

Package ‘NetworkSim’

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Type Package

Title Network Comparison Based on Structural Equivalence and Graphlets

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Description Functions to evaluate
pair-wise similarity of two networks especially on high-dimensional data.

Depends R (>= 3.4.0)

Imports igraph, incgraph

Suggests limma, DESeq2, edgeR, org.Hs.eg.db

License GPL-3

Encoding UTF-8

LazyData TRUE

RoxygenNote 6.1.1

NeedsCompilation no

Repository CRAN

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ADE2CAR.DEGs	<i>DEGs of the adenoma-carcinoma transition</i>
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Description

A dataset containing 1290 DEGs of the adenoma-carcinoma transition

Usage

ADE2CAR.DEGs

Format

A character vector

ADE2CAR.net	<i>PPI network of ADE2CAR.DEGs</i>
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Description

A dataset containing the PPI network consisted of DEGs between colonic adenomas and carcinomas

Usage

ADE2CAR.net

Format

A igraph object

databases.net	<i>integrated PPI network</i>
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Description

A dataset containing the integrated PPI network from Biogrid, HPRD and mentha databases

Usage

databases.net

Format

A igraph object

netGDD	<i>Calculate the Graphlet degree distribution (GDD) agreement between two networks</i>
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Description

Calculate the Graphlet degree distribution (GDD) agreement between two networks

Usage

```
netGDD(net1, net2, mean = "arithmetic", i2inc = T)
```

Arguments

net1	The input network, which should be one of incgraph and igraph objects
net2	The input network, which should be one of incgraph and igraph objects
mean	"arithmetic" or "geometric" mean to be used
i2inc	Whether the input graph object should to transformed into incgraph object

Details

```
netGDD(net1,net2,mean='arithmetic',i2inc=T)
```

Value

Agreement value between 0 and 1

Examples

```
nodes <-names(igraph::V(databases.net))  
net1 <-subnet(databases.net,sample(nodes,100))  
net2 <-subnet(databases.net,sample(nodes,100))  
netGDD(net1,net2)
```

netSE

Calculate the structural equivalence between two networks

Description

Calculate the structural equivalence between two networks

Usage

```
netSE(net1, net2, node, method = "cosine")
```

Arguments

net1	The input network, which should be a graph object
net2	The input network, which should be a graph object
node	Gene symbol, which is shared between two networks
method	The similarity measure to be used. This must be "cosine" or "euclidean".

Details

```
netSE(net1,net2,node,method='cosine')
```

Value

Similarity value between 0 and 1

Examples

```
netSE(NOR2ADE.net,ADE2CAR.net,'EREG')
```

nodesCom*Get the common nodes from two networks*

Description

Get the common nodes from two networks

Usage

```
nodesCom(net1, net2)
```

Arguments

net1 The input network, which should be a graph object
net2 The input network, which should be a graph object

Details

subnet(net1,net2)

Value

A vector of gene symbols

Examples

```
Aligned <- nodesCom(NOR2ADE.net,ADE2CAR.net)
```

NOR2ADE.DEGs *DEGs between colonic normals and adenomas*

Description

A dataset containing 4567 differentially expressed genes between normals and adenomas

Usage

NOR2ADE.DEGs

Format

A character vector

NOR2ADE.net *PPI network of NOR2ADE.DEGs*

Description

A dataset containing the PPI network consisted of DEGs between colonic normals and adenomas

Usage

NOR2ADE.net

Format

A igraph object

subnet	<i>Subnetwork from a network</i>
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Description

subnet generates a subnetwork from a network, which consists of specified nodes

Usage

```
subnet(net, nodes, impl = "auto", neighbors = F, delete = T)
```

Arguments

net	The original net, which should be a graph object
nodes	Gene symbol, which should match the nodes in original net
impl	Character scalar, to choose between two implementation of the subgraph calculation. Details are implemented in subgraph function of igraph package
neighbors	Logical scalar, whether to get the neighbors of input nodes
delete	Logical scalar, whether to remove the nodes which do not have any neighbors in the output network

Details

```
subnet(net,nodes,impl="auto",neighbors=F,delete=T)
```

Value

A new igraph graph object

Examples

```
NOR2ADE.net <-subnet(net=databases.net,nodes = NOR2ADE.DEGs)
```

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