Package ‘lmQCM’
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fastFilter  

*fastFilter: Subroutine for filtering expression matrix*

**Description**

Author: Zhi Huang

**Usage**

```r
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**

```r
lmQCM(data_in, gamma = 0.55, t = 1, lambda = 1, beta = 0.4,
       minClusterSize = 10, CCmethod = "pearson", normalization = F)
```
localMaximumQCM

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)

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: 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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