

# Package ‘MODA’

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**Type** Package

**Title** MODA: MOdule Differential Analysis for weighted gene  
co-expression network

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**Description** MODA can be used to estimate and construct condition-specific gene  
co-expression networks, and identify differentially expressed subnetworks as  
conserved or condition specific modules which are potentially associated with  
relevant biological processes.

**License** GPL (>= 2)

**Depends** R (>= 3.3)

**Imports** grDevices, graphics, stats, utils, WGCNA, dynamicTreeCut,  
igraph, cluster, AMOUNTAIN, RColorBrewer

**RoxygenNote** 5.0.1

**biocViews** GeneExpression, Microarray, DifferentialExpression, Network

**Suggests** BiocStyle, knitr, rmarkdown

**ignetteBuilder** knitr

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CompareAllNets	<i>Illustration of network comparison</i>
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**Description**

Compare the background network and a set of condition-specific network. Conserved or condition-specific modules are indicated by the plain files, based on the statistics

**Usage**

```
CompareAllNets(ResultFolder, intModules, indicator, intconditionModules,
conditionNames, specificTheta, conservedTheta)
```

**Arguments**

ResultFolder	where to store results
intModules	how many modules in the background network
indicator	identifier of current profile, served as a tag in name
intconditionModules	a numeric vector, each of them is the number of modules in each condition-specific network. Or just single number
conditionNames	a character vector, each of them is the name of condition. Or just single name
specificTheta	the threshold to define $\min(s) + \text{specificTheta}$ , less than which is considered as condition specific module. $s$ is the sums of rows in Jaccard index matrix. See supplementary file.
conservedTheta	The threshold to define $\max(s) - \text{conservedTheta}$ , greater than which is considered as condition conserved module. $s$ is the sums of rows in Jaccard index matrix. See supplementary file.

**Value**

None

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**See Also**

[WeightedModulePartitionHierarchical](#), [comparemodulestwonets](#)

**Examples**

```
data(synthetic)
ResultFolder = 'ForSynthetic' # where middle files are stored
CuttingCriterion = 'Density' # could be Density or Modularity
indicator1 = 'X' # indicator for data profile 1
indicator2 = 'Y' # indicator for data profile 2
specificTheta = 0.1 #threshold to define condition specific modules
conservedTheta = 0.1#threshold to define conserved modules
intModules1 <- WeightedModulePartitionHierarchical(datExpr1,ResultFolder,
indicator1,CuttingCriterion)
intModules2 <- WeightedModulePartitionHierarchical(datExpr2,ResultFolder,
indicator2,CuttingCriterion)
CompareAllNets(ResultFolder,intModules1,indicator1,intModules2,indicator2,
specificTheta,conservedTheta)
```

---

comparemodulestwonets *Illustration of two networks comparison*

---

**Description**

Compare the background network and a condition-specific network. A Jaccard index is used to measure the similarity of two sets, which represents the similarity of each module pairs from two networks.

**Usage**

```
comparemodulestwonets(sourcehead, nm1, nm2, ind1, ind2)
```

**Arguments**

sourcehead	prefix of where to store results
nm1	how many modules in the background network
nm2	how many modules in the condition-specific network
ind1	indicator of the background network
ind2	indicator of the condition-specific network

**Value**

A matrix where each entry is the Jaccard index of corresponding modules from two networks

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**Examples**

```

data(synthetic)
ResultFolder = 'ForSynthetic' # where middle files are stored
CuttingCriterion = 'Density' # could be Density or Modularity
indicator1 = 'X' # indicator for data profile 1
indicator2 = 'Y' # indicator for data profile 2
intModules1 <- WeightedModulePartitionHierarchical(datExpr1,ResultFolder,
indicator1,CuttingCriterion)
intModules2 <- WeightedModulePartitionHierarchical(datExpr2,ResultFolder,
indicator2,CuttingCriterion)
JaccardMatrix <- comparemodulestwonets(ResultFolder,intModules1,intModules2,
paste('/DenseModuleGene_',indicator1,sep=''),
paste('/DenseModuleGene_',indicator2,sep=''))

```

---

datExpr1

*datExpr1*


---

**Description**

Synthetic gene expression profile with 20 samples and 500 genes.

**Format**

A matrix with 20 rows and 500 columns.

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**Examples**

```

data(synthetic)
## plot the heatmap of the correlation matrix ...
## Not run: heatmap(cor(as.matrix(datExpr1)))

```

---

datExpr2

*datExpr2*


---

**Description**

Synthetic gene expression profile with 25 samples and 500 genes.

**Format**

A matrix with 25 rows and 500 columns.

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**Examples**

```
data(synthetic)
## plot the heatmap of the correlation matrix ...
## Not run: heatmap(cor(as.matrix(datExpr2)))
```

---

getPartition	<i>Get numeric partition from folder</i>
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---

**Description**

Get identified partitionAssignment, only for synthetic data where gene names are numbers

**Usage**

```
getPartition(ResultFolder)
```

**Arguments**

ResultFolder    folder used to save modules

**Value**

Number of partitions

---

MIcondition	<i>Modules detection by each condition</i>
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**Description**

Module detection on each condition-specific network, which is constructed from all samples but samples belonging to that condition

**Usage**

```
MIcondition(datExpr, conditionNames, ResultFolder, GeneNames, maxsize = 100,
  minsize = 30)
```

**Arguments**

datExpr	gene expression profile, rows are samples and columns genes, rowname should contain condition specifier
conditionNames	character vector, each as the condition name
ResultFolder	where to store the clusters
GeneNames	normally the gene official names to replace the colnames of datExpr
maxsize	the maximal nodes allowed in one module
minsize	the minimal nodes allowed in one module

**Value**

a numeric vector, each entry is the number of modules in condition-specific network

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

---

ModuleFrequency

*Statistics of all conditions*

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**Description**

Statistics of all conditions. To highlight conserved or condition-specific by counting how frequent each module is labelled as which, and then visualize the frequency by bar plot.

**Usage**

```
ModuleFrequency(ResultFolder, intModules, conditionNames, legendNames,  
indicator)
```

**Arguments**

ResultFolder	where to store results
intModules	how many modules in the background network
conditionNames	a character vector, each of them is the name
legendNames	a character vector, each of them is the condition name showing up in the frequency barplot of condition. Or just single name
indicator	identifier of current profile, served as a tag in name

**Value**

None

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**See Also**

[WeightedModulePartitionHierarchical](#), [WeightedModulePartitionLouvain](#), [WeightedModulePartitionSpectral](#), [WeightedModulePartitionAmoutain](#), [CompareAllNets](#)

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modulesRank	<i>Modules rank from recursive communities detection</i>
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---

**Description**

Assign the module scores by weights, and rank them from highest to lowest

**Usage**

```
modulesRank(foldername, indicator, GeneNames)
```

**Arguments**

foldername	folder used to save modules
indicator	normally a specific tag of condition
GeneNames	Gene symbols, sometimes we need them instead of probe ids

**Value**

The number of modules

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**See Also**

[recursiveigraph](#)

---

NMImatrix	<i>Illustration of network comparison by NMI</i>
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---

**Description**

Compare the background network and a set of condition-specific network. returning a pair-wise matrix to show the normalized mutual information between each pair of networks in terms of partitioning

**Usage**

```
NMImatrix(ResultFolder, intModules, indicator, intconditionModules,  
conditionNames, Nsize, legendNames = NULL, plt = FALSE)
```

**Arguments**

ResultFolder	where to store results
intModules	how many modules in the background network
indicator	identifier of current profile, served as a tag in name
intconditionModules	a numeric vector, each of them is the number of modules in each condition-specific network. Or just single number
conditionNames	a character vector, each of them is the name of condition. Or just single name
Nsize	The number of genes in total
legendNames	a character vector, each of them is the condition name showing up in the similarity matrix plot if applicable
plt	a boolean value to indicate whether plot the similarity matrix

**Value**

NMI matrix indicating the similarity between each two networks

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**See Also**

[CompareAllNets](#)

---

PartitionDensity      *Illustration of partition density*

---

**Description**

Calculate the average density of all resulting modules from a partition. The density of each module is defined as the average adjacency of the module genes.

**Usage**

```
PartitionDensity(ADJ, PartitionSet)
```

**Arguments**

ADJ	gene similarity matrix
PartitionSet	vector indicates the partition label for genes

**Value**

partition density, defined as average density of all modules

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>



## References

Langfelder, Peter, and Steve Horvath. "WGCNA: an R package for weighted correlation network analysis." *BMC bioinformatics* 9.1 (2008): 1.

## Examples

```
data(synthetic)
ADJ1=abs(cor(datExpr1,use="p"))^10
dissADJ=1-ADJ1
hierADJ=hclust(as.dist(dissADJ), method="average" )
groups <- cutree(hierADJ, h = 0.8)
pDensity <- PartitionDensity(ADJ1,groups)
```

---

PartitionModularity     *Illustration of modularity density*

---

## Description

Calculate the average modularity of a partition. The modularity of each module is defined from a natural generalization of unweighted case.

## Usage

```
PartitionModularity(ADJ, PartitionSet)
```

## Arguments

ADJ	gene similarity matrix
PartitionSet	vector indicates the partition label for genes

## Value

partition modularity, defined as average modularity of all modules

## Author(s)

Dong Li, <dxl466@cs.bham.ac.uk>

## References

Newman, Mark EJ. "Analysis of weighted networks." *Physical review E* 70.5 (2004): 056131.

## Examples

```
data(synthetic)
ADJ1=abs(cor(datExpr1,use="p"))^10
dissADJ=1-ADJ1
hierADJ=hclust(as.dist(dissADJ), method="average" )
groups <- cutree(hierADJ, h = 0.8)
pDensity <- PartitionModularity(ADJ1,groups)
```

---

recursiveigraph      *Modules identification by recursive community detection*

---

**Description**

Modules detection using igraph's community detection algorithms, when the resulted module is larger than expected, it is further divided by the same program

**Usage**

```
recursiveigraph(g, savefile, method = c("fastgreedy", "louvain"),
               maxsize = 200, minsize = 30)
```

**Arguments**

g	igraph object, the network to be partitioned
savefile	plain text, used to store module, each line as a module
method	specify the community detection algorithm
maxsize	maximal module size
minsize	minimal module size

**Value**

None

**Author(s)**

Dong Li, <dxl466@cs.bham.ac.uk>

**References**

Blondel, Vincent D., et al. "Fast unfolding of communities in large networks." *Journal of statistical mechanics: theory and experiment* 2008.10 (2008): P10008.

---

WeightedModulePartitionAmoutain  
*Modules detection by AMOUNTAIN algorithm*

---

**Description**

Module detection based on the AMOUNTAIN algorithm, which tries to find the optimal module every time and use a modules extraction way

**Usage**

```
WeightedModulePartitionAmoutain(datExpr, Nmodule, foldername, indicatename,
                               GeneNames, maxsize = 200, minsize = 3, power = 6, tao = 0.2)
```

**Arguments**

datExpr	gene expression profile, rows are samples and columns genes
Nmodule	the number of clusters(modules)
foldername	where to store the clusters
indicatename	normally a specific tag of condition
GeneNames	normally the gene official names to replace the colnames of datExpr
maxsize	the maximal nodes allowed in one module
minsize	the minimal nodes allowed in one module
power	the power parameter of WGCNA, $W_{ij} =  \text{cor}(x_i, x_j) ^{\text{pwr}}$
tao	the threshold to cut the adjacency matrix

**Value**

None

**Author(s)**

Dong Li, &lt;dxl466@cs.bham.ac.uk&gt;

**References**

Blondel, Vincent D., et al. "Fast unfolding of communities in large networks." Journal of statistical mechanics: theory and experiment 2008.10 (2008): P10008.

**Examples**

```
data(synthetic)
ResultFolder <- 'ForSynthetic' # where middle files are stored
GeneNames <- colnames(datExpr1)
intModules1 <- WeightedModulePartitionAmoutain(datExpr1,5,ResultFolder,'X',
GeneNames,maxsize=100,minsize=50)
truemodule <- c(rep(1,100),rep(2,100),rep(3,100),rep(4,100),rep(5,100))
#mymodule <- getPartition(ResultFolder)
#randIndex(table(mymodule,truemodule),adjust=F)
```

---

 WeightedModulePartitionHierarchical

*Modules detection by hierarchical clustering*

---

**Description**

Module detection based on the optimal cutting height of dendrogram, which is selected to make the average density or modularity of resulting partition maximal. The clustering and visualization function are from WGCNA.

**Usage**

```
WeightedModulePartitionHierarchical(datExpr, foldername, indicatename,
  cutmethod = c("Density", "Modularity"), power = 10)
```

**Arguments**

datExpr            gene expression profile, rows are samples and columns genes  
 foldername        where to store the clusters  
 indicatename     normally a specific tag of condition  
 cutmethod        cutting the dendrogram based on maximal average Density or Modularity  
 power            the power parameter of WGCNA,  $W_{ij}=|cor(x_i,x_j)|^power$

**Value**

The number of clusters

**Author(s)**

Dong Li, <dxl466@cs.bham.ac.uk>

**References**

Langfelder, Peter, and Steve Horvath. "WGCNA: an R package for weighted correlation network analysis." BMC bioinformatics 9.1 (2008): 1.

**See Also**

[PartitionDensity](#)  
[PartitionModularity](#)

**Examples**

```
data(synthetic)
ResultFolder = 'ForSynthetic' # where middle files are stored
CuttingCriterion = 'Density' # could be Density or Modularity
indicator1 = 'X'            # indicator for data profile 1
indicator2 = 'Y'            # indicator for data profile 2
specificTheta = 0.1 #threshold to define condition specific modules
conservedTheta = 0.1#threshold to define conserved modules
intModules1 <- WeightedModulePartitionHierarchical(datExpr1,ResultFolder,
indicator1,CuttingCriterion)
#mymodule <- getPartition(ResultFolder)
#randIndex(table(mymodule,truemodule),adjust=F)
```

---

WeightedModulePartitionLouvain

*Modules detection by Louvain algorithm*

---

**Description**

Module detection based on the Louvain algorithm, which tries to maximize overall modularity of resulting partition.

**Usage**

```
WeightedModulePartitionLouvain(datExpr, foldername, indicatename, GeneNames,
maxsize = 200, minsize = 30, power = 6, tao = 0.2)
```

**Arguments**

datExpr	gene expression profile, rows are samples and columns genes
foldername	where to store the clusters
indicatename	normally a specific tag of condition
GeneNames	normally the gene official names to replace the colnames of datExpr
maxsize	the maximal nodes allowed in one module
minsize	the minimal nodes allowed in one module
power	the power parameter of WGCNA, $W_{ij} =  \text{cor}(x_i, x_j) ^{\text{power}}$
tao	the threshold to cut the adjacency matrix

**Value**

The number of clusters

**Author(s)**

Dong Li, <dxl466@cs.bham.ac.uk>

**References**

Blondel, Vincent D., et al. "Fast unfolding of communities in large networks." *Journal of statistical mechanics: theory and experiment* 2008.10 (2008): P10008.

**Examples**

```
data(synthetic)
ResultFolder <- 'ForSynthetic' # where middle files are stored
indicator <- 'X' # indicator for data profile 1
GeneNames <- colnames(datExpr1)
intModules1 <- WeightedModulePartitionLouvain(datExpr1, ResultFolder, indicator, GeneNames)
truemodule <- c(rep(1,100), rep(2,100), rep(3,100), rep(4,100), rep(5,100))
#mymodule <- getPartition(ResultFolder)
#randIndex(table(mymodule, truemodule), adjust=F)
```

---

WeightedModulePartitionSpectral

*Modules detection by spectral clustering*

---

**Description**

Module detection based on the spectral clustering algorithm, which mainly solve the eigendecomposition on Laplacian matrix

**Usage**

```
WeightedModulePartitionSpectral(datExpr, foldername, indicatename, GeneNames,
power = 6, nn = 10, k = 2)
```

**Arguments**

datExpr	gene expression profile, rows are samples and columns genes
foldername	where to store the clusters
indicatename	normally a specific tag of condition
GeneNames	normally the gene official names to replace the colnames of datExpr
power	the power parameter of WGCNA, $W_{ij} =  \text{cor}(x_i, x_j) ^{\text{power}}$
nn	the number of nearest neighbor, used to construct the affinity matrix
k	the number of clusters(modules)

**Value**

None

**Author(s)**

Dong Li, <dx1466@cs.bham.ac.uk>

**References**

Von Luxburg, Ulrike. "A tutorial on spectral clustering." *Statistics and computing* 17.4 (2007): 395-416.

**Examples**

```
data(synthetic)
ResultFolder <- 'ForSynthetic' # where middle files are stored
indicator <- 'X' # indicator for data profile 1
GeneNames <- colnames(datExpr1)
WeightedModulePartitionSpectral(datExpr1, ResultFolder, indicator,
GeneNames, k=5)
truemodule <- c(rep(1,100), rep(2,100), rep(3,100), rep(4,100), rep(5,100))
#mymodule <- getPartition(ResultFolder)
#randIndex(table(mymodule, truemodule), adjust=F)
```

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