

Package ‘NCIgraph’

November 27, 2025

Title Pathways from the NCI Pathways Database

Version 1.59.0

Date 2012-04-27

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

biocViews Pathways, GraphAndNetwork

git_url <https://git.bioconductor.org/packages/NCIgraph>

git_branch devel

git_last_commit 5a91ea4

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2025-11-26

Contents

directedBFS	2
edgesToMerge	3
getNCIPathways	3
getSubtype.NCIgraph	5
is.NCIgraph	6
mergeNodes	6
NCI.demo.cyList	7

NCIgraph	8
parseNCInetwork	8
propagateRegulation	9
translateNCI2GeneID	10
Index	11

directedBFS	<i>Uses a breadth first search on a directed graph to identify which genes are regulated by a particular node in the graph</i>
-------------	--

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	<i>Identifies edges that should be merged to parse a NCI network</i>
--------------	--

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	<i>Loads networks from Cytoscape and parses them</i>
----------------	--

Description

Loads networks from Cytoscape and parses them.

Usage

```
getNCIPathways(cyList=NULL, parseNetworks=TRUE, entrezOnly=TRUE, verbose=FALSE)
```

Arguments

<code>cyList</code>	a list providing the networks loaded from Cytoscape. If NULL , the function will try to build the list from Cytoscape.
<code>verbose</code>	If TRUE , extra information is output.
<code>parseNetworks</code>	A logical . If FALSE , the raw NCI networks are returned as graphNEL objects. If TRUE , some additional parsing is performed by the <code>parseNCInetwork</code> function.
<code>entrezOnly</code>	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 @KEGGEEdgeSubType objects describing each edge of the NCI network
---------------------	---

Description

Returns a list of @KEGGEEdgeSubType objects describing each edge of the NCI network.

Usage

```
getSubtype.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	<i>Assess whether a graph is a NCI graph</i>
-------------	--

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	<i>Merges a given list of nodes in a graph</i>
------------	--

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	<i>10 raw NCI networks from Nature curated pathways and BioCarta imported as graphNEL objects, for demonstration purpose</i>
-----------------	--

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

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,mergeEntrezCopies=T
```

propagateRegulation	<i>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</i>
---------------------	---

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]])
```

Index

- * **classes**
 - NCIgraph, [8](#)
- * **datasets**
 - NCI.demo.cyList, [7](#)
- * **documentation**
 - NCIgraph, [8](#)
- character, [10](#)
- directedBFS, [2](#)
- edgesToMerge, [3](#)
- FALSE, [3](#), [6](#)
- getNCIPathways, [3](#)
- getSubtype.NCIgraph, [5](#)
- graph, [2](#), [3](#), [6–10](#)
- is.NCIgraph, [6](#)
- list, [2–5](#), [7](#)
- logical, [3](#), [6–8](#)
- mergeNodes, [6](#)
- NCI.demo.cyList, [7](#)
- NCIgraph, [5](#), [8](#)
- NCIgraph-class (NCIgraph), [8](#)
- NULL, [3](#)
- parseNCInetwork, [3](#), [4](#), [6](#), [7](#), [8](#), [9](#), [10](#)
- propagateRegulation, [2](#), [9](#)
- translateNCI2GeneID, [10](#)
- TRUE, [3](#), [6–8](#)