Package ‘biclust’

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### Description

Performs Bimax Biclustering based on the framework by Prelic et. al.(2006). It searches for submatrices of ones in a logical matrix. Uses the original C code of the authors.
Usage

```r
## S4 method for signature 'matrix,BCBimax'
biclust(x, method=BCBimax(), minr=2, minc=2, number=100)
## S4 method for signature 'matrix,BCrepBimax'
biclust(x, method=BCrepBimax(), minr=2, minc=2, number=100, maxc=12)
```

Arguments

- `x`: A logical matrix which represents the data.
- `method`: Here BCBimax, to perform Bimax algorithm
- `minr`: Minimum row size of resulting bicluster.
- `minc`: Minimum column size of resulting bicluster.
- `number`: Number of Bicluster to be found.
- `maxc`: Maximum column size of resulting bicluster.

Value

Returns an object of class Biclust.

Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

References


See Also

biclust, Biclust

Examples

```r
test <- matrix(rnorm(5000), 100, 50)
test[11:20,11:20] <- rnorm(100, 3, 0.1)
loma <- binarize(test, 2)
res <- biclust(x=loma, method=BCBimax(), minr=4, minc=4, number=10)
res
```
**Description**

Performs CC Biclustering based on the framework by Cheng and Church (2000). Searches for submatrices with a score lower than a specific threshold in a standardized data matrix.

**Usage**

```r
## S4 method for signature 'matrix,BCCC'
biclust(x, method=BCCC(), delta = 1.0, alpha=1.5, number=100)
```

**Arguments**

- `x` : Data matrix.
- `method` : Here BCCC, to perform CC algorithm
- `delta` : Maximum of accepted score.
- `alpha` : Scaling factor.
- `number` : Number of bicluster to be found.

**Value**

Returns an object of class Biclust.

**Author(s)**

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

**References**

Cheng, Y. & Church, G.M. Biclustering of Expression Data Proceedings of the Eighth International Conference on Intelligent Systems for Molecular Biology, 2000, 1, 93-103

**See Also**

biclust, Biclust

**Examples**

```r
test <- matrix(rbinom(400, 50, 0.4), 20, 20)
res <- biclust(test, method=BCCC(), delta=1.5, alpha=1, number=10)
res
```
Description

Performs Plaid Model Biclustering as described in Turner et al., 2003. This is an improvement of original 'Plaid Models for Gene Expression Data' (Lazzeroni and Owen, 2002). This algorithm models data matrices to a sum of layers, the model is fitted to data through minimization of error.

Usage

```r
## S4 method for signature 'matrix,BCPlaid'
biclust(x, method=BCPlaid(), cluster="b", fit.model = y ~ m + a + b,
    background = TRUE, background.layer = NA, background.df = 1, row.release = 0.7,
    col.release = 0.7, shuffle = 3, back.fit = 0, max.layers = 20, iter.startup = 5,
    iter.layer = 10, verbose = TRUE)
```

Arguments

- `x`: The data matrix where biclusters have to be found
- `method`: Here BCPlaid, to perform Plaid algorithm
- `cluster`: 'r', 'c' or 'b', to cluster rows, columns or both (default 'b')
- `fit.model`: Model (formula) to fit each layer. Usually, a linear model is used, that estimates three parameters: m (constant for all elements in the bicluster), a (constant for all rows in the bicluster) and b (constant for all columns). Thus, default is: \( y \sim m + a + b \).
- `background`: If 'TRUE' the method will consider that a background layer (constant for all rows and columns) is present in the data matrix.
- `background.layer`: If background='TRUE' a own background layer (Matrix with dimension of x) can be specified.
- `background.df`: Degrees of Freedom of background layer if background.layer is specified.
- `shuffle`: Before a layer is added, it's statistical significance is compared against a number of layers obtained by random defined by this parameter. Default is 3, higher numbers could affect time performance.
- `iter.startup`: Number of iterations to find starting values
- `iter.layer`: Number of iterations to find each layer
- `back.fit`: After a layer is added, additional iterations can be done to refine the fitting of the layer (default set to 0)
- `row.release`: Scalar in \([0,1]\) (with interval recommended \([0.5-0.7]\)) used as threshold to prune rows in the layers depending on row homogeneity
- `col.release`: As above, with columns
- `max.layers`: Maximum number of layer to include in the model
- `verbose`: If 'TRUE' prints extra information on progress.
Value

Returns an Biclust object.

Author(s)

Adaptation of original code from Heather Turner from Rodrigo Santamaria <rodri@usal.es>.

References


Examples

```r
# Random matrix with embedded bicluster
test <- matrix(rnorm(5000), 100, 50)
test[11:20, 11:20] <- rnorm(100, 3, 0.3)
res <- biclust(test, method=BCPlaid())
res

# Microarray matrix
data(BicatYeast)
res <- biclust(BicatYeast, method=BCPlaid(), verbose=FALSE)
res
```

Description

Performs Questmotif Biclustering a Bicluster algorithm for questionnaires based on the framework by Murali and Kasif (2003). Searches subgroups of questionnaires with same or similar answer to some questions.

Usage

```r
## S4 method for signature 'matrix,BCQuest'
biclust(x, method=BCQuest(), ns=10, nd=10, sd=5, alpha=0.05, number=100)
## S4 method for signature 'matrix,BCQuestord'
biclust(x, method=BCQuestord(), d=1, ns=10, nd=10, sd=5, alpha=0.05, number=100)
## S4 method for signature 'matrix,BCQuestmet'
biclust(x, method=BCQuestmet(), quant=0.25, vari=1, ns=10, nd=10, sd=5,
alpha=0.05, number=100)
```
**Arguments**

- x: Data Matrix.
- method: Here BCQuest, to perform Questmotif algorithm.
- ns: Number of questions chosen.
- nd: Number of repetitions.
- sd: Sample size in repetitions.
- alpha: Scaling factor for column result.
- number: Number of bicluster to be found.
- d: Half margin of interval question values should be in (Interval is mean-d, mean+d).
- quant: Which quantile to use on metric data.
- vari: Which variance to use for metric data.

**Value**

Returns an object of class `Biclust`.

**Extends**

Class "BiclustMethod", directly.

**Author(s)**

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

**References**

Murali, T. & Kasif, S. Extracting Conserved Gene Expression Motifs from Gene Expression Data Pacific Symposium on Biocomputing, sullivan.bu.edu, 2003, 8, 77-88

**See Also**

biclust, Biclust

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**BCSpectral**

*The Spectral Bicluster algorithm*

**Description**

Performs Spectral Biclustering as described in Kluger et al., 2003. Spectral biclustering supposes that normalized microarray data matrices have a checkerboard structure that can be discovered by the use of svd decomposition in eigenvectors, applied to genes (rows) and conditions (columns).
Usage

```r
## S4 method for signature 'matrix,BCSpectral'
biclust(x, method=BCSpectral(), normalization="log", numberOfEigenvalues=6,
    minr=2, minc=2, withinVar=1, n_clusters = NULL, n_best = 3)
```

Arguments

- **x**: The data matrix where biclusters are to be found.
- **method**: Here BCSpectral, to perform Spectral algorithm.
- **normalization**: Normalization method to apply to mat. Three methods are allowed as described by Kluger et al.: "log" (Logarithmic normalization), "irrc" (Independent Rescaling of Rows and Columns) and "bistochastization". If "log" normalization is used, be sure you can apply logarithm to elements in data matrix, if there are values under 1, it automatically will sum to each element in mat (1+abs(min(mat))) Default is "log", as recommended by Kluger et al.
- **numberOfEigenvalues**: the number of eigenValues considered to find biclusters. Each row (gene) eigenVector will be combined with all column (condition) eigenVectors for the first numberOfEigenvalues eigenvalues. Note that a high number could increase dramatically time performance. Usually, only the first eigenvectors are used. With "irrc" and "bistochastization" methods, first eigenvalue contains background (irrelevant) information, so it is ignored.
- **minr**: minimum number of rows that biclusters must have. The algorithm will not consider smaller biclusters.
- **minc**: minimum number of columns that biclusters must have. The algorithm will not consider smaller biclusters.
- **withinVar**: maximum within variation allowed. Since spectral biclustering outputs a checkerboard structure despite of relevance of individual cells, a filtering of only relevant cells is necessary by means of this within variation threshold.
- **n_clusters**: vector with first element the number of row clusters and second element the number of column clusters. If n_clusters = NULL, the number of clusters will be estimated.
- **n_best**: number of eigenvectors to which the data is projected for the final clustering step, recommended values are 2 or 3.

Value

Returns an object of class Biclust.

Author(s)

Sami Leon <Sami_Leon@URMC.Rochester.edu>
Rodrigo Santamaria <rodri@usal.es>
The Xmotifs Bicluster algorithm

Description

Performs XMotifs Biclustering based on the framework by Murali and Kasif (2003). Searches for a submatrix where each row as a similar motif through all columns. The Algorithm needs a discret matrix to perform.

Usage

```r
# S4 method for signature 'matrix,BCXmotifs'
biclust(x, method=BCXmotifs(), ns=10, nd=10, sd=5, alpha=0.05, number=100)
```
Arguments

x          Data Matrix.
method     Here BCXmotifs, to perform Xmotifs algorithm
ns         Number of columns choosen.
nd         Number of repetitions.
sd         Sample size in repetitions.
alpha      Scaling factor for column result.
number     Number of bicluster to be found.

Value

Returns an object of class Biclust.

Extends

Class "BiclustMethod", directly.

Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

References

Murali, T. & Kasif, S. Extracting Conserved Gene Expression Motifs from Gene Expression Data
Pacific Symposium on Biocomputing, sullivan.bu.edu, 2003, 8, 77-88

See Also

biclust, Biclust

Examples

data(BicatYeast)
x<-discretize(BicatYeast)
res <- biclust(x, method=BCXmotifs(), ns=20, nd=20, sd=5, alpha=0.01, number=10)
res
BicatYeast

BicatYeast

Description
Microarray data matrix for 80 experiments with Saccharomyces Cerevisiae organism extracted from BicAT example data set.

Usage
data(BicatYeast)

Format
Data structure with information about the expression levels of 419 probesets over 70 conditions Row names follow Affymetrix probeset notation

Source
BicAT datasets at http://www.tik.ee.ethz.ch/sop/bicat/

biclust

Description
The function biclust is the main function of the package. It calculates the bicluster in a data matrix using the algorithm specified in the method-argument. Currently the package contains 5 different methods for the use in biclust. For each algorithm see the class help files for further details. For some algorithms preprocessing is necessary, e.g. BCBimax only runs with a logical matrix.

Usage
## S4 method for signature 'matrix,BiclustMethod'
biclust(x,method,...)

## S4 method for signature 'matrix,character'
biclust(x,method,...)

Arguments
x Data matrix.
method An object of class "BiclustMethod" or a character string with the name of a "BiclustMethod"-class.
... Additional Parameters of the "BiclustMethod"
Value

Returns an object of class Biclust.

Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also

Biclust-class, BCCC, BCXmotifs, BCPlaid, BCSpectral, BCBimax, BCQuest, BiclustMethod-class

Examples

test <- matrix(rbinom(400, 50, 0.4), 20, 20)
res1 <- biclust(test, method=BCCC(), delta=1.5, alpha=1, number=10)

Biclust-class

The Biclust Class

Description

Biclust is the class structure for results of a bicluster algorithm. It contains all information needed for further processing. The show Method gives the Name of the Algorithm used and the first Bicluster found. The summary Method gives sizes of all bicluster found.

Objects from the Class

Objects can be created by performing a bicluster algorithm via the biclust() function.

Slots

Objects of class Biclust have the following slots:

Parameters: Saves input Parameters in a list
RowxNumber: Logical Matrix which contains 1 in [i,j] if Row i is in Bicluster j
NumberxCol: Logical Matrix which contains 1 in [i,j] if Col j is in Bicluster i
Number: Number of Bicluster
info: Additional Outputs from the different bicluster algorithms

Details

RowxNumber and NumberxCol are named after the arrangement of the data they contain. The column results are transposed in order to ensure a easy processing.

Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>
biclustbarchart

Description
Draws a barchart for a Bicluster result representing the columns

Usage
biclustbarchart(x, Bicres, which=NULL, ...)

Arguments
x The data matrix
Bicres BiclustResult object with a bicluster result set. If this value is set to NULL, the
data matrix is drawn as a heatmap, without any reordering. Default NULL.
which If specified gives the plotting order of the columns from bottom to top
... Additional plot options passed to barchart

Author(s)
Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also
bubbleplot for simultaneous representation of biclusters, parallelCoordinates for single representation of biclusters as lines of gene or condition profiles, drawHeatmap for Heatmap representation of biclusters and biclustmember for a membership graph.

Examples
set.seed(1)
x=matrix(rnorm(900),30,30)
x[1:5,1:5]=rnorm(25,3,0.3)
x[11:15,11:15]=rnorm(25,-3,0.3)
x[21:25,21:25]=rnorm(25,6,0.3)
colnames(x)<-paste("Var.",1:30)
bics <- biclust(x,BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b, iter.startup = 5, iter.layer = 30, verbose = TRUE)
biclustbarchart(x,bics, col="#A3E0D8")
ord<-bicorder(bics, cols=TRUE, rev=TRUE)
biclustbarchart(x,bics,which=ord)
biclusterm

**Description**

Function to extract the bicluster or the row and column numbers from a given bicluster result

**Usage**

```r
bicluster(x, BicRes, number = 1:BicRes@Number)
biclusternumber(BicRes, number = 1:BicRes@Number)
```

**Arguments**

- `x`: The data matrix
- `BicRes`: BiclustResult object
- `number`: Which bicluster to be extracted

**Value**

Returns a list containing all extracted bicluster

**Author(s)**

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

**See Also**

`writeclust`, `writeBiclusterResults`

**Examples**

```r
s2 <- matrix(rnorm(400), 20, 20)
s2[12:16, 12:16] <- rnorm(25, 3, 0.3)
set.seed()
bics <- biclust(s2, BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b, iter.startup = 5, iter.layer = 30, verbose = TRUE)
bicluster(s2, bics)
biclusternumber(bics)
```
biclustmember

**Bicluster Membership Graph**

**Description**

Draws a membership graph cluster x columns

**Usage**

```r
biclustmember(bicResult, x, mid = T, cl_label = "", which=NA, 
   main = "Bicluster Membership Graph", xlab="Cluster", 
   color=diverge_hcl(101, h = c(0, 130)), ...) 
clustmember(res, x, mid = T, cl_label = "", which=NA, 
   main = "Cluster Membership Graph", xlab="Cluster", 
   color=diverge_hcl(101, h = c(0, 130)), ...) 
bicorder(bicResult, cols=TRUE, rev=FALSE)
```

**Arguments**

- **x**
  The data matrix
- **bicResult**
  BiclustResult object with a bicluster result set.
- **res**
  Cluster Result (is converted into a kcca object)
- **mid**
  If TRUE, shows the value of the remaining objects inside the cluster value, else shows both aside each other.
- **cl_label**
  Ticks of x-axis
- **which**
  If specified gives the plotting order of the columns from bottom to top
- **main**
  Gives the title of the plot
- **xlab**
  Label of x-axis
- **color**
  Range of colors for the plot
- **...**
  Additional plot options or if necessary option for as.kcca
- **cols**
  If TRUE orders the column by appearance in the bicluster, else orders the rows.
- **rev**
  If TRUE reverses the order

**Author(s)**

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

**See Also**

- `bubbleplot` for simultaneous representation of biclusters,
- `parallelCoordinates` for single representation of biclusters as lines of gene or condition profiles,
- `drawHeatmap` for Heatmap representation of biclusters and
- `biclustbarchart` for a barchart.
Examples

```r
set.seed(1)
x=matrix(rnorm(900),30,30)
x[1:5,1:5]=rnorm(25,3,0.3)
x[11:15,11:15]=rnorm(25,-3,0.3)
x[21:25,21:25]=rnorm(25,6,0.3)
colnames(x)<-paste("Var.",1:30)
bics <- biclust(x,BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b,
iter.startup = 5, iter.layer = 30, verbose = TRUE)

biclustmember(bics,x)

ord<-bicorder(bics, cols=TRUE, rev=TRUE)

biclustmember(bics,x,which=ord)
```

**BiclustMethod-class**  
_The BiclustMethod Virtual Class_

**Description**

BiclustMethod is the virtual class structure for algorithms provided in the package. In order to use the `biclust()` function a algorithm has to have a class inherit from here.

**Algorithms**

Currently 6 classes inherit from BiclustMethod: BCCC, BCXmotifs, BCPlaid, BCSpectral, BCBimax, BCQuest

**Author(s)**

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

**See Also**

biclust, Biclust-class, BCCC, BCXmotifs, BCPlaid, BCSpectral, BCBimax, BCQuest, BiclustMethod-class
Parameter Grid for BCBimax Biclustering

Description
Generates a list containing parameter settings for the ensemble algorithm.

Usage
bimax.grid(method = "BCBimax", minr = c(10, 11), minc = c(10, 11), number = 10)

Arguments
- method: Here BCBimax, to perform Bimax algorithm
- minr: Minimum row size of resulting bicluster.
- minc: Minimum column size of resulting bicluster.
- number: Number of Bicluster to be found.

Value
A list containing parameter settings

Author(s)
Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also
ensemble, BCBimax

Examples
bimax.grid()

Binarize

Description
Methods to convert a real matrix to a binary matrix.

Usage
binarize(x, threshold=NA)
binarizeByPercentage(x, percentage, error=0.2, gap=0.1)
densityOnes(x)
Arguments

- **x**: The data matrix to be binarized.
- **threshold**: Threshold used to binarize. Values over threshold will be set to 1, the rest to 0. If threshold is NA, median is used as threshold. Default NA.
- **percentage**: Percentage of ones against zeros desired in the binary matrix.
- **error**: Percentage of ones against zeros in the final matrix will be in [percentage-error, percentage+error]. Default 0.2
- **gap**: Value used for incremental search of threshold. Default 0.1

Details

The `binarize` function returns a matrix binarized by input threshold, or by the median if no threshold is given.

The `binarizeByPercentage` function returns a matrix binarize by input percentage, given as desired density of ones against zeros.

The `densityOnes` function returns the percentage of ones against zeros in a logical matrix.

Author(s)

Rodrigo Santamaria <rodri@usal.es>

Examples

```r
data(BicatYeast)
m1=binarize(BicatYeast)
m2=binarize(BicatYeast, 0.2)
m3=binarizeByPercentage(BicatYeast, 5)
densityOnes(m3)
densityOnes(m2)
densityOnes(m1)
drawHeatmap(BicatYeast)
drawHeatmap(m1)
drawHeatmap(m2)
drawHeatmap(m3)
```

Description

Draws a bubble plot where each bicluster is represented as a circle (bubble). Color represents the bicluster set to which bicluster pertains (up to three bicluster sets can be represented simultaneously). Brightness represents the bicluster homogeneity (darker, less homogeneous). Size represents the size of the bicluster, as (number of genes)x(number of conditions). Location is a 2D-projection of gene and condition profiles.
Usage

```r
bubbleplot(x, bicResult1, bicResult2=NULL, bicResult3=NULL, projection="mean", showLabels=FALSE)
```

Arguments

- **x**: The data matrix from which biclusters were identified.
- **bicResult1**: BiclustResult object with a bicluster result set whose biclusters will be drawn in green.
- **bicResult2**: BiclustResult object with an optional second bicluster result set. Will be drawn in red (default NULL).
- **bicResult3**: BiclustResult object with an optional third bicluster result set. Will be drawn in blue (default NULL).
- **projection**: Projection algorithm used to position bubbles. Allowed projections are 'mean', 'isomds' and 'cmdscale' (default 'mean'). See details section for a broader explanation.
- **showLabels**: If 'TRUE', puts a label over each bubble that tells the number within the corresponding bicluster result (default 'FALSE').

Details

Position of circles depend on a 2D projection of the multidimensional point formed by rows and columns present in the bicluster. For example, if we have a 3x3 matrix to analyze and we find a bicluster with rows 1 and 3 and columns 2 and 3, the corresponding multidimensional point will be p=(1,0,1,0,1,1). For this example, 'mean' projection will map the bicluster with the point x=(1+3)/2=2 and y=(2+3)/2=2.5. Other projections will take the point p and project it following the corresponding algorithms (see the corresponding help pages for details).

Note

Bubbleplot 2D-projection, as any multidimensional scaling, loses information, trying to take the main relationships and trends of n-dimensional data. Thus, locations and intersections between bubbles-biclusters are only an estimate of its similarity. This visualization should be used just as a help to understand overall behavior of biclustering methods, detect trends and outliers, etc.

Author(s)

Rodrigo Santamaria <rodri@usal.es>

See Also

drawHeatmap for single representation of biclusters inside data matrix, parallelCoordinates for single representation of biclusters as lines of gene or condition profiles, cmdscale, isomds for multidimensional scaling and plot for other point representations.
Examples

```r
#Simplified yeast microarray data
## Not run:
data(BicatYeast)
set.seed(1)
bics1 <- biclust(BicatYeast,BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b,
row.release = 0.7, col.release = 0.7,
verbose = FALSE, max.layers = 10, iter.startup = 5,
iter.layer = 30)
bubbleplot(BicatYeast,bics1, showLabels=TRUE)

loma=binarize(BicatYeast,2)
bics2=biclust(loma,BCBimax(), minr=4, minc=4, number=10)
bubbleplot(BicatYeast,bics1,bics2)
## End(Not run)
```

ChiaKaruturi

Chia and Karuturi Function

Description

Function computing scores as described in the paper of Chia and Karuturi (2010)

Usage

```r
ChiaKaruturi(x, bicResult, number)
```

Arguments

- `x` : Data Matrix
- `bicResult` : Biclust object from biclust package
- `number` : Number of bicluster in the output for computing the scores

Details

The function computes row (T) and column (B) effects for a chosen bicluster. The scores for columns within bicluster have index 1, the scores for columns outside the bicluster have index 2. Ranking score is SB, stratification score is TS.

Value

Data.Frame with 6 slots: T, B scores for within and outside bicluster, SB and TS scores

Author(s)

Tatsiana KHAMIAKOVA <tatsiana.khamiakova@uhasselt.be>
## References


## See Also

`diagnosticPlot`, `computeObservedFstat`, `diagnoseColRow`

## Examples

```r
#---simulate dataset with 1 bicluster ---#
xmat <- matrix(rnorm(50*50,0,0.25),50,50) # background noise only
rowSize <- 20 #number of rows in a bicluster
colSize <- 10 #number of columns in a bicluster
a1 <- rnorm(rowSize,1,0.1) #sample row effect from N(0,0.1) #adding a coherent values bicluster:
b1 <- rnorm(colSize),2,0.25) #sample column effect from N(0,0.05)
mu <- 0.01 #constant value signal
for (i in 1 : rowSize){
  for(j in 1: (colSize)){
    xmat[i,j] <- xmat[i,j] + mu + a1[i] + b1[j]
  }
}
#--obtain a bicluster by running an algorithm---#
plaidmab <- biclust(x=xmat, method=BCPlaid(), cluster="b", fit.model = y ~ m + a+ b, background = TRUE, row.release = 0.6, col.release = 0.7, shuffle = 50, back.fit = 5, max.layers = 1, iter.startup = 100, iter.layer = 100, verbose = TRUE)

#Get Chia and Karuturi scores:
ChiaKaruturi(x=xmat, bicResult = plaidmab, number = 1)
```

<table>
<thead>
<tr>
<th>coherence</th>
<th>Coherence measures</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>

## Description

Different preliminary measures of how much constant or (additive, multiplicative, sign) coherent a bicluster is, following Madeira and Oliveira classification of biclusters.

## Usage

```r
constantVariance(x, resultSet, number, dimension="both")
additiveVariance(x, resultSet, number, dimension="both")
multiplicativeVariance(x, resultSet, number, dimension="both")
signVariance(x, resultSet, number, dimension="both")
```
Arguments

- **x**: The data matrix from which biclusters were identified.
- **resultSet**: BiclustResult object with a bicluster result set where is the bicluster to measure.
- **number**: Number of the bicluster within the result set.
- **dimension**: "both" for determining overall variance, "row" for gene variance and "col" for column variance. Default "both".

Details

Returns the corresponding variance of genes or conditions as the average of the sum of euclidean distances between all rows and/or columns of the bicluster. For additive, multiplicative and sign variance first a transformation of the bicluster is done, so variance is computed on a matrix that reflects difference, rest or change of sign between rows, columns or both.

The lower the value returned, the more constant or coherent the bicluster is. If the value returned is 0, the bicluster is ideally constant or coherent. Usually, a value above 1-1.5 is enough to determine the bicluster is not constant or coherent.

Note

There are preliminary measures for coherence. Since transformations are different, measures are not normalized and comparison between, for example, additive and multiplicative variance is not meaningful. Only comparisons between different measures of the same kind of variance are reliable by now.

Author(s)

Rodrigo Santamaria <rodri@usal.es>

Examples

```r
#Simplified yeast microarray data
data(BicatYeast)
set.seed(1)
bics1 <- biclust(BicatYeast,BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b,
row.release = 0.7, col.release = 0.7,
verbose = FALSE, max.layers = 10, iter.startup = 5,
iter.layer = 30)

constantVariance(BicatYeast, bics1,1,"row")
constantVariance(BicatYeast, bics1,1,"col")
constantVariance(BicatYeast, bics1,1,"both")
additiveVariance(BicatYeast, bics1,1,"both")
multiplicativeVariance(BicatYeast, bics1,1,"both")
signVariance(BicatYeast, bics1,1,"both")
```
computeObservedFstat  Diagnostic F Statistic Calculation

Description
Functions for obtaining F statistics within bicluster and the significance levels. The main effects considered are row, column and interaction effect.

Usage
computeObservedFstat(x, bicResult, number)

Arguments
- **x**: Data Matrix
- **bicResult**: Biclust object from biclust package
- **number**: Number of bicluster in the output for computing observed statistics

Details
F-statistics are calculated from the two-way ANOVA mode with row and column effect. The full model with interaction is unidentifiable, thus, Tukey's test for non-additivity is used to detect an interaction within a bicluster. p-values are obtained from asymptotic F distributions.

Value
Data frame with three rows ("Row Effect", "Column Effect", "Tukey test") and 2 columns for corresponding statistics (Fstat) and their p-values (PValue).

Author(s)
Tatsiana KHAMIAKOVA <tatsiana.khamiakova@uhasselt.be>

See Also
diagnosticTest, diagnosticPlot2, ChiaKaruturi, diagnoseColRow

Examples
```r
#---simulate dataset with 1 bicluster ---#
xmat<-matrix(rnorm(50*50,0,0.25),50,50) # background noise only
rowSize <- 20 #number of rows in a bicluster
colSize <- 10 #number of columns in a bicluster
a1<-rnorm(rowSize,1,0.1) #sample row effect from N(0,0.1) #adding a coherent values bicluster:
b1<-rnorm((colSize),2,0.25) #sample column effect from N(0,0.05)
muc<-0.01 #constant value signal
for ( i in 1 : rowSize){
  for(j in 1 : (colSize)){
```
```r
xmat[i,j] <- xmat[i,j] + mu + a1[i] + b1[j]
}
}
#--obtain a bicluster by running an algorithm--#
plaidmab <- biclust(x=xmat, method=BCPlaid(), cluster="b", fit.model = y ~ m + a+ b, background = TRUE, row.release = 0.6, col.release = 0.7, shuffle = 50, back.fit = 5, max.layers = 1, iter.startup = 100, iter.layer = 100, verbose = TRUE)

#Calculate statistics and their p-values to infer about the structure within bicluster:
Structure <- computeObservedFstat(x=xmat, bicResult = plaidmab, number = 1)
```

---

**diagnoseColRow**  
*Bootstrap Procedure for Bicluster Diagnostics*

**Description**

Calculate the significance of the discovered pattern in the data based on the bootstrapping procedure.

**Usage**

```r
diagnoseColRow(x, bicResult, number, nResamplings, replace = TRUE)
```

**Arguments**

- `x`: data matrix, which `biclust` function was applied to
- `bicResult`: object of class `biclust`, containing result of a biclustering algorithm
- `number`: number of bicluster from the output for the diagnostics
- `nResamplings`: number of bootstrap replicates
- `replace`: logical flag for bootstrap (TRUE), or sampling without replacement (FALSE)

**Details**

The function computes observed F statistics for row and column effect based on two-way ANOVA model. Bootstrap procedure is used to evaluate the significance of discovered bicluster. Based on `nResamplings` replicates, the distribution of F statistics for row and column effects are obtained. The p-value is computed as

\[
P(A) = \frac{\# \{ F^*(A)_b > F(A)^{obs} \}}{nResamplings + 1}
\]

Low p-values denote non-random selection of columns for a given bicluster. Large p-values show that in other columns for a given set of genes in the bicluster structure is similar. Hence, bicluster columns were just randomly picked by an algorithm for a set of co-regulated genes.
Value

bootstrapFstats
matrix with two columns, containing values of bootstrap F-statistics. The first column corresponds to row, the second column corresponds to column.

observedFstatRow
observed F-statistics for the row effect

observedFstatCol
observed F-statistics for the column effect

bootstrapPvalueRow
bootstrap p value for row effect

bootstrapPvalueCol
bootstrap p value for column effect

Author(s)

Tatsiana KHAMIAKOV A <tatsiana.khamiakova@uhasselt.be>

See Also
diagnosticTest, diagnosticPlot2, diagnosticPlot, computeObservedFstat, ChiaKaruturi

Examples

```r
#---simulate dataset with 1 bicluster ---#
xmat<-matrix(rnorm(50*50,0,0.25),50,50) # background noise only
rowSize <- 20 #number of rows in a bicluster
colSize <- 10 #number of columns in a bicluster
a1<-rnorm(rowSize,1,0.1) #sample row effect from N(0,0.1) #adding a coherent values bicluster:
b1<-rnorm((colSize),2,0.25) #sample column effect from N(0,0.05)
mu<-0.01 #constant value signal
for ( i in 1 : rowSize){
  for(j in 1: (colSize)){
    xmat[i,j] <- xmat[i,j] + mu + a1[i] + b1[j]
  }
}
#--obtain a bicluster by running an algorithm---#
plaidmab <- biclust(x=xmat, method=BCPlaid(), cluster="b", fit.model = y ~ m + a+ b, background = TRUE, row.release = 0.6, col.release = 0.7, shuffle = 50, back.fit = 5, max.layers = 1, iter.startup = 100, iter.layer = 100, verbose = TRUE)

#Run bootstrap procedure:
Bootstrap <- diagnoseColRow(x=xmat, bicResult = plaidmab, number = 1, nResamplings = 999, replace = TRUE)
diagnosticPlot(bootstrapOutput = Bootstrap) # plotting distribution of bootstrap replicates
```
diagnosticPlot

Diagnostic F Statistics Visualization

Description
Plots distributions of bootstrap replicates of F-statistics for row and column effect and highlights the observed statistics.

Usage

diagnosticPlot(bootstrapOutput)

Arguments

bootstrapOutput
output of diagnoseColRow function, containing bootstrap replicates and observed F-statistics.

Value
No value is returned. The plot is constructed in a current device.

Author(s)
Tatsiana KHAMIKA

See Also
diagnoseColRow, computeObservedFstat

Examples

#---simulate dataset with 1 bicluster ---#
xmat<-matrix(rnorm(50*50,0,0.25),50,50)  # background noise only
rowSize <- 20  #number of rows in a bicluster
colSize <- 10  #number of columns in a bicluster
a1<-rnorm(rowSize,1,0.1)  #sample row effect from N(0,0.1) 
#adding a coherent values bicluster:
b1<-rnorm(colSize),2,0.25)  #sample column effect from N(0,0.05)
mu<-0.01  #constant value signal
for (i in 1 : rowSize){
  for(j in 1 : (colSize)){
    xmat[i,j] <- xmat[i,j] + mu + a1[i] + b1[j]
  }
}
#--obtain a bicluster by running an algorithm---#
plaidmab <- biclust(x=xmat, method=BCPlaid(), cluster="b", fit.model = y ~ m + a+ b,
background = TRUE, row.release = 0.6, col.release = 0.7, shuffle = 50, back.fit = 5,
max.layers = 1, iter.startup = 100, iter.layer = 100, verbose = TRUE)
# Run bootstrap procedure:
Bootstrap <- diagnoseColRow(x=xmat, bicResult = plaidmab, number = 1,
  nResamplings = 999, replace = TRUE)

# plotting distribution of bootstrap replicates
diagnosticPlot(bootstrapOutput = Bootstrap)

diagnosticPlot2       Diagnostics F Statistics Visualization

**Description**

Plots distributions of bootstrap replicates of F-statistics for row, column and multiplicative effects obtained from `diagnosticTest` (when `save_F=TRUE`). Contains an option to highlight the observed statistics.

**Usage**

diagnosticPlot2(diagnosticTest, number = 1, StatVal = TRUE,
  binwidth = NULL)

**Arguments**

- **diagnosticTest**: output of `diagnosticTest` with `save_F=TRUE` which contains the F-statistics and sampling replicates.
- **number**: Number of which BC to plot. This needs to be one of the Biclusters requested in `diagnosticTest`.
- **StatVal**: Boolean value to draw the observed statistic on the distribution plots.
- **binwidth**: The width of the bins.

**Value**

Returns a ggplot object.

**Author(s)**

Ewoud De Troyer

**Examples**

```r
## Not run:
#Random matrix with embedded bicluster (with multiplicative effect)
test <- matrix(rnorm(5000),100,50)
```
```r
diagnosticTest <- function(BCresult, data, number = 1:BCresult@Number, verbose = TRUE, statistics = c("F", "Tukey"), sampling = TRUE, samplingtypes = NULL, nSim = 1000, alpha = 0.05, save_F = FALSE)
{
  # Apply Plaid Biclustering
  res <- biclust(test, method=BCPlaid())

  # Apply default diagnosticTest
  out <- diagnosticTest(BCresult=res, data=test, save_F=TRUE, number=1,
                        statistics=c("F","Tukey","ModTukey","Tukey2","Mandel","LBI","JandG"),
                        samplingtypes=c("Permutation","SemiparPerm","SemiparBoot","PermutationCor","SamplingCor","NormSim"))

  # Plot Distributions
  diagnosticPlot2(out, number=1)

  ## End(Not run)
```

---

**diagnosticTest**  
*Testing Procedure for Bicluster Diagnostics*

**Description**

Calculate the statistical value of the row, column and multiplicative effect based on discovered biclusters in the data. Additionally multiple sampling methods are available to compute the statistical significance through p-values.

**Usage**

```r
diagnosticTest(BCresult, data, number = 1:BCresult@Number, verbose = TRUE, statistics = c("F", "Tukey"), sampling = TRUE, samplingtypes = NULL, nSim = 1000, alpha = 0.05, save_F = FALSE)
```

**Arguments**

- **BCresult**: An object of class biclust containing the result of a biclustering algorithm
- **data**: data matrix, which biclust function was applied to
- **number**: Vector of bicluster numbers of which the diagnostics should be calculated. (default = all available biclusters)
- **verbose**: Boolean value to print progression of computed statistics.
- **statistics**: Vector select which statistics to compute. (default = c("F", "Tukey"))
  - "F" (Row and column F statistics of two-way ANOVA with one replicate for cell)
• "Tukey" (Tukey’s test for non-additivity)
• "ModTukey" (mtukey.test)
• "Tusell" (tusell.test)
• "Mandel" (mandel.test)
• "LBI" (lbi.test)
• "JandG" (johnson.graybill.test)

sampling
Boolean value to apply sampling methods to compute statistical significance (default=TRUE). If FALSE only the "Theoretical" p-values are computed. If TRUE, both the "Theoretical" and samplingtypes p-values are computed.

samplingtypes
Vector of sampling methods for sampling=TRUE. (default=NULL=c("Permutation","SemiparPerm"))

- "Permutation"
- "SemiparPerm"
- "SemiparBoot"
- "PermutationCor"
- "SamplingCor"
- "NormSim"

See Details for more info.

nSim
Number of permutations/bootstraps.

alpha
Significance level (default=0.05)

save_F
Option to save the permuted/bootstrapped statistics. This is necessary for diagnosticPlot2

Details
Due to the uncertainty of discovering the true bicluster(s) in the data, it’s often advisable to not rely on the theoretical p-values but instead retrieve the p-values through a sampling procedure.

Available p-values/sampling types for each statistical method:

- "F": "Theoretical" and "Permutation" for both row and column effect.
- "Tukey": "Theoretical", "SemiparPerm" and "SemiparBoot".
- "ModTukey": "Theoretical", "SemiparPerm", "SemiparBoot", "PermutationCor" and "SamplingCor".
- "Tusell": "SemiparPerm", "SemiparBoot" and "NormSim".
- "Mandel": "Theoretical", "SemiparPerm" and "SemiparBoot".
- "LBI": "SemiparPerm", "SemiparBoot" and "NormSim".
- "JandG": "SemiparPerm", "SemiparBoot" and "NormSim".

More info on the sampling types can be found in the section below. If available, the "Theoretical" will always be computed. By default when sampling=TRUE, a sampling method without replacement is chosen, namely "Permutation" and "SemiparPerm".

When save_F=TRUE, the null distributions of the statistics can be visualised with diagnosticPlot2.

Disclaimer: While their functionality did not change, some functions of the additivityTests package were altered in order to be able to return the permuted/bootstrapped statistics and p-values.
Value

Returns a list with `length(number)` elements. Each element corresponds with the requested bi-clusters and is a list containing:

- **table**: a data frame where each row is statistics and `samplingtypes` (including Theoretical) combination. The data frame contains the `Method`, `Type` (p-value type), `StatVal` (statistical value), `CritVal` (critical value), `pVal` and `Sign` (0/1 significance indicator based on `alpha`).

- **save_F**: if `save_F=TRUE`, a (`nSim` x number of permuted/bootstrapped p-values) matrix contained the sampled statistics.

Sampling Types

For each sampling type a permuted/bootstrapped BC is created as following:

- **"Permutation"**: Sample a BC from the entire dataset with replacement.

- **"SemiparPerm"**: A semi-parametric permutation procedure. Two-way ANOVA is applied on the original BC and the residual matrix extracted. A new residual matrix is created by sampling without replacement from the original residual matrix. The sampled BC is then generated by adding this sampled residual matrix on top the mean, row and column effect of the ANOVA procedure of the original BC.

- **"SemiparBoot"**: A semi-parametric bootstrapping procedure. Two-way ANOVA is applied on the original BC and the residual matrix extracted. A new residual matrix is created by sampling with replacement from the original residual matrix. The sampled BC is then generated by adding this sampled residual matrix on top the mean, row and column effect of the ANOVA procedure of the original BC.

- **"PermutationCor"**: See `correction=1` parameter of `mtukey.test`. More info in Simecek and Simeckova (2012).

- **"SamplingCor"**: See `correction=2` parameter of `mtukey.test`. More info in Simecek and Simeckova (2012).

- **"NormSim"**: Sample a BC from a standard normal distribution. This sampling procedure is used for some methods in the `additivityTests` package.

Author(s)

Ewoud De Troyer

References


## Not run:
# Random matrix with embedded bicluster (with multiplicative effect)
test <- matrix(rnorm(5000), 100, 50)
roweff <- sample(1:5, 10, replace=TRUE)
coleff <- sample(1:5, 10, replace=TRUE)
  matrix(coleff,nrow=10,ncol=10,byrow=TRUE) +
  matrix(roweff,nrow=10,ncol=10) +
  roweff %*% t(coleff)

# Apply Plaid Biclustering
res <- biclust(test, method=BCPlaid())

# Apply default diagnosticTest
out <- diagnosticTest(BCresult=res, data=test, save_F=TRUE, number=1,
  statistics=c("F","Tukey","ModTukey","Tusell","Mandel","LBI","JandG"),
  samplingtypes=c("Permutation","SemiparPerm","SemiparBoot",
  "PermutationCor","SamplingCor","NormSim"))

out[[1]]$table

## End(Not run)

### discretize

Create a discret matrix

#### Description

Some biclustering algorithms need a discret matrix to perform well. This function delivers a discret matrix with either a given number of levels of equally spaced intervals from minimum to maximum, or levels of same size using the quantiles.

#### Usage

```r
discretize(x, nof=10, quant=FALSE)
```

#### Arguments

- `x`: The data matrix from which should be dicretized
- `nof`: Number of levels
- `quant`: If TRUE using the quantiles, else using equally spaced levels
Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

Examples

# Discretize yeast microarray data
data(BicatYeast)
discretize(BicatYeast[1:10,1:10])

drawHeatmap

Draw Heatmap

Description

Draws a microarray data matrix as a heatmap, with rows and columns reordered so the rows and columns of the input bicluster will be at top-left of the matrix.

Usage

drawHeatmap(x,bicResult=NULL,number=NA,local=TRUE, beamercolor=FALSE,paleta,...)
drawHeatmap2(x,bicResult=NULL,number=NA,plotAll=FALSE)

Arguments

x The data matrix where the bicluster is to be drawn.
bicResult BiclustResult object with a bicluster result set. If this value is set to NULL, the data matrix is drawn as a heatmap, without any reordering. Default NULL.
number Bicluster to be drawn from the result set 'bicResult'. If bicResult is set to NULL, this value is ignored. Default NA
local If TRUE, only rows and columns of the bicluster were drawn.
plotAll If TRUE, all Bicluster of result set 'bicResult' were drawn.
beamercolor If TRUE, palate colors are used.
paleta Colors
... Additional plot options

Details

'plotAll' only works if there is a exclusive rows and column Result!

Author(s)

Rodrigo Santamaria <rodri@usal.es>, Sebastian Kaiser
EisenYeast

See Also

\bubbleplot\ for simultaneous representation of biclusters.\ parallelCoordinates for single representation of biclusters as lines of gene or condition profiles.

Examples

```r
#Random 100x50 matrix with a single, up-regulated 10x10 bicluster
s2=matrix(rnorm(5000),100,50)
s2[11:20,11:20]=rnorm(100,3,0.3)
set.seed(1)
bics <- biclust(s2,BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b,
iter.startup = 5, iter.layer = 30, verbose = TRUE)
drawHeatmap(s2,bics,1)
```

Description

Microarray data matrix for 80 experiments with Saccharomyces Cerevisiae organism by Eisen Lab.

Usage

```r
data(EisenYeast)
```

Format

Data frame with information about the expression levels of 6221 genes over 80 conditions. Missing values have been imputed using k-nearest neighbor averaging implemented in impute.knn() from library `impute` (using default k=10). Gene names follow ORF (Open Reading Format) notation.

Source

Eisen Lab at http://rana.lbl.gov/EisenData.htm
**ensemble**

*Ensemble Methods for Bicluster Algorithms*

**Description**

Calculates an ensemble of biclusters from different parameter setting of possible different bicluster algorithms.

**Usage**

```
ensemble(x, confs, rep = 1, maxNum = 5, similar = jaccard2, thr = 0.8, simthr = 0.7,
subs = c(1, 1), bootstrap = FALSE, support = 0, combine = firstcome, ...)
```

**Arguments**

- `x` : Data Matrix
- `confs` : Matrix containing parameter sets
- `rep` : Number of repetitions for each parameter set
- `maxNum` : Maximum number of biclusters taken from each run
- `similar` : Function to produce a similarity matrix of bicluster
- `thr` : Threshold for similarity
- `simthr` : Proportion of row column combinations in bicluster
- `subs` : Vector of proportion of rows and columns for subsampling. Default c(1,1) means no subsampling.
- `bootstrap` : Should bootstrap sampling be used (logical: replace=bootstrap).
- `support` : Which proportion of the runs must contain the bicluster to have enough support to report it (between 0 and 1).
- `combine` : Function to combine the single bicluster only firstcome and hcl for hierarchical clustering are possible at the moment.
- `...` : Arguments past to the combine function.

**Details**

Two different kinds (or both combined) of ensembling is possible. Ensemble of repeated runs or ensemble of runs on subsamples.

**Value**

Return an object of class Biclust

**Author(s)**

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>
See Also

Biclust-class, plaid.grid, bimax.grid

Examples

## Not run:
data(BicatYeast)
ensemble.plaid <- ensemble(BicatYeast, plaid.grid()[1:5], rep=1, maxNum=2, thr=0.5, subs = c(1,1))
ensemble.plaid
x <- binarize(BicatYeast)
ensemble.bimax <- ensemble(x, bimax.grid(), rep=10, maxNum=2, thr=0.5, subs = c(0.8, 0.8))
ensemble.bimax
## End(Not run)

heatmapBC

Overlapping Heatmap

Description

Other than drawHeatmap this function plots all or a chosen number of bicluster in one plot even if they were overlapping.

Usage

heatmapBC(x, bicResult, number = 0, local = TRUE, order = FALSE, outside = FALSE, ...)

Arguments

- **x**: The data matrix where the bicluster is to be drawn.
- **bicResult**: BiclustResult object with a bicluster result set.
- **number**: Number of bicluster to be drawn from the result set `bicResult`. If the default 0 is chosen all bicluster of the biclustResult are drawn.
- **local**: If TRUE, only rows and columns of the bicluster are drawn. This argument is only used if number is not set to 0.
- **order**: If TRUE, rows and columns are ordered by their values.
- **outside**: If TRUE, Boxes are drawn for overlapping
- **...**: Additional plot options

Details

Overlap plotting only works for two neighbor bicluster defined by the order in the number slot.
isoverlapp

Author(s)

Sebastian Kaiser

See Also

drawHeatmap, parallelCoordinates

Examples

set.seed(1234)
data(BicatYeast)
resplaid <- biclust(BicatYeast, BCPlaid(), verbose = FALSE)
heatmapBC(x = BicatYeast, bicResult = resplaid)

isoverlapp | Is Bicresult overlapping?
---|---

Description

Checks if Biclusterresult includes overlapping rows or columns

Usage

isoverlapp(bicResult)

Arguments

bicResult | Result of biclust function

Value

Overlapping | Is there overlapping
Max.bicluster.Rows | Maximal number of bicluster a single row is in
Max.bicluster.Cols | Maximal number of bicluster a single col is in

Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also

drawHeatmap
Description

An adaption of the Jaccard Index for clustering is calculated.

Usage

jaccardind(bicres1, bicres2)
jaccard2(Rows, Cols)

Arguments

bicres1 A object of class Biclust
bicres2 A object of class Biclust
Rows Matrix containing rows of biclusters
Cols Matrix containing cols of biclusters

Details

The function calculates the percentage of datapoints in the same bicluster structure from all datapoints at least included in one bicluster.

Value

jaccardind calculates the Jaccard index jaccard2 returns a similarity matrix containing the Jaccard index between all biclusters (upper triangle matrix)

Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

Examples

## Not run:
data(BicatYeast)
res1<-biclust(BicatYeast, method=BCPlaid(), back.fit = 2, shuffle = 3,
               fit.model = ~m + a + b, iter.startup = 5, iter.layer = 30, verbose = TRUE)
res2<-biclust(BicatYeast, method=BCCC())
jaccardind(res1,res2)

## End(Not run)
parallelCoordinates

Parallel Coordinates

Description

Represents expression levels through gene and/or condition profiles in a bicluster as lines.

Usage

parallelCoordinates(x, bicResult, number, plotBoth = FALSE, plotcol = TRUE,
compare = TRUE, info = F, bothlab = c("Rows", "Columns"), order = FALSE,
order2 = 0, ylab = "Value", col=1,...)

Arguments

x
bicResult
number
plotBoth
plotcol
compare
info
bothlab
order
order2
ylab
col
...

Plot Parameters

Author(s)

Rodrigo Santamaria, Martin Sill and Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also

drawHeatmap for alternative representation of biclusters and bubbleplot for simultaneous representation of biclusters.
Examples

# Random 100x50 matrix with a single, up-regulated 10x10 bicluster
s2 = matrix(rnorm(5000), 100, 50)
s2[11:20, 11:20] = rnorm(100, 3, 0.3)
set.seed(1)
bics <- biclust(s2, BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b,
iter.startup = 5, iter.layer = 30, verbose = TRUE)
parallelCoordinates(x = s2, bicResult = bics, number = 1, plotBoth = TRUE,
plotcol = TRUE, compare = TRUE, info = TRUE, bothlab = c("Genes Bicluster 1",
"Conditions Bicluster 1"), order = TRUE)
parallelCoordinates(x = s2, bicResult = bics, number = 1, plotBoth = FALSE, plotcol = TRUE,
compare = FALSE, info = TRUE)

plaid.grid

Parameter Grid for BCPlaid Biclustering

Description

Generates a list containing parameter settings for the ensemble algorithm.

Usage

plaid.grid(method = "BCPlaid", cluster = "b", fit.model = y ~ m + a + b,
background = TRUE, background.layer = NA, background.df = 1,
row.release = c(0.5, 0.6, 0.7), col.release = c(0.5, 0.6, 0.7),
shuffle = 3, back.fit = 0, max.layers = 20, iter.startup = 5,
iter.layer = 10, verbose = FALSE)

Arguments

method Here BCPlaid, to perform Plaid algorithm
cluster 'r', 'c' or 'b', to cluster rows, columns or both (default 'b')
fit.model Model (formula) to fit each layer. Usually, a linear model is used, that estimates
three parameters: m (constant for all elements in the bicluster), a (constant for all
rows in the bicluster) and b (constant for all columns). Thus, default is: y ~ m +
a + b.
background If 'TRUE' the method will consider that a background layer (constant for all
rows and columns) is present in the data matrix.
background.layer If background='TRUE' a own background layer (Matrix with dimension of x)
can be specified.
background.df Degrees of Freedom of backround layer if background.layer is specified.
shuffle Before a layer is added, it's statistical significance is compared against a number
of layers obtained by random defined by this parameter. Default is 3, higher
numbers could affect time performance.
plotclust

iter.startup  Number of iterations to find starting values
iter.layer   Number of iterations to find each layer
back.fit     After a layer is added, additional iterations can be done to refine the fitting of
             the layer (default set to 0)
row.release  Scalar in [0,1](with interval recommended [0.5-0.7]) used as threshold to prune
             rows in the layers depending on row homogeneity
col.release  As above, with columns
max.layers   Maximum number of layer to include in the model
verbose      If 'TRUE' prints extra information on progress.

Value
A list containing parameter settings

Author(s)
Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also
ensemble, BCPlaid

Examples
plaid.grid()

plotclust          Barplot of Bicluster

Description
Draws a graph to compare the values inside the different biclusters with the values outside the bicluster

Usage
plotclust(res, x, bicluster=TRUE, legende=FALSE, noC=5, wyld=3, Titel="Plotclust", ...)

Arguments
x           The data matrix
res         BiclustResult object if bicluster=TRUE else a normal kcca object.
bicluster   If TRUE, res is treated as a BiclustResult object
legende     Draws a legend.
noC         Number of Clusters drawn
wyld        Gives the distance between plot and axis.
Titel       Gives the title of the plot.
...         Additional plot options
predictBimax

Author(s)
Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also
bubbleplot for simultaneous representation of biclusters. parallelCoordinates for single representation of biclusters as lines of gene or condition profiles. drawHeatmap for Heatmap representation of biclusters.

Examples

```r
s2 <- matrix(rnorm(400), 20, 20)
s2[12:16, 12:16] <- rnorm(25, 3, 0.3)
set.seed(1)
bics <- biclust(s2, BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b, iter.startup = 5, iter.layer = 30, verbose = TRUE)
plotclust(bics, s2)
```

predictBimax

Predict from a BCrepBimax Result

Description
Predicts cluster membership for new data rows given a BCrepBimax Result

Usage
`predictBimax(BCrepBimax, x)`

Arguments
- `BCrepBimax`: Result of biclust function with method BCrepBimax
- `x`: The data matrix which clustermembership should be predicted

Value
Returns a vector with clustermembership of data x of class.

Author(s)
Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

See Also
BCrepBimax
**Description**

Synthetic microarray data matrix generated by SynTrEN for 20 experiments using 200 genes from Transcription Regulatory Network of Shen-Orr et al. (2002).

**Usage**

data(SyntrenEcoli)

**Format**

Data structure with information about the expression levels of 200 genes over 20 conditions. Conditions are named as C1... C20

**Source**

SynTrEN software can be downloaded at http://homes.esat.kuleuven.be/~kmarchal/SynTrEN/index.html

**References**


---

**Description**

Write bicluster results to a file

**Usage**

writeBiclusterResults(fileName, bicResult, bicName, geneNames, arrayNames, append=FALSE, delimiter=" ")
**Arguments**

- **fileName**: Path to the file were biclusters are written.
- **bicResult**: Biclusters results as a Biclust class.
- **bicName**: Brief description for the biclustering algorithm used.
- **geneNames**: Array of strings with gene (row) names in the analyzed data matrix.
- **arrayNames**: Array of strings with condition (column) names in the analyzed data matrix.
- **append**: If true, adds the bicluster results to previous information in the text file, if it exists. Default false.
- **delimiter**: Delimiter string between gene and condition names. Default " ".

**Author(s)**

Rodrigo Santamaria <rodri@usal.es>

**Examples**

```r
## Not run:
data(BicatYeast)
res <- biclust(BicatYeast, method=BCCC(), delta=1.5, alpha=1, number=10)
writeBiclusterResults("results.txt", res,"CC with delta 1.5", dimnames(BicatYeast)[1][[1]],
dimnames(BicatYeast)[2][[1]])
## End(Not run)
```

---

**writeclust**

*Write a Bicluster as a Cluster Result*

**Description**

Draws a graph to compare the values inside the different biclusters with the values outside the bicluster.

**Usage**

```r
writeclust(BiclusterResult,row=TRUE,noC=10)
```

**Arguments**

- **BiclusterResult**: BiclustResult object.
- **row**: If TRUE, cluster of rows were written.
- **noC**: Number of Clusters written.
Author(s)

Sebastian Kaiser <sebastian.kaiser@stat.uni-muenchen.de>

Examples

```r
s2 = matrix(rnorm(400), 20, 20)
s2[12:16, 12:16] = rnorm(25, 3, 0.3)
set.seed(1)
bics <- biclust(s2, BCPlaid(), back.fit = 2, shuffle = 3, fit.model = ~m + a + b,
iter.startup = 5, iter.layer = 30, verbose = TRUE)
writeclust(bics)
```
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