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, GraphAndNetwork

NeedsCompilation no

R topics documented:

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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
getNCIPathways

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
###-------------------------------
getSubtype.NCIgraph

## 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

gSubtype.NCIgraph(object)

Arguments

object An NCIgraph object.

Value

A list of KEGGEedgeSubType 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.
eentrezOnly
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

\begin{verbatim}
data("NCIgraphVignette")
length(NCI.demo.cyList)
library(Rgraphviz)
plot(NCI.demo.cyList[[1]])
\end{verbatim}

NCIgraph     Class NCIgraph

Description

Package: NCIgraph
Class NCIgraph

public static class NCIgraph
extends graphNELObject

Class extending graphNEL for graphs built 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

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.
propagateRegulation

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=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

**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**

```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 gene ids for the first of them
uids <- translateNCI2GeneID(grList[[1]])
```
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