

# Package ‘lmQCM’

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**Type** Package

**Title** An Algorithm for Gene Co-Expression Analysis

**Version** 0.1.2

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**Author** Zhi Huang [aut, cre],  
Jie Zhang [aut, ctb],  
Kun Huang [aut, ctb],  
Zhi Han [aut, ctb]

**Maintainer** Zhi Huang <huang898@purdue.edu>

**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, nnet, stats

**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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lmQCM

*lmQCM: Main Routine for Gene Co-expression Analysis*

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## 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

mergedCluster - An merged clusters group

## Examples

```
library(lmQCM)  
library(Biobase)  
data(sample.ExpressionSet)  
data = assayData(sample.ExpressionSet)$exprs  
lmQCM(data)
```

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localMaximumQCM	<i>localMaximumQCM: Subroutine for Creating Gene Clusters</i>
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**Description**

Author: Zhi Huang

**Usage**

```
localMaximumQCM(cMatrix, gamma = 0.55, t = 1, lambda = 1)
```

**Arguments**

cMatrix	a correlation matrix
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	<i>merging_lmQCM: Subroutine for Merging Gene Clusters</i>
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**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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