

# Package ‘mogsa’

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**Type** Package

**Title** Multiple omics data integrative clustering and gene set analysis

**Version** 1.38.0

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

**License** GPL-2

**Depends** R (>= 3.4.0)

**Imports** methods, graphite, genefilter, BiocGenerics, gplots, GSEABase, Biobase, parallel, corpcor, svd, cluster, grDevices, graphics, stats, utils

**VignetteBuilder** knitr

**Suggests** BiocStyle, knitr, org.Hs.eg.db

**biocViews** GeneExpression, PrincipalComponent, StatisticalMethod, Clustering, Software

**NeedsCompilation** no

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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  
Date: 2016-01-19  
License: GPL-2  
Depends: methods

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

## 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", stasis = TRUE)

# using moa as input
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", stasis = 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)
```

---

`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 the information about presence and absence of a feature for a specific data set.

## Usage

```
annotate.gs(mgsa, gs)
```

## Arguments

<code>mgsa</code>	An object of class <code>mgsa-class</code> or <code>moa.sup-class</code> .
<code>gs</code>	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

```
# 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", stasis = TRUE)
allgs <- colnames(NCI60_4array_supdata[[1]])
annotate.gs(mgsa, allgs[1])
```

---

biSoftK	<i>NIPALS algorithm with soft thresholding operator on rows and columns</i>
---------	---

---

### Description

An internal function called by [mbpca](#).

### Usage

```
biSoftK(x, maxiter, kp, kt, weight.p, weight.t, pos = FALSE, unit.pb = TRUE, unit.tb = FALSE)
```

### Arguments

x	The input matrix, rows are observations, columns are variables
maxiter	Number of maximum iteration the algorithm can run
kp	The number ( $\geq 1$ ) 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.
kt	The number ( $\geq 1$ ) or proportion ( $< 1$ ) of non-zero scores for obvservations.
weight.p	The weight of variables. It could be 1) a vector has the same length as x, one value for each table/block; 2) one number, all variables share the same weight or 3) a list of vectors, the length of each vector should be the same with the columns numbers of the corresponding table/block, so every variables has a unique weight.
weight.t	The weight for observation. For accepted values or formats, see weight.p.
pos	Logical value, if only non-negative values in the loading and score vectors.
unit.pb	Logical value, whether the length of table/block loading should be unit length.
unit.tb	Logical value, whether the length of table/block score should be unit length.

### Details

This function also use the NIPALS algorithm, but it generalized nipalsSoftK from several aspects: 1. Allowing sparsity on both columns and rows of matrices 2. Allowing weights for columns and rows 3. Allowing loading and/or score vectors of blocks to be unit length 4. Allowing only positive number in loading and score vectors

### Value

an list object contains the following elements:

tb - the block scores

pb - the block loadings

t - the global scores

w - the wegihts of block scores to construct the global score.

**Author(s)**

Chen Meng

**See Also**[msvd](#)

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**

```
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 <a href="#">moa</a> returned by <a href="#">mbpca</a> .
mc.cores	Integer; number of cores used in bootstrap. This value is passed to function <code>mclapply</code>
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 <a href="#">mbpca</a> . In most of cases, user do not need to specify this argument because it could be inferred from moa.
method	Passed to function <a href="#">mbpca</a> . In most of cases, user do not need to specify this argument because it could be inferred from moa.
maxiter	Passed to function <a href="#">mbpca</a> . In most of cases, user do not need to specify this argument because it could be inferred from moa.
svd.solver	Passed to function <a href="#">mbpca</a> . 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**

Bootstrap method were used to determine the components that are presenting significant concordant structure between datasets.

**Value**

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

**Author(s)**

Chen Meng

**Examples**

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

---

bootMbpcaK	<i>An internal function called by <a href="#">bootMbpca</a>.</i>
------------	--

---

**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 <code>mclapply</code>
resample	Could be one of "sample", "gene" or "total". "sample" and "gene" means sample-wise and variable-wise resampling, repectively. "total" means total resampling.
ncomp	passed to <a href="#">mbpca</a> .
method	passed to <a href="#">mbpca</a> .
k	passed to <a href="#">mbpca</a> .
center	passed to <a href="#">mbpca</a> .
scale	passed to <a href="#">mbpca</a> .
option	passed to <a href="#">mbpca</a> .
maxiter	passed to <a href="#">mbpca</a> .
svd.solver	passed to <a href="#">mbpca</a> .

**Value**

A matrix of mbpca eigenvalues resulted from bootstrap samples

**Author(s)**

Chen Meng

**See Also**

[bootMbpca](#)

---

bootMoa

*Significant components in "moa" returned by function "moa".*

---

**Description**

Using bootstrap method to extract the components representing significant concordance structures between datasets from "moa" (returned by function "moa").

**Usage**

```
bootMoa(moa, proc.row="center_ssq1", w.data="inertia", w.row=NULL, stasis=FALSE,
        mc.cores=1, B = 100, replace=TRUE, resample=c("sample", "gene", "total"),
        plot=TRUE, log="y", tol = 1e-7)
```

**Arguments**

moa	An object of <a href="#">moa</a> returned by <a href="#">moa</a> .
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.
stasis	A logical indicates whether STATIS method should be used. See details.
mc.cores	Integer; number of cores used in bootstrap. This value is passed to function <code>mclapply</code>



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.
plot	Logical; whether the result should be plotted.
log	Could be "x", "y" or "xy" for plot log axis.
tol	The minimum eigenvalues shown in the plot.

### Details

set plot=TRUE to help selecting significant components.

### Value

A matrix where columns are components and rows are variance of PCs from bootstrap samples.

### Author(s)

Chen Meng

### References

Herve Abdi, Lynne J. Williams, Dominique Valentin and Mohammed Bannani-Dosse. STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat 2012. Volume 4, Issue 2, pages 124-167  
 Herve Abdi, Lynne J. Williams, Dominique Valentin. Multiple factor analysis: principal component analysis for multitable and multiblock data sets. WIREs Comput Stat 2013

### See Also

[moa](#), [sup.moa](#), [mogsa](#). More about plot see [moa-class](#).

### Examples

```
# see function moa
```

---

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	An object of class <code>mgsa-class</code> or <code>moa.sup-class</code>
gs	Gene set want to be explored
moa	An object of class <code>moa</code> . It is required if x is an object of class <code>moa.sup-class</code>
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 <code>boxplot</code>

**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_ssq1", w.data = "inertia", stasis = 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(1:4, 2, 2))
```

---

combine-methods	<i>Combine two objects of class mgsa into one.</i>
-----------------	--

---

### Description

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

### Usage

```
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

```
# 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
mgsa1 <- mogsa(x = NCI60_4arrays, sup=sup1, nf=9,
              proc.row = "center_ssq1", w.data = "inertia", stasis = TRUE)
mgsa2 <- mogsa(x = NCI60_4arrays, sup=sup2, nf=9,
              proc.row = "center_ssq1", w.data = "inertia", stasis = 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.group      *Data-wise or PC-wise decomposition of gene set scores for all observations.*

---

### Description

Data-wise or PC-wise decomposition of gene set scores (GSS) across all observations. The predefined group/cluster information should be given so that the mean decomposed GSSs for each group are returned and plotted.

### Usage

```
decompose.gs.group(x, gs, group, decomp = "data", nf = 2, x.legend = "bottomleft",
  y.legend = NULL, plot = TRUE, main = NULL, ...)
```

### Arguments

x	An object of class <code>mgsa-class</code> or <code>moa.sup-class</code>
gs	The gene set want to exam.
group	An vector or factor to indicate the group of observations, such as clusters. See examples.
decomp	A charater string either "data" or "pc" to indicate how the gene set scores should be decomposed (with respect to data or PC.
nf	The number of axes/PCs to be calculated and plotted.
x.legend	Used to control the position of legends.
y.legend	Used to control the position of legends.
plot	A logical indicates if a plot should be drawn.
main	The main title of plot.
...	Other arguments passed to <code>barplot</code> .

### Details

This function could be used when the number of observation is large and there are cluster/group information is available. In this case, the means of decomposed gene set scores over each group is calculated. The vertical bar on the end of each bar indicates the 95% confident interval of the means.

### Value

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

### 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
mogsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
               proc.row = "center_ssqr1", w.data = "inertia", statis = TRUE)

colcode <- as.factor(sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\\."), "[", 1))
decompose.gs.group(x = mogsa, gs = 2, group = colcode, decomp = "data", plot = TRUE)
decompose.gs.group(x = mogsa, gs = 2, group = colcode, decomp = "pc", nf = 3, plot = TRUE)
```

---

decompose.gs.ind	<i>Data-wise or PC-wise decomposition of gene set scores for a single observation.</i>
------------------	--

---

**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 <a href="#">mogsa-class</a> or <a href="#">moa.sup-class</a>
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

```
# 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", stasis = 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 <a href="#">msvd</a> or <a href="#">nipalsSoftK</a>
tb	The block scores returned by <a href="#">msvd</a> or <a href="#">nipalsSoftK</a>
pb	The block loadings returned by <a href="#">msvd</a> or <a href="#">nipalsSoftK</a>
method	A charater to specify the deflation strateg, could be one of c("globalScore", "blockLoading", "blockScore").

**Value**

A list of deflated matrix

**Author(s)**

Chen Meng

---

distMoa	<i>Calculate the distance matrix from an object of class <a href="#">moa-class</a>.</i>
---------	---

---

**Description**

A convenient function to calculate the distance matrix from an object of class [moa-class](#).

**Usage**

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

**Arguments**

x	An object of class <a href="#">moa-class</a> .
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 <code>dist</code>
diag	passed to function <code>dist</code>
upper	passed to function <code>dist</code>
p	passed to function <code>dist</code>

**Value**

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

**Author(s)**

Chen Meng

**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)

dst <- distMoa(moa)
```

---

getmgsa

*get values in an object of class "mgsa".*

---

**Description**

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

**Usage**

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

**Arguments**

<code>mgsa</code>	An object of class <code>mgsa-class</code> .
<code>value</code>	The name of the value want to extract from <code>"mgsa"</code> . See detail for options.

**Details**

if value in `c("call", "moa", "sup")`, the function equal function `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 extact corresponding value from `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 `moa.sup-class`.

**Value**

The function return the selected value in `"mgsa"`.



**Author(s)**

Chen Meng

**References**

TBA

**Examples**

```
# library(mogsa)
# loading gene expression data and supplementary data
data(NCI60_4array_supdata)
data(NCI60_4arrays)
mogsa <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, nf=9,
               proc.row = "center_ssq1", w.data = "inertia", stasis = TRUE)
part.eig <- getmogsa(mogsa, "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 <code>mgsa-class</code> .
geneSet	A character string or number to indicate 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	A positive integer specifying the number of top influencers that should be returned.
plot	A logical indicating if the result should be plotted.
Fvalue	A logical indicating 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 indicating whether to use correlation between reconstructed expression and 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:

$$\log_2(\text{var}(\text{GS}_{-i})/\text{var}(\text{GS}))$$

where GS is the gene set score, and the GS<sub>-i</sub> is a recalculation 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:

$$\log_2(F(\text{GS}_{-i})/F(\text{GS}))$$

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 column is the gene influential score. The third column indicates from where the feature/gene is selected.

## Author(s)

Chen Meng

## References

TBA

## See Also

see [annotate.gs](#)

## 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_ssq1", w.data = "inertia", stasis = 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**

```
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**

```
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"),
      k.obs = "all", w = NA, w.obs = NA,
      unit.p = FALSE, unit.obs = FALSE, pos = FALSE)
```

**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 $k \geq 1$ ) 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 <code>moa-class</code>
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.

<code>k.obs</code>	The absolute number (if $k \geq 1$ ) or the proportion (if $0 < k < 1$ ) of non-zero coefficients for the observations. Sparse factor scores for observation are used by sparse concordance analysis. (New arguments from v1.12)
<code>w</code>	The weight of variables. It could be given in the following format: 1) NA or a numeric value: all variables have the same weight; 2) A vector of numeric values, the vector has the same length as <code>x</code> : variables in each block shares the same weight; 3) A list of vector, each vector in the list has the same length as the number of row in the corresponding table/block, then each variable use a different weight. See detail how to select weight. (New arguments from v1.12)
<code>w.obs</code>	The weight of observations, see <code>w</code> . (New arguments from v1.12)
<code>unit.p</code>	A logical value, whether the loading vectors (for variables) for each table/block should be unit length.
<code>unit.obs</code>	A logical value, whether the score vectors (for observations) for each table/block should be unit length. (New arguments from v1.12)
<code>pos</code>	A logical value, whether only retain non-negative coefficients in loading and score vectors. (New arguments from v1.12)

### Details

Select of weight for variables: In omics data, it is often true that low intensity variables suffers more noise. Therefore, The variables with higher intensities are more reliable. If we consider this, we can use the total sum intensity of a variable (or a tranform of it) as weight, the model would prefer to select high intensity variables.

### 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 wegihts of block scores to construct the global scor

### Note

no note

### Author(s)

Chen Meng

### References

For clustering problem: Meng et al. 2015 moCluster: Identifying Joint Patterns Across Multiple Omics Data Sets. Journal of proteome research.

### 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)

genes <- moaCoef(moas)
genes$nonZeroCoef$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**

**combine** 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.

**show** signature(x = "moa", y = "missing"): show the "mgsa" result.

**Author(s)**

Chen Meng

**See Also**

[moa](#) and [moa.sup](#)

**Examples**

```
showClass("mgsa")
# 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
mgsa1 <- mogsa(x = NCI60_4arrays, sup=sup1, nf=9,
               proc.row = "center_ssq1", w.data = "inertia", stasis = TRUE)
mgsa2 <- mogsa(x = NCI60_4arrays, sup=sup2, nf=9,
               proc.row = "center_ssq1", w.data = "inertia", stasis = 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, stasis=FALSE, moa=TRUE)
```

**Arguments**

data	A list of <code>data.frame</code> or <code>matrix</code> 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.
stasis	A logical indicates whether STATIS method should be used. See details.
moa	Logical; whether the output should be converted to an object of class <code>moa-class</code>

**Details**

Different methods employs different precessing of row and datasets. For multiple 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=center\_ssq1, w.data="lambda1"). This algorithm does not have a well defined criterion to be optimized (see reference).

If stasis=TRUE, the stasis 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 and Mohammed Bennani-Dosse. STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat 2012. Volume 4, Issue 2, pages 124-167 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**

```
# library(mogsa)
# loading data
data(NCI60_4arrays)
# run analysis
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", stasis = 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")

# to extract the components representing significant concordance structures between datasets
bt <- bootMoa(moa = ana, proc.row = "center_ssq1", w.data = "inertia", stasis = TRUE, B = 20)
```

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 sparately.  
**partial.eig:** matrix, rows indicate the partial eigenvalues from each data.  
**eig.vec:** a matrix, eigenvectors.  
**loading:** the coordinate of variables/features.  
**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" could 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  
**show** signature(x = "moa", y = "missing"): show "moa" object

### Author(s)

Chen Meng

### References

Herve Abdi, Lynne J. Williams, Dominique Valentin and Mohammed Bennani-Dosse. STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat 2012. Volume 4, Issue 2, pages 124-167

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

### Examples

```

showClass("moa")
# load("R/mogsa/data/NCI60_4arrays.rda")
data(NCI60_4arrays)
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", stasis = TRUE)

plot(ana, value="eig")
plot(ana, value="tau", type=2)

```

---

moa.sup-class	Class "moa.sup"
---------------	-----------------

---

### 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 information on each separate data.  
**coord.comb:** The projection of geneset information 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.  
**p.val.corrected:** the matrix of corrected p values.

**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

**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", stasis = TRUE)
plot(ana, value="eig")
smoa <- sup.moa(ana, sup=NCI60_4array_supdata, nf=5)

```

---

moaCoef

---

*Extract the loadings/coefficients from an object of class [moa-class](#).*


---

**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 \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)
```

---

moaScore

*Extract global scores from an object of class [moa-class](#).*

---

**Description**

Extract global scores from an object of class [moa-class](#).

**Usage**

```
moaScore(moa)
```

**Arguments**

moa                    An object of class [moa-class](#)

**Value**

A matrix of global score

**Author(s)**

Chen Meng

**See Also**

[moaCoef](#)

**Examples**

```
# see examples in \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)
```

---

moGap

*Gap statistic for clustering latent variables in [moa-class](#).*

---

**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**

```
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 <code>moa-class</code> returned by <code>mbpca</code> .
K.max	The maximum number of clusters to consider, passed to <code>clusGap</code>
B	The number of bootstrap, passed to <code>clusGap</code>
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**

Tibshirani, R., Walther, G. and Hastie, T. (2001). Estimating the number of data clusters via the Gap statistic. *Journal of the Royal Statistical Society B*, 63, 411-423.

Maechler, M., Rousseeuw, P., Struyf, A., Hubert, M., Hornik, K.(2015). `cluster`: Cluster Analysis Basics and Extensions. R package version 2.0.1.

**See Also**

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

## Examples

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

data("NCI60_4arrays")
moa <- mbpca(NCI60_4arrays, ncomp = 10, k = "all", method = "globalScore", option = "lambda",
            center=TRUE, scale=FALSE)
gap <- moGap(moa, K.max = 12, cluster = "hc1")

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

moa2 <- moa(NCI60_4arrays, proc.row="center_ssq1", w.data="inertia", w.row=NULL, stasis=FALSE)
gap2 <- moGap(moa, K.max = 12, cluster = "hc1")
```

---

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 [moa](#) and [sup.moa](#).

## Usage

```
mogsa(x, sup, nf=NULL, factors = NULL, proc.row=NULL, w.data=NULL, w.row=NULL, stasis=FALSE, ks.stat=
```

## Arguments

x	An object of class <code>list</code> or <a href="#">moa-class</a> . A list would be a list of data frame.
sup	An object of class <code>list</code> or <a href="#">moa.sup-class</a> . A list would be a list of supplementary data.
nf	The number of principal components used to reconstruct, only used when x is a an object of <code>list</code> .
factors	The index of principal components used in the projection, used when non-consecutive PC to be included in the analysis.
proc.row	Preprocessing of rows. If x is a object of <code>list</code> , it is passed moa
w.data	Weights of datasets. If x is a object of <code>list</code> , it is passed moa
w.row	Weight of row. If x is a object of <code>list</code> , it is passed moa
stasis	A logical indicates if stasis algorithm should be used. If x is a object of <code>list</code> , it is passed moa
ks.stat	The logical indicates if the p-value should be calculated using K-S statistic (the method used in "ssgsea" in GSEA package). Default is FALSE, which means using the z-score method. See <a href="#">sup.moa</a> .



<code>ks.B</code>	An integer to indicate the number of bootstrapping samples to calculate the p-value of KS statistic.
<code>ks.cores</code>	An integer to indicate the number of cores to be used in bootstrapping. It is passed to function <code>mclapply</code> in the <code>parallel</code> package.
<code>p.adjust.method</code>	The method of p value adjustment, passed to <code>p.adjust</code> function.

### 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

Preprint: Meng, C., Kuster, B., Peters, B., Culhane, AC., Moghaddas Gholami, A., moGSA: integrative single sample gene-set analysis of multiple omics data. doi: <http://dx.doi.org/10.1101/046904>  
 Haenzelmann, S., Castelo, R. and Guinney, J. GSVA: Gene set variation analysis for microarray and RNA-Seq data. *BMC Bioinformatics*, 14:7, 2013. Barbie, D.A. et al. Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. *Nature*, 462(5):108-112, 2009.

### 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", stasis = TRUE)
mgsa1x <- mogsa(x = NCI60_4arrays, sup=NCI60_4array_supdata, factors = c(1,3,6),
              proc.row = "center_ssq1", w.data = "inertia", stasis = TRUE)

# using moa as input
ana <- moa(NCI60_4arrays, proc.row = "center_ssq1", w.data = "inertia", stasis = 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	<i>SVD based algorithm to calculate block Score and global scores for <a href="#">mbpca</a>.</i>
------	--

---

### 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 operators in this function.

### Usage

```
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 <code>svd</code> .

### 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

[nipalsSoftK](#)

---

NCI60_4arrays	<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, which could be used as input to `mcia` directly.

## Usage

```
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

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

---

NCI60\_4array\_supdata *supp data for Microarray gene expression profiles of the NCI 60 cell lines from 4 different platforms*

---

### Description

Supplimentary 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.

---

nipalsSoftK *NIPALS algorithm with soft thresholding operator*

---

### 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 iteration the algorithm can run
k	The number ( $\geq 1$ ) 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](#)

---

`pairwise.rv`      *pairwise RV coefficients.*

---

**Description**

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

**Usage**

```
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  $R_v = \text{trace}(XX'YY') / \sqrt{\text{trace}(XX'XX') * \text{trace}(YY'YY')}$

**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**

Robert, P.; Escoufier, Y. (1976). A Unifying Tool for Linear Multivariate Statistical Methods: The RV-Coefficient. *Applied Statistics* 25 (3): 257-265.

**Examples**

```
data(NCI60_4arrays)
pairwise.rv(NCI60_4arrays)
```

plot-methods

*Methods for function plot***Description**

Methods for function plot

**Methods**

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

---

plotGS	<i>Plot the gene set space</i>
--------	--------------------------------

---

**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, ...)
```

**Arguments**

<code>x</code>	An object of class <code>mgsa-class</code> or <code>moa.sup-class</code>
<code>axes</code>	An integer vector in the length 2 to indicate the axes to be drawn.
<code>center.only</code>	A logical to indicate whether the separate gene set spaces from each of the data set should be plotted. Default is FALSE.
<code>topN</code>	An integer specify N gene set from the most positive and negative end of axes to be labeled
<code>data.pch</code>	The shape for plotting each data set. This argument is passed to points function, so only used when separate gene set spaces are plotted (i.e. <code>center.only = FALSE</code> ).
<code>data.col</code>	The col for plotting each data set. This argument is passed to points function, so only used when separate gene set spaces are plotted (i.e. <code>center.only = FALSE</code> ).
<code>highlight.col</code>	The color used to highlight the selected gene sets
<code>label</code>	Either a character vector or NULL (default). The character vector should be the name of some gene sets want ot be labeled.
<code>label.cex</code>	Passed to <code>text</code> function to adjust the the labels
<code>layout</code>	A matrix passed to the layout function.
<code>...</code>	Other arguments passed to <code>points</code>

**Details**

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

```
# 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)

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

---

prepGraphite

*Prepare pathway gene sets from graphite package*

---

## Description

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

## Usage

```
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

Sales G, Calura E and Romualdi C (2014). graphite: GRAPH Interaction from pathway Topological Environment. R package version 1.10.1.



**See Also**

See Also as [prepMsigDB](#) and [prepSupMoa](#).

**Examples**

```
library(graphite)
keggdb <- prepGraphite(db = pathways("hsapiens", "kegg")[1:3], id = "entrez")
```

---

prepMsigDB	<i>Conver gmt format file to a list</i>
------------	---

---

**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 supplementary tables for projection by sup.moa or mogsa.*

---

### Description

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

### Usage

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

### 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 be 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 be used as supplementary tables by "sup.moa" or "mogsa".

### Author(s)

Chen Meng

### See Also

See Also as [prepGraphite](#) and [prepMsigDB](#).

### Examples

```
library(graphite)
data(NCI60_4arrays)
kegg <- pathways(species = "hsapiens", "kegg")
pw <- c("Purine metabolism", "MAPK signaling pathway")
gss <- prepGraphite(db = kegg[pw], id="symbol")
gss <- lapply(gss, function(x) sub("SYMBOL:", "", x))
sup_data1 <- prepSupMoa(NCI60_4arrays, geneSets=gss)
```

```
gene_list <- lapply(NCI60_4arrays, rownames)
sup_data2 <- prepSupMoa(gene_list, geneSets=gss)
```

---

print-methods                      *Methods for function print*

---

### Description

Methods for function print

### Methods

```
signature(object = "moa") print "moa" class
signature(object = "moa.sup") print "sup.moa" class
signature(object = "mgsa") print "mgsa" class
```

---

processOpt                      *preprocessing of input data in mbpca.*

---

### Description

An internal function called by [mbpca](#).

### Usage

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

### 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 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.

### Value

A list of normalized matrix.

### Author(s)

Chen Meng

---

show-methods                      *Methods for function show*

---

### Description

Methods for function show

### Methods

```
signature(object = "moa") show "moa" class
signature(object = "moa.sup") show "sup.moa" class
signature(object = "mgsa") show "mgsa" class
```

---

softK                                      *Soft-thresholding operator*

---

### Description

Weighted soft-thresholding operator, which is called by [mbpca](#).

### Usage

```
softK(x, k, w = 1, pos = FALSE)
```

### Arguments

x	A numerical vector
k	Number of non-zero elements want to keep
w	weight for each element. The actual thresholding is base on $x*w$ , the default setting equals to ordinary soft thresholding.
pos	A logical value, if only positive values are retained.

### Value

A thresholded numerical vector

### Author(s)

Chen Meng

### Examples

```
v <- rnorm(10)
softK(v, k = 2)
```

---

summary-methods	<i>Methods for function summary</i>
-----------------	-------------------------------------

---

**Description**

Methods for function summary

**Methods**

signature(object = "moa") summary "moa" class

signature(object = "moa.sup") summary "sup.moa" class

signature(object = "mgsa") summary "mgsa" class

---

sup.moa	<i>Projecting supplementary tables on object of class moa-class.</i>
---------	--

---

**Description**

Projecting supplementary tables on [moa-class](#)

**Usage**

```
sup.moa(X, sup, nf = 2, factors = NULL, ks.stat=FALSE, ks.B = 1000, ks.cores = NULL, p.adjust.method =
```

**Arguments**

X	An object of class <a href="#">moa-class</a>
sup	A list of data.frames contains supplementary data.
nf	The number of principal components used in the projection.
factors	The index of principal components used in the projection, used when non-consecutive PC to be included in the analysis.
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.
p.adjust.method	The method of p value adjustment, passed to p.adjust function.

**Details**

Projecting supplementary tables on [moa-class](#), for details see reference.

**Value**

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

**Author(s)**

Chen Meng

**References**

Herve Abdi, Lynne J. Williams, Dominique Valentin and Mohammed Bennani-Dosse. STATIS and DISTATIS: optimum multitable principal component analysis and three way metric multidimensional scaling. WIREs Comput Stat 2012. Volume 4, Issue 2, pages 124-167 Haenzelmann, S., Castelo, R. and Guinney, J. GSEA: Gene set variation analysis for microarray and RNA-Seq data. BMC Bioinformatics, 14:7, 2013. Barbie, D.A. et al. Systematic RNA interference reveals that oncogenic KRAS-driven cancers require TBK1. Nature, 462(5):108-112, 2009.

**Examples**

```
# 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
smao <- sup.moa(ana, sup=NCI60_4array_supdata, nf=3)
# heatmap visualize the gene set scores
heatmap(slot(smao, "score"))
```

---

toMoa

*convert mbpca result to moa-class*

---

**Description**

An internal function called by `mbpca`.

**Usage**

```
toMoa(data, x, call)
```

**Arguments**

<code>data</code>	The preprocessed data in <code>mbpca</code>
<code>x</code>	The object calculated in <code>mbpca</code>
<code>call</code>	The call of <code>mbpca</code>

**Value**

An object of moa-class.

**Author(s)**

Chen Meng

---

wsvd

*Weighted singular value decomposition (SVD)*


---

**Description**

The weighted version of singular value decomposition.

**Usage**

```
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**

Herve Abdi. Singular Value Decomposition (SVD) and Generalized Singular Value Decomposition (GSVD) <http://www.utdallas.edu/~herve/Abdi-SVD2007-pretty.pdf>

**See Also**

svd

**Examples**

```
set.seed(56)
m <- matrix(rnorm(15), 5, 3)
w1 <- rnorm(5)
wr <- runif(3)
s <- wsvd(X=m, D1=w1, D2=wr)
# t(s$u) %*% diag(w1) %*% s$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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