

Package ‘NCIgraph’

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Title Pathways from the NCI Pathways Database

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Description Provides various methods to load the pathways from the NCI Pathways Database in R graph objects and to re-format them.

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LazyLoad yes

Imports graph, KEGGgraph, methods, RBGL, RCy3, R.oo

Depends R (>= 4.0.0)

Suggests Rgraphviz

Enhances DEGraph

biocViews Pathways, GraphAndNetwork

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| | |
|-------------|--|
| directedBFS | <i>Uses a breadth first search on a directed graph to identify which genes are regulated by a particular node in the graph</i> |
|-------------|--|

Description

Uses a breadth first search on a directed graph to identify which genes are regulated by a particular node in the graph.

Usage

```
directedBFS(g, node)
```

Arguments

| | |
|------|---------------------------------|
| g | A graph object. |
| node | A node of g. |

Value

A structured [list](#) containing the regulated genes and the type of interaction between node and each gene.

Author(s)

Laurent Jacob

See Also

[propagateRegulation\(\)](#)

| | |
|--------------|--|
| edgesToMerge | <i>Identifies edges that should be merged to parse a NCI network</i> |
|--------------|--|

Description

Identifies edges that should be merged to parse a NCI network.

Usage

```
edgesToMerge(g)
```

Arguments

`g` A [graph](#) object.

Value

A [list](#) of edges to be merged

Author(s)

Laurent Jacob

See Also

[parseNCInetwork\(\)](#)

| | |
|----------------|--|
| getNCIPathways | <i>Loads networks from Cytoscape and parses them</i> |
|----------------|--|

Description

Loads networks from Cytoscape and parses them.

Usage

```
getNCIPathways(cyList=NULL, parseNetworks=TRUE, entrezOnly=TRUE, verbose=FALSE)
```

Arguments

`cyList` a [list](#) providing the networks loaded from Cytoscape. If [NULL](#), the function will try to build the [list](#) from Cytoscape.

`verbose` If [TRUE](#), extra information is output.

`parseNetworks` A [logical](#). If [FALSE](#), the raw NCI networks are returned as [graphNEL](#) objects. If [TRUE](#), some additional parsing is performed by the [parseNCInetwork](#) function.

`entrezOnly` A [logical](#). If [TRUE](#), only keep nodes with an [entrezID](#) property.

Value

A **list** of two elements: pList, a **list** of graphNEL objects, and failedW a **list** containing the names of the networks that R failed to read from cytoscape.

Author(s)

Laurent Jacob

See Also

[parseNCInetwork\(\)](#)

Examples

```
##-----  
## Load NCIgraph  
##-----  
  
library(NCIgraph)  
  
##-----  
## Example 1: with Cytoscape  
##-----  
  
## Must have Cytoscape running with some networks open and CyREST plugin started.  
  
## In this case, getNCIPathways will both read the raw networks from Cytoscape and parse them.  
  
## Not run:  
grList <- getNCIPathways(cyList=NULL, parseNetworks=TRUE, entrezOnly=TRUE, verbose=TRUE)$pList  
  
## End(Not run)  
  
##-----  
## Example 2: without Cytoscape  
##-----  
  
## Get some raw networks  
  
data("NCIgraphVignette", package="NCIgraph")  
  
## When passed a non null cyList argument (a list of networks),  
## getNCIPathways will simply parse the list of networks  
  
grList <- getNCIPathways(cyList=NCI.demo.cyList, parseNetworks=TRUE, entrezOnly=TRUE, verbose=TRUE)$pList
```

getSubtype.NCIgraph *Returns a list of @KEGGEdgeSubType objects describing each edge of the NCI network*

Description

Returns a list of @KEGGEdgeSubType objects describing each edge of the NCI network.

Usage

```
getSubtype.NCIgraph(object)
```

Arguments

object An [NCIgraph](#) object.

Value

A [list](#) of KEGGEdgeSubType objects.

Author(s)

Laurent Jacob

Examples

```
##-----  
## Load NCIgraph  
##-----  
  
library(NCIgraph)  
  
##-----  
## Get some raw networks  
##-----  
  
data("NCIgraphVignette", package="NCIgraph")  
  
##-----  
## Parse them  
##-----  
  
grList <- getNCIPathways(cyList=NCI.demo.cyList, parseNetworks=TRUE, entrezOnly=TRUE, verbose=TRUE)$pList  
  
##-----  
##  
## Get the subtype of the second network. Some activation and some  
## inhibition edges.  
##
```

```
##-----  
getSubtype.NCIgraph(grList[[2]])
```

| | |
|-------------|--|
| is.NCIgraph | <i>Assess whether a graph is a NCI graph</i> |
|-------------|--|

Description

Assess whether a graph is a NCI graph.

Usage

```
is.NCIgraph(gr)
```

Arguments

gr A [graph](#) object.

Value

A [logical](#), [TRUE](#) if the graph is a NCI graph, [FALSE](#) otherwise.

Author(s)

Laurent Jacob

See Also

[parseNCInetwork\(\)](#)

| | |
|------------|--|
| mergeNodes | <i>Merges a given list of nodes in a graph</i> |
|------------|--|

Description

Merges a given list of nodes in a graph.

Usage

```
mergeNodes(g, mEdges, separateEntrez=TRUE, entrezOnly=TRUE)
```

Arguments

`g` A [graph](#) object.
`mEdges` A [list](#) of nodes to be merged.
`separateEntrez` A [logical](#). If `TRUE`, don't merge two nodes with `entrezID`.
`entrezOnly` A [logical](#). If `TRUE`, only keep nodes with an `entrezID` property.

Value

The updated [graph](#) object

Author(s)

Laurent Jacob

See Also

[parseNCInetwork\(\)](#)

| | |
|-----------------|--|
| NCI.demo.cyList | <i>10 raw NCI networks from Nature curated pathways and BioCarta imported as graphNEL objects, for demonstration purpose</i> |
|-----------------|--|

Description

These are the ten first elements of the full list of raw networks that can be downloaded using the `downloadCyLists.R` script.

Usage

```
NCI.demo.cyList
```

Format

A list of 10 `graphNEL` objects.

Author(s)

Laurent Jacob

Examples

```
data("NCIgraphVignette")
length(NCI.demo.cyList)

library(Rgraphviz)
plot(NCI.demo.cyList[[1]])
```

| | |
|----------|-----------------------|
| NCIgraph | <i>Class NCIgraph</i> |
|----------|-----------------------|

Description

Package: NCIgraph

Class NCIgraph

public static class **NCIgraph**
 extends graphNELObject

Class extending graphNEL fro graphs build from NCI gene networks.

Author(s)

Laurent Jacob

| | |
|-----------------|---|
| parseNCInetwork | <i>Takes a NCI network and transforms it into a simpler graph only representing inhibition/activation relationships between genes</i> |
|-----------------|---|

Description

Takes a NCI network and transforms it into a simpler graph only representing inhibition/activation relationships between genes.

Usage

```
parseNCInetwork(g, propagateReg=TRUE, separateEntrez=TRUE, mergeEntrezCopies=TRUE, entrezOnly=TRUE)
```

Arguments

| | |
|-------------------|--|
| g | A graph object. |
| propagateReg | A logical . If TRUE , use propagateRegulation to transform the network before parsing it. |
| separateEntrez | A logical . If TRUE , don't merge two nodes with entrezID. |
| mergeEntrezCopies | A logical . If TRUE , merge resulting nodes that have the same entrezID. |
| entrezOnly | A logical . If TRUE , only keep nodes with an entrezID property. |

Value

The new [graph](#) object.

Author(s)

Laurent Jacob

Examples

```
## Load NCIgraph
library(NCIgraph)

## Get some raw networks
data("NCIgraphVignette", package="NCIgraph")

## Parse the first of them

parsedNetwork <- parseNCInetwork(NCI.demo.cyList[[1]],propagateReg=TRUE,separateEntrez=TRUE,mergeEntrezCopies=T
```

`propagateRegulation` *Transforms the network in a way that each Biochemical Reaction node pointing to a Complex points to what is regulated by the complex and updates the interaction types accordingly*

Description

Transforms the network in a way that each Biochemical Reaction node pointing to a Complex points to what is regulated by the complex and updates the interaction types accordingly.

Usage

```
propagateRegulation(g)
```

Arguments

`g` A [graph](#) object.

Value

The updated [graph](#) object

Author(s)

Laurent Jacob

See Also

[parseNCInetwork\(\)](#)

translateNCI2GeneID *Gives the entrezID corresponding to the nodes of a graph*

Description

Gives the entrezID corresponding to the nodes of a graph.

Usage

```
translateNCI2GeneID(g)
```

Arguments

`g` A [graph](#) object.

Value

A vector of [character](#) giving the entrez ID of the nodes of `g`.

Author(s)

Laurent Jacob

See Also

[parseNCInetwork\(\)](#)

Examples

```
##-----  
## Load NCIgraph  
##-----  
  
library(NCIgraph)  
  
## Get some raw networks  
  
data("NCIgraphVignette", package="NCIgraph")  
  
## Parse them  
  
grList <- getNCIPathways(cyList=NCI.demo.cyList, parseNetworks=TRUE, entrezOnly=TRUE, verbose=TRUE)$pList  
  
## Get the gene ids for the first of them  
  
gids <- translateNCI2GeneID(grList[[1]])
```

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