

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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deal_net	<i>Title deal with network</i>
----------	--------------------------------

Description

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	<i>a vector of disease related genes</i>
-----------	--

Description

some genes

Usage

dise_gene

Format

A matrix with 79 rows and 1 column

edge_weight	<i>weights of edges of a net</i>
-------------	----------------------------------

Description

the first two columns are a net, and third column is their weight

Usage

edge_weight

Format

A matrix with 25 rows and 3 columns

genes_mat	<i>a one-to-many matrix of GO term and gene</i>
-----------	---

Description

the first column is the gene symbol, the second column is the go terms

Usage

genes_mat

Format

A matrix with 45 rows and 3 columns

Details

the third column is the number of go terms

get_edge_weight	<i>Title weight edge</i>
-----------------	--------------------------

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)
```

get_gene_mat	<i>Get a one-to-many matrix of gene and GO term</i>
--------------	---

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

Examples

```
get_gene_mat(net_disease)
```

get_neighbor *Title get neighbor of a node*

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	<i>Title weight node</i>
-----------------	--------------------------

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	<i>Title get the disease risk transition probability matrix</i>
-------	---

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

```
get_R(node_weight, net_disease_term, bet, R_0, 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

```
net_disease <- deal_net(net,dise_gene)
genes_mat <- get_gene_mat(net_disease)
node_weight <- get_node_weight(genes_mat)
net_disease_term <- get_net_disease_term(genes_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

```
get_R_0(disease_gene, node_weight, f = 1)
```

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)
```

get_W	<i>Title</i>
-------	--------------

Description

Title

Usage

```
get_W(node1, node2)
```

Arguments

node1	a gene
node2	a gene

Value

a number

metabolic_net	<i>a matrix, Human metabolic network</i>
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Description

a matrix, Human metabolic network

Usage

```
metabolic_net
```

Format

A matrix with 589,199 rows and 2 columns

net	<i>a network of genes</i>
-----	---------------------------

Description

a network of genes

Usage

net

Format

A matrix with 2000 rows and 2 columns

net_disease	<i>a network of disease related genes</i>
-------------	---

Description

a network of disease related genes

Usage

net_disease

Format

A matrix with 26 rows and 2 columns

net_disease_term	<i>GO terms for each pair of nodes in the network</i>
------------------	---

Description

the first two columns is the network

Usage

net_disease_term

Format

A matrix with 25 rows and 4 columns

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	<i>a matrix, genes and their weights</i>
-------------	--

Description

a matrix, genes and their weights

Usage

node_weight

Format

A matrix with 45 rows and 2 columns

R_0	<i>the vector of initial disease risk scores for all genes</i>
-----	--

Description

the vector of initial disease risk scores for all genes

Usage

R_0

Format

A vector of 45 number

terms_mat	<i>a matrix, GO terms and GO genes</i>
-----------	--

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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