

Package ‘SpidermiR’

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Type Package

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

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Depends R (>= 3.0.0)

Imports httr, igraph, utils, stats, miRNAatap, miRNAatap.db,
AnnotationDbi, org.Hs.eg.db, 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 (mir-Walk, miRTarBase, miRandola, Miranda, PicTar and TargetScan). Furthermore, we also present a statistical test to identify pharmaco-mir relationships using the gene-drug interactions derived by DGIdb and MATADOR database.

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biocViews GeneRegulation, miRNA, Network

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

VignetteBuilder knitr

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

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

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R topics documented:

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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_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', 'FOXO1'), gB=c('FOXO1', 'KPNA4'), stringsAsFactors=FALSE)
biomark_of_interest<-c("hsa-let-7a", "CDK", "FOXO1", "hsa-miR-27a")
GI_direct_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_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_drug_gene

Download drug-gene interactions in DGldb

Description

SpidermiRdownload_drug_gene will download drug gene interactions

Usage

```
SpidermiRdownload_drug_gene(drug_gene)
```

Arguments

drug_gene parameter

Value

a dataframe with miRNA target validated interactions

Examples

```
drug_genetarget<-SpidermiRdownload_drug_gene(drug_gene)
```

SpidermiRdownload_miRNAPrediction

Download human 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_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)
```

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[,])
```

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)
```


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