

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> Normalized lmQCM: 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, nnet, stats

Suggests devtools, roxygen2

LazyData true

RoxygenNote 6.0.1

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

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

NeedsCompilation no

Repository CRAN

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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", 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".
normalization	Determine if normalization is needed on massive correlation coefficient matrix.

Value

mergedCluster - An merged clusters group

Examples

```
library(lmQCM)  
library(Biobase)  
data(sample.ExpressionSet)  
data = assayData(sample.ExpressionSet)$exprs  
lmQCM(data)
```

localMaximumQCM	<i>localMaximumQCM: Subroutine for Creating Gene Clusters</i>
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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	<i>merging_lmQCM: Subroutine for Merging Gene Clusters</i>
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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

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