Package ‘Mirsynergy’

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Type Package
Title Mirsynergy
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Description Detect synergistic miRNA regulatory modules by overlapping neigbourhood expansion.
Depends R (>= 3.0.2), igraph, ggplot2
Imports graphics, grDevices, gridExtra, Matrix, parallel, RColorBrewer, reshape, scales, utils
Suggests glmnet, RUnit, BiocGenerics, knitr
License GPL-2
URL http://www.cs.utoronto.ca/~yueli/Mirsynergy.html
biocViews Clustering
Lazyload yes
VignetteBuilder knitr
NeedsCompilation no

R topics documented:

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Description

Mirsynergy is a deterministic overlapping clustering algorithm adapted from a recently developed framework. Mirsynergy operates in two stages that first forms MRM based on co-occurring miRNAs and then expand the MRM by greedily including (excluding) mRNA into (from) the MRM to maximize the synergy score, which is a function of miRNA-mRNA and gene-gene interactions.

Details

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The main function `mirsynergy` takes as inputs the mRNA and miRNA interaction matrix and gene-gene interaction matrix provided by the user or generated from existing techniques described in the manuscript (in preparation). The function then outputs a list with each item as a miRNA regulatory module (MRM) containing miRNA and mRNA ID and and other results for diagnostic purpose.

Author(s)

Yue Li Maintainer: Yue Li <yueli@cs.toronto.edu>

References

Li, Y. et al. Mirsynergy: detect synergistic miRNA regulatory modules by overlapping neighbourhood expansion. (in preparation).


See Also

`mirsynergy`
**Description**

Detect synergistic miRNA regulatory modules by overlapping neighbourhood expansion using a deterministic overlapping clustering algorithm adapted from a recently developed framework. Mirsynergy operates in two stages that first forms MRM based on co-occurring miRNAs and then expand the MRM by greedily including (excluding) mRNA into (from) the MRM to maximize the synergy score, which is a function of miRNA-mRNA and gene-gene interactions.

**Usage**

```r
mirsynergy(W, H, alpha = 2, merge.tol = 0.8, density1.tol = 1e-2, density2.tol = 5e-3, verbose = FALSE)
```

**Arguments**

- `W`: An N by M edge weight matrix containing interaction strength between N mRNA and M miRNA.
- `H`: An N by N edge weight matrix containing the binary interaction among the N mRNA (genes).
- `alpha`: Penalty for including a node into the growing module (advanced option). See manuscript or Nepusz et al. (2012) for more details.
- `merge.tol`: Threshold with range [0,1] to merge modules based on the percentage of nodes shared between the two modules.
- `density1.tol`: Threshold with range [0,1] to filter modules by the density function at stage 1 clustering.
- `density2.tol`: Threshold with range [0,1] to filter modules by the density function 2 at stage 2 clustering.
- `verbose`: Binary indicator to show running info.

**Details**

The weight matrix `W` can be obtained by various approaches such as Pearson correlation or linear regression on mRNA and miRNA expression profiles across multiple samples. Matrix `H` can be obtained from public database such as TRANSFAC and BioGrid.

**Value**

A nested list containing each item as a miRNA regulatory module (MRM). Each item itself is a list containing the following information:

- `miRNA`: miRNA included in the MRM
- `mRNA`: mRNA included in the MRM
- `v.in`: miRNA and mRNA
- `v.bound`: miRNA and mRNA disregard or excluded from the MRM but still have nonzero connection with the internal nodes
- `card.m`: Number of miRNA in the MRM
- `card.t`: Number of mRNA targets in the MRM
- `card`: Total number of miRNA and mRNA targets in the MRM
- `density`: Density of the MRM
Author(s)
Yue Li

References

Examples
###---- Should be DIRECTLY executable !! ----
###-- ==> Define data, use random,
###--or do help(data=index) for the standard data sets.
#
# simulate N mRNA and M miRNA and their interaction matrices
load(system.file("extdata/toy_modules.RData", package="Mirsynergy"))

# run mirsynergy clustering
V <- mirsynergy(W, H, verbose=TRUE)

summary_modules(V)

---

plot_modules

Plot module assignments.

Description
Plot as network graphical view of the output from mirsynergy V. NB: small network only.

Usage
plot_modules(V, W, H, legend.pos = "topright", ...)

Arguments
V Outputs from mirsynergy
W An N by M edge weight matrix containing interaction strength between N mRNA and M miRNA.
H An N by N edge weight matrix containing the binary interaction among the N mRNA (genes).
legend.pos Specify legend position
... Other parameters passed to plot

Details
Each node will be coloured by the modules they belong to. If a node belongs to multiple modules, it will be coloured differently based on the exact combination of the module indexes. The legend displays the corresponding colours and module assignments.
Note

Only for small network. For large network please use `tabular_module` to create a pairwise table as input to Cytoscape.

Author(s)

Yue Li

Examples

```r
load(system.file("extdata/toy_modules.RData", package="Mirsynergy"))
plot_modules(V,W,H)
```

---

**plot_module_summary**  
*Plot module statistics*

Description

Plot module statistics using output from `mirsynergy`.

Usage

```r
plot_module_summary(V)
```

Arguments

- `V`  
  Outputs from `mirsynergy`

Author(s)

Yue Li

Examples

```r
load(system.file("extdata/toy_modules.RData", package="Mirsynergy"))
plot_module_summary(V)
```
**summary_modules**

Print summary information of the formed modules

**Description**

Return summary information of the formed modules, which are the outputs from `mirsynergy`.

**Usage**

```r
summary_modules(V)
```

**Arguments**

- `V` Output from `mirsynergy`.

**Value**

- `moduleSummaryInfo` Summary information per module
- `miRNA.internal` miRNA count distribution across modules
- `mRNA.internal` mRNA count distribution across modules

**Author(s)**

Yue Li
**tabular_module**

**Examples**

```r
load(system.file("extdata/toy_modules.RData", package="Mirsynergy"))
summary_modules(V)
```

---

**Description**

Generate tabulated module assignments and nodes for input to Cytoscape.

**Usage**

```r
tabular_module(V, W, H, outdir)
```

**Arguments**

- **V**: Output from `mirsynergy`.
- **W**: An N by M edge weight matrix containing interaction strength between N mRNA and M miRNA.
- **H**: An N by N edge weight matrix containing the binary interaction among the N mRNA (genes).
- **outdir**: Path to save the nodes and edges files.

**Value**

- **nodes**: data.frame containing edges in each indexed module. Each edge (row) contain the edge weights, the edge type (MMI or GGI), and which module they belong to.
- **edges**: data.frame containing nodes in each indexed module. Each node (row) contain the node name, type (mRNA/miRNA), and which module they belong to.

**Author(s)**

Yue Li

**Examples**

```r
load(system.file("extdata/toy_modules.RData", package="Mirsynergy"))
tabular_module(V,W,H)
```
tcga_brca_testdata  Breast cancer expression test data from TCGA

Description
Test data of 2661 mRNA and 142 miRNA (i.e., 0.2 of the whole data) across 15 tumor samples from breast cancer (BRCA) patients. The data were downloaded from TCGA (The Cancer Genome Atlas). The full BRCA expression data contain expression measurements for 13306 and 710 distinct mRNAs and miRNAs across 331 samples.

Format
A list containing the follow items:

- $X, Z$  N-by-T and M-by-T Expression matrices for N mRNA and M miRNA measured across T samples
- $C, H$  N-by-M and N-by-N matrices for sequence-based miRNA-targets downloaded from TargetScan-Human 6.2 and gene-gene interactions from TRANSFAC and BioGrid involving transcription factor binding sites (TFBS) and protein-protein interactions, respectively.

References

Examples
load(system.file("extdata/tcga_brca_testdata.RData", package="Mirsynergy"))

toy_modules  Test data of 20 mRNA and 20 miRNA.

Description
Test data of 20 mRNA and 20 miRNA generated from simulation.

Format
A list containing the follow items:

- $V$  Outputs from mirsynergy
- $W, H$  Inputs used to generate $V$

Examples
load(system.file("extdata/toy_modules.RData", package="Mirsynergy"))
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