Package ‘ARNetMiT’

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Type Package

Title Association Rules based Gene Network of miRNA Targets

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Description This package infers gene-gene interactions from miRNA-target gene interactions dataset using association rules based algorithm (Eclat).

License GPL (>= 2.10)

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buildmiRNATargetTable  Create miRNA-targets table for gene network inference

Description

buildmiRNATargetTable Take miRNA target interactions in binary format then converts it into machine processable format.

Usage

buildmiRNATargetTable(dataset)

Arguments

dataset  miRNA-target gene interactions dataset. The first column must contain miRNAs and the second column must contain target genes.

Value

buildmiRNATargetTable returns miRNA-targets table

See Also

buildNetworkbyARules, visualizeNet, inferNet2BinaryFormat, createMirnaListFromDisease

Examples

data(prostateData)
table=buildmiRNATargetTable(prostateData)

buildNetworkbyARules  All in one function to infer network of miRNA targets using association rules

Description

buildNetworkbyARules takes a miRNA-target gene dataset as input and then infers gene co-expression networks using hash based association rules based algorithm.

Usage

buildNetworkbyARules(dataset, support, confidenceVal, supportType="rank", filtering="s")
createMirnaListfromDisease

Arguments

dataset miRNA-target gene interactions dataset. The first column must contain miRNAs and the second column must contain target genes.
support The support value of association rules based algorithm. Users can determine the support value when supportType parameter is selected as "rank"
confidenceVal The confidence value of association rules based algorithm.
supportType It enables users to choose the support value types. It can be "rank", "firstQuartile", "median", "thirdQuartile" and "mean". If this parameter is determined as "rank" then the support parameter become active.
filtering It is a filtering (or pruning) parameter to eliminate some weak associations to build robust GCN. This parameter can be "s" that indicates usage of only support value for interaction pruning or it can be "sc" that indicates usage of support and confidence value for interaction pruning.

Value

buildNetworkbyARules returns environment res that returns final interactions as $finalNetwork, the common miRNAs of gene-gene interactions are given as $geneMirna, the lift values of the interactions are given as $liftTable, the confidence values of the interactions are given as $confidenceTable, the support values of the interactions are given as $binaryInteractions and the filtered genes of the first elimination steps are given as $firstStep.

See Also

createMirnaListfromDisease, visualizeNet, inferNet2BinaryFormat, buildmiRNATargetTable

Examples

data(prostateData)

res <- buildNetworkbyARules(prostateData,0.3,0.5,supportType="rank", filtering="s")

net <- res$finalNetwork

createMirnaListfromDisease

To obtain disease related miRNA-target genes dataset

Description

createMirnaListfromDisease It returns the disease related miRNA-target genes dataset.

Usage

createMirnaListfromDisease(mirnaGeneData,diseaseMirnaData,disease,diseaseIndice)
Arguments

mirnaGeneData miRNAs-target genes dataset which consists of two columns. First column contains miRNAs and the second columns contains target genes.
diseaseMirnaData miRNAs-diseases dataset which consists of two columns. First column contains miRNAs and the second columns contains diseases.
disease It shows the disease list.
diseaseIndice It indicates the disease indice of the disease list. ex: the prostate cancer indice is 11 in disease list

Value

createMirnaListfromDisease Return the disease related miRNA-target genes dataset.

See Also

buildNetworkbyARules, visualizeNet, inferNet2BinaryFormat, buildmiRNATargetTable

Examples

data(mirnaGeneData)
data(diseaseMirnaData)
data(disease)

prostateData= createMirnaListfromDisease(mirnaGeneData,diseaseMirnaData,disease,11);

disease The disease list

Description

disease It returns the disease list

Usage

data( disease )

Arguments

disease It is a dataset that contains disease list

Details

It consists of unique 152 diseases that are obtained from miR2Disease dataset.
Value

disease returns the disease list

References


Examples

data(disease)

diseaseMirnaData miRNA-disease relations

Description

diseaseMirnaData Experimentally validated miRNA-disease relations

Usage

data( diseaseMirnaData )

Arguments

diseaseMirnaData

It is a dataset that contains experimentally validated miRNA-disease relations

Details

It consists of unique 2429 miRNA-disease relations. These relations are obtained from 477 unique miRNAs and 152 unique diseases. This dataset is derived from "miR2Disease".

Value

diseaseMirnaData returns experimentally validated miRNA-disease relations

References


Examples

data(diseaseMirnaData)
inferNet2BinaryFormat  

Convert inferred interactions to binary interaction format

Description

inferNet2BinaryFormat Convert inferred interactions to binary interaction format.

Usage

inferNet2BinaryFormat (net, genes, filtering="s")

Arguments

- **net**: It can be either n*n matrix of support values of interactions or n*n matrix of confidence values of interactions.
- **genes**: The data contains gene names.
- **filtering**: It is a filtering (or pruning) parameter to eliminate some weak associations to build robust GCN. This parameter can be "s" that indicates usage of only support value for interaction pruning or it can be "sc" that indicates usage of support and confidence value for interaction pruning.

Value

inferNet2BinaryFormat returns environment res that returns gene-gene interactions in binary format as res$interactions and it also returns indices of interactions as res$indices.

See Also

buildNetworkbyARules, visualizeNet, createMirnaListFromDisease, buildmiRNATargetTable

Examples

data(prostateData)

temp <- buildNetworkbyARules(prostateData, 0.3, 0.5, supportType="rank", filtering="s")
net <- temp$binaryInteractions;
genesis <- temp$firstStep;

res <- inferNet2BinaryFormat (net, genes, filtering="s")
binaryFormat <- res$interactions;
**mirnaGeneData**

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### Description

**mirnaGeneData** Experimentally validated miRNA-target gene interactions

### Usage

```r
data(mirnaGeneData)
```

### Arguments

- **mirnaGeneData**
  
  It is a dataset that contains experimentally validated miRNA-target gene interactions

### Details

mirnaGeneData consists of two validated miRNA-target gene datasets. First datasets is the release 6.1 of miRTarBase that contains the experimentally validated microRNA-target interactions database. It has 322,389 unique miRNA-target gene interactions from 410,620 miRNA-target gene interactions. The second data set is miR2Disease and it has 637 unique miRNA-target gene interactions from 805 miRNA-target gene interactions. The integrated data consists of experimentally validated 322,994 unique miRNA-target gene interactions.

### Value

**mirnaGeneData** returns miRNA-target gene interactions whose first column contains miRNAs and the second column contains target genes

### References


### Examples

```r
data(mirnaGeneData)
```
### prostateData

**The prostate cancer related miRNA-target gene dataset**

**Description**

prostateData It returns The prostate cancer related miRNA-target gene dataset

**Usage**

```r
data(prostateData)
```

**Arguments**

- **prostateData** The prostate cancer related miRNA-target gene dataset

**Details**

This dataset is derived from miRTarBase and miR2Disease datasets by using "createMirnaList-fromDisease" function.

**Value**

prostateData returns the prostate cancer related miRNA-target gene dataset

**References**


**Examples**

```r
data(prostateData)
```

### visualizeNet

**Plot the target gene network**

**Description**

visualizeNet Plot the target network

**Usage**

```r
visualizeNet(network)
```
Arguments

network It is the binary format network that has edge weights.

Value

visualizeNet It only plots the gene network and it returns void.

See Also

buildNetworkbyARules, inferNet2BinaryFormat, createMirnaListfromDisease, buildmiRNAATargetTable

Examples

data(prostateData)

temp <- buildNetworkbyARules(prostateData, 0.3, 0.5, supportType="rank", filtering="sc")
net <- temp$finalNetwork;

visualizeNet(net);
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