Package ‘prioGene’

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Type Package

Title Candidate Gene Prioritization for Non-Communicable Diseases Based on Functional Information

Version 1.0.1

biocViews GraphAndNetwork, FunctionalGenomics, Genetics, Network

Description In gene sequencing methods, the topological features of protein-protein interaction (PPI) networks are often used, such as ToppNet <https://toppgene.cchmc.org>. In this study, a candidate gene prioritization method was proposed for non-communicable diseases considering disease risks transferred between genes in weighted disease PPI networks with weights for nodes and edges based on functional information.

Depends R (>= 3.6.0)

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Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Imports AnnotationDbi, org.Hs.eg.db

NeedsCompilation no

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R topics documented:

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deal_net

Title deal with network

Usage

deal_net(net, dise_gene)

Arguments

net a network
dise_gene a matrix with one column of genes

Value

a matrix

Examples

deal_net(net, dise_gene)
### dise_gene

- **Description**: A vector of disease related genes
- **Usage**: `dise_gene`
- **Format**: A matrix with 79 rows and 1 column

### edge_weight

- **Description**: Weights of edges of a net
- **Usage**: `edge_weight`
- **Format**: A matrix with 25 rows and 3 columns

### genes_mat

- **Description**: A one-to-many matrix of GO term and gene
- **Usage**: `genes_mat`
- **Format**: A matrix with 45 rows and 3 columns
get_gene_mat

Description
Get a one-to-many matrix of gene and GO term

Usage
get_gene_mat(net_disease)

Arguments
net_disease  a disease related network, matrix

Value
a matrix

get_edge_weight

Description
Title weight edge

Usage
get_edge_weight(net_disease_term, terms_mat)

Arguments
net_disease_term  GO terms for each pair of nodes in the network
terms_mat  result of get_term_mat()

Value
a matrix

Examples
get_edge_weight(net_disease_term, terms_mat)

details
the third column is the number of go terms
get_neighbor

Examples
get_gene_mat(net_disease)

description
Title get neighbor of a node

Usage
get_neighbor(node, net)

Arguments
node a gene
net a network

Value
a vector of gene

get_net_disease_term

Title Get the GO terms for each pair of nodes in the network

Description
Title Get the GO terms for each pair of nodes in the network

Usage
get_net_disease_term(genes_mat, net_disease)

Arguments
genes_mat a one-to-many matrix of GO term and gene
net_disease a disease related network, matrix

Value
a matrix

Examples
get_net_disease_term(genes_mat, net_disease)
get_node_weight

**Title**: weight node

**Description**

Title weight node

**Usage**

get_node_weight(genes_mat)

**Arguments**

- **genes_mat**: a one-to-many matrix of GO term and gene

**Value**

a matrix

**Examples**

get_node_weight(genes_mat)

---

get_Q

**Title**: get the disease risk transition probability matrix

**Description**

Title get the disease risk transition probability matrix

**Usage**

get_Q(node_weight, net_disease_term)

**Arguments**

- **node_weight**: a matrix, genes and their weights
- **net_disease_term**: GO terms for each pair of nodes in the network

**Value**

a matrix
*get_R*

**Title** get the final genetic disease risk scores

**Description**

Title get the final genetic disease risk scores

**Usage**

\[
\text{get}_R(\text{node\_weight}, \text{net\_disease\_term}, \text{bet}, R_0, \text{threshold} = 10^{-9})
\]

**Arguments**

- node\_weight: a matrix, genes and their weights
- net\_disease\_term: GO terms for each pair of nodes in the network
- bet: a parameter to measure the importance of genes and interactions
- R\_0: the vector of initial disease risk scores for all genes
- threshold: a threshold for terminating iterations

**Value**

a matrix

**Examples**

```r
net\_disease <- deal\_net(net, dise\_gene)
gen\_mat <- get\_gene\_mat(net\_disease)
node\_weight <- get\_node\_weight(gen\_mat)
net\_disease\_term <- get\_net\_disease\_term(gen\_mat, net\_disease)
R\_0 <- get\_R\_0(dise\_gene, node\_weight, f=1)
result <- get\_R(node\_weight, net\_disease\_term, bet = 0.5, R\_0 = R\_0, threshold = 10^{-9})
```

*get_R\_0*

**Title** get the vector of initial disease risk scores for all genes

**Description**

Title get the vector of initial disease risk scores for all genes

**Usage**

\[
\text{get}_R(0(disease\_gene, node\_weight, f = 1)
\]

**Examples**

```r
net\_disease <- deal\_net(net, dise\_gene)
gen\_mat <- get\_gene\_mat(net\_disease)
node\_weight <- get\_node\_weight(gen\_mat)
net\_disease\_term <- get\_net\_disease\_term(gen\_mat, net\_disease)
R\_0 <- get\_R\_0(dise\_gene, node\_weight, f=1)
result <- get\_R(node\_weight, net\_disease\_term, bet = 0.5, R\_0 = R\_0, threshold = 10^{-9})
```
get_term_mat

Arguments

disease_gene  a matrix of a column of genes
node_weight   a matrix, genes and their weights
f             an integer parameter to measure the significance of disease genes and candidate genes

Value

a vector

Examples

get_R_0(dise_gene,node_weight,1)

get_term_mat

Get a one-to-many matrix of GO term and gene

Description

Get a one-to-many matrix of GO term and gene

Usage

get_term_mat(net_disease)

Arguments

net_disease   a disease related network, matrix

Value

a matrix

Examples

get_term_mat(net_disease)
Description
Title

Usage
get_W(node1, node2)

Arguments
node1 a gene
tnode2 a gene

Value
a number

metabolic_net a matrix, Human metabolic network

Description
a matrix, Human metabolic network

Usage
metabolic_net

Format
A matrix with 589,199 rows and 2 columns
### net

**Description**

A network of genes

**Usage**

`net`

**Format**

A matrix with 2000 rows and 2 columns

### net_disease

**Description**

A network of disease related genes

**Usage**

`net_disease`

**Format**

A matrix with 26 rows and 2 columns

### net_disease_term

**Description**

GO terms for each pair of nodes in the network

**Usage**

`net_disease_term`

**Format**

A matrix with 25 rows and 4 columns
**node_weight**

Details
- the third column is the go terms, the fourth column is the number of go terms
- the fourth column is the number of go terms

| node_weight | a matrix, genes and their weights |

Description
- a matrix, genes and their weights

Usage
- node_weight

Format
- A matrix with 45 rows and 2 columns

---

**R_0**

Description
- the vector of initial disease risk scores for all genes

Usage
- R_0

Format
- A vector of 45 number

---

**terms_mat**

Description
- a one-to-many matrix of GO term and gene

Usage
- terms_mat

Format
- A matrix with 1172 rows and 3 columns
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