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, 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**

```r
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**

```r
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

**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

```r
data("NCIgraphVignette", package="NCIgraph")
```

### Parse them

```r
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.

```r
getSubtype.NCIgraph(grList[[2]])
```

---

### 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()`
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**

```r
NCI.demo.cyList
```

**Format**

A list of 10 graphNEL objects.

**Author(s)**

Laurent Jacob
NCIgraph

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

g
propagateReg
separateEntrez
mergeEntrezCopies
entrezOnly

A graph object.
A logical. If TRUE, use propagateRegulation to transform the network before parsing it.
A logical. If TRUE, don’t merge two nodes with entrezID.
A logical. If TRUE, merge resulting nodes that have the same entrezID.
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 frac{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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