Package ‘NCIgraph’

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Title Pathways from the NCI Pathways Database

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Author Laurent Jacob

Maintainer Laurent Jacob <laurent.jacob@gmail.com>

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` *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`()

`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()

---

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

`parseNCInetwork` *Takes a NCI network and transforms it into a simpler graph only representing 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=TRU
```

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,mergeEntrezCopi
```

`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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