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

LazyData true

RoxygenNote 6.1.0

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

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

NeedsCompilation no

Repository CRAN

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R topics documented:

`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", 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'

`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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