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**

`directedBFS(g, node)`

**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>node</td>
<td>A node of g.</td>
</tr>
</tbody>
</table>

**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**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>g</td>
<td>A graph object.</td>
</tr>
</tbody>
</table>

**Value**

A list of edges to be merged
getNCIPathways

Author(s)
Laurent Jacob

See Also
parseNCInetwork()

getNCIPathways

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

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)
```
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**

```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()`

---

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
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 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.
etrezOnly A logical. If TRUE, only keep nodes with an entrezID property.
**propagateRegulation**

Value

The new graph object.

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

```r
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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