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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