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, progress, stats, methods

Suggests devtools, roxygen2

LazyData true

RoxygenNote 7.1.1

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

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

NeedsCompilation no

Repository CRAN

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R topics documented:

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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

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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

QCMObject - 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)
```

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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

An unmerged clusters group '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 - An merged clusters group

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