

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, RCytoscape, R.methodsS3

Depends graph, R (>= 2.10.0)

Suggests Rgraphviz

Enhances DEGraph

biocViews Pathways, GraphsAndNetworks

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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>
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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>
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Description

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

Usage

```
edgesToMerge(g)
```

Arguments

g	A graph object.
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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>
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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 Cytoscape RPC 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 @KEGGEEdgeSubType objects describing each edge of the NCI network*

Description

Returns a list of @KEGGEEdgeSubType 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

Assess whether a graph is a NCI graph

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

Merges a given list of nodes in a graph

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>
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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.cylList[[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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