Package ‘superbiclust’

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Type Package

Title Generating Robust Biclusters from a Bicluster Set (Ensemble Biclustering)

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Depends biclust, fabia

Imports methods, Matrix, graphics, stats

Description Biclusters are submatrices in the data matrix which satisfy certain conditions of homogeneity. Package contains functions for generating robust biclusters with respect to the initialization parameters for a given bicluster solution contained in a bicluster set in data, the procedure is also known as ensemble biclustering. The set of biclusters is evaluated based on the similarity of its elements (the overlap), and afterwards the hierarchical tree is constructed to obtain cut-off points for the classes of robust biclusters. The result is a number of robust (or super) biclusters with none or low overlap.

License GPL (>= 2)

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superbiclust-package    generating robust biclusters from the set of biclusters

Description

The package contains a number of functions for computing similarity matrix of the biclusters obtained by a variety of methods, initialization seeds or various parameter settings. It uses biclustering output as generated by biclust or fabia. isa2 package can be used to generate the biclusters as well, however, a prior conversion is needed to a bicluster object by using isa2.biclust() function. The matrix is used for the construction of hierarchical tree based on overall similarity, row similarity or column similarity to obtain cut-off points for the similarity metric of choice. Various statistics are output per bicluster set: a number of a given gene(compound) or gene (compound) set has been present in any bicluster of output or per run. After the tree is cut, the robust or super biclusters are obtained in a form of biclust object, which can further be used for plotting of biclusters. Biclusters are sub-matrices in the data which satisfy certain conditions of homogeneity. For more details on biclusters and biclustering see Madeira and Oliveira (2004).

Details

Package:    superbiclust
Type:       Package
Version:    0.99
Date:       2012-08-23
License:    GPL
LazyLoad:   yes
**Author(s)**

Tatsiana Khamiakova <tatsiana.khamiakova@uhasselt.be>

**References**


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**BiclustSet-class**

**Class**

BiclustSet

**Description**

BiclustSet Class contains the biclustering result in a form: bicluster rows and bicluster columns

**Objects from the Class**

Objects can be created by calls of the form new("BiclustSet", ...). The variety of inputs variety of inputs (isa2, fabia, biclust,...) can be used.

**Slots**

GenesMembership: logical, object of class "matrix", with row membership within a bicluster

ColumnMembership: logical, object of class "matrix", with column membership within a bicluster

Number: code "numeric", number of biclusters in the set

**Author(s)**

Tatsiana Khamiakova
BiclustSet-methods  

Constructor of BiclustSet object

Description

The method extract relevant information from a variety of biclustering input and constructs a Bi-clustSet object

Methods

signature(x = "ANY")
signature(x = "Biclust") Converts Biclust objects into BiclustSet object
signature(x = "Factorization") Converts FABIA Factorization object into BiClustSet
signature(x = "list") Converts a list with biclustering results into BiClustSet

See Also

BiclustSet

Examples

test <- matrix(rnorm(5000), 100, 50)
test[11:20,11:20] <- rnorm(100, 3, 0.1)
test[17:26,21:30] <- rnorm(100, 3, 0.1)

#Run FABIA
set.seed(1)
FabiaRes1 <- fabia(test)
#construct BiclustSet object from FABIA output
FabiabiclustSet <- BiclustSet(FabiaRes1)
FabiabiclustSet

combine  

Combine two Biclust objects into one

Description

Combine two Biclust objects into one

Usage

combine(x,y)

Arguments

x  
1st Biclust object containing bicluster results

y  
2nd Biclust object containing bicluster results
getStats

Details

If a biclust function returns empty set, joined result contains only results of non-empty object. Info and Parameters slots of a "Biclust" object contain information about both biclustering runs.

Value

object of a class Biclust

Author(s)

Tatsiana Khamiakova

See Also

BiclustSet

Examples

#combine output of two biclust objects
test <- matrix(rnorm(5000), 100, 50)
test[11:20,11:20] <- rnorm(100, 3, 0.1)
test[17:26,21:30] <- rnorm(100, 3, 0.1)
set.seed(1)
PlaidRes1 <- biclust(x=test, method=BCPlaid())
set.seed(2)
PlaidRes2 <- biclust(x=test, method=BCPlaid())
combinedRes <- combine(PlaidRes1,PlaidRes2)
summary(combinedRes)

getStats

Get frequency statistic for the columns and rows membership

Description

For a given Bicluster set, for each row and column in data, compute frequency of apperance within a bicluster

Usage

getStats(x)

Arguments

x

Biclust object containing bicluster results

Value

a list of column and row frequencies
HCLtree

Hierarchical structure of bicluster output

Description

Constructs and plots hierarchical tree of biclusters output based on the similarity matrix

Usage

HCLtree(x)

Arguments

x

Similarity object containing pairwise similarity indices for all biclusters in the output

Details

This function operates on a similarity matrix, which is converted to the distance between biclusters according to \( \text{dist}(a, b) = 1 - \text{sim}(a, b) \), where the smaller the distance, the higher is overlap in terms of rows and columns. The tree is constructed using complete method and plotted. Further, the structure must be explored and robust or super-biclusters obtained after cutting the tree. identify function can be applied to the hierarchical tree to see the partition and get the plots of biclusters.

Value

tree

Author(s)

Tatsiana Khamiakova

See Also

similarity, plotSuper

Examples

# compute sensitivity for BiMAX biclusters
test <- matrix(rnorm(5000), 100, 50)
test[11:20,11:20] <- rnorm(100, 3, 0.1)
test[17:26,21:30] <- rnorm(100, 3, 0.1)
testBin <- binarize(test, 2)
res <- biclust(x=testBin, method=BCBimax(), minr=4, minc=4, number=10)
BiMaxBiclustSet <- BiclustSet(res)
SensitivityMatr <- similarity(BiMaxBiclustSet, index = "sensitivity")
# construct hierarchical clustering based on the sensitivities
HCLsensitivity <- HCLtree(SensitivityMatr)
plot(HCLsensitivity, main = "structure of bicluster solution")

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**jaccardMat**

**Jaccard similarity Matrix for bicluster output**

**Description**

computes jaccard similarity matrix for biclusters in two bicluster sets

**Usage**

jaccardMat(x, y, type = c("rows", "cols", "both"))

**Arguments**

- **x** BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **y** BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **type** whether to compute Jaccard index in two dimensions, row dimension or column dimension

**Details**

This function operates on BiclustSet objects and computes pairwise similarity based on the common elements between biclusters. The Jaccard similarity score $j_a$ for two biclusters $A$ and $B$ is computed as

$$j_a = \frac{|A \cap B|}{|A \cup B|}$$

**Value**

matrix of pairwise Jaccard indices

**Author(s)**

Tatsiana Khamiakova

**See Also**

similarity, kulczynskiMat, ochiaiMat, sensitivityMat, specificityMat, sorensenMat
**kulczynskiMat**

*Kulczynski similarity Matrix for bicluster output*

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**Description**

computes Kulczynski similarity matrix for biclusters in two bicluster sets

**Usage**

kulczynskiMat(x, y, type=c("rows", "cols", "both"))

**Arguments**

- **x**: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **y**: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **type**: whether to compute Kulczynski index in two dimensions, row dimension or column dimension

**Details**

This function operates on BiclustSet objects and computes pairwise similarity based on the common elements between biclusters. Kulczynski similarity score $ku$ for two biclusters $A$ and $B$ is computed as

$$ku = 2|A \cap B| \left( \frac{1}{|A|} + \frac{1}{|B|} \right)$$

**Value**

matrix of pairwise Kulczynski indices

**Author(s)**

Tatsiana Khamiakova

**See Also**

similarity, jaccardMat, ochiaiMat, sensitivityMat, specificityMat, sorensenMat
Ochiai similarity Matrix for bicluster output

Description

Computes Ochiai similarity matrix for biclusters in two bicluster sets.

Usage

```r
ochiaiMat(x, y, type=c("rows", "cols", "both"))
```

Arguments

- `x`: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters.
- `y`: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters.
- `type`: whether to compute Ochiai index in two dimensions, row dimension or column dimension.

Details

This function operates on BiclustSet objects and computes pairwise similarity based on the common elements between biclusters. The Ochiai similarity score $ja$ for two biclusters $A$ and $B$ is computed as

$$ oc = \frac{|A \cap B|}{\sqrt{|A||B|}} $$

Value

matrix of pairwise Ochiai indices.

Author(s)

Tatsiana Khamiakova

See Also

`similarity`, `jaccardMat`, `ochiaiMat`, `sensitivityMat`, `specificityMat`, `sorensenMat`
**plotProfilesAcrossAllSamples**  

*Plot Gene Expression Profiles Across All Samples of the Original Data*

**Description**

Plot Gene Expression Profiles Across All Samples of the Original Data

**Usage**

```r
plotProfilesAcrossAllSamples(x, coreBiclusterGenes, coreBiclusterSamples)
```

**Arguments**

- `x`: data
  - `coreBiclusterGenes`: vector of genes belonging to bicluster
  - `coreBiclusterSamples`: vector of samples belonging to bicluster

**Details**

The plot re-sorts the samples by bicluster membership and highlights them in red. Only the genes of a bicluster are plotted.

**Value**

no return value; a plot is drawn to the current device

**Author(s)**

Tatsiana Khamiakova

**See Also**

`BiclustSet.plotSuperAll`
plotProfilesWithinBicluster

Plot Gene Expression Profiles within a (Core) Bicluster

Description

Plot Gene Expression Profiles within a (Core) Bicluster

Usage

plotProfilesWithinBicluster(x, main = "", sampleNames, geneNames = NULL)

Arguments

x        expression matrix (of class 'matrix') for the subset of genes and samples corresponding to the bicluster under study
main     main title for the graph
sampleNames     names of the samples to be used for annotating the x axis (character vector of length equal to the number of columns of the expression matrix 'x' (representing the bicluster)
geneNames names of the genes to be plotted in a legend (character vector of length equal to the number of rows of the expression matrix 'x'); only suitable for biclusters containing a small number of genes

Value

no return value; a plot is drawn to the current device

Author(s)

Tatsiana Khamiakova

See Also

plotSuper
plotSuper

Plot gene profiles within biclusters

Description

Function for plotting gene profiles for compounds within constructed super-bicluster

Usage

plotSuper(x, data, BiclustSet)

Arguments

x  a vector, containing indices of biclusters, to be joined for obtaining the robust bicluster
data  matrix, dataset, from which the bicluster results are obtained
BiclustSet  a BiclustSet object containing bicluster output

Details

This function constructs a robust bicluster from a set of biclusters identified in a hierarchical tree and plots gene profiles for columns in a robust bicluster. Each line represents a gene from a bicluster. The bicluster is saved as Biclust object which can be further plotted by available functions from biclust package. The information about the number of biclusters used to generate the resulting robust bicluster is saved in Call slot of the object. This information is important to see how often the bicluster has been discovered under different parameter settings (e.g. initialization seeds) Indices used as an input can be obtained by identify function or by cutting the tree.

Value

biclust object containing bicluster and the information about bicluster subset used to generate it

Author(s)

Tatsiana Khamiakova

See Also

HCLtree, plotSuperAll, plotProfilesWithinBicluster
plotSuperAll

Plot gene profiles for all samples in the data

Description
Function for plotting bicluster gene profiles for all samples in the data

Usage
plotSuperAll(x, data, BiclustSet)

Arguments
- x: a vector, containing indices of biclusters, to be joined for obtaining the robust bicluster
- data: matrix, dataset, from which the bicluster results are obtained
- BiclustSet: a BiclustSet object containing bicluster output

Details
This function constructs a robust bicluster from a subset of biclusters specified in x argument and plots the expression profiles

Value
biclust object

Author(s)
Tatsiana Khamiakova

See Also
HCLtree, plotProfilesAcrossAllSamples

sensitivityMat

Sensitivity Matrix for bicluster output

Description
Computes sensitivity matrix for biclusters in two bicluster sets

Usage
sensitivityMat(x, y, type=c("rows", "cols", "both"))
Arguments

- **x**: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **y**: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **type**: whether to compute sensitivity in two dimensions, row dimension or column dimension

Details

This function operates on BiclustSet objects and computes pairwise similarity based on the common elements between biclusters. Sensitivity inclusion score \( sen \) of biclusters A and B is computed as

\[
    sen = \frac{|A \cap B|}{|A|}
\]

Value

matrix of pairwise sensitivities

Author(s)

Tatsiana Khamiakova

See Also

similarity, jaccardMat, ochiaiMat, kulczynskiMat, specificityMat, sorensenMat

Description

computes similarity matrix for the biclustering output based on one of the pairwise similarity indices of biclusters in a given bicluster set

Usage

```
similarity(x, index = "jaccard", type="rows")
```

Arguments

- **x**: BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- **index**: similarity index for the biclusters in output
- **type**: whether to perform similarity in two dimensions, "both" (recommended for biclustering), row dimension, "rows" (default, requires less computations) or column dimension "cols"
sorensenMat

Details

This function operates on BiclustSet object and computes pairwise similarity based on the common elements between biclusters. The type variable controls whether similarity index is constructed for all elements, or in one dimension (rows or columns) only. In general, similarity indices for one dimension (row or column) are higher than for two-dimensions. Several options for similarity indices are offered: jaccard (default), kulczynski, sensitivity, specificity, sorensen and ochiai indices.

Value

a "similarity" object containing similarity matrix

Author(s)

Tatsiana Khamiakova

See Also

HCLtree, plotSuper, jaccardMat, kulczynskiMat, ochiaiMat, sensitivityMat, specificityMat, sorensenMat

Examples

#compute sensitivity for BiMAX biclusters
test <- matrix(rnorm(5000), 100, 50)
test[11:20,11:20] <- rnorm(100, 3, 0.1)
test[17:26,21:30] <- rnorm(100, 3, 0.1)
testBin <- binarize(test,2)
res <- biclust(x=testBin, method=BCBimax(), minr=4, minc=4, number=10)
BiMaxBiclustSet <- BiclustSet(res)
SensitivityMatr <- similarity(BiMaxBiclustSet, index="sensitivity", type="rows")
SensitivityMatr

sorensenMat

Sorensen similarity Matrix for bicluster output

Description

Computes Sorensen similarity matrix for biclusters in two bicluster sets

Usage

sorensenMat(x, y, type=c("rows", "cols", "both"))

Arguments

x BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
y BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
type whether to compute Sorensen index in two dimensions, row dimension or column dimension
Details
This function operates on BiclustSet objects and computes pairwise similarity based on the common elements between biclusters. Sorensen similarity score $so$ for two biclusters $A$ and $B$ is computed as
\[ so = \frac{2|A \cap B|}{|A| + |B|} \]

Value
matrix of pairwise Sorensen indices

Author(s)
Tatsiana Khamiakova

See Also
similarity, jaccardMat, ochiaiMat, sensitivityMat, specificityMat, kulczynskiMat

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specificityMat

Specificity Matrix for bicluster output

Description
Computes specificity matrix for biclusters in two bicluster sets

Usage
`specificityMat(x, y, type=c("rows", "cols", "both"))`

Arguments
- `x` BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- `y` BiclustSet object containing row and column indicators of bicluster membership, number of biclusters
- `type` whether to compute specificity in two dimensions, row dimension or column dimension

Details
This function operates on BiclustSet objects and computes pairwise similarity based on the common elements between biclusters. Sensitivity inclusion score $spe$ of biclusters $A$ and $B$ is computed as
\[ spe = \frac{|A \cap B|}{|B|} \]
**specificityMat**

**Value**
matrix of pairwise specificities

**Author(s)**
Tatsiana Khamiakova

**See Also**
similarity, jaccardMat, ochiaiMat, kulczynskiMat, sensitivityMat, sorensenMat
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