

Package ‘LncPriCNet’

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Type Package

Title Prioritizing Candidate LncRNAs Based on a Composite Multi-Level Network

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Description

Prioritizing the disease lncRNAs based on random walking on a composite Multi-level network.

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LncPriNet-package *Description of LncPriNet Package*

Description

A R platform to prioritize candidate disease lncRNAs by LncPriNet method which extend random walk analysis on multi-omics network.

Introduction

The main goal of LncPriNet is to prioritize candidate disease lncRNAs by LncPriNet method.

Author(s)

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DiseaseInfList *All Known Disease Information.*

Description

A dataframe contains known disease information, including disease phenotype, disease genes and disease lncRNAs.

Usage

```
data("DiseaseInfList")
```

Format

A data frame with 53 observations on the following 6 variables.

OMIMId a numeric vector
DLncs known disease lncRNAs
DGenes known disease genes
DGenNum a numeric vector
DLncNum a numeric vector
OMIMName disease phenotype name

Examples

```
data(DiseaseInfList)  
head(DiseaseInfList)  
## maybe str(DiseaseInfList) ;
```

getCoExpGeneofLncs *Get Co-expressed Genes of LncRNAs*

Description

Get co-expressed genes of one or some lncRNAs based on the multi-omics network.

Usage

```
getCoExpGeneofLncs(lncRNAs, GLNet, scoreCutoff = 0.6)
```

Arguments

lncRNAs	A character or a character vector. The names of lncRNAs.
GLNet	An adjacency matrix of the gene-lncRNA network with colnames representing lncRNAs and rownames representing genes. The value represents co-expression relation and it ranges from 0 to 1.
scoreCutoff	A numeric donotes if the co-expression scores between genes and lncRNAs above this value, the genes would be retained. A value ranges from 0 to 1. The default value is 0.6.

Value

A vector of gene names.

Author(s)

Qianlan Yao <yaoqianlan@yahoo.com>

See Also

[getTopDiseaseLncRNAs](#)

Examples

```
## Not run:
##### getCoExpGeneofLncs #####
##breast cancer
data("GLNetExample")
diseaseInf<-getDiseaseInf("114480")
lncRNA<-diseaseInf$lncRNAs[1]
genes<-getCoExpGeneofLncs(lncRNA, GLNet=GLNetExample, scoreCutoff = 0.6)
print(genes[1:5])

## End(Not run)
```

getDiseaseInf	<i>Get All Disease Information based on phenotype id (OMIM Id) Provided by LncPriCNet Package</i>
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Description

Get all disease information provided by LncPriCNet package by OMIMID. This function will provide you known disease genes and lncRNAs corresponding phenotype.

Usage

```
getDiseaseInf(OMIMID)
```

Arguments

OMIMID A character. OMIM ID of one disease or phenotype.

Value

A list.

Author(s)

Qianlan Yao <yaoqianlan@yahoo.com>

See Also

[DiseaseInfList](#)

Examples

```
## Not run:
##### Get disease information #####
##breast cancer
diseaseInf<-getDiseaseInf("114480")
diseaseInf
##
data(DiseaseInfList)
head(DiseaseInfList)

## End(Not run)
```

getTopDiseaseLncRNAs *Get the Disease Risk LncRNAs*

Description

prioritize the disease candidate lncRNAs by integrated multi-omics information.

Usage

```
getTopDiseaseLncRNAs(pheSeed = NULL, genSeed = NULL, lncSeed = NULL,
candidates = NULL, showTop = 30, gamma = 0.7, x = 1/3, y = 1/3,
a = 1/3, b = 1/3, GNet, PNet, LNet, GLNet, PGNet, PLNet)
```

Arguments

pheSeed	A character vector, represents the disease users want to study. Users should input diseaseName.
genSeed	A character vector, The gene seeds are the known disease genes of corresponding phenotype. Users should input a gene seed vector.
lncSeed	A character vector, The lncRNA seeds are the known disease lncRNAs of corresponding phenotype. Users should input a lncRNA seed vector.
candidates	A character vector. Users should input lncRNA candidates, a lncRNA seed vector.
showTop	An integer. The number of top ranked candidate lncRNAs users want to show.
gamma	Restart probability in RWR method. A value ranges from 0 to 1. The default value is 0.7.
x	Jumping probability between gene network and phenotype network. A value ranges from 0 to 1. The default value is 1/3.
y	Jumping probability between gene network and lncRNA network. A value ranges from 0 to 1. The default value is 1/3.
a	a denote the importance of the gene network. A value ranges from 0 to 1. The default value is 1/3.
b	b denote the importance of the phenotype network. A value ranges from 0 to 1. The default value is 1/3.
GNet	An adjacency matrix of the gene network with colnames and rownames representing genes. The value in it ranges from 0 to 1.
PNet	An adjacency matrix of the phenotype network with colnames and rownames representing phenotypes. The value in it ranges from 0 to 1.
LNet	An adjacency matrix of the lncRNA network with colnames and rownames representing lncRNAs. The value in it ranges from 0 to 1.
GLNet	An adjacency matrix of the gene-lncRNA network with colnames representing lncRNAs and rownames representing genes. The value in it ranges from 0 to 1.

PGNet	An adjacency matrix of the phenotype-gene network with colnames representing genes and rownames representing phenotypes. The value in it ranges from 0 to 1.
PLNet	An adjacency matrix of the phenotype-lncRNA network with colnames representing lncRNAs and rownames representing phenotypes. The value in it ranges from 0 to 1.

Details

The function `getTopDiseaseLncRNAs` could get the top ranked candidate lncRNAs by prioritization of the disease candidate lncRNAs using known disease seed nodes to perform random walk on multi-omics network. Note: If users want to use seeds we provided, `pheSeed`, `genSeed` and `lncSeed` can be obtained by `getDiseaseInf`.

Value

A dataframe.

Author(s)

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See Also

[DiseaseInfList](#), [getCoExpGeneofLncs](#), [getDiseaseInf](#).

Examples

```
## Not run:
##### Prioritize candidate lncRNAs #####

## Here we use six fake matrix(networks).
data("GNetExample")
data("GLNetExample")
data("PNetExample")
data("LNetExample")
data("PGNetExample")
data("PLNetExample")

## Get three types seeds from DiseaseInfList we provided.
diseaseName<-"BREAST CANCER" ;
data("DiseaseInfList")
loci<-match(diseaseName,DiseaseInfList[["OMIMName"]]);
pheSeedExample<-DiseaseInfList[loci,"OMIMId"];
genSeedExample<-unlist(strsplit(as.character(DiseaseInfList[loci,"DGenes"]),";"));
lncSeedExample<-unlist(strsplit(as.character(DiseaseInfList[loci,"DLncs"]),";"));
PNodes<-colnames(PNetExample) ;
GNodes<-colnames(GNetExample);
LNodes<-colnames(LNetExample);
pheSeedResult<-pheSeedExample;
genSeedResult<-genSeedExample;
```

```

lncSeedResult<-lncSeedExample;

## Get candidates.
candidateResult<-setdiff(LNodes,lncSeedResult);
##Run getTopDiseaseLncRNAs
example<-getTopDiseaseLncRNAs(pheSeed=pheSeedResult,genSeed=genSeedResult,lncSeed=lncSeedResult,
  candidates=candidateResult,showTop=30,GNet=GNetExample,PNet=PNetExample,LNet=LNetExample,
  GLNet=GLNetExample,PGNet=PGNetExample,PLNet=PLNetExample);
head(example)

## End(Not run)

```

GLNetExample	<i>An Example of Gene-LncRNA Network.</i>
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Description

An adjacency matrix of gene-lncRNA network. An Example of gene-lncRNA Network, which would be used to construct multi-omics composite network.

Usage

```
data("GLNetExample")
```

Examples

```
data(GLNetExample)
## maybe str(GLNetExample) ;
```

GNetExample	<i>An Example of Gene Network.</i>
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Description

An adjacency matrix of gene network. An Example of gene Network, which would be used to construct multi-omics composite network.

Usage

```
data("GNetExample")
```

Examples

```
data(GNetExample)
## maybe str(GNetExample) ;
```

LNetExample	<i>An Example of LncRNA Network.</i>
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Description

An adjacency matrix of lncRNA network. An Example of lncRNA Network, which would be used to construct multi-omics composite network.

Usage

```
data("LNetExample")
```

Examples

```
data(LNetExample)  
## maybe str(LNetExample) ;
```

PGNetExample	<i>An Example of Phenotype-gene Network.</i>
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Description

An adjacency matrix of phenotype-gene network. An Example of Phenotype-gene Network, which would be used to construct multi-omics composite network.

Usage

```
data("PGNetExample")
```

Examples

```
data(PGNetExample)  
## maybe str(PGNetExample) ;
```

PLNetExample	<i>An Example of Phenotype-lncRNA Network.</i>
--------------	--

Description

An adjacency matrix of phenotype-lncRNA network. An Example of Phenotype-lncRNA Network, which would be used to construct multi-omics composite network.

Usage

```
data("PLNetExample")
```

Examples

```
data(PLNetExample)
## maybe str(PLNetExample) ;
```

PNetExample	<i>An Example of Phenotype Network.</i>
-------------	---

Description

An adjacency matrix of phenotype network. An Example of Phenotype Network, which would be used to construct multi-omics composite network.

Usage

```
data("PNetExample")
```

Examples

```
data(PNetExample)
## maybe str(PNetExample) ;
```

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