

# Package ‘NCIgraph’

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**Title** Pathways from the NCI Pathways Database

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**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, RCytoscape, R.methodsS3

**Depends** graph, R (>= 2.10.0)

**Suggests** Rgraphviz

**Enhances** DEGraph

**biocViews** Pathways, GraphAndNetwork

**NeedsCompilation** no

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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>
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**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 <a href="#">graph</a> 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	<i>Identifies edges that should be merged to parse a NCI network</i>
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**Description**

Identifies edges that should be merged to parse a NCI network.

**Usage**

```
edgesToMerge(g)
```

**Arguments**

g	A <a href="#">graph</a> object.
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**Value**

A [list](#) of edges to be merged

**Author(s)**

Laurent Jacob

**See Also**

[parseNCInetwork\(\)](#)

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getNCIPathways	<i>Loads networks from Cytoscape and parses them</i>
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**Description**

Loads networks from Cytoscape and parses them.

**Usage**

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

**Arguments**

cyList	a <a href="#">list</a> providing the networks loaded from Cytoscape. If <a href="#">NULL</a> , the function will try to build the <a href="#">list</a> from Cytoscape.
verbose	If <a href="#">TRUE</a> , extra information is output.
parseNetworks	A <a href="#">logical</a> . If <a href="#">FALSE</a> , the raw NCI networks are returned as graphNEL objects. If <a href="#">TRUE</a> , some additional parsing is performed by the <a href="#">parseNCInetwork</a> function.
entrezOnly	A <a href="#">logical</a> . If <a href="#">TRUE</a> , 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 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*

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**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 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\(\)](#)

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mergeNodes

*Merges a given list of nodes in a graph*

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**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\(\)](#)

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

**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	<i>Class NCIgraph</i>
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**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	<i>Takes a NCI network and transforms it into a simpler graph only representing inhibition/activation relationships between genes</i>
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---

### 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 <a href="#">graph</a> object.
propagateReg	A <a href="#">logical</a> . If <a href="#">TRUE</a> , use propagateRegulation to transform the network before parsing it.
separateEntrez	A <a href="#">logical</a> . If <a href="#">TRUE</a> , don't merge two nodes with entrezID.
mergeEntrezCopies	A <a href="#">logical</a> . If <a href="#">TRUE</a> , merge resulting nodes that have the same entrezID.
entrezOnly	A <a href="#">logical</a> . If <a href="#">TRUE</a> , 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.cylList[[1]], propagateReg=TRUE, separateEntrez=TRUE, mergeEntrezCopies=TRUE)
```



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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\(\)](#)

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translateNCI2GeneID    *Gives the entrezID corresponding to the nodes of a graph*

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**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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