Package: MODA (via r-universe)

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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

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ignetteBuilder knitr

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Contents

`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

```
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)+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)-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

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)
```

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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, <dxl466@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=''))
```

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

Examples

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

`getPartition` *Get numeric partition from folder*

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 *Modules detection by each condition*

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>

ModuleFrequency *Statistics of all conditions*

Description

Statistics of all conditions. To highlight conserved or condition-specific by counting how frequent each module is lablelled 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 *Modules rank from recursive communities detection*

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

See Also

recursiveigraph

NMImatrix *Illustration of network comparison by NMI*

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

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, <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` *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 devided 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=|cor(x_i,x_j)|^pwr
tao	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

`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=|cor(x_i,x_j)|^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=|cor(x_i,x_j)|^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, <dxl466@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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