Package ‘omicade4’
March 29, 2017

Type Package
Title Multiple co-inertia analysis of omics datasets
Version 1.14.0
Date 2015-06-10
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Imports made4
Depends R (>= 3.0.0), ade4
Suggests BiocStyle
Description Multiple co-inertia analysis of omics datasets


License GPL-2
LazyLoad yes
biocViews Software, Clustering, Classification, MultipleComparison

R topics documented:

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omicade4-package

multiple co-inertia analysis of omics datasets

Description
The main function in the package performing multiple co-inertia analysis on omics datasets

Details

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Multiple co-inertia analysis (MCIA) is a multivariate analysis method that could be used to analyze multiple tables measuring the same set of individuals, this package provides a one-stop function for MCIA and functions for subsequent analysis especially for multiple omics datasets.

Author(s)
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References
Meng C, Kuster B, Culhane AC and Gholami AM. A multivariate approach to the integration of multi-omics datasets. (Manuscript under preparation)


See Also
ade4 and package made4

Examples

data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
mcia

multiple co-inertia analysis

Description

The main function in omicade4. Performing multiple co-inertia analysis on a list of data.frames or matrix

Usage

mcia(df.list, cia.nf = 2, cia.scan = FALSE, nsc = T, svd = TRUE)
## S3 method for class 'mcia'
plot(x, axes = 1:2,
    sample.lab = TRUE, sample.legend = TRUE, sample.color = 1,
    phenovec = NULL, df.color = 1,
    df.pch = NA, gene.nlab = 0, ...)

Arguments

df.list A list of data.frames, matrix or ExpressionSet is going to be analyzed, the column number must be the same and mapped across all data.frame/matrix

cia.nf An integer indicating the number of kept axes

cia.scan A logical indicating whether the co-inertia analysis eigenvalue (scree) plot should be shown so that the number of axes, (cia.nf) can be selected interactively. Default value is FALSE.

nsc A logical indicating whether multiple co-inertia analysis should be performed using multiple non-symmetric correspondence analyses dudi.nsc. The default =TRUE is highly recommended. If FALSE, COA dudi.coa will be performed on the first data.frame, and row weighted COA dudi.rwcoa will be performed on the rest ones using the row weights from the first one.

svd A logical indicates which function should be used to perform singular value decomposition.

sample.lab A logical indicating if the samples should be labelled, the default is TRUE.

sample.color Defining colours of samples for plotting sample space, the length of this argument should be either one (uniform color) or the same with the column number of data.frame in df.list.

sample.legend A logical indicating if the legend for sample space should be drawn.

df.color Defining the colours for plotting variables (genes) from different data.frame. The length of this argument should be either one (all datasets use the same colour) or the same number of datasets (each dataset has a specified colour, the repetitive use of colour code is allowed.)

df.pch Defining the pch for plotting variable (gene) space. The default is NA, the function will distinguish datasets by default. Otherwise, the length of this argument should be either one (all datasets use the same pch) or the same number of datasets (each dataset has a specified pch).

phenovec A factor for plotting sample space, phenovec could be used to distinguish individuals in the data.frames.

x An object of class mcia
Axes A vector of integer in length 2 to indicate the axes are going to be plotted. The
default are first two axes.

gene.nlab An integer indicating how many top weighted genes on each axis should be
labelled

... Other arguments

Details

The column number of data.frame in the df.list must be the same, and the same column from
different data.frame should be matchable. For example, Microarray profiling for the same set of
cell lines, patients and etc.

cmia calls dudi.nsc, ktab and mcoa in ade4 packages.

Plotting and visualizing mcia results

Two functions could be used to visualize the result of mcia: The first is plot.mcia, which results
in four plots. Top left represents the sample space. Individuals from the same column of different
data.frames are linked by edges. Different platforms are distinguished by the shape of points. Top
right shows the variable space, datasets are marked by different colours. Bottom left represents the
eigenvalue scree plot. The pseudo-eigenvalue space of all data.frames are visualized in the bottom
right panel. The second function is plotVar.mcia, which could be used to plot the variable space
for different datasets as well as finding and visualizing the variables (genes) across datasets.

Other methods

selectVar.mcia: selecting variables (genes) according to the their coordinates.

Value

call the function called

mcoa The results returned by mcoa

coa The results returned by separate analysis (applying dudi.nsc or dudi.coa on
each data.frame separately)

Author(s)

Chen Meng

See Also

See Also as mcoa, plotVar, plotVar

Examples

data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
plot(mcoin, sample.lab=FALSE, df.col=4:7)

colcode <- sapply(strsplit(colnames(NCI60_4arrays$agilent), split="\."),
    function(x) x[1])
plot(mcoin, sample.lab=FALSE, sample.color=as.factor(colcode))
**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.

**Source**


**References**


**Examples**

```r
data(NCI60_4arrays)
summary(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
```
plotVar

Plot variable (gene) spaces of result from MCIA or CIA

Description

The user level function for plotting variable space of mcia or cia, which could be used to visualize selected variables (genes) across datasets. It calls plotVar.cia or plotVar.mcia.

Usage

plotVar(x, var = NA, axes = 1:2, var.col = "red", var.lab = FALSE, bg.var.col = "gray", nlab = 0, sepID.data=NULL, sepID.sep="_", ...)

Arguments

x An object of class cia or mcia
var A character vector defining the variables (genes) are going to be labelled and coloured. The default NA means no variables (genes) selected.
axes An integer vector in length 2 indicating which axes are going to be plotted. Default are the first two axes.
var.col The colour of selected variables (genes), the length of this argument should be either 1 (uniform colour) or the length of var (each var has a specified colour).
var.lab A logical indicating if the variables (genes) selected should be labelled, the default is FALSE
bg.var.col Colour code for unselected variables (genes) in all datasets.
nlab An integer indicating how many top weighted genes on each axis should be labelled.
sepID.data This argument enables a more generalized mapping of identifiers in different datasets. For example, if there is a PTM (post-transcriptional modification) dataset in one of the data.frames, the corresponding protein could be detected with setting this argument. For more details, see "details" section.
sepID.sep Used to help determine the separator of variables (genes) in the sepID.data. For more details, see "details" section.
... Other arguments

Details

For the sepID.data, a typical example is the post-transcriptional modification (PTM) data. The name of variables (genes) have a general form like "proteinName_modificationSite". The sepID.data specifies the IDs from dataset that should be separated, sepID.sep specifies the separator of protein name and modification site. This is used to determine the same proteins/genes across different datasets.

Value

If var is not NA, a data frame is returned, with rows for variables (genes) of interest and columns of logical values indicating which dataset contains which variables (genes).
plotVar.cia

Author(s)

Chen Meng

See Also

See Also as plotVar.cia, plotVar.mcia

Examples

data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
plotVar(mcoin, var=c("S100B", "S100A1"), var.lab=TRUE)

# an example for the usage of sepID.data and sepID.sep
nci60_mod <- NCI60_4arrays
rownames(nci60_mod$hgu95) <- paste(rownames(nci60_mod$hgu95), "s1", sep="._")
mcoin_mod <- mcia(nci60_mod)
# without specifying
plotVar(mcoin_mod, var=c("S100B", "S100A1"), var.lab=TRUE)
# specifying the sepID.data and sepID.sep
plotVar(mcoin_mod, var=c("S100B", "S100A1"), var.lab=TRUE, sepID.data=4, sepID.sep="._")

---

plotVar.cia  

Plot variable space of result from cia

Description

Plot variable space of mcia and visualize selected variables across datasets.

Usage

```r
## S3 method for class 'Var
plotVar(x, var = NA, axes = 1:2,
       var.col = "red", var.lab = FALSE, bg.var.col = "gray",
       nlab = 0, sepID.data = NULL, sepID.sep = ",", ...)
```

Arguments

- `x`  
  An object of class cia
- `var`  
  see plotVar
- `axes`  
  see plotVar
- `var.col`  
  see plotVar
- `var.lab`  
  see plotVar
- `bg.var.col`  
  see plotVar
- `nlab`  
  see plotVar
- `sepID.data`  
  see plotVar
- `sepID.sep`  
  see plotVar
- `...`  
  Other arguments
Value

If `var` is not NA, a data frame is return, with rows for variables of interest and columns of logical value indicating which data.frames contains which variables.

Author(s)

Chen Meng

See Also

See Also as `plotVar.mcia`

---

**plotVar.mcia**

*Plot variable space of result from mcia*

---

Description

Plot variable space of `mcia` and visualize selected variables across datasets, the function is called by `plotVar`.

Usage

```r
## S3 method for class 'mcia'
plotVar(x, var = NA, axes = 1:2,
    var.col = "red", var.lab = FALSE, bg.var.col = "gray",
    nlab = 0, sepID.data = NULL, sepID.sep = ",",
    df = NA, layout = NA, ...)
```

Arguments

- `x` 
  An object of class `mcia`, the result returned by `mcia`.
- `var` 
  See `plotVar`
- `axes` 
  See `plotVar`
- `var.col` 
  See `plotVar`
- `var.lab` 
  See `plotVar`
- `bg.var.col` 
  See `plotVar`
- `nlab` 
  See `plotVar`
- `sepID.data` 
  See `plotVar`
- `sepID.sep` 
  See `plotVar`
- `df` 
  Integers indicating which dataset should be plotted, the default NA means all datasets are plotted.
- `layout` 
  The layout of multiple plots.
- `...` 
  Other arguments

Value

If `var` is not NA, a data frame is return, with rows for variables of interest and columns of logical values indicating which data.frames contains which variables.
**selectVar**

**Author(s)**

Chen Meng

**See Also**

See Also as `plotVar.cia, plotVar`

**Examples**

```r
data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
plot.mcia(mcoin, sample.lab=FALSE, df.col=4:7)
plotVar(mcoin, var=NA, bg.var.col=1:4, var.lab=TRUE)
plotVar(mcoin, var=c("SPOPL", "CAPN2", "SNX8"),
        df=1:4, var.lab=TRUE, var.col=c("red", "green", "blue"))
```

---

**Description**

The user level function calls `selectVar.mcia` or `selectVar.cia`. Function `cia` or `mcia` projects variables (genes) from different datasets to a 2 dimensional space. This function supplies a method selecting variables (genes) according to the coordinates of variables.

**Usage**

```r
selectVar(x, axis1 = 1, axis2 = 2, ...)
```

**Arguments**

- `x` An object of class `cia` or `mcia`, the result returned by `cia` or `mcia` respectively.
- `axis1` Integer, the column number for the x-axis. The default is 1.
- `axis2` Integer, the column number for the y-axis. The default is 2.
- `...` Other arguments

**Value**

Returns a data.frame describing which variables (genes) are presented on which data.frames within the limited region(s).

**Author(s)**

Chen Meng

**See Also**

See Also as `selectVar.mcia, selectVar.cia`
Examples

data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
selectVar(mcoin, a1.lim=c(2, Inf), a2.lim=c(-Inf, Inf))

# an example for the usage of sepID.data and sepID.sep
nci60_mod <- NCI60_4arrays
rownames(nci60_mod$hgu95) <- paste(rownames(nci60_mod$hgu95), "s1", sep="_")
mcoin_mod <- mcia(nci60_mod)
# without specifying
selectVar(mcoin_mod, a1.lim=c(2, Inf), a2.lim=c(-Inf, Inf))
# specifying the sepID.data and sepID.sep
selectVar(mcoin_mod, a1.lim=c(2, Inf), a2.lim=c(-Inf, Inf), sepID.data=4, sepID.sep="_")

selectVar.cia

Selecting variables from result of CIA

Description

To select variables in CIA variable space, the function is called by `selectVar`.

Usage

```r
## S3 method for class 'Var.cia'
selectVar(x, axis1 = 1, axis2 = 2,
df1.a1.lim = c(-Inf, Inf), df1.a2.lim = c(-Inf, Inf),
df2.a1.lim = df1.a1.lim, df2.a2.lim = df1.a2.lim,
sepID.data = NULL, sepID.sep = "_")
```

Arguments

- **x**: The result returned by `cia`
- **axis1**: Integer, the column number for the x-axis. The default is 1.
- **axis2**: Integer, the column number for the y-axis. The default is 2.
- **df1.a1.lim**: A vector containing 2 numbers indicating the range of X axis of selected on the 1st data.frame. The first value limiting the lower boundary, the second value limiting the upper boundary.
- **df1.a2.lim**: The range of Y axis of selected on the 1st datasets.
- **df2.a1.lim**: The range of X axis of selected on the 2nd dataset.
- **df2.a2.lim**: The range of Y axis of selected on the 2nd dataset.
- **sepID.data**: See `plotVar.mcia`
- **sepID.sep**: See `plotVar.mcia`
- **...**: Other arguments

Details

cia projecting variables from different datasets to a two dimensional space. This function supplies a method selecting variables according to the co-ordinates of variables.
selectVar.mcia

Value

Returns a data.frame describing which variables are presented on which data.frame within the limited region(s).

Author(s)

Chen Meng

See Also

See Also as selectVar.mcia

selectVar.mcia  Selecting variables from result of MCIA

Description

The selection of variables based on co-ordinates of MCIA variable space. The function is called by selectVar

Usage

## S3 method for class 'mcia'
selectVar(x, axis1 = 1, axis2 = 2,
a1.lim = c(-Inf, Inf), a2.lim = c(-Inf, Inf),
sepID.data = NULL, sepID.sep = "_", ...)

Arguments

x  An object of class mcia, the result returned by mcia.

axis1  Integer, the column number for the x-axis. The default is 1.

axis2  Integer, the column number for the y-axis. The default is 2.

a1.lim  The limited range of x-axis of selected. It could be either a vector (containing 2 numbers, the first value limiting the lower boundary, the second value limiting the upper boundary) or a list of vectors, each of which contains two number. If it is a list, the length of the list should be the same with number of data.frames in mcia.

a2.lim  The limited range of y-axis.

sepID.data  See plotVar.mcia

sepID.sep  See plotVar.mcia

...  Other arguments

Details

mcia projecting variables (genes) from different datasets to a lower dimensional space. This function supplies a method selecting variables according to the co-ordinates of variables.
topVar

Description

The user level function calls `topVar.mcia` or `topVar.cia`. This function provides a method selecting top weighted variables (genes) on an axis (either positive side or negative side or both).

Usage

```r
topVar(x, axis = 1, end = "both", topN = 5)
```

Arguments

- **x**: an object of class `mcia` or `cia`
- **axis**: an integer to specify which axis to check
- **end**: which end of the axis to check, could be positive, negative or both. Any unambiguous substring can be given.
- **topN**: An integer. The number of top weighted variable to return.

Value

Returns a data.frame contains selected variables.

Author(s)

Chen Meng

Examples

```r
data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
selectVar(mcoin, a1.lim=c(1, Inf))
```

---

**Description**

Selecting top weighted variables (genes) from result of MCIA or CIA

**Usage**

```r
topVar(x, axis = 1, end = "both", topN = 5)
```

**Arguments**

- **x**: an object of class `mcia` or `cia`
- **axis**: an integer to specify which axis to check
- **end**: which end of the axis to check, could be positive, negative or both. Any unambiguous substring can be given.
- **topN**: An integer. The number of top weighted variable to return.

**Value**

Returns a data.frame contains selected variables.

**Author(s)**

Chen Meng

**Examples**

```r
data(NCI60_4arrays)
mcoin <- mcia(NCI60_4arrays)
topVar(mcoin, axis = 1, end = "both", topN = 3)
```
**topVar.cia**

Selecting top weighted variables (genes) from result of CIA

**Description**

This function provides a method selecting top weighted variables (genes) on an axis (either positive side or negative side or both) from an object of class `cia` (see made4 package).

**Usage**

```r
## S3 method for class 'cia'
topVar(x, axis = 1, end = "both", topN = 5)
```

**Arguments**

- `x` See `plotVar.mcia`
- `axis` See `plotVar.mcia`
- `end` See `plotVar.mcia`
- `topN` See `plotVar.mcia`

**Value**

See `plotVar.mcia`

**Author(s)**

Chen Meng

---

**topVar.mcia**

Selecting top weighted variables (genes) from result of MCIA

**Description**

This function provides a method selecting top weighted variables (genes) on an axis (either positive side or negative side or both) from an object of class `mcia`.

**Usage**

```r
## S3 method for class 'mcia'
topVar(x, axis = 1, end = "both", topN = 5)
```

**Arguments**

- `x` See `plotVar.mcia`
- `axis` See `plotVar.mcia`
- `end` See `plotVar.mcia`
- `topN` See `plotVar.mcia`
Value

See plotVar.mcia

Author(s)

Chen Meng
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