

Package ‘SpidermiR’

October 18, 2017

Type Package

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

Version 1.7.4

Date 09-20-2017

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Depends R (>= 3.0.0)

Imports networkD3, httr, igraph, utils, stats, miRNAAtap, miRNAAtap.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, miR2Disease, miRTar, 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 6.0.1

NeedsCompilation no

R topics documented:

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`Case_Study1_loading_1_network`*Loading 1 network of shared protein domain*

Description

`Case_Study1_loading_1_network` loads shared protein domain in HomoSapiens

Usage

```
Case_Study1_loading_1_network(species)
```

Arguments

`species` `variable`

Value

dataframe with interactions

Examples

```
## Not run:  
a<-Case_Study1_loading_1_network(species)  
  
## End(Not run)
```

`Case_Study1_loading_2_network`*Loading 2 network of shared protein domain*

Description

`Case_Study1_loading_2_network` loads shared protein domain in HomoSapiens including only miRNAs already found deregulated in PC,

Usage

```
Case_Study1_loading_2_network(data)
```

Arguments

`data` the output of `Case_Study1_loading_1_network`

Value

dataframe with selected interactions

Examples

```
## Not run:  
b<-Case_Study1_loading_2_network(data=a)  
  
## End(Not run)
```

Case_Study1_loading_3_network

Loading 3 network of shared protein domain

Description

Case_Study1_loading_3_network loads shared protein domain in HomoSapiens including only the DEGs with a direct interaction among them

Usage

```
Case_Study1_loading_3_network(data, dataFilt, dataClin)
```

Arguments

| | |
|----------|---|
| data | the output of Case_Study1_loading_2_network |
| dataFilt | TCGA matrix |
| dataClin | clinical data matrix |

Value

dataframe with selected interactions

Examples

```
## Not run:  
c<-Case_Study1_loading_3_network(data=b,dataFilt=dataFilt,dataClin=dataClin)  
  
## End(Not run)
```

Case_Study1_loading_4_network

Loading 4 network of shared protein domain

Description

Case_Study1_loading_4_network loads network community with the higher number of elements in the 3 network

Usage

```
Case_Study1_loading_4_network(TERZA_NET)
```

Arguments

TERZA_NET the output of Case_Study1_loading_3_network

Value

dataframe with selected interactions

Examples

```
## Not run:  
d<-Case_Study1_loading_4_network(TERZA_NET=c)  
  
## End(Not run)
```

Case_Study2_loading_1_network

Loading 1 network of Protein Interactions (PI)

Description

Case_Study2_loading_1_network loads PI in HomoSapiens

Usage

```
Case_Study2_loading_1_network(species)
```

Arguments

species variable

Value

dataframe with interactions

Examples

```
## Not run:  
a2<-Case_Study2_loading_1_network(species)  
## End(Not run)
```

Case_Study2_loading_2_network

Loading 2 network of Protein Interactions (PI) with miRNAs

Description

Case_Study2_loading_2_network loads PI in HomoSapiens with miRNAs already found as deregulated in BC (only interaction miRNA-gene)

Usage

```
Case_Study2_loading_2_network(data)
```

Arguments

data output of Case_Study2_loading_1_network

Value

dataframe with interactions

Examples

```
## Not run:
b2<-Case_Study2_loading_2_network(data=a2)

## End(Not run)
```

Case_Study2_loading_3_network

Loading 3 network of Protein Interactions (PI) with miRNAs

Description

Case_Study2_loading_2_network loads PI in HomoSapiens with miRNAs already found as deregulated in BC (only interaction miRNA-gene)

Usage

```
Case_Study2_loading_3_network(sdas, miRNA_NET)
```

Arguments

sdas output of Case_Study2_loading_1_network
miRNA_NET output of Case_Study2_loading_2_network

Value

dataframe with interactions

Examples

```
## Not run:
c2<-Case_Study2_loading_3_network(sdas=a2,miRNA_NET=b2)

## End(Not run)
```

 SpidermiR

Download data

Description

SpidermiR allows you to Download data of samples from GeneMania

Details

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('FOXO1', 'KPN4'), 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 biomarker

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('FOXO1', '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 neighbors for each gene of the network

Examples

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

SpidermiRanalyze_DEnetworkTCGA
Integration with TCGA data in order to obtain a network of differentially expressed (DE) genes or miRNAs.

Description

SpidermiRanalyze_DEnetworkTCGA integrates the information of differential analysis of TCGA data in the network. The final result will be a network with only DE genes or miRNAs depending whether the user chooses to mRNA or miRNA TCGA data.

Usage

```
SpidermiRanalyze_DEnetworkTCGA(data, TCGAmatrix, tumour, normal)
```

Arguments

| | |
|------------|---|
| data | network data (e.g. shared protein domains, co-expression,...) |
| TCGAmatrix | gene or miRNA expression matrix |
| tumour | barcode TCGA tumour data |
| normal | barcode TCGA normal data |

Value

a network miRNA-gene differentially expressed as calculated by TCGAbiolinks package. The user can select the samples and cancer type from TCGA portal.

Examples

```
miRNA_cN <-data.frame(gA=c('IGFL3', 'GABRA1'), gB=c('IGFL2', 'KRT13'), stringsAsFactors=FALSE)
tumour<-c("TCGA-E9-A1RD-01A", "TCGA-E9-A1RC-01A")
normal<-c("TCGA-BH-A18P-11A", "TCGA-BH-A18L-11A")
de_int<-SpidermiRanalyze_DEnetworkTCGA(data=miRNA_cN,
                                       TCGAmatrix=Data_CANCER_normUQ_filt,
                                       tumour,
                                       normal
                                       )
```

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 interactions.

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', 'FOXO1'),gB=c('FOXO1', '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 integration 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('FOXO1', 'KPNA4'),stringsAsFactors=FALSE)
mol<-SpidermiRanalyze_mirnanet_pharm(mir_ph=mir_p,net=net_p)
```

SpidermiRanalyze_mirna_gene_complnet

Integration of microRNA target gene networks.

Description

SpidermiRanalyze_mirna_gene_complnet creates a data frame with miRNA target gene interaction. The user can filter the search by disease.

Usage

```
SpidermiRanalyze_mirna_gene_complnet(data, miR_trg, mirna_t = NULL,
  disease = NULL)
```

Arguments

| | |
|---------|---|
| data | SpidermiRprepare_NET output |
| miR_trg | a parameter to indicate miRNA target database used. The user can use: 1) validated database (val) or 2) predicted database (pred) |
| mirna_t | a list given by the user with miRNA list of interest |
| disease | miRNA target gene interaction can be filtered by disease using the parameters obtained from SpidermiRquery_disease |

Value

dataframe with miRNA target gene interaction data

Examples

```
GS_net <- data.frame(gA=c('SMAD', 'MYC'),gB=c('FOXO1', 'KRAS'),stringsAsFactors=FALSE)
miRNA_cNT<-SpidermiRanalyze_mirna_gene_complnet(data=GS_net,disease="prostate cancer",miR_trg="val")
```

 SpidermiRanalyze_mirna_network

Integration of microRNA target networks.

Description

SpidermiRanalyze_mirna_network creates a data frame with miRNA gene interaction. The user can filter the search by disease.

Usage

```
SpidermiRanalyze_mirna_network(data, miR_trg, mirna_t = NULL,
  disease = NULL)
```

Arguments

| | |
|---------|---|
| data | SpidermiRprepare_NET output |
| miR_trg | a parameter to indicate miRNA target database used. The user can use: 1) validated database (val) or 2) predicted database (pred) |
| mirna_t | a list given by the user with miRNA list of interest |
| disease | miRNA gene interaction can be filtered by disease using the parameters obtained from SpidermiRquery_disease |

Value

dataframe with miRNA gene interaction data

Examples

```
GS_net <- data.frame(gA=c('SMAD', 'MYC'), gB=c('FOXMI1', 'KRAS'), stringsAsFactors=FALSE)
miRNA_NET<-SpidermiRanalyze_mirna_network(data=GS_net, disease="prostate cancer", miR_trg="val")
```

 SpidermiRanalyze_subnetwork_neigh

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

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('FOXO1', '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_miRNALNC_miRNA

Download microRNAs binding sites on long non coding RNA from lncRNome database

Description

SpidermiRdownload_miRNALNC_miRNA-RNA will download microRNAs binding sites on long non coding RNA

Usage

```
SpidermiRdownload_miRNALNC_miRNA(miRNALNC_miRNA)
```

Arguments

miRNALNC_miRNA parameter

Value

a dataframe with miRNALNC_miRNA

Examples

```
list_LNC_miRNA<-SpidermiRdownload_miRNALNC_miRNA(miRNALNC_miRNA)
```

SpidermiRdownload_miRNALNC_RNA

Download Long Non-Coding RNA (LNC-RNA) from lncRNome database

Description

SpidermiRdownload_LNC-RNA will download LNC-RNA

Usage

```
SpidermiRdownload_miRNALNC_RNA(miRNALNC_RNA)
```

Arguments

miRNALNC_RNA parameter

Value

a dataframe with miRNALNC_RNA

Examples

```
list<-SpidermiRdownload_miRNALNC_RNA(miRNALNC_RNA)
```

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 from 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('FOXO1','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('FOXO1','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

| | |
|-------------------|--|
| <code>data</code> | The input data is a dataframe containing miRNA network data (e.g. output of <code>SpidermiRanalyze_mirna_network</code>). |
|-------------------|--|

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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