Package 'lmQCM'

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Type Package

Title lmQCM: An Algorithm for Gene Co-Expression Analysis

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Description An Algorithm for Detecting Weak Quasi-Cliques in Weighted Graph with Applications in Gene Co-Expression Module Discovery in Cancers.

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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

R topics documented:

| 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")
```

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".

Value

mergedCluster

| 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 matirx
gamma	gamma value (default = 0.55)
t	t value (default = 1)
lambda	lambda value (default = 1)

Value

C

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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

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