

Package ‘NCIgraph’

January 30, 2026

Title Pathways from the NCI Pathways Database

Version 1.58.0

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 RELEASE_3_22

git_last_commit eb4dd86

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-29

Contents

directedBFS	2
edgesToMerge	2
getNCIPathways	3
getSubtype.NCIgraph	4
is.NCIgraph	5
mergeNodes	6
NCI.demo.cyList	6
NCIgraph	7
parseNCInetwork	7
propagateRegulation	8
translateNCI2GeneID	9

Index

10

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

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  
##-----
```

```

## 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

```

##-----
## 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	<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, mergeEntrezCopi
```

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