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.

License GPL-3

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

---

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](#)()

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edgesToMerge	*Identifies edges that should be merged to parse a NCI network*

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](#)()

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getNCIPathways	*Loads networks from Cytoscape and parses them*

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 *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	*10 raw NCI networks from Nature curated pathways and BioCarta imported as graphNEL objects, for demonstration purpose*

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   *Class NCIgraph*

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

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parseNCInetwork   *Takes a NCI network and transforms it into a simpler graph only rep-
                                   resenting inhibition/activation relationships between genes*

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()

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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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