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.
License GPL-3
LazyLoad yes
Imports graph, KEGGgraph, methods, RBGL, RCy3, R.oo
Depends R (>= 4.0.0)
Suggests Rgraphviz
Enhances DEGraph
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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.
getNCIPathways

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

```r
##------------------------------
## 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

```r
#-----------------------------
# 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.
```
## is.NCIgraph

Assess whether a graph is a NCI graph

### Description

Assess whether a graph is a NCI graph.

### Usage

```r
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()`

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## mergeNodes

Merges a given list of nodes in a graph

### Description

Merges a given list of nodes in a graph.

### Usage

```r
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()`

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### 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=TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>g</td>
<td>A graph object.</td>
</tr>
<tr>
<td>propagateReg</td>
<td>A logical. If TRUE, use propagateRegulation to transform the network before parsing it.</td>
</tr>
<tr>
<td>separateEntrez</td>
<td>A logical. If TRUE, don’t merge two nodes with entrezID.</td>
</tr>
<tr>
<td>mergeEntrezCopies</td>
<td>A logical. If TRUE, merge resulting nodes that have the same entrezID.</td>
</tr>
<tr>
<td>entrezOnly</td>
<td>A logical. If TRUE, only keep nodes with an entrezID property.</td>
</tr>
</tbody>
</table>

Value
The new graph object.
propagateRegulation

Author(s)
Laurent Jacob

Examples

```r
## 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=TRUE)
```

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
gList <- getNCIPathways(cyList=NCI.demo.cyList, parseNetworks=TRUE, entrezOnly=TRUE, verbose=TRUE)$pList

## Get the gene ids for the first of them
gids <- translateNCI2GeneID(gList[[1]])
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