Package 'SpidermiR'

October 16, 2019

Type Package

Title SpidermiR: An R/Bioconductor package for integrative network analysis with miRNA data

Version 1.14.0

Date 02-04-2019

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Depends R (>= 3.0.0)

Imports networkD3, httr, igraph, utils, stats, miRNAtap, miRNAtap.db, AnnotationDbi, org.Hs.eg.db, ggplot2, gridExtra, gplots, grDevices, lattice, latticeExtra, visNetwork, TCGAbiolinks, gdata

Description The aims of SpidermiR are : i) facilitate the network open-access data retrieval from GeneMania data, ii) prepare the data using the appropriate gene nomenclature, iii) integration of miRNA data in a specific network, iv) provide different standard analyses and v) allow the user to visualize the results. In more detail, the package provides multiple methods for query, prepare and download network data (GeneMania), and the integration with validated and predicted miRNA data (mirWalk, miRTarBase, miRandola,Pharmaco-miR,DIANA, Miranda, PicTar and TargetScan) and the use of standard analysis (igraph) and visualization methods (networkD3).

License GPL (>= 3)

biocViews GeneRegulation, miRNA, Network

Suggests BiocStyle, knitr, rmarkdown, testthat, devtools, roxygen2

VignetteBuilder knitr

LazyData true

URL https://github.com/claudiacava/SpidermiR

BugReports https://github.com/claudiacava/SpidermiR/issues

RoxygenNote 6.1.1

NeedsCompilation no

git_url https://git.bioconductor.org/packages/SpidermiR

git_branch RELEASE_3_9

git_last_commit dd1a07c

git_last_commit_date 2019-05-02

Date/Publication 2019-10-15

R topics documented:

`SpidermiR` *SpidermiR allows you to Download data of samples from GeneMania*

Description

The functions you're likely to need from **SpidermiR** is `SpidermiR` Otherwise refer to the vignettes to see how to format the documentation.

SpidermiRanalyze_Community_detection
Find community detection

Description

SpidermiRanalyze_Community_detection try to find dense subgraphs in directed or undirected graphs, by optimizing some criteria.

Usage

```
SpidermiRanalyze_Community_detection(data, type)
```

Arguments

data	SpidermiRanalyze_mirna_network output or SpidermiRanalyze_mirna_gene_complnet
type	with the parameter type the user can choose the algorithm to calculate the community structure EB edge.betweenness.community FC fastgreedy.community WC walktrap.community SC spinglass.community LE leading.eigenvector.community LP label.propagation.community

Value

a list of clusters with their number of genes

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','hsa-miR-300'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
comm<-  SpidermiRanalyze_Community_detection(data=miRNA_cN,type="FC")
```

SpidermiRanalyze_Community_detection_bi
Community detection from biomarkers of interest

Description

SpidermiRanalyze_Community_detection_bi find the cluster with biomarkers of interest

Usage

```
SpidermiRanalyze_Community_detection_bi(data, BI)
```

Arguments

data	SpidermiRanalyze_Community_detection output
BI	a set of biomarkers of interest

Value

a list with the cluster for each biomarkers of interest

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','hsa-miR-300'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
comm<-  SpidermiRanalyze_Community_detection(data=miRNA_cN,type="FC")
biomark_of_interest<-c("hsa-let-7a","CDK","FOXO1","hsa-miR-27a")
mol<-SpidermiRanalyze_Community_detection_bi(data=comm,BI=biomark_of_interest)
```

SpidermiRanalyze_Community_detection_net

Find the network of community detection and direct biormarker

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Description

SpidermiRanalyze_direct_net find the direct interactions from a specific community

Usage

```
SpidermiRanalyze_Community_detection_net(data, comm_det, size)
```

Arguments

data	SpidermiRanalyze_mirna_network output or SpidermiRanalyze_mirna_gene_complnet
comm_det	SpidermiRanalyze_Community_detection
size	the index of community detection obtained from SpidermiRanalyze_Community_detection

Value

dataframe with the interatcions

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','hsa-miR-300'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
comm<-  SpidermiRanalyze_Community_detection(data=miRNA_cN,type="FC")
cd_net<-SpidermiRanalyze_Community_detection_net(data=miRNA_cN,comm_det=comm,size=1)
```

SpidermiRanalyze_degree_centrality

Ranking degree centrality genes

Description

SpidermiRanalyze_degree_centrality provides degree centrality, defined as the total number of direct neighbors for each gene.

Usage

```
SpidermiRanalyze_degree_centrality(data, cut = NULL)
```

Arguments

data	SpidermiRanalyze_mirna_network output or SpidermiRanalyze_mirna_gene_complnet
cut	parameter cut is able to cut off other genes

Value

dataframe with the ranked number of direct neighobors for each gene of the network

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','hsa-miR-300'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
biomark_of_interest<-c("hsa-let-7a","CDK","FOXO1","hsa-miR-27a")
top10_cent<-SpidermiRanalyze_degree_centrality(miRNA_cN)
```

SpidermiRanalyze_direct_net

Searching by biomarkers of interest with direct interaction

Description

SpidermiRanalyze_direct_net finds other biomarkers that are related to a set of biomarkers of interest (the input of user) with direct interations.

Usage

```
SpidermiRanalyze_direct_net(data, BI)
```

Arguments

data	SpidermiRanalyze_mirna_network output or SpidermiRanalyze_mirna_gene_complnet
BI	a set of biomarkers of interest

Value

dataframe with direct interaction of biomarkers of interest

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','FOXM1'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
biomark_of_interest<-c("hsa-let-7a","CDK","FOXO1","hsa-miR-27a")
GIdirect_net<-SpidermiRanalyze_direct_net(data=miRNA_cN,BI=biomark_of_interest)
```

SpidermiRanalyze_direct_subnetwork

Searching by biomarkers of interest with direct interaction by ONLY the nodes in BI

Description

SpidermiRanalyze_direct_subnetwork creates a sub network composed by ONLY the nodes in genes of interest and the edges between them

Usage

```
SpidermiRanalyze_direct_subnetwork(data, BI)
```

Arguments

data	SpidermiRanalyze_mirna_network output or SpidermiRanalyze_mirna_gene_complnet
BI	a set of biomarkers of interest

Value

dataframe with direct interaction of biomarkers of interest

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','FOXM1'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
biomark_of_interest<-c("hsa-let-7a","CDK","FOXO1","hsa-miR-27a")
subnet<-SpidermiRanalyze_direct_subnetwork(data=miRNA_cN,BI=biomark_of_interest)
```

SpidermiRanalyze_mirnanet_pharm

Integration of pharmacomiR in the network

Description

SpidermiRanalyze_mirnanet_pharm integrates both miRNA targeting of the gene and the gene-drug interaction from PharmacomiR database in the network

Usage

```
SpidermiRanalyze_mirnanet_pharm(mir_ph, net)
```

Arguments

mir_ph	SpidermiRdownload_pharmacomir output
net	a network data (e.g. SpidermiRanalyze_mirna_network or SpidermiRanalyze_mirna_gene_complnet output)

Value

a dataframe with the integation of network and pharmacomiR data

Examples

```
mir_p <-data.frame(gA=c('hsa-let-7a','CASP3'),gB=c('CASP3','paclitaxel'),stringsAsFactors=FALSE)
net_p <-data.frame(gA=c('hsa-let-7a','hsa-miR-300'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
mol<-SpidermiRanalyze_mirnanet_pharm(mir_ph=mir_p,net=net_p)
```

SpidermiRanalyze_subnetwork_neigh

Searching by biomarkers of interest and all the edges among this bunch of nodes

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Description

SpidermiRanalyze_subnetwork_neigh create a sub network composed by the nodes in BI and, if some of them are connected to other nodes (even if not in BI), take also them (include all the edges among this bunch of nodes).

Usage

```
SpidermiRanalyze_subnetwork_neigh(data, BI)
```

Arguments

data	SpidermiRanalyze_mirna_network output or SpidermiRanalyze_mirna_gene_complnet
BI	a set of biomarkers of interest

Value

dataframe with interactions

Examples

```
miRNA_cN <-data.frame(gA=c('hsa-let-7a','hsa-miR-300'),gB=c('FOXM1','KPNA4'),stringsAsFactors=FALSE)
biomark_of_interest<-c("hsa-let-7a","CDK","FOXO1","hsa-miR-27a")
GIdirect_net_neigh<-SpidermiRanalyze_subnetwork_neigh(data=miRNA_cN,BI=biomark_of_interest)
```

SpidermiRdownload_miRNAextra_cir
Download miRNA validated database

Description

SpidermiRdownload_miRNAprediction will download miRNA validated target

Usage

```
SpidermiRdownload_miRNAextra_cir(miRNAextra_cir)
```

Arguments

miRNAextra_cir	parameter

Value

a dataframe with miRNA target validated interactions

Examples

```
list<-SpidermiRdownload_miRNAextra_cir(miRNAextra_cir)
```

SpidermiRdownload_miRNAprediction
Download miRNA predicted database

Description

SpidermiRdownload_miRNAprediction will download miRNA predicted target

Usage

```
SpidermiRdownload_miRNAprediction(mirna_list)
```

Arguments

mirna_list	miRNA list of interest

Value

a dataframe with miRNA target validated interactions

Examples

```
mirna<-c('hsa-miR-567')
list<-SpidermiRdownload_miRNAprediction(mirna_list=mirna)
```

SpidermiRdownload_miRNAvalidate *Download miRNA validated database*

Description

SpidermiRdownload_miRNAprediction will download miRNA validated target

Usage

```
SpidermiRdownload_miRNAvalidate(validated)
```

Arguments

validated	parameter

Value

a dataframe with miRNA target validated interactions

Examples

```
list<-SpidermiRdownload_miRNAvalidate(validated)
```

SpidermiRdownload_net *Download the network from GeneMania.*

Description

SpidermiRdownload_net function will download the data

Usage

```
SpidermiRdownload_net(data)
```

Arguments

data	The SpidermiRquery_spec_networks output

Value

Download GeneMania network

Examples

```
org<-SpidermiRquery_species(species)
net_shar_prot<-SpidermiRquery_spec_networks(organismID = org[9,],
network = "SHpd")
out_net<-SpidermiRdownload_net(data=net_shar_prot)
```

SpidermiRdownload_pharmacomir *Download both miRNA target and the gene-drug interaction from PharmacomiR database*

Description

SpidermiRdownload_pharmacomir will download miRNA Pharmacogenomic data

Usage

```
SpidermiRdownload_pharmacomir(pharmacomir)
```

Arguments

pharmacomir	variable

Value

a dataframe with gene-drug, and miR-gene associations

Examples

```
mir_pharmaco<-SpidermiRdownload_pharmacomir(pharmacomir=pharmacomir)
```

SpidermiRprepare_NET *Prepare matrix of gene network from Genamania with Ensembl Gene ID, and gene symbols*

Description

The user in this step obtained a gene network matrix with the integration of gene symbols ID.

Usage

```
SpidermiRprepare_NET(organismID, data)
```

Arguments

organismID	is the index of SpidermiRquery_spec_networks output
data	is the output of function SpidermiRdownload_net

Value

A list of tables.

Examples

```
org<-SpidermiRquery_species(species)
net_shar_prot<-SpidermiRquery_spec_networks(organismID = org[9,],
network = "SHpd")
out_net<-SpidermiRdownload_net(data=net_shar_prot)
geneSymb_net<-SpidermiRprepare_NET(organismID = org[9,],
                                   data = out_net)
```

SpidermiRquery_disease

Visualize disease categories

Description

The user can visualize the disease supported by SpidermiR

Usage

```
SpidermiRquery_disease(diseaseID)
```

Arguments

diseaseID	variable name

Value

a list of disease.

Examples

```
disease<-SpidermiRquery_disease(diseaseID)
```

SpidermiRquery_networks_type

Network categories

Description

The user can visualize the network types supported by GeneMania for a specific specie using SpidermiRquery_networks_type

Usage

```
SpidermiRquery_networks_type(organismID)
```

Arguments

organismID	describes index of a specific specie obtained by SpidermiRquery_species output

Value

a list of network categories in a specie indicated.

Examples

```
org<-SpidermiRquery_species(species)
net_type<-SpidermiRquery_networks_type(organismID=org[9,])
```

SpidermiRquery_species

Searching by network species

Description

The user can visualize the species supported by GeneMania, using the function SpidermiRquery_species .

Usage

```
SpidermiRquery_species(species)
```

Arguments

species	a variable parameter

Value

table of species

Examples

```
org<-SpidermiRquery_species(species)
```

SpidermiRquery_spec_networks

Searching by network categories

Description

The user can visualize the database or reference where the information came from

Usage

```
SpidermiRquery_spec_networks(organismID, network)
```

Arguments

organismID	describes index of a specific specie obtained by SpidermiRquery_species output
network	The network type the user is interested in. Example:

COexp	Co-expression
PHint	Physical_interactions
COloc	Co-localization
GENint	Genetic_interactions
PATH	Pathway
SHpd	Shared_protein_domains
pred	Predicted

Value

a list of the database or reference where the information came from.

Examples

```
org<-SpidermiRquery_species(species)
net_shar_prot<-SpidermiRquery_spec_networks(organismID = org[9,],
                                            network = "SHpd")
```

`SpidermiRvisualize_3Dbarplot`
plots the 3D barplot

Description

It shows a barplot of 5 networks given by the user with a summary representation of number of nodes, edges, and miRNAs (log values)

Usage

```
SpidermiRvisualize_3Dbarplot(Edges_1net, Edges_2net, Edges_3net,
  Edges_4net, Edges_5net, NODES_1net, NODES_2net, NODES_3net, NODES_4net,
  NODES_5net, nmiRNAs_1net, nmiRNAs_2net, nmiRNAs_3net, nmiRNAs_4net,
  nmiRNAs_5net)
```

Arguments

`Edges_1net`	int number of edges in the 1 net
`Edges_2net`	int number of edges in the 2 net
`Edges_3net`	int number of edges in the 3 net
`Edges_4net`	int number of edges in the 4 net
`Edges_5net`	int number of edges in the 5 net
`NODES_1net`	int number of nodes in the 1 net
`NODES_2net`	int number of nodes in the 2 net
`NODES_3net`	int number of nodes in the 3 net
`NODES_4net`	int number of nodes in the 4 net
`NODES_5net`	int number of nodes in the 5 net
`nmiRNAs_1net`	int number of miRNAs in the 1 net

nmiRNAs_2net	int number of miRNAs in the 2 net
nmiRNAs_3net	int number of miRNAs in the 3 net
nmiRNAs_4net	int number of miRNAs in the 4 net
nmiRNAs_5net	int number of miRNAs in the 5 net

Value

barplot

Examples

```
SpidermiRvisualize_3Dbarplot(Edges_1net=1041003,Edges_2net=100016,Edges_3net=3008,
Edges_4net=1493,Edges_5net=1598,NODES_1net=16502,NODES_2net=13338,NODES_3net=1429,NODES_4net=675,
NODES_5net=712,nmiRNAs_1net=0,nmiRNAs_2net=74,nmiRNAs_3net=0,nmiRNAs_4net=0,nmiRNAs_5net=37)
```

SpidermiRvisualize_adj_matrix

plots the adjacency matrix of the network

Description

It shows a plot OF the adjacency matrix of the network

Usage

```
SpidermiRvisualize_adj_matrix(data)
```

Arguments

data	The input data is a network

Value

plot

Examples

```
cd<-data.frame(gA=c('hsa-let-7a','hsa-miR-141'),gB=c('FOXM1','CDK'),stringsAsFactors=FALSE)
SpidermiRvisualize_adj_matrix(data=cd)
```

SpidermiRvisualize_BI *Visualize results obtained by SpidermiR analysis starting form a set of biomarker of interest*

Description

Visualize miRNA-target interaction and miRNA-target-gene starting from a set of biomarker of interest

Usage

```
SpidermiRvisualize_BI(data, BI)
```

Arguments

data	The input data is a dataframe containing network data.
BI	a set of biomarkers of interest

Value

3D graphic

Examples

```
miRNA_cNET <-data.frame(gA=c('hsa-let-7a','hsa-miR-141'),gB=c('FOXM1','CDK'),stringsAsFactors=FALSE)
biomark_of_interest<-c("hsa-let-7a","CDK","FOXO1","hsa-miR-27a")
SpidermiRvisualize_BI(data=miRNA_cNET,BI=biomark_of_interest)
```

SpidermiRvisualize_degree_dist *plots the degree distribution of the network*

Description

It shows a plot of the degree distribution of the network

Usage

```
SpidermiRvisualize_degree_dist(data)
```

Arguments

data	The input data is a network

Value

plot

Examples

```
cd<-data.frame(gA=c('hsa-let-7a','hsa-miR-141'),gB=c('FOXM1','CDK'),stringsAsFactors=FALSE)
SpidermiRvisualize_degree_dist(data=cd)
```

SpidermiRvisualize_direction

Visualize results obtained by SpidermiR analysis with the direction of the interaction (pharmaco-gene and miRNA-gene)

Description

Visualize the network

Usage

```
SpidermiRvisualize_direction(data)
```

Arguments

data	The input data is a dataframe containing network data.

Value

3D graphic

Examples

```
miRNA_cNET <-data.frame(gA=c('hsa-let-7a','hsa-miR-141'),gB=c('FOXM1','CDK'),stringsAsFactors=FALSE)
SpidermiRvisualize_direction(data=miRNA_cNET)
```

SpidermiRvisualize_mirnanet

Visualize results obtained by SpidermiR analysis

Description

Visualize the network

Usage

```
SpidermiRvisualize_mirnanet(data)
```

Arguments

data	The input data is a dataframe containing network data.

Value

3D graphic

Examples

```
miRNA_cNET <-data.frame(gA=c('hsa-let-7a','hsa-miR-141'),gB=c('FOXM1','CDK'),stringsAsFactors=FALSE)
SpidermiRvisualize_mirnanet(data=miRNA_cNET)
```

SpidermiRvisualize_plot_target *Visualize results obtained by SpidermiRanalyze_mirna_network*

Description

It shows a plot with miRNAs and the number of their targets in the network

Usage

```
SpidermiRvisualize_plot_target(data)
```

Arguments

data	The input data is a dataframe containing miRNA network data (e.g. output of SpidermiRanalyze_mirna_network.

Value

plot

Examples

```
cd<-data.frame(gA=c('hsa-let-7a','hsa-miR-141'),gB=c('FOXM1','CDK'),stringsAsFactors=FALSE)
SpidermiRvisualize_plot_target(data=cd)
```

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