

# Package ‘MODA’

August 16, 2025

**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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## Contents

|                                 |   |
|---------------------------------|---|
| CompareAllNets . . . . .        | 2 |
| comparemodulestwonets . . . . . | 3 |
| datExpr1 . . . . .              | 4 |
| datExpr2 . . . . .              | 4 |
| getPartition . . . . .          | 5 |

|                                               |    |
|-----------------------------------------------|----|
| MIcondition . . . . .                         | 5  |
| ModuleFrequency . . . . .                     | 6  |
| modulesRank . . . . .                         | 7  |
| NMImatrix . . . . .                           | 7  |
| PartitionDensity . . . . .                    | 8  |
| PartitionModularity . . . . .                 | 9  |
| recursiveigraph . . . . .                     | 10 |
| WeightedModulePartitionAmoutain . . . . .     | 10 |
| WeightedModulePartitionHierarchical . . . . . | 11 |
| WeightedModulePartitionLouvain . . . . .      | 12 |
| WeightedModulePartitionSpectral . . . . .     | 13 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>15</b> |
|--------------|-----------|

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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> |
|--------------|------------------------------------------|

---

**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> |
|-------------|--------------------------------------------|

---

**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, <dxl466@cs.bham.ac.uk>

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|                 |                                     |
|-----------------|-------------------------------------|
| ModuleFrequency | <i>Statistics of all conditions</i> |
|-----------------|-------------------------------------|

---

**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, <dxl466@cs.bham.ac.uk>

**See Also**

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

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

---

**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 numeber of modules

**Author(s)**

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

**See Also**

[recursiveigraph](#)

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

---

**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, <dxl466@cs.bham.ac.uk>

**See Also**

[CompareAllNets](#)

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|                  |                                          |
|------------------|------------------------------------------|
| PartitionDensity | <i>Illustration of partition density</i> |
|------------------|------------------------------------------|

---

**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, <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.

## 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 | <i>Modules identification by recursive community detection</i> |
|-----------------|----------------------------------------------------------------|

---

### 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 | <i>Modules detection by AMOUNTAIN algorithm</i> |
|---------------------------------|-------------------------------------------------|

---

### 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**

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

**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.

**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 visulization function are from WGCNA.

**Usage**

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

**Arguments**

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

**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**

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

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

# Index

- \* **NMI**
  - NMImatrix, [7](#)
- \* **Statistics**
  - ModuleFrequency, [6](#)
- \* **community**
  - recursiveigraph, [10](#)
- \* **comparison**
  - comparemodulestwonets, [3](#)
- \* **cutting**
  - WeightedModulePartitionHierarchical, [11](#)
  - WeightedModulePartitionLouvain, [12](#)
  - WeightedModulePartitionSpectral, [13](#)
- \* **data**
  - datExpr1, [4](#)
  - datExpr2, [4](#)
- \* **dendrogram**
  - WeightedModulePartitionHierarchical, [11](#)
  - WeightedModulePartitionLouvain, [12](#)
  - WeightedModulePartitionSpectral, [13](#)
- \* **density**
  - PartitionDensity, [8](#)
- \* **detection**
  - recursiveigraph, [10](#)
- \* **differential**
  - CompareAllNets, [2](#)
  - ModuleFrequency, [6](#)
  - NMImatrix, [7](#)
- \* **modularity**
  - PartitionModularity, [9](#)
- \* **module**
  - CompareAllNets, [2](#)
  - comparemodulestwonets, [3](#)
  - ModuleFrequency, [6](#)
  - NMImatrix, [7](#)
- \* **multiplecondition**
  - MIcondition, [5](#)
- \* **optimization**
  - WeightedModulePartitionAmoutain, [10](#)
  - CompareAllNets, [2](#), [6](#), [8](#)
  - comparemodulestwonets, [3](#), [3](#)
  - datExpr1, [4](#)
  - datExpr2, [4](#)
  - getPartition, [5](#)
  - MIcondition, [5](#)
  - ModuleFrequency, [6](#)
  - modulesRank, [7](#)
  - NMImatrix, [7](#)
  - PartitionDensity, [8](#), [12](#)
  - PartitionModularity, [9](#), [12](#)
  - recursiveigraph, [7](#), [10](#)
  - WeightedModulePartitionAmoutain, [6](#), [10](#)
  - WeightedModulePartitionHierarchical, [3](#), [6](#), [11](#)
  - WeightedModulePartitionLouvain, [6](#), [12](#)
  - WeightedModulePartitionSpectral, [6](#), [13](#)