Package ‘rqubic’

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Type Package

Title Qualitative biclustering algorithm for expression data analysis in R

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Description This package implements the QUBIC algorithm introduced by Li et al. for the qualitative biclustering with gene expression data.

Imports methods, Biobase, BiocGenerics, biclust

Suggests RColorBrewer

Collates onload.R AllClasses.R AllMethods.R c_output_parser.R
   r_qubic_implementation.R rqubic_to_c_funcs.R combineBiclust.R

biocViews Clustering

License GPL-2

LazyLoad yes

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Description

QUBIC is a qualitative biclustering algorithm for high-throughput expression data analysis. rqubic package implements this algorithm in R, partly with the codes contributed by Haibao Tang and Qin Ma (version 0.23 released without any limitation).

The rqubic package also provides parsers for the command line tool of qubic written in C.

Details

Package: rqubic
Type: Package
Version: 1.5
Date: 2011-04-11
License: LGPL-2
LazyLoad: yes

Part of the source code in C is modified from the source code of the QUBIC command line tool (in C) provided by Haibao Tang and Qin Ma <maqin@csbl.bmb.uga.edu>, downloaded from http://csbl.bmb.uga.edu/~maqin/bicluster/ on 01.03.2011, version 0.23.

Source code of QUBIC also uses open-source data structure library codes. See the README file included in the QUBIC command line tool source.

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>, Laura Badi and Martin Ebeling Maintainer: Jitao David Zhang <jitao_david.zhang@roche.com>
References

Li et al. (2009) QUBIC: a qualitative biclustering algorithm for analyses of gene expression data
Nucleic Acids Research 37:e101

Description

Combining two or more Biclust objects into one object. These objects must be of same dimension,
namely have same numbers of features and samples, although the numbers of biclusters do not have
to be the same (and usually are not).

Methods

signature(x = "Biclust", y = "Biclust") Method for any Biclust objects
signature(x = "QUBICBiclusterSet", y = "QUBICBiclusterSet") Method for QUBICBiclusterSet
only. Besides combining biclusters, they will also combine parameters and information stored
in each QUBICBiclusterSet into the returning object.
signature(x = "list", y = "missing") Method for a list of Biclust or QUBICBiclusterSet
objects.

Examples

data(sample.ExpressionSet, package="Biobase")
re1.discret <- quantileDiscretize(sample.ExpressionSet, rank=1L)
re1.sel.seeds <- generateSeeds(re1.discret, minColWidth=2L)
re1.blocks <- quBicluster(re1.sel.seeds,
                         re1.discret,
                         report.no=50L,
                         filter.proportion=0.1)

re2.discret <- quantileDiscretize(sample.ExpressionSet, rank=2L)
re2.sel.seeds <- generateSeeds(re2.discret, minColWidth=2L)
re2.blocks <- quBicluster(re2.sel.seeds,
                         re2.discret,
                         report.no=50L,
                         filter.proportion=0.1)

re3.discret <- quantileDiscretize(sample.ExpressionSet, rank=3L)
re3.sel.seeds <- generateSeeds(re3.discret, minColWidth=2L)
re3.blocks <- quBicluster(re3.sel.seeds,
                         re3.discret,
                         report.no=50L,
                         filter.proportion=0.1)

re12.blocks <- combineBiclusts(re1.blocks, re2.blocks)
eSetDimName

Get dimname from an eSet object

Description
This function is implemented to automatically validate and choose feature (sample) names from the user input. This function is exported for the purpose of easing other Bioconductor developers performing the similar job, and is not tended to be called by end-user directly.

Usage
eSetDimName(eset, input, type = c("feature", "sample"))

Arguments
- eset: An object of eSet class, mostly an ExpressionSet class.
- input: The user input, see details below
- type: Either ‘feature’ or ‘sample’, indicating which dimension should be determined

Details
The input can be one of the following three possibilities:
- Missing. Depending on the type, the results of calling featureNames (“feature”) or sampleNames (“sample”) on the eset object will be returned.
- A character string of length 1. Depending on the type, it is first to be matched to the column names of either fData or pData results of the eset object. If found, the values in that column are returned (coerced to characters if necessary). If not found, the function stops by raising an error.
- A character vector of the length equal to one of the two dimensions of the eset. In this scenario, the function only validates the equality of the length, coerces the input into characters, and return them.

If none of the scenarios above was met, the function stops by raising an error.

Value
A vector of characters, the length of which determined by the dimension of the input object.

Note
A special case arises if one of the dimensions of the eset object is 1: In this case, the input value is interpreted as the new name and returned. No column name match will take place in this case.
Author(s)
Jitao David Zhang <jitao_david.zhang@roche.com>

See Also
sampleNames, featureNames, fData, pData
writeQubicInputFile calls the function.

Examples

data(sample.ExpressionSet, package="Biobase")
sub.eset <- sample.ExpressionSet[1:3, 1:3]

## usage one:
eSetDimName(sub.eset, type="feature")
eSetDimName(sub.eset, type="sample")

## usage two
## "sex" is one column in the pData(sub.eset)
eSetDimName(sub.eset, input="sex", type="sample")
## Not run: eSetDimName(sub.eset, input="foo", type="sample")

## usage three
eSetDimName(sub.eset, input=paste("Sample", 1:3), type="sample")
## Not run: eSetDimName(sub.eset, input=paste("Sample", 1:4),
## type="sample")
## End(Not run)

## special case: dim equals to one
eSetDimName(sub.eset[,1], input="foo", type="sample")

---

**fcFilter**  
Feature-Condition Filter

Description
Filter Biclusters by feature and condition counts. Biclusters with fewer features or conditions than specified thresholds are removed.

Usage
fcFilter(object, ...)

Arguments

object  
A Biclust object

...  
Two parameters are accepted: feat.min and cond.min. They indicate the minimum number of features (conditions) in biclusters, which are to be accepted. It is allowed to only specify one threshold. If both are specified, only biclusters fulfilling both criterion are accepted.
Value

A Biclust object.

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>

Examples

data(sample.ExpressionSet, package="Biobase")
rqubic.example.discret <- quantileDiscretize(sample.ExpressionSet, rank=2L)

rqubic.example.sel.seeds <- generateSeeds(rqubic.example.discret, minColWidth=2L)

rqubic.example.blocks <- quBicluster(rqubic.example.sel.seeds,
rqubic.example.discret,
  report.no=200L,
  filter.proportion=0.1)

print(rqubic.example.blocks)
print(fcFilter(rqubic.example.blocks, feat.min=10))
print(fcFilter(rqubic.example.blocks, cond.min=2))
print(fcFilter(rqubic.example.blocks, feat.min=10, cond.min=2))

fcFilter-methods Feature-Condition Filter

Description

Feature-Condition Filter for biclusters

Methods

signature(object = "Biclust") Use help("fcFilter") see help and examples

features-methods Extract features and conditions

Description

Generic function features and conditions, as well as auxillary count functions, are implemented for Biclust objects.

They can be used in one of the following forms:
1. Used on a `Biclust`, and without specifying index, `features` or `conditions` returns the unique and ordered features or conditions involved in at least one bicluster, and `featureCount` or `conditionCount` returns the length of respective vectors. To get the feature/condition numbers in each bicluster of the set, use `BCfeatureCount/BCconditionCount`.

2. Used on a `Biclust` and provided index (indices), the features/conditions or their counts are returned for specified biclusters.

In addition, `featureNames` and `sampleNames` are of the same implementation as `features` and `conditions`.

**Methods**

- `signature(object = "QUBICBicluster")` Information about all the biclusters.
- `signature(object = "Biclust", index = "missing")` Information about all the biclusters in the set.
- `signature(object = "Biclust", index = "ANY")` Information about selected biclusters in the set, the index can be integers or logical variables for subsetting.

**Author(s)**

Jitao David Zhang <jitao_david.zhang@roche.com>

**References**


**See Also**

See other methods implemented for the `Biclust` class in the `biclust` package. And the methods specific for `QUBICBiclusterSet`.

**Examples**

```r
library(Biobase)
library(biclust)
example.file <- system.file("extdata", "sampleExpressionSet.blocks", package="rqubic")

example.block <- parseQubicBlocks(example.file)

head(features(example.block))
featureCount(example.block)
head(conditions(example.block))
conditionCount(example.block)

BCfeatureCount(example.block)
BCfeatures(example.block)[1:2]
BCconditionCount(example.block)
BCconditions(example.block)[1:2]
```
generateSeeds-methods

**generateSeeds**

*Description*

generateSeeds takes either matrix or an ExpressionSet object to generate seeds. Seeds are defined as pairs of genes (edges) which share coincident expression levels in samples. The higher the coincidence, the higher the score of the seeds will be. The seeds are generated by subsequent comparing each pair of genes. When all seeds have been produced, they are sorted by the coincidence scores and returned as an object. See the details section for notes on implementation.

**Methods**

In the rqubic package, generateSeeds currently supports two data types: ExpressionSet (an inherited type of eSet, or numeric matrix).

Both methods requires in addition a parameter, `minColWidth`, specifying the minimum number of conditions shared by the two genes of each seed. Its default value is 2. When this default value is used, the minimum coincidence score is defined as \( \text{max}(2, \frac{\text{ncol}}{20}) \), where \( \text{ncol} \) represents the number of conditions. When a non-default value is provided, the value is used to select seeds.

```
signature(object = "eSet")  An object representing expression data. Note that the exprs must be a matrix of integers, otherwise the method warns and coerces the storage mode of matrix into integer.

signature(object = "matrix")  A matrix of integers. In case filled by non-integers, the method warns and coerces the storage mode into integer
```

**Details**

The function compares all pairs of genes, namely all edges of a complete graph composed by genes. The weight of each edge is defined as the number of samples, in which two genes have the same expression level. This weight, also known as the coincidence score, reflects the co-regulation relationship between two genes.

The seed is chosen by picking edges with higher scores than the minimum score, provided by the `minColWidth` parameter (default: 2).

To implement such a selection algorithm, a Fibonacci heap is constructed in the C codes. Its size is predefined as a constant, which should be reduced in case the gene number is too large to run the algorithm. A new seed, which was selected by having a higher coincidence score than the minimum, is inserted to the heap. And dependent on whether the heap is full or not, it is either inserted by squeezing the minimum seed out, or put into the heap directly.

Once the heap is filled by examining all pairs of genes, it is dumped into an array of edge pointers, with decreasingly ordered edge pointers by their scores. This array is captured as an external pointer, attached as an attribute of an rqubicSeeds object.

An rqubicSeeds object holds an integer, which records the height of the heap. It has (besides the class identifier) two attributes: one for the external pointer, and the other one for the threshold of the coincidence score.
Note

In the rqubic implementation, the variable arr_c[i][j] holds the level symbols \((-1, 0, 1\) in the default case), whereas in the QUBIC implementation, this variable holds the index of level symbols, and the level symbols are saved in the global variable symbols.

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>

Examples

data(sample.ExpressionSet, package="Biobase")
sample.disc <- quantileDiscretize(sample.ExpressionSet)
sample.seeds <- generateSeeds(sample.disc)
sample.seeds

## with higher threshold of incidence score
sample.seeds.higher <- generateSeeds(sample.disc, minColWidth=5)
sample.seeds.higher

parseQubicBlocks

Parse QUBIC Command Line Tool Output Files

Description

These functions parse output files of the QUBIC command line tool developed by Ma et al.

Usage

parseQubicRules(filename)
parseQubicChars(file, check.names=FALSE, ...)
parseQubicBlocks(filename)

Arguments

filename Input filename
date Input filename
check.names logical, should the column names be checked?
... other parameters passed to the read.csv function

Details

Parse QUBIC Command Line Tool Output Files

Value

parseQubicRules and parseQubicChars both return a data frame.
parseQubicBlocks returns an instance of QUBICBiclustetSet class.
### quantileDiscretize

**Discretize expression matrix for qualitative biclustering**

**Description**

Performs recursive quantilizations on gene expression data across samples, to quantileDiscretize gene expression matrix. The quantile parameter \( q \) determines the estimated proportion of differentially expressed genes (2\( q \) as for both up- and down-regulations). The rank parameter \( r \) determines how many discrete levels should differentially expressed genes (or outliers) have. See details below.

**Usage**

\[
\text{quantileDiscretize}(x, \ldots)
\]

**Arguments**

- \( x \) It can be an object of the \texttt{eSet} class or inheriting it. The most commonly used form is an \texttt{linkS4class(\texttt{ExpressionSet})} class. Alternatively, it can be a numeric matrix.

- \( \ldots \) Currently, the \( \ldots \) accepts two parameter: \( q \) and \( \text{rank} \), explained below.

- \( q \) Estimated proportion of conditions where gene is up- or down-regulated, value between \((0, 0.5)\), default value is set to 0.06. By specifying \( q \) one estimates that in 2\( q \) of all conditions, the expression value of a gene is considered as outlier.
quantileDiscretize

- rankRanks (levels) of outliers, a positive integer, default is 1L. By default, all conditions get one label for each gene in \(-1, 0, 1\), representing down expression, not changing and high expression respectively. In case \(rank > 1\), the outliers are further divided into \(rank\) levels by applying recursive quantilization with equal intervals.

Details

Parameter q corresponds to the command line option \(-q\) in the QUBIC command line tool, and the rank option corresponds to \(-r\).

For each gene, the algorithm applies quantile discretization first to divide conditions into negative (lower), un-changed and positive (higher) expressions. Negative and positive expressed conditions are considered as outliers. For outliers in each direction, the algorithm tries to further quantileDiscretize the expression values in case \(rank > 1\).

This second discretization step is performed by dividing the sorted outliers into \(rank\) tandem groups with equal conditions. A label is assigned to each of these tandem groups, in the following order:

\[-1, -2, \ldots, -rank\]

for outliers with negative expression, from the most negative group to the least negative group (not the other way around!).

Similarly, for positive outliers, labels in the order of

\[rank, rank - 1, \ldots, 1\]

are assigned to tandem groups from the least positive group to the most positive group.

That is, signs of labels indicate the direction of gene expression change, and the absolute value represents the quantileDiscretized \(rank\) in the outliers.

Value

An object of the same class as the input parameter, with the \(\text{exprs}\) slot replaced by the quantileDiscretized matrix, which is a matrix of integer.

Note

Note that the resulting discrete matrix of this implementation can be slightly different from the one used by the QUBIC command line tool.

The main reason for this is the internal data type: while QUBIC uses \(\text{float}\) to represent expression matrix, we use \(\text{double}\) to represent the matrix.

It has the advantages of interfacing to R, having higher precision and avoiding errors caused by floating presentation. It is implemented with potential larger costs of memory, however for test data sets (for example the ALL dataset with more than 120 samples and 12000 genes) the peak memory use (<100M) as well as the execution time (CPU time 0.028s) are well under control.

The differentially is especially often observed when there are many tied values. These cases however are very rare cases and we assume they will not affect the results to a large extent.

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>
QUBICBiclusterSet-class

References

Li et al. (2009) QUBIC: a qualitative biclustering algorithm for analyses of gene expression data
Nucleic Acids Research 37:e101

See Also

parseQubicChars parses the quantileDiscretized matrix by the QUBIC command line tool into a
data frame.

Examples

library(Biobase)
data(sample.ExpressionSet, package="Biobase")
sample.disc <- quantileDiscretize(sample.ExpressionSet)
exprs(sample.disc)[1:6, 1:6]

## Equivalent to pass a numeric matrix
sample.mat.disc <- quantileDiscretize(exprs(sample.ExpressionSet))
sample.mat.disc[1:6, 1:6]
## Not run: identical(exprs(sample.disc),sample.mat.disc)

## with multiple ranks
sample.rank3 <- quantileDiscretize(sample.ExpressionSet, rank=3)
exprs(sample.rank3)[1:6, 1:6]

QUBICBiclusterSet-class

Class "QUBICBiclusterSet"

Description

Object representing a set of biclusters identified by the QUBIC algorithm. The class structure
inherits the Biclust class in the biclust package.

Objects from the Class

Created by functions parsing the output files of QUBIC command line tool, or functions calling
QUBIC algorithm implementations in R.

Not intended to be created manually by end-users. However, interested users are invited to review
the source code or use the showClass method to view the construction of the class.

Slots

See the class structure of Biclust. The slots Parameter and Info have been filled with lists
relevant to the QUBIC algorithm, and all items should be accessed by S4-methods to make
sure the consistency.
quBicluster

Methods

Svalue signature(object = "QUBICBiclusterSet", index = "missing"): Return S values of QUBIC biclusters as a vector

Svalue signature(object = "QUBICBiclusterSet", index = "numeric"): S values of specified bicluster(s) are returned. Index is one or a vector of integers. Non-integers will be coerced.

[ signature(x = "QUBICBiclusterSet", i = "ANY", j = "missing", drop = "missing"): Returning a subset of the current QUBICBiclusterSet.

parameter signature(object = "Biclust", index = "character"): return an input parameter specified by the parameter name

parameter signature(object = "Biclust", index = "missing"): return a list of input parameters used by the biclustering algorithm, for example QUBIC

info signature(object = "Biclust", index = "ANY"): return information of the biclusters. For end-users, specific information accessors should be preferred, for example features, conditions and Svalue

info signature(object = "Biclust", index = "missing"): return all information of the biclusters in a list. For end-users, specific information accessors should be preferred, for example features, conditions and Svalue

show signature(object = "QUBICBiclusterSet"): showing method

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>

References


See Also

Biclust is the basic block accommodating biclusters identified by the QUBIC algorithm.

Examples

showClass("QUBICBiclusterSet")

<table>
<thead>
<tr>
<th>quBicluster</th>
<th>Qualitative Biclustering</th>
</tr>
</thead>
</table>

Description

The function takes seeds and quantileDiscretized ExpressionSet as input, biclusters the data and returns an object holding biclusters. Users may control the report number of clusters, tolerance of incoherent genes (or conditions), as well as the filtering of redundant clusters.
Usage

quBicluster(seeds, eset, report.no = 100L, tolerance = 0.95, filter.proportion = 1)

Arguments

seeds 
An object of the S3-class rqubicSeeds, representing seeds generated from the quantileDiscretized expression data

eset 
Discretized expression data

report.no 
Number of biclusters that should be reported. Detected biclusters are ranked by the S-score, which is defined by the product of gene counts and sample counts. They are ordered and the top ones are reported.

tolerance 
Percentage of tolerated incoherent samples, 0.95 by default

filter.proportion 
Proportion of a cluster, over which the cluster is considered as redundant. Each bicluster is compared to all better ranking biclusters, and the overlapping proportion is measured by the proportion of the product of overlapping samples and overlapping genes, to the product samples and genes. If the proportion is larger than the given threshold, the block will be considered redundant and therefore not reported. Setting the threshold to 1 (default) does not perform any filtering.

Details

The function calls a C routine to perform the biclustering. Currently the routine returns blocks with fewer samples specified by the minimum column number, due to the set of tolerance values. This might be changed in the fewer versions.

Value

An object of the QUBICBiclusterSet-class, holding all biclusters.

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>

References


See Also

quantileDiscretize and generateSeeds
### Examples

```r
data(sample.ExpressionSet, package="Biobase")
rqubic.example.discret <- quantileDiscretize(sample.ExpressionSet, rank=2L)

rqubic.example.sel.seeds <- generateSeeds(rqubic.example.discret, minColWidth=2L)

rqubic.example.blocks <- quBicluster(rqubic.example.sel.seeds,
                                   rqubic.example.discret,
                                   report.no=200L,
                                   filter.proportion=0.1)

## print features in each bicluster
BCfeatures(rqubic.example.blocks)
```

---

### Description

This function complements the functionality of `writeBiclusterResults` in the biclust package. It constructs a `Biclust` object from a plain text file.

### Usage

```r
readBiclusterResults(filename, featureNames, sampleNames, delimiter = ";", ...)
```

### Arguments

- `filename`: Character, name of the file storing biclustering information
- `featureNames`: Optional character vector, feature names of the underlying expression dataset. See details.
- `sampleNames`: Optional character vector, sample names of the underlying expression dataset. See details.
- `delimiter`: Character used to separate features, samples and counts of them.
- `...`: Other parameters passed to the `readLines` function.

### Details

Currently output files written by the `writeBiclusterResults` function does not contain original feature names or sample names in the expression dataset from which biclusters were mined. The `featureNames` and `sampleNames` allow to use this information to construct a `Biclust` object that has the same dimension as the original expression dataset.

### Value

A `Biclust` object
writeQubicInputFile

Author(s)

Jitao David Zhang <jitao_david.zhang@roche.com>

See Also

In case several biclustering algorithms were applied to the same expression dataset, they can be combined with combineBiclusts once the results were read from plain texts.

Examples

```r
temp <- tempfile()
library(biclust)
data(BicatYeast, package="biclust")
res <- biclust(BicatYeast, method=BCBimax(), number=5)
writeBiclusterResults(temp, res,"CC with delta 1.5",dimnames(BicatYeast)[[1]],dimnames(BicatYeast)[[2]], delimiter=";")
res.back <- readBiclusterResults(temp, delimiter=";")
res.full.back <- readBiclusterResults(temp,featureNames=rownames(BicatYeast), sampleNames=colnames(BicatYeast),delimiter=";")
```

Description

The QUBIC command line tool (developed by Ma et al.) requires a tab-limited data matrix as input file, with some special requirements (see details below). This function takes an object of ExpressionSet and outputs the file.

Usage

```r
writeQubicInputFile(x, file = "", featureNames, sampleNames)
```

Arguments

- `x`: An object inheriting the eSet class, most commonly an ExpressionSet object, representing expression data of features across samples.
- `file`: Filename to output, or a connection to write to (e.g. stdout()).
- `featureNames`: Specifies the feature names. It can be left blank, in which case the result of calling featureNames on x will be used. Alternatively, it can be one character string, specifying which column in the fData should be used. The third possibility, it can be a vector of characters, with the same length as features in the object. In the last option, all other types will be converted to characters.
- `sampleNames`: Specifies the sample names. It can be left blank, in which case the result of calling sampleNames on x will be used. Alternatively, it can be one character string, specifying which column in the pData should be used. The third possibility, it can be a vector of characters, with the same length as features in the object. In the last option, all other types will be converted to characters.
writeQubicInputFile

Details
The description of the data format can be checked by running the QUBIC tool in the command line mode, with the option -h (for help). A special requirement, which makes it different from the results of the write.table function in R, is that before the sample names (column names), an “o” must be added.

Value
No visible value will be returned, the function is called for its side effect.

Author(s)
Jitao David Zhang <jitao_david.zhang@roche.com>

See Also
eSetDimName, write.table

Examples

tmpfile <- tempfile()
data(sample.ExpressionSet, package="Biobase")
sub.eset <- sample.ExpressionSet[1:3, 1:3]

## write to standard output
writeQubicInputFile(sub.eset)

## write to a temporary file
writeQubicInputFile(sub.eset, tmpfile)
head(readLines(tmpfile))

## specify names with one column name in fData/pData
writeQubicInputFile(sub.eset, file="", sampleNames="sex")

## alternatively specify names manually
writeQubicInputFile(sub.eset, file="",sampleNames=paste("Sample", 1:3))
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