proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)

part.eig <- getmgsa(mgsa, "partial.eig")
barplot(as.matrix(part.eig))

GIS  
calculate gene influential scores of genes in a gene set.

Description

Calculate the gene influential score of individual feature to the overall variance of GS score. Using a leave-one-out procedure (See detail).

Usage

GIS(x, geneSet, nf=NA, barcol=NA, topN=NA, plot=TRUE, Fvalue=FALSE, ff=NA, cor=FALSE)

Arguments

- **x**: An object of class `mgsa-class`.
- **geneSet**: A character string or number to indicated the gene sets under consideration.
- **nf**: The number of PCs used in the calculation of gene set scores. The default is NA, which means using all the PCs in the mogsa. This should work for most of the cases.
- **barcol**: The color of the bars, which is used to distinguish features/genes from different datasets, so its length should be the same as the number of data sets.
- **topN**: An positive integer specify the number of top influencers that should to returned.
- **plot**: A logical indicate if the result should be plotted.
- **Fvalue**: A logical indicate if the GIS should be calculated in a supervised manner.
- **ff**: The vector indicates the group of columns for calculating the F-ratio when Fvalue=TRUE.
- **cor**: A logical indicates whether use correlation between reconstructed expression with GSS. This is faster than the standard GIS.

Details

The evaluation of the importance of a single feature is calculated in the supervised or unsupervised manner.

In the unsupervised manner, the value is calculated by:

\[
\log_2 \frac{\text{var}(\text{GS}_{-i})}{\text{var}(\text{GS})}
\]

where GS is the gene set score, and the GS_{-i} is a recalculate of gene set score without i’th feature. var() is the variance.

In the supervised manner, the value is calculated as the F-ratio over a class vector:
\[ \log_2(F(GS_{-i})/F(GS)) \]

Where \( F() \) is the calculation of F-ratio. The unsupervised GIS is encouraged since it works better for most of the cases in practice.

**Value**

An object of class `data.frame` contains three columns. The first column is the feature name, the second columns is the gene influential score. The third columns indicates from where the feature/gene is selected.

**Author(s)**

Chen Meng

**References**

TBA

**See Also**

see `annotate.gs`

**Examples**

```r
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
mgsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
              proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
allgs <- colnames(NCI60_4array_supdata[[1]])

# unsupervised measurement
GIS(mgsa, allgs[1], topN = 5)

# supervised measurement
tissueType <- as.factor(sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\."), 
                                
       "[", 1))
GIS(mgsa, allgs[1], topN = 5, Fvalue = TRUE, ff = tissueType)
# more PCs to calculate
GIS(mgsa, allgs[1], nf = 20, topN = 5, Fvalue = TRUE, ff = tissueType)
```

---

**matpower**

*compute the power of a matrix*

**Description**

the power of a matrix

**Usage**

`matpower(x, n, nf = min(dim(x)), tol = 1e-07)`
**Arguments**

- **x**: a numerical matrix object that the power of which should be calculated.
- **n**: The matrix to the power of.
- **nf**: The number of axes kept in the calculation of SVD and reconstruction.
- **tol**: The tolerance of the axis, singular vectors with singular value lower than tol will be ignored in the reconstruction.

**Details**

The power of a matrix is calculated in two steps: decomposition step: $x = UDV'$ and the reconstruction step: $x^n = U D^n V'$. In the reconstruction, the singular vectors with a singular value more than tol are kept.

**Value**

A matrix $x^n$

**Note**

Called by the wsvd function.

**Author(s)**

Chen Meng

**See Also**

See Also `wsvd`

**Examples**

```r
set.seed(56)
m <- matrix(rnorm(15), 5, 3)
s <- matpower(m, 2)
s <- matpower(m, -2)
```

---

**mbpca**

*Extension of PCA to analyze multiple data sets*

**Description**

Three approaches are supplied in this function, consensus PCA (CPCA), generalized CCA (GCCA) and multiple co-inertia analysis (MCIA).

**Usage**

```r
mbpca(x, ncomp, method, k = "all", center = TRUE, scale = FALSE, option = "uniform", maxiter = 1000, moa = TRUE, verbose = TRUE, svd.solver = c("svd", "fast.svd", "propack"))
```
Arguments

x A list of matrix or data.frame, where rows are variables and columns are samples. The columns among the matrices need to be match but the variables do not need to be.

ncomp An integer; the number of components to calculate. To calculate more components requires longer computational time.

method A character string could be one of c("globalScore", "blockScore", "blockLoading"). The "globalScore" approach equals consensus PCA; The "blockScore" approach equals generalized canonical correlation analysis (GCCA); The "blockLoading" approach equals multiple co-inertia analysis (MCIA);

k The absolute number (if k >= 1) or the proportion (if 0<k<1) of non-zero coefficients for the variable loading vectors. It could be a single value or a vector has the same length as x so the sparsity of individual matrix could be different.

center Logical; if the variables should be centered

scale Logical; if the variables should be scaled

option A character string could be one of c("lambda1", "inertia", "uniform") to indicate how the different matrices should be normalized. If "lambda1", the matrix is divided by its the first singular value, if "inertia", the matrix is divided by its total inertia (sum of square), if "uniform", none of them would be done.

maxiter Integer; Maximum number of iterations in the algorithm

moa Logical; whether the output should be converted to an object of class moa-class

verbose Logical; whether the process (# of PC) should be printed

svd.solver A character string could be one of c("svd", "fast.svd", "propack"). The default "fast.svd" has a good compromise between the robustness and speed. "propack" is the fastest but may failed to converge in practice.

Details
details need to update

Value
An object of class moa-class (if moa=TRUE) or an list object contains the following elements:
tb - the block scores
pb - the block loadings
t - the global scores
w - the weights of block scores to construct the global scor

Note
no note now

Author(s)
Chen Meng

References
reference need to be updated
See Also

see `moa` for non-iterative algorithms for multi-block PCA.

Examples

data("NCI60_4arrays")
tumorType <- sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\."), "[", 1)
colcode <- as.factor(tumorType)
levels(colcode) <- c("red", "green", "blue", "cyan", "orange",
                    "gray25", "brown", "gray75", "pink")
colcode <- as.character(colcode)

moa <- mbpca(NCI60_4arrays, ncomp = 10, k = "all", method = "globalScore", option = "lambda1",
               center=TRUE, scale=FALSE)
plot(moa, value="eig", type=2)
r <- bootMbpca(moa, mc.cores = 1, B=6, replace = FALSE, resample = "sample")

moas <- mbpca(NCI60_4arrays, ncomp = 3, k = 0.1, method = "globalScore", option = "lambda1",
               center=TRUE, scale=FALSE)

scr <- moaScore(moa)
scrs <- moaScore(moas)
diag(cor(scr[, 1:3], scrs))

layout(matrix(1:2, 1, 2))
plot(scrs[, 1:2], col=colcode, pch=20)
legend("topright", legend = unique(tumorType), col=unique(colcode), pch=20)
plot(scrs[, 2:3], col=colcode, pch=20)

gap <- moGap(moas, K.max = 12, cluster = "hcl")
gap$nClust

hcl <- hclust(dist(scrs))
cls <- cutree(hcl, k=4)
clsColor <- as.factor(cls)
levels(clsColor) <- c("red", "blue", "orange", "pink")
clsColor <- as.character(clsColor))

heatmap(t(scrs[hcl$order, ]), ColSideColors = colcode[hcl$order], Rowv = NA, Colv=NA)
heatmap(t(scrs[hcl$order, ]), ColSideColors = clsColor[hcl$order], Rowv = NA, Colv=NA)
genesis <- moaCoef(moas)
genesis$nonZeroCoef$agilent.V1.neg
Description

mgsa class here.

Objects from the Class

Objects can be created by calls of the form `new("mgsa", ...)`.

Slots

- `call`: call
- `moa`: Object of class `moa`
- `sup`: Object of class `moa.sup`

Methods

`signature(x = "mgsa", y = "mgsa")` To combine two objects of class "mgsa"

This function could only be used to combine two "mgsa" objects, using "Reduce" function to combine more.

Author(s)

Chen Meng

See Also

`moa` and `moa.sup`

Examples

```r
showClass("mgsa")
# library(mgsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
# split gene set annotation into two sets.
sup1 <- lapply(NCI60_4array_supdata, function(x) x[, 1:10])
sup2 <- lapply(NCI60_4array_supdata, function(x) x[, -(1:10)])
# project two sets of annotation
mgsa1 <- mogsa(x = NCI60_4arrays, sup=sup1, nf=9,
               proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
mgsa2 <- mogsa(x = NCI60_4arrays, sup=sup2, nf=9,
               proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
# combine two independent mgsa sets
mgsa_comb <- combine(mgsa1, mgsa2)
dim(getmgsa(mgsa1, "fac.scr"))
dim(getmgsa(mgsa2, "fac.scr"))
dim(getmgsa(mgsa_comb, "Fac.scr"))
```
moa

Multiple omics data analysis using MFA or STATIS

Description
Analysis multiple omics data using MFA or STATIS. The input multiple tables are in a form that columns are samples and rows are variables/features.

Usage
moa(data, proc.row="center_ssq1", w.data="inertia", w.row=NULL, statis=FALSE)

Arguments
- **data**: A list of data.frame or matrix that contains the input datas, the columns in all datasets should be samples/observations (which need to be matched) and rows should be variables.
- **proc.row**: Preprocessing of rows of datasets, should be one of none - no preprocessing, center - center only, center_ssq1 - center and scale (sum of squared values equals 1), center_ssqN - center and scale (sum of squared values equals the number of columns), center_ssqNm1 - center and scale (sum of squared values equals the number of columns - 1) MFA corresponds to "proc.row=center_ssq1" and "w.data="lambda1"".
- **w.data**: The weights of each separate dataset, should be one of uniform - no weighting, lambda1 - weighted by the reverse of the first eigenvalue of each individual dataset or inertia - weighted by the reverse of the total inertia. See detail.
- **w.row**: If it is not null, it should be a list of positive numerical vectors, the length of which should be the same with the number of rows of each dataset to indicated the weight of rows of datasets.
- **statis**: A logical indicates whether STATIS method should be used. See details.

Details
Different methods employs different precessing of row and datasets. For multipple factorial analysis (MFA), the rows of each dataset are first centered and scaled, then each dataset is weighted by the reverse of its first eigenvalue (proc.row=\text{center\_ssq1}, w.data="\text{lambda1}"). This algorithm does not have a well defined criterion to be optimized (see reference).

If statis=TRUE, the statis algorithm will be used, that is, each dataset will be further weighted so that datasets closer to the overall structure will receive a higher weight.

Value
An object of class moa-class.

Author(s)
Chen Meng
**References**


Herve Abdi, Lynne J. Williams, Domininique Valentin. Multiple factor analysis: principal component analysis for multitable and multiblock data sets. WIREs Comput Stat 2013

**See Also**

sup.moa, mogsa. More about plot see moa-class.

**Examples**

```r
# library(mogsa)
# loading data
data(NCI60_4arrays)
# run analysis
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
# plot
# plot eigen value
plot(ana, value = "eig", type = 2)
# plot the normalized (percentage) eigen value
plot(ana, value = "tau", type = 2)
# plotting the observations
colcode <- as.factor(sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\\."), ",\[", 1))
plot(ana, type = 1, value = "obs", col=colcode)
plot(ana, type = 2, value = "obs", col=colcode, data.pch=1:4)
# plot variables/features in each data sets
plot(ana, value = "var", layout=matrix(1:4, 2, 2))
# plot the RV coefficients for the data sets
plot(ana, value = "RV")
```

**moa-class**

**Class** "moa"

**Description**

moa class object

**Objects from the Class**

Objects can be created by calls of the form `new("moa", ...)`.  

**Slots**

- `eig`: eigen values
- `tau`: The percentage of explained variance by each datasets separately.
- `partial.eig`: matrix, rows indicate the partial eigenvalues from each data.
- `eig.vec`: a matrix, eigenvectors.
- `loading`: the coordinate of variables/features.
moa-class

fac.scr: factor score of observations.
partial.fs: partial factor score.
ctr.obs: contribution of each observation to the total factor score.
ctr.var: contribution of each variables to the total variance.
ctr.tab: contribution of each data to the total variance.
RV: pairwise RV coefficients
w.row: weight of rows
w.data: weight of datasets
data: the original input data
tab.dim: the dimension of each input data
call: call

Methods

plot signature(x = "moa", y = "missing"): Argument "value" sould be one of "eig", "tau", "obs", "var" and "RV"
    if value = "eig", the eigenvalue would be plotted as scree plot. The following arguments could be set:
type=1 - The type of plot to show eigenvalues. (type=1: the eigenvalue are plotted; type=2: partial eigenvalue shown as concatenated bars; type=3: partial eigenvalue shown as bars side by side; type=4: matplot view of eigenvalues, lty need to be set; type=5: the two dimensional plot of partial eigenvalues, axes and pch need to be set in this case.)
axes=NULL - The axes selected to plot
n=NULL - Top n eigenvalues to be drawn
tol=1e-5 - The tolerance of eigenvalue, eigenvalues lower than this value will not be shown.
legend=NULL - legend to put, a character string as calling legend function
col=NULL - The color of partial eigenvalues from each data set
lty=1 - The line type used in the matplot, used when type =4
pch=NULL - the pch to draw 2D partial eigen plot, when type = 5 used
lg.x="topright" - The position of legend
lg.y=NULL - Position argument passed to function "legend"
... - other arguments passed to functions
    if value = "tau", the same with eig, but in the eigenvalues are scaled to 1
    if value = "obs", the observation space will be shown, the following argument could be set:
axes=1:2 - Which axes should be draw
type=1 - Which type, see below (for type=1: the center points draw; type=2: the separate factor scores linked by lines; ... will be passed to function "points")
data.pch=20 - the pch of dataset, if type=1, the first one is used
col=1 - the color of observations, recycled used by data.frame
label=FALSE - A logical indicates if labels should be shown
lg.x="topright" - Position of legend
lg.y=NULL - Position of legend
xlim=NULL - The x limit
ylim=NULL - The y limit
label.cex=1 - the cex of text

var - the separate gene view, layout can be specified
RV - the heatmap of RV coefficients
Author(s)
Chen Meng

References
Herve Abdi, Lynne J. Williams, Domininique Valentin. Multiple factor analysis: principal component analysis for multitable and multiblock data sets. WIREs Comput Stat 2013

Examples

```r
showClass("moa")
# load("R/mogsa/data/NCI60_4arrays.rda")
data(NCI60_4arrays)
a <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
plot(a, value="eig")
plot(a, value="tau", type=2)
```

Description
moa.sup class desc.

Objects from the Class
Objects can be created by calls of the form `new("moa.sup", ...).

Slots
sup: Object of class "list", the matrix of supplementary data.
coord.sep: The projection of geneset infomation on each separate data.
coord.comb: The projection of geneset infomation on total dataset.
score: the gene set-sample pathway score
score.data: the gene set-sample pathway score, data separate
score.pc: the gene set-sample pathway score, PC separate
score.sep: the gene set-sample pathway score, separate.
p.val: the p value matrix have the same dimension with score matrix.

Methods
There is no generic function for objects of "moa.sup", but have specific function, including: - decompose.gs.ind - box.gs.feature - plotGS - decompose.gs.group
**moaCoef**

**Author(s)**
Chen Meng

**See Also**
objects to See Also as `decompose.gs.ind, box.gs.feature, plotGS, decompose.gs.group`.

**Examples**
```
showClass("moa.sup")
data(NCI60_4array_supdata)
data(NCI60_4arrays)
sapply(NCI60_4array_supdata, dim)
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
plot(ana, value="eig")
smoa <- sup.moa(ana, sup=NCI60_4array_supdata, nf=5)
```

---

**Description**
Extract the loadings/coefficients from an object of class **moa-class**.

**Usage**
```
moaCoef(moa)
```

**Arguments**

- **moa**  
  An object of class **moa-class**.

**Value**
It returns a list consist of two components:

- `coefMat` - the loading matrix
- `nonZeroCoef` - it is a list of data frame to list the non-zero coefficient variable in each of loading vectors and data sets. The element names are in a format as
  
  "xxxx.yy.zzz"
  
  xxxx - are the data names, tells the data set where a variable is from
  
  yy - the number of Axes, for example, "V1" indicate the variable has a non-zero coefficient in the first loading vector.
  
  zzz - could be either "pos" (coefficient >0) or "neg" (coefficient < 0)

  The data frame has two columns, the first column is the ID of a variable the second column is the coefficient/loading.

---

**Author(s)**
Chen Meng
See Also

moaScore

Examples

# see examples in \code{\link{mbpca}}

data("NCI60_4arrays")
moa <- mbpca(NCI60_4arrays, ncomp = 10, k = "all", method = "globalScore", option = "lambda1",
               center=TRUE, scale=FALSE)

genes <- moaCoef(moa)
scr <- moaScore(moa)
Description

Gap statistic is a measurement of goodness of clustering result. This is a convenient function to calculate the gap statistic of clustering "moa".

Usage

```r
moGap(x, K.max, B = 100, cluster = c("kmeans", "hclust"), plot = TRUE, 
      dist.method = "euclidean", dist.diag = FALSE, dist.upper = FALSE, dist.p = 2, 
      hcl.method = "complete", hcl.members = NULL, 
      km.iter.max = 10, km.nstart = 10, 
      km.algorithm = c("Hartigan-Wong", "Lloyd", "Forgy", "MacQueen"), km.trace = FALSE)
```

Arguments

- `x`: An object of class `moa-class` returned by `mbpca`.
- `K.max`: The maximum number of clusters to consider, passed to `clusGap`.
- `B`: The number of bootstrap, passed to `clusGap`.
- `cluster`: A character string could be either "kmeans" or "hclust" to specify the clustering algorithm.
- `plot`: Logical; whether return the gap statistic plot.
- `dist.method`: Distance measurement, passed to function "dist".
- `dist.diag`: Passed to function "dist".
- `dist.upper`: Passed to function "dist".
- `dist.p`: Passed to function "dist".
- `hcl.method`: Hierarchical clustering method, passed to "hclust".
- `hcl.members`: Passed to "hclust".
- `km.iter.max`: Maximum number of iteration in kmeans, passed to "kmeans".
- `km.nstart`: An integer to specify how many random sets should be chosen. passed to "kmeans".
- `km.algorithm`: Kmeans algorithm, passed to "kmeans".
- `km.trace`: See function "kmeans".

Value

It returns a list consists of five components:

- "Tab", "n", "B", "FUNcluster" - see `clusGap`
- "nClust" - the estimated number of clusters using different method, see `maxSE`

Author(s)

Chen Meng
References


See Also

Function "clusGap" in "cluster" package Function "dist", "hclust", "kmeans"

Examples

# see examples in \code{\link{mbpca}}

data("NCI60_4arrays")
moa <- mbpca(NCI60_4arrays, ncomp = 10, k = "all", method = "globalScore", option = "lambda1",
             center=TRUE, scale=FALSE)
gap <- moGap(moa, K.max = 12, cluster = "hcl")
genesis <- moaCoef(moa)
scr <- moaScore(moa)

mogsa

multiple omics data integration and gene set analysis

Description

The main function called by users, omics data analysis and gene set annotation. A wrapper function of \code{moa} and \code{sup.moa}.

Usage

\code{mogsa(x, sup, nf=NULL, proc.row=NULL, w.data=NULL, w.row=NULL, statis=FALSE, ks.stat=FALSE, ks.B = 1000, ks.cores = NULL)}

Arguments

\code{x} An object of class \code{list} or \code{moa-class}. A list would be a list of data frame.

\code{sup} An object of class \code{list} or \code{moa.sup-class}. A list would be a list of supplementary data.

\code{nf} The number of principal components used to reconstruct, only used when \code{x} is a an object of list.

\code{proc.row} Preprocessing of rows. If \code{x} is a object of list, it is passed \code{moa}

\code{w.data} Weights of datasets. If \code{x} is a object of list, it is passed \code{moa}

\code{w.row} Weight of row. If \code{x} is a object of list, it is passed \code{moa}

\code{statis} A logical indicates if statis algrithm should be used. If \code{x} is a object of list, it is passed \code{moa}
ks.stat  The logical indicates if the p-value should be calculated using K-S statistic (the method used in "ssgsea" in GSVA package). Default is FALSE, which means using the z-score method. See sup.moa.

ks.B  An integer to indicate the number of bootstrapping samples to calculated the p-value of KS statistic.

ks.cores  An integer indicate the number of cores to be used in bootstrapping. It is passed to function mclapply in the parallel package.

Details

A wrapper function of moa and sup.moa.

Value

An object of class mgsa-class.

Note

This function will be changed to a generic function for "S4-style" programming.

Author(s)

Chen Meng

References


See Also

moa and sup.moa

Examples

# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)

# using a list of data.frame as input
mgsa1 <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
               proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)

# using moa as input
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
smoa <- sup.moa(ana, sup=NCI60_4array_supdata, nf=3)
mgsa2 <- mogsa(x = ana, sup=NCI60_4array_supdata, nf=9)
mgsa3 <- mogsa(x = ana, sup=smoa)
**msvd**

*SVD based algorithm to calculate block Score and global scores for mbpca.*

**Description**

An internal function called by `mbpca`. It returns the result comparable with nipalsSoftK, but way faster since it uses the SVD algorithm. No sparse operations in this function.

**Usage**

```r
msvd(x, svd.sol = svd)
```

**Arguments**

- **x**
  
  The input matrix, rows are observations, columns are variables

- **svd.sol**
  
  A function object to specify the preferred SVD solver, default is svd.

**Value**

An list object contains the following elements:

- **tb** - the block scores
- **pb** - the block loadings
- **t** - the global scores
- **w** - the weights of block scores to construct the global scores

**Author(s)**

Chen Meng

**See Also**

- `nipalsSoftK`

---

**NCI60_4arrays**

*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, which could be used as input to `mcia` directly.

**Usage**

```r
data(NCI60_4arrays)
```
Format

The format is: List of 4 data.frames

- \$agilent: data.frame containing 300 rows and 60 columns. 300 gene expression log ratio measurements of the NCI60 cell lines, by Agilent platform.
- \$hgu133: data.frame containing 298 rows and 60 columns. 298 gene expression log ratio measurements of the NCI60 cell lines, by H-GU133 platform.
- \$hgu133p2: data.frame containing 268 rows and 60 columns. 268 gene expression log ratio measurements of the NCI60 cell lines, by H-GU133 plus 2.0 platform.
- \$hgu95: data.frame containing 288 rows and 60 columns. 288 gene expression log ratio measurements of the NCI60 cell lines, by H-GU95 platform.

Value

NCI60_4arrays will be loaded in your working space.

Source


References


NCI60_4array_supdata [supp data for Microarray gene expression profiles of the NCI 60 cell lines from 4 different platforms](http://discover.nci.nih.gov/cellminer/)

Description

Supplementary to NCI60_4arrays.

Usage

data(NCI60_4arrays)

Format

The format is: List of 4 matrix

- \$agilent: matrix containing 300 rows and 60 columns. 300 gene expression log ratio measurements of the NCI60 cell lines, by Agilent platform.
- \$hgu133: matrix containing 298 rows and 60 columns. 298 gene expression log ratio measurements of the NCI60 cell lines, by H-GU133 platform.
- \$hgu133p2: matrix containing 268 rows and 60 columns. 268 gene expression log ratio measurements of the NCI60 cell lines, by H-GU133 plus 2.0 platform.
- \$hgu95: matrix containing 288 rows and 60 columns. 288 gene expression log ratio measurements of the NCI60 cell lines, by H-GU95 platform.
Value

NCI60_4array_supdata will be loaded in your working space.

Description

An internal function called by mbpca.

Usage

nipalsSoftK(x, maxiter, k)

Arguments

x The input matrix, rows are observations, columns are variables
maxiter # of maximum interation the algorithm can run
k The number (>=1) or proportion (<1) of variables want to keep. It could be a single value or a vector has the same length as x so the sparsity of individual matrix could be different.

Value

an list object contains the following elements:
tb - the block scores
pb - the block loadings
t - the global scores
w - the weights of block scores to construct the global score.

Author(s)

Chen Meng

See Also

msvd
Description
Calculating pairwise RV coefficients for a list of matrices or data.frame.

Usage
```r
pairwise.rv(data.list, match="col")
```

Arguments
- `data.list`: A list of data.frame or matrix, either rows or columns in each data set should be matched.
- `match`: Whether columns or rows of data.frame/matrix should be matched.

Details
The RV coefficient for each pair of matrices is calculated as $R_v = \frac{\text{trace}(X'Y')}{\sqrt{\text{trace}(X'X') \text{trace}(Y'Y')}}$

Value
The function will return a matrix containing the pairwise RV coefficients.

Note
The variable in matrices are not automatically centered or scaled in this function. So these step may need to be performed before calling this function.

Author(s)
Chen Meng

References

Examples
```r
data(NCI60_4arrays)
pairwise.rv(NCI60_4arrays)
```
Methods

signature(x = "moa", y = "missing") plot moa object

Argument "value" should be one of "eig", "tau", "obs", "var" and "RV". If value = "eig", the eigenvalue would be plotted as scree plot. The following arguments could be set:

- type=1 - The type of plot to show eigenvalues. (type=1: the eigenvalue are plotted; type=2: partial eigenvalue shown as concatenated bars; type=3: partial eigenvalue shown as bars side by side; type=4: matplot view of eigenvalues, lty need to be set; type=5: the two dimensional plot of partial eigenvalues, axes and pch need to be set in this case.)
- axes=NULL - The axes selected to plot
- n=NULL - Top n eigenvalues to be drawn
- tol=1e-5 - The tolerance of eigenvalue, eigenvalues lower than this value will not be shown.
- legend=NULL - Legend to put, a character string as calling legend function
- col=NULL - The color of partial eigenvalues from each data set
- lty=1 - The line type used in the matplot, used when type =4 \ pch=NULL
- pch=NULL - The pch to draw 2D partial eigen plot, when type = 5 used \ lg.x="topright"
- lg.x="topright" - The position of legend
- lg.y=NULL - Position argument passed to function "legend" \... - other arguments passed to functions

If value = "tau", the same with eig, but in the eigenvalues are scaled to 1

If value = "obs", the observation space will be shown, the following argument could be set:
- axes=1:2 - Which axes should be drawn
- type=1 - Which type, see below (for type=1: the center points draw; type=2: the separate factor scores linked by lines; ... will be passed to function "points")
- data.pch=20 - The pch of dataset, if type=1, the first one is used
- data.col=1 - The color of observations, recycled used by data.frame
- label=FALSE - A logical indicates if labels should be shown
- lg.x="topright" - Position of legend
- lg.y=NULL - Position of legend
- xlim=NULL - The x limit
- ylim=NULL - The y limit
- label.cex=1 - The cex of text
- var - The separate gene view, layout can be specified
- RV - The heatmap of RV coefficients

plotGS

Plot the gene set space

Description

Plot the gene set space of objects of "moa" and "mgsa"

Usage

plotGS(x, axes=1:2, center.only=FALSE, topN=1, data.pch=20, data.col=1, highlight.col = 2, label=NULL, label.cex=1, layout=NULL, ...)

plotGS

Plot the gene set space
plotGS

Arguments

x An object of class \texttt{mgsa-class} or \texttt{moa.sup-class}

axes An integer vector in the length 2 to indicate the axes to be drawn.

center.only A logical to indicate whether the separate gene set spaces from each of the data set should be plotted. Default is \texttt{FALSE}.

topN An integer specify N gene set from the most positive and negative end of axes to be labeled.

data.pch The shape for plotting each data set. This argument is passed to \texttt{points} function, so only used when separate gene set spaces are plotted (i.e. \texttt{center.only = FALSE}).

data.col The col for plotting each data set. This argument is passed to \texttt{points} function, so only used when separate gene set spaces are plotted (i.e. \texttt{center.only = FALSE}).

highlight.col The color used to highlight the selected gene sets

label Either a character vector or \texttt{NULL} (default). The character vector should be the name of some gene sets want ot be labeled.

label.cex Passed to \texttt{text} function to adjust the the labels

layout A matrix passed to the \texttt{layout} function.

... Other arguments passed to \texttt{points}

Details

This is a convenience function to explore the gene set space so not very flexible. For customized plot, please use the object of \texttt{data@coord.comb} and \texttt{data@coord.sep}.

Value

If assign to variable, A list of selected/highlighted gene set at the (positive and negative) end of each axis will be returned.

Author(s)

Chen Meng

Examples

```R
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
mgsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
               proc.row = "center_ssq!", w.data = "inertia", statis = TRUE)

plotGS(mgsa, center.only = TRUE, topN=5)
res <- plotGS(mgsa, center.only = FALSE, data.pch=1:4, data.col=1:4)
res
```
**Description**

Prepare pathway gene sets from "graphite" package, which could be passed to "prepSupMoa" function.

**Usage**

```r
prepGraphite(db, id = c("entrez", "symbol"))
```

**Arguments**

- `db`: The database to be used, an object of class either 'PathwayList' create by "pathways" function.
- `id`: Which identifier for output, either "entrez" or "symbol".

**Details**

Only support "entrez" or "symbol" output currently.

**Value**

This function returns an object of list containing gene set information, which could be further processed by function "prepSupMoa" to convert to the object that can be used as input of "sup.moa" or "mogsa".

**Author(s)**

Chen Meng

**References**


**See Also**

See Also as `prepMsigDB` and `prepSupMoa`.

**Examples**

```r
library(graphite)
keggdb <- prepGraphite(db = pathways("hsapiens", "kegg")[1:3], id = "entrez")
```
**prepMsigDB**  
*Convert gmt format file to a list*

**Description**  
Convert a gmt file (Could be downloaded from MSigDB) to a list of gene sets information.

**Usage**  
```
prepMsigDB(file)
```

**Arguments**  
- `file`  
The directory and file name of the gmt file.

**Value**  
This function returns an object of list containing gene set information, which could be further processed by function "prepSupMoa" to convert to the object that can be used as input of "sup.moa" or "mogsa".

**Author(s)**  
Chen Meng

**See Also**  
See Also as prepGraphite and prepSupMoa.

**Examples**  
```
# not run
dir <- system.file(package = "mogsa")
preGS <- prepMsigDB(file=paste(dir, 
"/extdata/example_msigdb_data.gmt.gz", sep = ""))
```

---

**prepSupMoa**  
*Prepare sumpplementary tables for projection by sup.moa or mogsa.*

**Description**  
Convert a list of gene set information to a set of sumpplementary tables that can be used as input of function "sup.moa" or "mogsa".

**Usage**  
```
prepSupMoa(X, geneSets, minMatch = 10, maxMatch = 500)
```
processOpt

Arguments

\( X \)  
A matrix/data.frame or a list of matrix/data.frame or a list of character vector. If it is a list of matrix/data.frame, row names of matrix/data.frame will be used to create the projection matrix. Otherwise the character vectors will used to create the supplementary matrix.

geneSets  
Gene sets list or an object of class "GeneSet" or "GeneSetCollection". A gene set list could be returned by prepGraphite or prepMolsigDB.

minMatch  
The minimum match of geneset.

maxMatch  
The maximum match genesets.

Details

Details here

Value

A list of matrix could used as supplementary tables by "sup.moa" or "mogsa".

Author(s)

Chen Meng

See Also

See Also as prepGraphite and prepMsigDB.

Examples

```r
library(graphite)
data(NCI60_4arrays)
gss <- prepGraphite(db = kegg[6:10], id="symbol")
sup_data1 <- prepSupMoa(NCI60_4arrays, geneSets=gss)
gene_list <- lapply(NCI60_4arrays, rownames)
sup_data2 <- prepSupMoa(gene_list, geneSets=gss)
```

Description

An internal function called by mbpca.

Usage

```
processOpt(x, center = TRUE, scale = FALSE, option = c("lambda1", "inertia", "uniform"))
```
softK

Arguments

x A list of matrices, rows are observations and columns are variables
center A logical variable indicates whether columns should be centered
scale A logical variable indicates whether columns should be scaled
option A character string could be one of c("lambda1", "inertia", "uniform") to indicate how the different matrices should be normalized. If "lambda1", the matrix is divided by its first singular value, if "inertia", the matrix is divided by its total inertia (sum of square), if "uniform", none of them would be done.

Value

A list of normalized matrix.

Author(s)

Chen Meng

softK

Soft-thresholding operator

Description

Soft-thresholding operator, which is called by mbpcas.

Usage

softK(x, k)

Arguments

x A numerical vector
k Number of non-zero elements want to keep

Value

A numerical vector

Author(s)

Chen Meng

Examples

v <- rnorm(10)
softK(v, k = 2)
sup.moa

Projecting supplementary tables on object of class moa-class.

Description

Projecting supplementary tables on moa-class

Usage

sup.moa(X, sup, nf = 2, ks.stat=FALSE, ks.B = 1000, ks.cores = NULL)

Arguments

- **X**: An object of class moa-class
- **sup**: A list of data.frames contains supplementary data.
- **nf**: The number of principal components used in the projection.
- **ks.stat**: The logical indicates if the p-value should be calculated using K-S statistic (the method used in "ssgsea" in GSVA package). Default is FALSE, which means using the z-score method.
- **ks.B**: An integer to indicate the number of bootstrapping samples to calculated the p-value of KS statistic.
- **ks.cores**: An integer indicate the number of cores to be used in bootstrapping. It is passed to function mclapply in the parallel package.

Details

Projecting supplementary tables on moa-class, for details see reference.

Value

An object of class moa.sup-class.

Author(s)

Chen Meng

References


Examples

```r
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
# check the dimension of each supplementary data to see how many gene set annotated the data
sapply(NCI60_4array_supdata, dim)
# run analysis
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", statis = TRUE)
plot(ana, value="eig")
# projectin supplementary data
smoa <- sup.moa(ana, sup=NCI60_4array_supdata, nf=3)
# heatmap visualize the gene set scores
heatmap(slot(smoa, "score"))
```

toMoa

Convert mbpcas result to moa-class

Description

An internal function called by mbpcas.

Usage

toMoa(data, x, call)

Arguments

data The preprocessed data in mbpcas
x The object calculated in mbpcas
call The call of mbpcas

Value

An object of moa-class.

Author(s)

Chen Meng
Weighted singular value decomposition (SVD)

Description

The weighted version of singular value decomposition.

Usage

```r
wsvd(X, D1 = diag(1, nrow(X)), D2 = diag(1, ncol(X)))
```

Arguments

- `X`: A numeric matrix whose wSVD decomposition is to be computed.
- `D1`: A square matrix or vector. The left constraint/weight matrix (symmetric and positive in diagonal). The dimension of D1 should be the same with the number of rows in X. A vector input will be converted to a diagonal matrix.
- `D2`: A square matrix or vector. The right constraint/weight matrix (symmetric, positive in diagonal). The dimension of D1 should be the same with the number of columns in X. A vector input will be converted to a diagonal matrix.

Details

The weighted version of generalized singular value decomposition (SVD) of matrix A = UDV' with the constraints U'D1U = I and V'D2V = I. D1 and D2 are two matrices express constraints imposed on the rows and the columns of matrix A.

Value

- `d`: singular values
- `u`: left singular vectors
- `v`: right singular vectors
- `D1`: the left weight matrix (directly from input)
- `D2`: the right weight matrix (directly from input)

Author(s)

Chen Meng

References


See Also

`svd`
Examples

```r
set.seed(56)
m <- matrix(rnorm(15), 5, 3)
wl <- rnorm(5)
wr <- runif(3)
s <- wsvd(X=m, D1=wl, D2=wr)
# t(s$u) %*% diag(wl) %*% s$u
# t(s$v) %*% diag(wr) %*% s$v
# all.equal(m, as.matrix(s$u) %*% diag(s$d) %*% t(s$v))
```
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