Package ‘Mfuzz’

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R topics documented:

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acore

Extraction of alpha cores for soft clusters

Description
This function extracts genes forming the alpha cores of soft clusters.

Usage
acore(eset, cl, min.acore = 0.5)

Arguments
eset object of the class ExpressionSet.
cl An object of class flcust as produced by mfuzz.
min.acore minimum membership values of gene belonging to the cluster core.

Value
The function produces an list of alpha cores including genes and their membership values for the corresponding cluster.

Author(s)
Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

Examples
if (interactive()){
  ### Data loading and pre-processing
  data(yeast) # data set includes 17 measurements
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  ### Soft clustering and visualisation
  cl <- mfuzz(yeastF, c = 20, m = 1.25)
  acore.list <- acore(yeastF, cl = cl, min.acore = 0.7)
}
cselection

**Description**

This function performs repeated soft clustering for a range of cluster numbers \( c \) and reports the number of empty clusters detected.

**Usage**

```r
cselection(eset, m, crange=seq(4,32,4), repeats=5, visu=TRUE,...)
```

**Arguments**

- `eset` object of class `ExpressionSet`
- `m` value of fuzzy c-means parameter \( m \)
- `crange` range of number of clusters \( c \)
- `repeats` number of repeated clusterings.
- `visu` If `visu=TRUE` plot of number of empty clusters is produced.
- `...` additional arguments for underlying `mfuzz`.

**Details**

A soft cluster is considered as empty, if none of the genes has a corresponding membership value larger than 0.5

**Value**

A matrix with the number of empty clusters detected is generated.

**Note**

The `cselection` function may help to determine an accurate cluster number. However, it should be used with care, as the determination remains difficult especially for short time series and overlapping clusters. A better way is likely to perform clustering with a range of cluster numbers and subsequently assess their biological relevance e.g. by GO analyses.

**Author(s)**


**References**


L. Kumar and M. Futschik, Mfuzz: a software package for soft clustering of microarray data, Bioinformation, 2(1) 5-7, 2007
Dmin

Calculation of minimum centroid distance for a range of cluster numbers for estimation of optimised number of clusters

Description

This function performs repeated soft clustering for a range of cluster numbers c and reports the minimum centroid distance.

Usage

Dmin(eset,m,crange=seq(4,40,4),repeats=3,visu=TRUE)

Arguments

- eset: object of class ExpressionSet.
- m: value of fuzzy c-means parameter m.
- crange: range of number of clusters c.
- repeats: number of repeated clusterings.
- visu: If visu=TRUE plot of average minimum centroid distance is produced

Details

The minimum centroid distance is defined as the minimum distance between two cluster centers produced by the c-means clusterings.

Examples

if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)
  
  #### parameter selection
  # Empty clusters should not appear
  cl <- mfuzz(yeastF,c=20,m=1.25)
  mfuzz.plot(yeastF,cl=cl,mfrow=c(4,5))
  
  # Note: The following calculation might take some time
  tmp <- cselection(yeastF,m=1.25,crange=seq(5,40,5),repeats=5,visu=TRUE)
  # derivation of number of non-empty clusters (crosses) from diagonal
  # line indicate appearance of empty clusters
  
  # Empty clusters might appear
  cl <- mfuzz(yeastF,c=40,m=1.25)
  mfuzz.plot(yeastF,cl=cl,mfrow=c(4,5))
}
Value

The average minimum centroid distance for the given range of cluster number is returned.

Note

The minimum centroid distance can be used as cluster validity index. For an optimal cluster number, we may see a ‘drop’ of minimum centroid distance when plotted versus a range of cluster number and a slower decrease of the minimum centroid distance for higher cluster number. More information and some examples can be found in the study of Schwaemmle and Jensen (2010). However, it should be used with care, as the determination remains difficult especially for short time series and overlapping clusters. Alternatively, the function cselection can be used or functional enrichment analysis (e.g. using Gene Ontology) can help to adjust the cluster number.

Author(s)

Matthias E. Futschik (http://www.cbme.ualg.pt/mfutschik_cbme.html)

References


L. Kumar and M. Futschik, Mfuzz: a software package for soft clustering of microarray data, Bioinformation, 2(1) 5-7, 2007

Schwaemmle and Jensen, Bioinformatics, Vol. 26 (22), 2841-2848, 2010

Examples

if (interactive()){  
data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)
  #### parameter selection
  # For fuzzifier m, we could use mestimate
  m1 <- mestimate(yeastF)
  m1 # 1.15
  # or the function partcoef (see example there)

  # For selection of c, either cselection (see example there)
  # or

  tmp <- Dmin(eset,m=m1,crange=seq(4,40,4),repeats=3,visu=TRUE)# Note: This calculation might take some time

  # It seems that the decrease for c ~ 20 - 25 24 and thus 20 might be
  # a suitable number of clusters
}

if (interactive()){
fill.NA

Replacement of missing values

Description

Methods for replacement of missing values. Missing values should be indicated by NA in the expression matrix.

Usage

fill.NA(eset, mode="mean", k=10)

Arguments

- eset: object of the class ExpressionSet.
- mode: method for replacement of missing values:
  - mean: missing values will be replaced by the mean expression value of the gene,
  - median: missing values will be replaced by the median expression value of the gene,
  - knn: missing values will be replaced by the averaging over the corresponding expression values of the k-nearest neighbours,
  - knnw: same replacement method as knn, but the expression values averaged are weighted by the distance to the corresponding neighbour
- k: Number of neighbours, if one of the knn method for replacement is chosen (knn, knnw).

Value

The function produces an object of the ExpressionSet class with missing values replaced.

Note

The replacement methods knn and knnw can computationally intensive for large gene expression data sets. It may be a good idea to run these methods as a ‘lunchtime’ or ‘overnight’ job.

Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik) and Lokesh Kumar

Examples

```r
if (interactive()){
  data(yeast) # data set includes 17 measurements
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  }
```
filter.NA

Filtering of genes based on number of non-available expression values.

Description

This function can be used to exclude genes with a large number of expression values not available.

Usage

filter.NA(eset, thres=0.25)

Arguments

eset  object of the class “ExpressionSet”.

thres  threshold for excluding genes. If the percentage of missing values (indicated by NA in the expression matrix) is larger than thres, the corresponding gene will be excluded.

Value

The function produces an object of the ExpressionSet class. It is the same as the input eset object, except for the genes excluded.

Author(s)

Matthias E. Futschik (http://www.sysbiolab.eu)

Examples

if (interactive()){
  data(yeast) # data set includes 17 measurements
  yeastF <- filter.NA(yeast) # genes are excluded if more than 4 measurements are missing
}

filter.std

Filtering of genes based on their standard deviation.

Description

This function can be used to exclude genes with low standard deviation.

Usage

filter.std(eset, min.std, visu=TRUE)
kmeans2

K-means clustering for gene expression data

Description

This function is a wrapper function for kmeans of the e1071 package. It performs hard clustering of genes based on their expression values using the k-means algorithm.

Usage

kmeans2(eset,k,iter.max=100)

Arguments

eset object of the class ExpressionSet.
k number of clusters.
iter.max maximal number of iterations.

Value

An list of clustering components (see kmeans).

Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

Examples

data(yeast) # data set includes 17 measurements
yeastF <- filter.NA(yeast) # filtering of genes based on missing values
yeastF <- filter.std(yeastF,min.std=0.3) # filtering of genes based on standard deviation

kmeans2

K-means clustering for gene expression data

Value

The function produces an object of the ExpressionSet class. It is the same as the input eset object, except for the genes excluded.

Note

As soft clustering is noise robust, pre-filtering can usually be avoided. However, if the number of genes with small expression changes is large, such pre-filtering may be necessary to reduce noise.

Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)
**kmeans2.plot**

**See Also**

kmeans

**Examples**

```r
if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  # K-means clustering and visualisation
  kl <- kmeans2(yeastF,k=20)
  kmeans2.plot(yeastF,kl=kl,mfrow=c(2,2))
}
```

**kmeans2.plot**  
Plotting results for k-means clustering

**Description**

This function visualises the clusters produced by kmeans2.

**Usage**

`kmeans2.plot(eset, kl, mfrow=c(1,1))`

**Arguments**

- `eset`  
  object of the class "ExpressionSet".
- `kl`  
  list produced by kmeans2.
- `mfrow`  
  determines splitting of graphic window.

**Value**

The function displays the temporal profiles of clusters detected by k-means.

**Author(s)**

Matthias E. Futschik ([http://itb.biologie.hu-berlin.de/~futschik](http://itb.biologie.hu-berlin.de/~futschik))

**Examples**

```r
if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  # K-means clustering and visualisation
  kl <- kmeans2(yeastF,k=20)
```
Calculating of membership values for new data based on existing clustering

Description

Function that calculates the membership values of genes based on provided data and existing clustering.

Usage

`membership(x, clusters, m)`

Arguments

- `x`: expression vector or expression matrix
- `clusters`: cluster centroids from existing clustering
- `m`: fuzzification parameter

Value

Matrix of membership values for new genes

Note

This function calculates membership values for new data based on existing cluster centroids and fuzzification parameter. It can be useful, for instance, when comparing two time series, to assess whether the same gene in the different time series changes its cluster association.

Author(s)

Matthias E. Futschik ([http://www.sysbiolab.eu](http://www.sysbiolab.eu))

Examples

```r
if (interactive()){
  data(yeast)
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF) # for illustration only; rather use knn method
  yeastF <- standardise(yeastF)

  cl <- mfuzz(yeastF,c=20,m=1.25)
  m <- 1.25
  clusters <- cl[[1]]
  x <- matrix(rnorm(2*17),nrow=2) # new expression matrix with two genes
  mem.tmp <- membership(x,clusters=clusters,m=m) # membership values
}
```
**mestimate**

*Estimate for optimal fuzzifier m*

**Description**

This function estimates an optimal setting of fuzzifier m.

**Usage**

```r
mestimate(eset)
```

**Arguments**

- `eset` object of class “ExpressionSet”

**Details**

Schwaemmle and Jensen proposed a method to estimate of \( m \), which was motivated by the evaluation of fuzzy clustering applied to randomized datasets. The estimated \( m \) should give the minimum fuzzifier value which prevents clustering of randomized data.

**Value**

Estimate for optimal fuzzifier.

**Author(s)**

Matthias E. Futschik ([http://itb.biologie.hu-berlin.de/~futschik](http://itb.biologie.hu-berlin.de/~futschik))

**References**

Schwaemmle and Jensen, Bioinformatics, Vol. 26 (22), 2841–2848, 2010

**Examples**

```r
if (interactive()){  
data(yeast)  
  # Data pre-processing  
  yeastF <- filter.NA(yeast)  
  yeastF <- fill.NA(yeastF)  
  yeastF <- standardise(yeastF)  

  #### parameter selection  
  # For fuzzifier m, we could use mestimate  
  m1 <- mestimate(yeastF)  
  m1 # 1.15  

  cl <- mfuzz(yeastF,c=20,m=m1)  
  mfuzz.plot(yeastF,cl=cl,mfrow=c(4,5))  
}
```
mfuzz

Function for soft clustering based on fuzzy c-means.

Description

This function is a wrapper function for `cmeans` of the e1071 package. It performs soft clustering of
genes based on their expression values using the fuzzy c-means algorithm.

Usage

`mfuzz(eset, centers, m, ...)`

Arguments

- `eset`: object of the class “ExpressionSet”.
- `centers`: number of clusters.
- `m`: fuzzification parameter.
- `...`: additional parameters for `cmeans`.

Details

This function is the core function for soft clustering. It groups genes based on the Euclidean distance
and the c-means objective function which is a weighted square error function. Each gene is assigned
a membership value between 0 and 1 for each cluster. Hence, genes can be assigned to different
clusters in a gradual manner. This contrasts hard clustering where each gene can belongs to a single
cluster.

Value

An object of class `flcust` (see `cmeans`) which is a list with components:

- `centers`: the final cluster centers.
- `size`: the number of data points in each cluster of the closest hard clustering.
- `cluster`: a vector of integers containing the indices of the clusters where the data points
  are assigned to for the closest hard clustering, as obtained by assigning points to
  the (first) class with maximal membership.
- `iter`: the number of iterations performed.
- `membership`: a matrix with the membership values of the data points to the clusters.
- `withinerror`: the value of the objective function.
- `call`: the call used to create the object.

Note

Note that the clustering is based soley on the `exprs` matrix and no information is used from the
`phenoData`. In particular, the ordering of samples (arrays) is the same as the ordering of the columns
in the `exprs` matrix. Also, replicated arrays in the `exprs` matrix are treated as independent by the
`mfuzz` function i.e. they should be averagered prior to clustering or placed into different distinct
“ExpressionSet” objects.
Author(s)

Matthias E. Futschik (http://www.sysbiolab.eu)

References


L. Kumar and M. Futschik, Mfuzz: a software package for soft clustering of microarray data, Bioinformation, 2(1) 5-7, 2007

See Also
cmeans

Examples

if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF) # for illustration only; rather use knn method
  yeastF <- standardise(yeastF)

  # Soft clustering and visualisation
  cl <- mfuzz(yeastF,c=20,m=1.25)
  mfuzz.plot(yeastF,cl=cl,mfrow=c(2,2))

  # Plotting center of cluster 1
  X11(); plot(cl[[1]][1,],type="l",ylab="Expression")

  # Getting the membership values for the first 10 genes in cluster 1
  cl[[4]][1:10,1]
}
min.mem  Genes with membership values below min.mem will not be displayed.
time.labels labels can be given for the time axis.
new.window should a new window be opened for graphics.

Value
The function generates plots where the membership of genes is color-encoded.

Author(s)
Matthias E. Futschik (http://www.sysbiolab.eu/matthias)

Examples
if (interactive()){  
data(yeast)  
  # Data pre-processing  
yeastF <- filter.NA(yeast)  
yeastF <- fill.NA(yeastF)  
yeastF <- standardise(yeastF)  

  # Soft clustering and visualisation  
  cl <- mfuzz(yeastF,c=20,m=1.25)  
  mfuzz.plot(yeastF,cl=cl,mfrow=c(2,2))  

  # display of cluster cores with alpha = 0.5  
  mfuzz.plot(yeastF,cl=cl,mfrow=c(2,2),min.mem=0.5)  

  # display of cluster cores with alpha = 0.7  
  mfuzz.plot(yeastF,cl=cl,mfrow=c(2,2),min.mem=0.7)  
}

mfuzz.plot2
Plotting results for soft clustering with additional options

Description
This function visualises the clusters produced by mfuzz. It is similar to mfuzz.plot, but offers more options for adjusting the plots.

Usage
mfuzz.plot2(eset,cl,mfrow=c(1,1),colo,min.mem=0,time.labels,time.points, ylim.set=c(0,0), xlab="Time",ylab="Expression changes",x11=TRUE, ax.col="black",bg = "white",col.axis="black",col.lab="black", col.main="black",col.sub="black",col="black",centre=FALSE, centre.col="black",centre.lwd=2, Xwidth=5,Xheight=5,single=FALSE,...)
### Arguments

- `eset`: object of the class `ExpressionSet`.
- `cl`: object of class `flclust`.
- `mfrow`: determines splitting of graphic window. Use `mfrow=NA` if layout is used (see example).
- `colo`: color palette to be used for plotting. If the color argument remains empty, the default palette is used. If the `colo = "fancy"`, an alternative (fancier) palette will be used.
- `min.mem`: Genes with membership values below `min.mem` will not be displayed.
- `time.labels`: labels for ticks on x axis.
- `time.points`: numerical values for the ticks on x axis. These can be used if the measured time points are not equidistant.
- `ylim.set`: Vector of min. and max. y-value set for plotting. If `ylim.set=c(0,0)`, min. and max. value will be determined automatically.
- `xlab`: label for x axis
- `ylab`: label for y axis
- `x11`: If `TRUE`, a new window will be open for plotting.
- `ax.col`: Color of axis line.
- `bg`: Background color.
- `col.axis`: Color for axis annotation.
- `col.lab`: Color for axis labels.
- `col.main`: Color for main titles.
- `col.sub`: Color for sub-titles.
- `col`: Default plotting color.
- `centre`: If `TRUE`, a line for the cluster centre will be drawn.
- `centre.col`: Color of the line for the cluster centre
- `centre.lwd`: Width of the line for the cluster centre
- `Xwidth`: Width of window.
- `Xheight`: Height of window.
- `single`: Integer if a specific cluster is to be plotted, otherwise it should be set to `FALSE`.
- `...`: Additional, optional plotting arguments passed to `plot.default` and `axes` functions such as `cex.lab`, `cex.main`, `cex.axis`.

### Value

The function generates plots where the membership of genes is color-encoded.

### Author(s)

Matthias E. Futschik ([http://www.sysbiolab.eu/matthias](http://www.sysbiolab.eu/matthias))
Examples

if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  # Soft clustering and visualisation
  cl <- mfuzz(yeastF,c=20,m=1.25)
  mfuzz.plot2(yeastF,cl=cl,mfrow=c(2,2)) # same output as mfuzz.plot
  mfuzz.plot2(yeastF, cl=cl,mfrow=c(2,2),centre=TRUE) # lines for cluster centres will be included

  # More fancy choice of colors
  mfuzz.plot2(yeastF,cl=cl,mfrow=c(2,2),colo="fancy",
  ax.col="red",bg = "black",col.axis="red",col.lab="white",
  col.main="green",col.sub="blue",col="blue",cex.main=1.3,cex.lab=1.1)

  ### Single cluster with colorbar (cluster # 3)
  X11(width=12)
  mat <- matrix(1:2,ncol=2,nrow=1,byrow=TRUE)
  l <- layout(mat,width=c(5,1))
  mfuzz.plot2(yeastF,cl=cl,mfrow=NA,colo="fancy", ax.col="red",bg = "black",col.axis="red",col.lab="white",
  col.main="green",col.sub="blue",col="blue",cex.main=2, single=3,x11=FALSE)
  mfuzzColorBar(col="fancy",main="Membership",cex.main=1)

  ### Single cluster with colorbar (cluster # 3
  X11(width=14)
  mat <- matrix(1:2,ncol=2,nrow=1,byrow=TRUE)
  l <- layout(mat,width=c(5,1))
  mfuzz.plot2(yeastF,cl=cl,mfrow=NA,colo="fancy", ax.col="red",bg = "black",col.axis="red",col.lab="white",time.labels = c(paste(seq(0,160,10),"min")),
  col.main="green",col.sub="blue",col="blue",cex.main=2, single=3,x11=FALSE)
  mfuzzColorBar(col="fancy",main="Membership",cex.main=1)

  )
**Mfuzzgui**

**Arguments**

- **col**: vector of colours used. If missing, the same vector as the default vector for `mfuzz.plot` is used. If col="fancy", an alternative color palette is used (see `mfuzz.plot2`).
- **horizontal**: If TRUE, a horizontal colour bar is generated, otherwise a vertical one will be produced.

... additional parameter passed to `maColorBar` (see also example in `mfuzz.plot2`)

**Author(s)**

Matthias E. Futschik ([http://itb.biologie.hu-berlin.de/~futschik](http://itb.biologie.hu-berlin.de/~futschik))

**See Also**

- `maColorBar`

**Examples**

```r
if (interactive()){  
  X11(w=1.5,h=5);  
  par(mar=c(1,1,1,5))  
  mfuzzColorBar();  
  mfuzzColorBar(col=“fancy”,main=“Membership value”)  
}
```

**Mfuzzgui**  

*Graphical user interface for Mfuzz package*

**Description**

The function `Mfuzzgui` provides a graphical user interface for clustering of microarray data and visualisation of results. It is based on the functions of the Mfuzz package.

**Usage**

`Mfuzzgui()`

**Details**

The function `Mfuzzgui` launches a graphical user interface for the *Mfuzz* package. It is based on Tk widgets using the R TclTk interface by Peter Dalgaard. It also employs some pre-made widgets from the tkWidgets Bioconductor-package by Jianhua Zhang for the selection of objects/files to be loaded.

`Mfuzzgui` provides a convenient interface to most functions of the Mfuzz package without restriction of flexibility. An exception is the batch processes such as partcoeff and cselection routines which are used for parameter selection in fuzzy c-means clustering of microarray data. These routines are not included in `Mfuzzgui`. To select various parameters, the underlying Mfuzz routines may be applied.

Usage of `Mfuzzgui` does not require an pre-built exprSet object but can be used with tab-delimited text files containing the gene expression data. Note, however, that the clustering is based
on the ordering of samples (arrays) as of the columns in the expression matrix of the exprSet object or in the uploaded table, respectively. Also, replicated arrays in the expression matrix (or table) are treated as independent by the mfuzz function and, thus, should be averaged prior to clustering.

For a overview of the functionality of Mfuzzgui, please refer to the package vignette. For a description of the underlying functions, please refer to the Mfuzz package.

Value

Mfuzzgui returns a tclObj object.

Note

The newest versions of Mfuzzgui can be found at the Mfuzz webpage (http://itb.biologie.hu-berlin.de/~futschik/software/R/Mfuzz).

Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik) and Lokesh Kumar

References


See Also

mfuzz

Description

This function calculates the overlap of clusters produced by mfuzz.

Usage

overlap(cl)

Arguments

c1 object of class flclust

Value

The function generates a matrix of the normalised overlap of soft clusters. The overlap indicates the extent of “shared” genes between clusters. For a mathematical definiton of the overlap, see the vignette of the package or the reference below.
Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

References


Examples

if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  # Soft clustering and visualisation
  cl <- mfuzz(yeastF,c=20,m=1.25)
  mfuzz.plot(yeastF,cl=cl,mfrow=c(4,5))

  # Calculation of cluster overlap and visualisation
  O <- overlap(cl)
  X11()
  Ptmp <- overlap.plot(cl,over=O,thres=0.05)
}

overlap.plot

Visualisation of cluster overlap and global clustering structure

Description

This function visualises the cluster overlap produced by overlap.

Usage

overlap.plot(cl,overlap,thres=0.1,scale=TRUE,magni=30,P=NULL)

Arguments

cl
object of class “flclust”
overlap
matrix of cluster overlap produced by overlap
thres
threshold for visualisation. Cluster overlaps below the threshold will not be visualised.
scale
Scale parameter for principal component analysis by prcomp
magni
Factor for increase the line width for cluster overlap.
P
Projection matrix produced by principal component analysis.
Value

A plot is generated based on a principal component analysis of the cluster centers. The overlap is visualised by lines with variable width indicating the strength of the overlap. Additionally, the matrix of principal components is returned. This matrix can be re-used for other projections to compare the overlap and global cluster structure of different clusterings.

Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

See Also

prcomp

Examples

if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  # Soft clustering
  cl <- mfuzz(yeastF,c=20,m=1.25)
  X11();mfuzz.plot(yeastF,cl=cl,mfrow=c(4,5))
  O <- overlap(cl)
  X11();Ptmp <- overlap.plot(cl,over=O,thres=0.05)

  # Alternative clustering
  cl <- mfuzz(yeastF,c=10,m=1.25)
  X11();mfuzz.plot(yeastF,cl=cl,mfrow=c(3,4))
  O <- overlap(cl)
  X11();overlap.plot(cl,over=O,P=Ptmp,thres=0.05)

  # visualisation based on principal compents from previous projection
}

partcoef

Calculation of the partition coefficient matrix for soft clustering

Description

This function calculates partition coefficient for clusters within a range of cluster parameters. It can be used to determine the parameters which lead to uniform clustering.

Usage

partcoef(eset,crange=seq(4,32,4),mrange=seq(1.05,2,0.1),...)

Part coef
partcoef

Arguments

- `eset` object of class “ExpressionSet”.
- `c.range` range of number of clusters c.
- `m.range` range of clustering parameter m.
- `...` additional arguments for underlying `mfuzz`.

Details

Introduced by Bezdek (1981), the partition coefficient F is defined as the sum of squares of values of the partition matrix divided by the number of values. It is maximal if the partition is hard and reaches a minimum for \( U = 1/c \) when every gene is equally assigned to every cluster.

It is well-known that the partition coefficient tends to decrease monotonically with increasing n. To reduce this tendency we defined a normalized partition coefficient where the partition for uniform partitions are subtracted from the actual partition coefficients (Futschik and Kasabov, 2002).

Value

The function generates the matrix of partition coefficients for a range of c and m values. It also produces a matrix of normalised partition coefficients as well as a matrix with partition coefficient for uniform partitions.

Author(s)

Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

References

1. J.C. Bezdek, Pattern recognition with fuzzy objective function algorithms, Plenum, 1981

Examples

```r
if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  #### parameter selection
  yeastFR <- randomise(yeastF)
  cl <- mfuzz(yeastFR,c=20,m=1.1)
  mfuzz.plot(yeastFR,cl=cl,mfrow=c(4,5)) # shows cluster structures (non-uniform partition)

  tmp <- partcoef(yeastFR) # This might take some time.
  F <- tmp[[1]];F.n <- tmp[[2]];F.min <- tmp[[3]]

  # Which clustering parameters result in a uniform partition?
  F > 1.01 * F.min

  cl <- mfuzz(yeastFR,c=20,m=1.25) # produces uniform partition
}
mfuzz.plot(yeastFR,cl=cl,mfrow=c(4,5))
# uniform coloring of temporal profiles indicates uniform partition

randomise

Randomisation of data

Description
This function randomise the time order for each gene separately.

Usage
randomise(eset)

Arguments
- eset: object of the class ExpressionSet.

Value
The function produces an object of the ExpressionSet class with randomised expression data.

Author(s)
Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

Examples
data(yeast) # data set includes 17 measurements
yeastR <- randomise(yeast)

standardise

Standardization of microarray data for clustering.

Description
Standardisation of the expression values of every gene is performed, so that the average expression value for each gene is zero and the standard deviation is one.

Usage
standardise(eset)

Arguments
- eset: object of the class ExpressionSet.

Value
The function produces an object of the ExpressionSet class with standardised expression values.
standardise2

Author(s)
Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

Examples
if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)

  # Soft clustering and visualisation
  cl <- mfuzz(yeastF,c=20,m=1.25)
  mfuzz.plot(yeastF,cl=cl,mfrow=c(4,5))
}

standardise2 Standardization in regards to selected time-point

Description
Standardisation of the expression values of every gene is performed, so that the expression values at a chosen time point are zero and the standard deviations are one.

Usage
standardise2(eset,timepoint=1)

Arguments
eset object of the class ExpressionSet.
timepoint integer: which time point should have expression values of zero.

Value
The function produces an object of the ExpressionSet class with standardised expression values.

Author(s)
Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

Examples
if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise2(yeastF,timepoint=1)

  # Soft clustering and visualisation
  cl <- mfuzz(yeastF,c=20,m=1.25)
mfuzz.plot(yeastF, cl=cl, mfrow=c(4,5))

### table2eset

*Conversion of table to Expression set object.*

#### Description

A expression matrix stored as a table (in a defined format) is read and converted to Expression Set object.

#### Usage

```r
table2eset(filename)
```

#### Arguments

- **filename** name of file to be scanned in

#### Details

The expression matrix stored as table in the file has to follow some conventions in order to be able to be converted to an Expression Set object: The first row of the file contains sample labels and optionally, the second column can contain the time points. If the second row is used for the input the time, the first field in the second row must contain “Time”. Similarly, the first column contains unique gene IDs and optionally second row can contain gene names. If the second row contains gene names, the second field in the first row must contain “Gene.Name”. The rest of the file contains expression data. As example, two tables with expression data are provided. These examples can be viewed by inputing `data(yeast.table)` and `data(yeast.table2)` in the R console.

#### Value

An Expression Set object is generated.

#### Author(s)

Matthias E. Futschik ([http://www.sysbiolab.eu](http://www.sysbiolab.eu))

### top.count

*Determines the number for which each gene has highest membership value in all cluster*

#### Description

This function calculates the number, for which each gene appears to have the top membership score in the partition matrix of clusters produced by *mfuzz*.

#### Usage

```r
top.count(cl)
```
yeast

Arguments

cl object of class “flclust”

Value

The function generates a vector containing a count for each gene, which is just the number of times that particular gene has acquired the top membership score.

Author(s)

Lokesh Kumar and Matthias E. Futschik (http://itb.biologie.hu-berlin.de/~futschik)

Examples

if (interactive()){
  data(yeast)
  # Data pre-processing
  yeastF <- filter.NA(yeast)
  yeastF <- fill.NA(yeastF)
  yeastF <- standardise(yeastF)
  # Soft clustering and visualisation
  cl <- mfuzz(yeastF,c=20,m=1.25)
  top.count(cl)
}

yeast Gene expression data of the yeast cell cycle

Description

The data contains gene expression measurements for 3000 randomly chosen genes of the yeast mutant cdc28 as performed and described by Cho et al. For details, see the reference.

Usage

data(yeast)

Format

An object of class “ExpressionSet”.

Source

The data was downloaded from Yeast Cell Cycle Analysis Project webpage and converted to an ExpressionSet object.

References

**Description**

The data serves as an example for the format required for uploading tables with expression data into *Mfuzzgui*. The first row contains the names of the samples, the second row contains the measured time points. Note that “TIME” has to placed in the first field of the second row. The first column contains unique identifiers for genes; optionally the second row can contain gene names if “GENE.NAMES” is in the second field in the first row. An example for an table without optional fields is the dataset `yeast.table2`. The exemplary tables can be found in the data sub-folder of the *Mfuzzgui* package.

**References**


**See Also**

`yeast.table2`
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