

# Package: prioGene (via r-universe)

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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)

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

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**VignetteBuilder** knitr

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**NeedsCompilation** no

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deal_net	<i>Title deal with network</i>
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### 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)
```

---

<code>get_neighbor</code>	<i>Title get neighbor of a node</i>
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---

**Description**

Title get neighbor of a node

**Usage**

```
get_neighbor(node, net)
```

**Arguments**

<code>node</code>	a gene
<code>net</code>	a network

**Value**

a vector of gene

---

<code>get_net_disease_term</code>	<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**

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

---

**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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