

Package ‘lmQCM’

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Type Package

Title An Algorithm for Gene Co-Expression Analysis

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Description

Implementation based on Zhang, Jie & Huang, Kun (2014) <[doi:10.4137/CIN.S14021](https://doi.org/10.4137/CIN.S14021)> Normalized ImQCM: An Algorithm for Detecting Weak Quasi-Cliques in Weighted Graph with Applications in Gene Co-Expression Module Discovery in Cancers. Cancer informatics, 13, CIN-S14021.

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Encoding UTF-8

Depends genefilter, Biobase, progress, stats, methods

Suggests devtools, roxygen2

RoxygenNote 7.2.1

URL <https://github.com/huangzhii/lmQCM/>

BugReports <https://github.com/huangzhii/lmQCM/issues/>

NeedsCompilation no

Repository CRAN

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R topics documented:

fastFilter	2
lmQCM	2
localMaximumQCM	3
merging_lmQCM	4

Index	5
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fastFilter *fastFilter: Subroutine for filtering expression matrix*

Description

Author: Zhi Huang

Usage

```
fastFilter(  
  RNA,  
  lowest_percentile_mean = 0.2,  
  lowest_percentile_variance = 0.2,  
  var.func = "var"  
)
```

Arguments

RNA an expression matrix (rows: genes; columns: samples)
lowest_percentile_mean a float value range 0-1
lowest_percentile_variance a float value range 0-1
var.func specify variance function

Value

An filtered expression matrix

lmQCM *lmQCM: Main Routine for Gene Co-expression Analysis*

Description

Author: Zhi Huang

Usage

```
lmQCM(  
  data_in,  
  gamma = 0.55,  
  t = 1,  
  lambda = 1,  
  beta = 0.4,  
  minClusterSize = 10,
```

```

    CCmethod = "pearson",
    positiveCorrelation = F,
    normalization = F
  )

```

Arguments

data_in	real-valued expression matrix with rownames indicating gene ID or gene symbol
gamma	gamma value (default = 0.55)
t	t value (default = 1)
lambda	lambda value (default = 1)
beta	beta value (default = 0.4)
minClusterSize	minimum length of cluster to retain (default = 10)
CCmethod	Methods for correlation coefficient calculation (default = "pearson"). Users can also pick "spearman".
positiveCorrelation	This determines if correlation matrix should convert to positive (with abs function) or not.
normalization	Determine if normalization is needed on massive correlation coefficient matrix.

Value

QCMLObject - An S4 Class with lmQCM results

Examples

```

library(lmQCM)
library(Biobase)
data(sample.ExpressionSet)
data = assayData(sample.ExpressionSet)$exprs
data = fastFilter(data, 0.2, 0.2)
lmQCM(data)

```

localMaximumQCM

localMaximumQCM: Subroutine for Creating Gene Clusters

Description

Author: Zhi Huang

Usage

```
localMaximumQCM(cMatrix, gamma = 0.55, t = 1, lambda = 1)
```

Arguments

cMatrix	a correlation matrix
gamma	gamma value (default = 0.55)
t	t value (default = 1)
lambda	lambda value (default = 1)

Value

An unmerged clusters group 'C'

merging_lmQCM

merging_lmQCM: Subroutine for Merging Gene Clusters

Description

Author: Zhi Huang

Usage

```
merging_lmQCM(C, beta = 0.4, minClusterSize = 10)
```

Arguments

C	Resulting clusters
beta	beta value (default = 0.4)
minClusterSize	minimum length of cluster to retain (default = 10)

Value

mergedCluster - An merged clusters group

Index

`fastFilter`, 2

`lmQCM`, 2

`localMaximumQCM`, 3

`merging_lmQCM`, 4