

# Package ‘prioGene’

July 23, 2025

**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)

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**Imports** AnnotationDbi, org.Hs.eg.db

**NeedsCompilation** no

**Author** Erqiang Hu [aut, cre]

**Maintainer** Erqiang Hu <13766876214@163.com>

**Repository** CRAN

**Date/Publication** 2020-02-01 17:00:02 UTC

## Contents

|                     |   |
|---------------------|---|
| deal_net . . . . .  | 2 |
| dise_gene . . . . . | 3 |

|                                |           |
|--------------------------------|-----------|
| edge_weight . . . . .          | 3         |
| genes_mat . . . . .            | 3         |
| get_edge_weight . . . . .      | 4         |
| get_gene_mat . . . . .         | 4         |
| get_neighbor . . . . .         | 5         |
| get_net_disease_term . . . . . | 5         |
| get_node_weight . . . . .      | 6         |
| get_Q . . . . .                | 6         |
| get_R . . . . .                | 7         |
| get_R_0 . . . . .              | 7         |
| get_term_mat . . . . .         | 8         |
| get_W . . . . .                | 9         |
| metabolic_net . . . . .        | 9         |
| net . . . . .                  | 10        |
| net_disease . . . . .          | 10        |
| net_disease_term . . . . .     | 10        |
| node_weight . . . . .          | 11        |
| R_0 . . . . .                  | 11        |
| terms_mat . . . . .            | 11        |
| <b>Index</b>                   | <b>12</b> |

---

|          |                                |
|----------|--------------------------------|
| 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 | <i>Title get neighbor of a node</i> |
|--------------|-------------------------------------|

---

**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 | <i>Title Get the GO terms for each pair of nodes in the network</i> |
|----------------------|---------------------------------------------------------------------|

---

**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 | <i>Title get the final genetic disease risk scores</i> |
|-------|--------------------------------------------------------|

---

**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 | <i>Title get the vector of initial disease risk scores for all genes</i> |
|---------|--------------------------------------------------------------------------|

---

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

---

**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> |
|---------------|------------------------------------------|

---

**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

# Index

## \* datasets

- dise\_gene, 3
- edge\_weight, 3
- genes\_mat, 3
- metabolic\_net, 9
- net, 10
- net\_disease, 10
- net\_disease\_term, 10
- node\_weight, 11
- R\_0, 11
- terms\_mat, 11

- deal\_net, 2
- dise\_gene, 3

- edge\_weight, 3

- genes\_mat, 3
- get\_edge\_weight, 4
- get\_gene\_mat, 4
- get\_neighbor, 5
- get\_net\_disease\_term, 5
- get\_node\_weight, 6
- get\_Q, 6
- get\_R, 7
- get\_R\_0, 7
- get\_term\_mat, 8
- get\_W, 9

- metabolic\_net, 9

- net, 10
- net\_disease, 10
- net\_disease\_term, 10
- node\_weight, 11

- R\_0, 11

- terms\_mat, 11