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 (>= 3.1.0)

Imports WGCNA,dynamicTreeCut,igraph

RoxygenNote 5.0.1

biocViews GeneExpression, Microarray, DifferentialExpression, Network

Suggests BiocStyle, knitr

VignetteBuilder knitr

NeedsCompilation no

\textbf{R topics documented:}

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CompareAllNets

**Illustration of network comparison**

**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**

\[
\text{CompareAllNets}(\text{ResultFolder}, \text{intModules}, \text{speciesName}, \text{intconditionModules}, \\
\quad \text{conditionNames}, \text{specificTheta}, \text{conservedTheta})
\]

**Arguments**

- **ResultFolder**: where to store results.
- **intModules**: how many modules in the background network.
- **speciesName**: 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, <dxl466@cs.bham.ac.uk>

**See Also**

- WeightedModulePartitionDensity.
- comparemodulestwonets

**Examples**

```r
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 <- WeightedModulePartitionDensity(datExpr1,ResultFolder,
intModules2 <- WeightedModulePartitionDensity(datExpr2,ResultFolder,
```
**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**

```r
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, `<dxl466@cs.bham.ac.uk>`

**Examples**

```r
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 <- WeightedModulePartitionDensity(datExpr1,ResultFolder,
indicator1,CuttingCriterion)
intModules2 <- WeightedModulePartitionDensity(datExpr2,ResultFolder,
indicator2,CuttingCriterion)
JaccardMatrix <- comparemodulestwonets(ResultFolder,intModules1,intModules2,
paste('"/DenseModuleGene_",indicator1,sep=""),
paste('"/DenseModuleGene_",indicator2,sep=""))
```
Description

Synthetic gene expression profile with 20 samples and 500 genes.

Format

A matrix with 20 rows and 500 columns.

Author(s)

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

Examples

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

Description

Synthetic gene expression profile with 25 samples and 500 genes.

Format

A matrix with 25 rows and 500 columns.

Author(s)

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

Examples

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

\[ \text{PartitionDensity}(\text{ADJ}, \text{PartitionSet}) \]

**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, \(<\text{dxl466@cs.bham.ac.uk}>\)

**References**


**Examples**

```r
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**

\[ \text{PartitionModularity}(\text{ADJ}, \text{PartitionSet}) \]

**Examples**

```r
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)
```
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, <dxl1466@cs.bham.ac.uk>

References


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)

Usage

WeightedModulePartitionDensity(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}

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.
Value

The number of clusters

Author(s)

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References


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 <- WeightedModulePartitionDensity(datExpr1,ResultFolder, indicator1,CuttingCriterion)
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