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 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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Contents

`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

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)
```

`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'

`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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