

# Package ‘RCyjs’

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**Type** Package

**Title** Display and manipulate graphs in cytoscape.js

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**Suggests** RUnit, BiocStyle, knitr, rmarkdown

## Description

Interactive viewing and exploration of graphs, connecting R to Cytoscape.js, using websockets.

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---

addGraph,RCyjs-method *addGraph*

---

**Description**

addGraph send these nodes and edges (with attributes) to RCyjs for display

**Usage**

```
## S4 method for signature 'RCyjs'  
addGraph(obj, graph)
```

**Arguments**

obj	an RCyjs instance
graph	a graphNEL

**Details**

This version transmits a graph (nodes, edges and attributes) to the browser by writing the data to a file, and sending that filename to be read in the browser by javascript.

**Value**

nothing

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  g <- simpleDemoGraph()  
  setGraph(rcy, g)  
}
```

---

addGraphFromFile,RCyjs-method  
*addGraphFromFile*

---

**Description**

addGraphFromFile add graph from specified file, which contains a cytoscape.js JSON graph

**Usage**

```
## S4 method for signature 'RCyjs'  
addGraphFromFile(obj, jsonFileName)
```

**Arguments**

obj	an RCyjs instance
jsonFileName	path to the file

**Details**

More description

**Value**

nothin

**Examples**

```
if(interactive()){
  rcy <- RCyjs()
  filename <- system.file(package="RCyjs", "extdata", "sampleGraph.json")
  addGraphFromFile(rcy, filename)
  layout(rcy, "cose")
  fit(rcy, 200)
}
```

---

*clearSelection,RCyjs-method*

*clearSelection*

---

**Description**

`clearSelection` deselect all selected nodes, all selected edges, or both

**Usage**

```
## S4 method for signature 'RCyjs'
clearSelection(obj, which = "both")
```

**Arguments**

`obj` an RCyjs object  
`which` a character string: "both" (the default), "nodes" or "edges"

**Value**

no return value

**Examples**

```
if(interactive()){
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())
  selectNodes(rcy, c("A", "B"))
  clearSelection(rcy)
}
```

---

createTestGraph	<i>createTestGraph</i>
-----------------	------------------------

---

**Description**

createTestGraph With as many nodes and edges as you wish, but neither edge nor node attributes.

**Usage**

```
createTestGraph(nodeCount, edgeCount)
```

**Arguments**

nodeCount	1 or more
edgeCount	0 or more

**Value**

a graphNEL with nodeCount nodes and edgeCount edges

**Examples**

```
g <- createTestGraph(5, 3)
```

---

dataFramesToJSON	<i>Create a cytoscape.js JSON graph from one or two data.frames.</i>
------------------	--

---

**Description**

Create a cytoscape.js JSON graph from one or two data.frames.

**Usage**

```
dataFramesToJSON(tbl.edges, tbl.nodes = NULL)
```

**Arguments**

tbl.edges	data.frame, with source, target and interaction columns, others option for edge attributes
tbl.nodes	data.frame, options, useful for orphan nodes, and necessary for adding node attributes

---

`deleteGraph,RCyjs-method`  
*deleteGraph*

---

## Description

`deleteGraph` Remove all nodes and edges, the elements of the current graph.

## Usage

```
## S4 method for signature 'RCyjs'  
deleteGraph(obj)
```

## Arguments

`obj`                    `RCyjs` instance

## Details

This method will remove any previous graph in the browser

## Value

nothing

## See Also

[addGraph](#) [setGraph](#)

## Examples

```
if(interactive()){  
  sampleGraph <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=sampleGraph)  
  deleteGraph(rcy)  
}
```

---

```
deleteSelectedNodes,RCyjs-method
      deleteSelectedNodes
```

---

### Description

deleteSelectedNodes put somewhat more detailed description here

### Usage

```
## S4 method for signature 'RCyjs'
deleteSelectedNodes(obj)
```

### Arguments

obj                    an RCyjs instance

### Details

multi-line description goes here with continuations on subsequent lines if you like

### Value

explain what the method returns

### Examples

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  target <- nodes(g)[1]
  selectNodes(rcy, target)
  deleteSelectedNodes(rcy)
}
```

---

```
eda                    eda
```

---

### Description

eda retrieve the node/attribute-value pairs, for the specified node attribute category

### Usage

```
eda(graph, edge.attribute.name)
```



**Arguments**

graph            a graphNEL  
edge.attribute.name  
                  a character string

**Value**

character strings, the names of the unique edge attribute categories on the graph

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  edaNames(g) # discover the attribute category names  
  eda(g, "edgeType")  
  eda(g, "score")  
}
```

---

edaNames

*edaNames*

---

**Description**

edaNames the names of the unique edge attribute categories on the graph (not their values)

**Usage**

```
edaNames(graph)
```

**Arguments**

graph            a graphNEL

**Value**

character strings, the names of the unique edge attribute categories on the graph

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  edaNames(g)  
}
```

fit,RCyjs-method      *fit*

---

**Description**

fit zoom in (or out) to display all nodes in the current graph

**Usage**

```
## S4 method for signature 'RCyjs'  
fit(obj, padding = 30)
```

**Arguments**

obj                    an RCyjs instance  
padding                numeric, in pixels

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  setZoom(rcy, 0.5) # zoom out  
  fit(rcy)  
}
```

---

fitSelection,RCyjs-method  
                          *fitSelection*

---

**Description**

fitSelection zoom in to include only currently selected nodes

**Usage**

```
## S4 method for signature 'RCyjs'  
fitSelection(obj, padding = 30)
```

**Arguments**

obj                    an RCyjs instance  
padding                numeric, in pixels

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  selectNodes(rcy, "A")  
  fitSelection(rcy, padding=100)  
}
```

---

*getEdgeCount,RCyjs-method*  
*getEdgeCount*

---

**Description**

*getEdgeCount* the number of edges in the current cytoscape.js graph

**Usage**

```
## S4 method for signature 'RCyjs'  
getEdgeCount(obj)
```

**Arguments**

obj                    RCyjs instance

**Value**

numeric count

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  getEdgeCount(rcy)  
}
```

---

*getJSON,RCyjs-method*    *getJSON*

---

**Description**

`getJSON` a JSON string from the browser, describing the graph in cytoscape.js terms

**Usage**

```
## S4 method for signature 'RCyjs'  
getJSON(obj)
```

**Arguments**

`obj`                    an RCyjs instance

**Value**

a JSON string

**Examples**

```
if(interactive()){  
  sampleGraph <- simpleDemoGraph()  
  rcy <- RCyjs(title="getJSON", graph=sampleGraph)  
  s <- getJSON(rcy)  
  s.asList <- fromJSON(s) # easier to inspect if you wish to a  
}
```

---

*getLayoutStrategies,RCyjs-method*  
*getLayoutStrategies*

---

**Description**

`getLayoutStrategies` return a list of those currently offered

**Usage**

```
## S4 method for signature 'RCyjs'  
getLayoutStrategies(obj)
```

**Arguments**

`obj`                    an RCyjs instance

**Value**

a list of character strings

**Examples**

```
if(interactive()){  
  g <- createTestGraph(nodeCount=20, edgeCount=20)  
  rcy <- RCyjs(title="layouts", graph=g)  
  strategies <- getLayoutStrategies(rcy)  
}
```

---

*getNodeCount,RCyjs-method*  
*getNodeCount*

---

**Description**

`getNodeCount` the number of nodes in the current cytoscape.js graph

**Usage**

```
## S4 method for signature 'RCyjs'  
getNodeCount(obj)
```

**Arguments**

`obj` RCyjs instance

**Value**

numeric count

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  getNodeCount(rcy)  
}
```

---

`getNode`s,RCyjs-method *getNode*s

---

### Description

`getNode`s returns a data.frame, one row per node, providing id and (if present) name and label columns

### Usage

```
## S4 method for signature 'RCyjs'  
getNode(obj, which = "all")
```

### Arguments

`obj` an RCyjs instance  
`which` a character string, either "all", "visible" or "hidden"

### Details

Every node is guaranteed to have an "id" attribute. Because "name" and "label" are commonly used as well, they are returned as columns in the data.frame if present

### Value

a data.frame with at least an "id" column

### Examples

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  getNode(rcy)  
}
```

---

`getPosition`,RCyjs-method  
*getPosition*

---

### Description

`getPosition` for all or specified nodes

### Usage

```
## S4 method for signature 'RCyjs'  
getPosition(obj, nodeIDs = NA)
```

**Arguments**

obj                    an RCyjs instance  
nodeIDs                a vector of character strings, default NA

**Value**

a data.frame with "id", "x" and "y" columns

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="getPosition", graph=g)  
  layout(rcy, "cose")  
  tbl.pos <- getPosition(rcy)  
  tbl.posA <- getPosition(rcy, "A")  
}
```

---

*getSelectedNodes,RCyjs-method*  
*getSelectedNodes*

---

**Description**

*getSelectedNodes* get the selected nodes

**Usage**

```
## S4 method for signature 'RCyjs'  
getSelectedNodes(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

a data.frame with (at least) an id column

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  nodes.to.select <- getNodes(rcy)$id  
  selectNodes(rcy, nodes.to.select)  
}
```

---

*getSupportedEdgeDecoratorShapes,RCyjs-method*  
*getSupportedEdgeDecoratorShapes*

---

**Description**

`getSupportedEdgeDecoratorShapes` return a list of those currently offered

**Usage**

```
## S4 method for signature 'RCyjs'  
getSupportedEdgeDecoratorShapes(obj)
```

**Arguments**

`obj` an `RCyjs` instance

**Value**

a list of character strings

**Examples**

```
if(interactive()){  
  g <- createTestGraph(nodeCount=20, edgeCount=20)  
  rcy <- RCyjs(title="shapes", graph=g)  
  shapes <- getSupportedEdgeDecoratorShapes(rcy)  
}
```

---

*getSupportedNodeShapes,RCyjs-method*  
*getSupportedNodeShapes*

---

**Description**

`getSupportedNodeShapes` return a list of those currently offered

**Usage**

```
## S4 method for signature 'RCyjs'  
getSupportedNodeShapes(obj)
```



**Arguments**

obj                    an RCyjs instance

**Value**

a list of character strings

**Examples**

```
if(interactive()){  
  g <- createTestGraph(nodeCount=20, edgeCount=20)  
  rcy <- RCyjs(title="shapes", graph=g)  
  shapes <- getSupportedNodeShapes(rcy)  
}
```

---

*getZoom,RCyjs-method*    *getZoom*

---

**Description**

*getZoom* learn the zoom level of the current display

**Usage**

```
## S4 method for signature 'RCyjs'  
getZoom(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  getZoom(rcy)  
  Sys.sleep(1)  
  setZoom(rcy, 5)  
  getZoom(rcy)  
}
```

---

`graphNELtoJSON.string` *Convert R graphNEL object to cytoscape.js JSON.*

---

**Description**

Convert R graphNEL object to cytoscape.js JSON.

**Usage**

```
graphNELtoJSON.string(g)
```

**Arguments**

`g` a graphNEL

**Examples**

```
## Not run:  
g.json <- graphNELtoJSON.string(graphNEL())  
  
## End(Not run)
```

---

`hAlign,RCyjs-method` *hAlign*

---

**Description**

`hAlign` horizontally align selected nodes

**Usage**

```
## S4 method for signature 'RCyjs'  
hAlign(obj)
```

**Arguments**

`obj` an RCyjs instance

**Details**

The shared y coordinate will be the mean of the y coordinates of selected nodes. The x coordinates are preserved.

**Value**

no return value

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  layout(rcy, "cose")  
  selectNodes(rcy, nodes(g)[1:2])  
  hAlign(rcy)  
}
```

---

hideAllEdges,RCyjs-method  
*hideAllEdges*

---

**Description**

hideAllEdges

**Usage**

```
## S4 method for signature 'RCyjs'  
hideAllEdges(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

no return value

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  layout(rcy, "cose")  
  hideAllEdges()  
  showAll(rcy, "edges")  
}
```

---

hideEdges,RCyjs-method  
*hideEdges*

---

## Description

hideEdges hide all edges of the specified type

## Usage

```
## S4 method for signature 'RCyjs'  
hideEdges(obj, edgeType)
```

## Arguments

obj	an RCyjs instance
edgeType	a character string

## Details

edgeType is a crucial feature for RCyjs. We assume it is an attribute found on every edge in every graph.

## Value

no return value

## Examples

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  getNodes(rcy)  
  edaNames(rcy)      # includes "edgeType"  
  eda(rcy, "edgeType") # includes "phosphorylates"  
  hideEdges(rcy, edgeType="phosphorylates")  
  showEdges(rcy, edgeType="phosphorylates")  
}
```

---

hideNodes,RCyjs-method

*hideNodes*

---

## Description

hideNodes hide the named nodes from view

## Usage

```
## S4 method for signature 'RCyjs'  
hideNodes(obj, nodeIDs)
```

## Arguments

obj                    an RCyjs instance

## Details

The hidden nodes are not deleted from the graph

## Value

no return value

## See Also

[showAll](#)

## Examples

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  target <- nodes(g)[1]  
  selectNodes(rcy, target)  
  hideNodes(rcy)  
  getNodes(rcy, "hidden")  
  getNodes(rcy, "visible")  
  showAll(rcy, which="nodes")  
}
```

---

hideSelectedNodes,RCyjs-method  
*hideSelectedNodes*

---

**Description**

hideSelectedNodes hide selected nodes from view

**Usage**

```
## S4 method for signature 'RCyjs'  
hideSelectedNodes(obj)
```

**Arguments**

obj                    an RCyjs instance

**Details**

The hidden nodes are not deleted from the graph

**Value**

no return value

**See Also**

[showAll](#)

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  target <- nodes(g)[1]  
  selectNodes(rcy, target)  
  hideSelectedNodes(rcy)  
  getNodes(rcy, "hidden")  
  getNodes(rcy, "visible")  
  showAll(rcy, which="nodes")  
}
```

---

invertNodeSelection,RCyjs-method  
*invertNodeSelection*

---

**Description**

invertNodeSelection deselect all selected nodes, select all previously unselected nodes

**Usage**

```
## S4 method for signature 'RCyjs'  
invertNodeSelection(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

no return value

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  target <- nodes(g)[1]  
  selectNodes(rcy, target)  
  invertNodeSelection(rcy)  
}
```

---

layout,RCyjs-method    *layout*

---

**Description**

layout apply a layout algorithm to the current grap

**Usage**

```
## S4 method for signature 'RCyjs'  
layout(obj, strategy = "random")
```

**Arguments**

obj                    an RCyjs instance  
strategy                a character string, one of the supported algorithms

**Value**

explain what the method returns

**See Also**

[getLayoutStrategies](#)

**Examples**

```
if(interactive()){  
  g <- createTestGraph(nodeCount=20, edgeCount=20)  
  rcy <- RCyjs(title="layouts", graph=g)  
  strategies <- getLayoutStrategies(rcy)  
  for(strategy in strategies){  
    layout(rcy, strategy)  
    Sys.sleep(1)  
  }  
}
```

---

layoutSelectionInGrid,RCyjs-method  
*layoutSelectionInGrid*

---

**Description**

layoutSelectionInGrid arrange selected nodes in this region

**Usage**

```
## S4 method for signature 'RCyjs'  
layoutSelectionInGrid(obj, x, y, w, h)
```

**Arguments**

obj	an RCyjs instance
x	numeric this will be the top left x coordinate of the grid
y	numeric the top right
w	numeric width of the grid
h	numeric height of the grid

**Value**

no return value



**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  layout(rcy, "cose")
  fit(rcy, 100)
  loadStyleFile(rcy, system.file(package="RCyjs", "extdata", "sampleStyle2.js"));
  selectNodes(rcy, nodes(g))
  layoutSelectionInGrid(rcy, -1000, 10, 100, 400)
}
```

---

layoutSelectionInGridInferAnchor,RCyjs-method  
*layoutSelectionInGridInferAnchor*

---

**Description**

layoutSelectionInGridInferAnchor the top-most, left-most of the selected nodes is the anchor

**Usage**

```
## S4 method for signature 'RCyjs'
layoutSelectionInGridInferAnchor(obj, w, h)
```

**Arguments**

obj	an RCyjs instance
w	numeric, the width of the grid box
h	numeric, the height of the grid box

**Details**

anchor (the top left) of the grid is the location of the topmost/leftmost node, then arrange all the selected nodes in a box anchored here.

**Value**

explain what the method returns

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  layout(rcy, "cose")
  fit(rcy, 100)
  loadStyleFile(rcy, system.file(package="RCyjs", "extdata", "sampleStyle2.js"));
}
```

```
selectNodes(rcy, nodes(g))
layoutSelectionInGrid(rcy, -1000, 10, 100, 400)
}
```

---

loadStyleFile,RCyjs-method

*loadStyleFile*

---

### Description

loadStyleFile load a named JSON cytoscape.js style file into the browser

### Usage

```
## S4 method for signature 'RCyjs'
loadStyleFile(obj, filename)
```

### Arguments

obj	an RCyjs instance
filename	contains json in the proper cytoscape.js format

### Value

nothing

### References

<https://js.cytoscape.org/#style>

Though we provide access to individual styling rules (see below) we often find it convenient to express all aspects of a visual style in a single JSON file

### Examples

```
if(interactive()){
  rcy <- demo()
  filename <- system.file(package="RCyjs", "extdata", "sampleStyle1.js");
  loadStyleFile(rcy, filename)
}
```

---

noa	<i>noa</i>
-----	------------

---

**Description**

noa retrieve the node/attribute-value pairs, for the specified node attribute category

**Usage**

```
noa(graph, node.attribute.name)
```

**Arguments**

graph	a graphNEL
node.attribute.name	a character string

**Value**

character strings, the names of the unique edge attribute categories on the graph

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  noa(g, "lfc")
}
```

---

noaNames	<i>noaNames</i>
----------	-----------------

---

**Description**

noaNames the names of the unique node attribute categories on the graph (not their values)

**Usage**

```
noaNames(graph)
```

**Arguments**

graph	a graphNEL
-------	------------

**Value**

character strings, the names of the unique node attribute categories on the graph

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  noaNames(g)
}
```

---

 RCyjs-class

 Create an RCyjs object
 

---

**Description**

The RCyjs class provides an R interface to cytoscape.js, a rich, interactive, full-featured, javascript network (graph) library. One constructs an RCyjs instance on a specified port (default 9000), the browser code is loaded, and a websocket connection opened.

**Usage**

```
RCyjs(
  portRange = 16000:16100,
  title = "RCyjs",
  graph = graphNEL(),
  quiet = TRUE
)
```

**Arguments**

portRange	The constructor looks for a free websocket port in this range. 16000:16100 by default
title	Used for the web browser window, "RCyjs" by default
graph	a Bioconductor graphNEL object
quiet	A logical variable controlling verbosity during execution

**Value**

An object of the RCyjs class

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  setNodeLabelRule(rcy, "label");
  setNodeSizeRule(rcy, "count", c(0, 30, 110), c(20, 50, 100));
  setNodeColorRule(rcy, "count", c(0, 100), c(colors$green, colors$red), mode="interpolate")
  redraw(rcy)
  layout(rcy, "cose")
}
```

---

readAndStandardizeJSONNetworkFile

*Read in a JSON network file, identify (or add) elements field return JSON*

---

**Description**

Read in a JSON network file, identify (or add) elements field return JSON

**Usage**

readAndStandardizeJSONNetworkFile(filename)

**Arguments**

file            a json file

---

readAndStandardizeJSONStyleFile

*Read in a JSON file, extract the selector elements, return JSON*

---

**Description**

Read in a JSON file, extract the selector elements, return JSON

**Usage**

readAndStandardizeJSONStyleFile(filename)

**Arguments**

file            a json file

---

redraw,RCyjs-method     *redraw*

---

**Description**

redraw re-render the graph, using the latest style rules and assignments

**Usage**

```
## S4 method for signature 'RCyjs'  
redraw(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

explain what the method returns

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  layout(rcy, "cose")  
  fit(rcy, 100)  
  setNodeAttributes(rcy, "lfc", c("A", "B", "C"), c(0, 0, 0))  
  redraw(rcy)  
}
```

---

restoreLayout,RCyjs-method  
                          *restoreLayout*

---

**Description**

restoreLayout restore a previously-saved layout

**Usage**

```
## S4 method for signature 'RCyjs'  
restoreLayout(obj, filename = "layout.RData")
```

**Arguments**

obj                    an RCyjs instance  
filename                a character string, default "layout.RData"

**Value**

no return value

**See Also**

[saveLayout](#)

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  layout(rcy, "grid")  
  saveLayout(rcy, filename="gridLayout.RData")  
  layout(rcy, "circle")  
  restoreLayout(rcy, "gridLayout.RData")  
}
```

---

saveJPG,RCyjs-method    *saveJPG*

---

**Description**

saveJPG write current cytoscape view, at current resolution, to a JPG file.

**Usage**

```
## S4 method for signature 'RCyjs'  
saveJPG(obj, filename, resolutionFactor = 1)
```

**Arguments**

obj                    an RCyjs instance  
filename                a character string  
resolutionFactor  
                        numeric, default 1, higher values multiply resolution beyond screen dpi

**Value**

no return value

## Examples

```
if(interactive()){
  rcy <- RCyjs(title="layouts", graph=createTestGraph(nodeCount=20, edgeCount=20))
  style.filename <- system.file(package="RCyjs", "extdata", "sampleStyle1.js");
  loadStyleFile(rcy, style.filename)
  layout(rcy, "cose")
  fit(rcy)
  filename <- tempfile(fileext=".jpg")
  saveJPG(rcy, filename, resolutionFactor)
}
```

---

saveLayout,RCyjs-method

*saveLayout*

---

## Description

saveLayout to a named file

## Usage

```
## S4 method for signature 'RCyjs'
saveLayout(obj, filename = "layout.RData")
```

## Arguments

obj	a RCyjs instance
filename	"layout.RData" by default

## Details

All node positions are saved to a functionally opaque RData object, in a file whose name you supply. These files are used by restoreLayout.

## Value

no return value

## See Also

[restoreLayout](#)



## Examples

```
if(interactive()){
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())
  layout(rcy, "grid")
  saveLayout(rcy, filename="gridLayout.RData")
  layout(rcy, "circle")
  restoreLayout(rcy, "gridLayout.RData")
}
```

---

savePNG,RCyjs-method    *savePNG*

---

## Description

savePNG write current cytoscape view, at current resolution, to a PNG file.

## Usage

```
## S4 method for signature 'RCyjs'
savePNG(obj, filename)
```

## Arguments

obj	an RCyjs instance
filename	a character string

## Value

no return value

## Examples

```
if(interactive()){
  rcy <- RCyjs(title="layouts", graph=createTestGraph(nodeCount=20, edgeCount=20))
  style.filename <- system.file(package="RCyjs", "extdata", "sampleStyle1.js");
  loadStyleFile(rcy, style.filename)
  layout(rcy, "cose")
  fit(rcy)
  filename <- tempfile(fileext=".png")
  savePNG(rcy, filename)
}
```

---

`selectFirstNeighborsOfSelectedNodes,RCyjs-method`  
*selectFirstNeighborsOfSelectedNodes*

---

**Description**

`selectFirstNeighborsOfSelectedNodes`

**Usage**

```
## S4 method for signature 'RCyjs'  
selectFirstNeighborsOfSelectedNodes(obj)
```

**Arguments**

`obj`                    an RCyjs instance

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  selectNodes(rcy, "A")  
  getSelectedNodes(rcy) # just one  
  selectFirstNeighborsOfSelectedNodes()  
  getSelectedNodes(rcy) # now three  
}
```

---

`selectNodes,RCyjs-method`  
*selectNodes*

---

**Description**

`selectNodes` by node id

**Usage**

```
## S4 method for signature 'RCyjs'  
selectNodes(obj, nodeIDs)
```

**Arguments**

obj                    an RCyjs instance  
nodeIDs                character strings

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  selectNodes(rcy, c("A", "B"))  
}
```

---

setBackgroundColor,RCyjs-method  
*setBackgroundColor*

---

**Description**

setBackgroundColor of the entire cytoscape.js div

**Usage**

```
## S4 method for signature 'RCyjs'  
setBackgroundColor(obj, newValue)
```

**Arguments**

obj                    an RCyjs instance  
newValue              a character string, any valid CSS color

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  setBackgroundColor(rcy, "lightblue")  
}
```

---

setDefaultEdgeColor,RCyjs-method  
*setDefaultEdgeColor*

---

**Description**

setDefaultEdgeColor

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultEdgeColor(obj, newValue)
```

**Arguments**

obj                    an RCyjs instance  
newValue              a character string, any valid CSS color

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodeColor", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeFontColor(rcy, "red")  
}
```

---

setDefaultEdgeLineColor,RCyjs-method  
*setDefaultEdgeLineColor*

---

**Description**

setDefaultEdgeLineColor

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultEdgeLineColor(obj, newValue)
```

**Arguments**

obj            an RCyjs instance  
newValue      a character string, and valid CSS color

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultEdgeLineColor", graph=g)  
  layout(rcy, "cose")  
  setDefaultEdgeLineColor(rcy, "red")  
}
```

---

setDefaultEdgeLineStyle,RCyjs-method  
*setDefaultEdgeLineStyle*

---

**Description**

setDefaultEdgeLineStyle put somewhat more detailed description here

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultEdgeLineStyle(obj, newValue = c("solid", "dotted", "dashed"))
```

**Arguments**

obj            an RCyjs instance  
newValue      a character string, one of "solid", "dotted", or "dashed"

**Details**

multi-line description goes here with continuations on subsequent lines if you like

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultEdgeLineStyle", graph=g)
  layout(rcy, "cose")
  setDefaultEdgeLineColor(rcy, "dashed")
}
```

---

setDefaultEdgeSourceArrowColor,RCyjs-method  
*setDefaultEdgeSourceArrowColor*

---

**Description**

setDefaultEdgeSourceArrowColor

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultEdgeSourceArrowColor(obj, newValue)
```

**Arguments**

obj                    an RCyjs instance  
newValue              a character string, and valid CSS color

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultEdgeSourceArrowColor", graph=g)
  layout(rcy, "cose")
  setDefaultEdgeSourceArrowColor(rcy, "red")
}
```

---

setDefaultEdgeSourceArrowShape,RCyjs-method  
*setDefaultEdgeSourceArrowShape*

---

## Description

setDefaultEdgeSourceArrowShape put somewhat more detailed description here

## Usage

```
## S4 method for signature 'RCyjs'
setDefaultEdgeSourceArrowShape(
  obj,
  newValue = c("triangle", "triangle-tee", "triangle-cross", "triangle-backcurve", "vee",
              "tee", "square", "circle", "diamond", "none")
)
```

## Arguments

obj	an RCyjs instance
newValue	a character string, one of "triangle", "triangle-tee", "triangle-cross", "triangle-backcurve", "vee", "tee", "square", "circle", "diamond", "none"

## Details

multi-line description goes here with continuations on subsequent lines if you like

## Value

no value returned

## Examples

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultEdgeSourceArrowShape", graph=g)
  layout(rcy, "cose")
  setDefaultEdgeSourceArrowShape(rcy, "tee")
}
```

---

```
setDefaultEdgeTargetArrowColor,RCyjs-method
      setDefaultEdgeTargetArrowColor
```

---

**Description**

```
setDefaultEdgeTargetArrowColor
```

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultEdgeTargetArrowColor(obj, newValue)
```

**Arguments**

```
obj          an RCyjs instance
newValue     a character string, and valid CSS color
```

**Value**

```
no value returned
```

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultEdgeTargetArrowColor", graph=g)
  layout(rcy, "cose")
  setDefaultEdgeTargetArrowColor(rcy, "red")
}
```

---

```
setDefaultEdgeTargetArrowShape,RCyjs-method
      setDefaultEdgeTargetArrowShape
```

---

**Description**

```
setDefaultEdgeTargetArrowShape put somewhat more detailed description here
```

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultEdgeTargetArrowShape(
  obj,
  newValue = c("triangle", "triangle-tee", "triangle-cross", "triangle-backcurve", "vee",
    "tee", "square", "circle", "diamond", "none")
)
```



**Arguments**

obj	an RCyjs instance
newValue	a character string, one of "triangle", "triangle-tee", "triangle-cross", "triangle-backcurve", "vee", "tee", "square", "circle", "diamond", "none"

**Details**

multi-line description goes here with continuations on subsequent lines if you like

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultEdgeTargetArrowShape", graph=g)
  layout(rcy, "cose")
  setDefaultEdgeTargetArrowShape(rcy, "tee")
}
```

---

setDefaultEdgeWidth,RCyjs-method  
*setDefaultEdgeWidth*

---

**Description**

setDefaultEdgeWidth in pixels

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultEdgeWidth(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	a numeric

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultEdgeWidth", graph=g)  
  layout(rcy, "cose")  
  setDefaultEdgeWidth(rcy, 1)  
}
```

---

setDefaultNodeBorderColor,RCyjs-method  
*setDefaultNodeBorderColor*

---

**Description**

setDefaultNodeBorderColor put somewhat more detailed description here

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultNodeBorderColor(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	any CSS color

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodeBorderColor", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeBorderColor(rcy, "red")  
}
```

---

setDefaultNodeBorderWidth,RCyjs-method  
*setDefaultNodeBorderWidth*

---

**Description**

setDefaultNodeBorderWidth in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultNodeBorderWidth(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	numeric, in pixels

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodeBorderWidth", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeBorderWidth(rcy, 2)  
}
```

---

setDefaultNodeColor,RCyjs-method  
*setDefaultNodeColor*

---

**Description**

setDefaultNodeColor put somewhat more detailed description here

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultNodeColor(obj, newValue)
```

**Arguments**

obj            an RCyjs instance  
newValue      a character string, any valid CSS color name

**Details**

multi-line description goes here with continuations on subsequent lines if you like

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodeColor", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeColor(rcy, "lightblue")  
}
```

---

setDefaultNodeFontColor,RCyjs-method  
*setDefaultNodeFontColor*

---

**Description**

setDefaultNodeFontColor

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultNodeFontColor(obj, newValue)
```

**Arguments**

obj            an RCyjs instance  
newValue      any CSS color

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultNodeColor", graph=g)
  layout(rcy, "cose")
  setDefaultNodeFontColor(rcy, "red")
}
```

---

setDefaultNodeFontSize,RCyjs-method  
*setDefaultNodeFontSize*

---

**Description**

setDefaultNodeFontSize put somewhat more detailed description here

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultNodeFontSize(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	numeric, in points

**Details**

multi-line description goes here with continuations on subsequent lines if you like

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultNodeFontSize", graph=g)
  layout(rcy, "cose")
  setDefaultNodeFontSize(rcy, 8)
}
```

---

setDefaultNodeHeight,RCyjs-method  
*setDefaultNodeHeight*

---

**Description**

setDefaultNodeHeight set all nodes to the same specified width, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultNodeHeight(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	a numeric, in pixels

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodeHeight", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeHeight(rcy, 80)  
}
```

---

setDefaultNodeShape,RCyjs-method  
*setDefaultNodeShape*

---

**Description**

setDefaultNodeShape change the shape of all nodes

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultNodeShape(
  obj,
  newValue = c("ellipse", "triangle", "rectangle", "roundrectangle",
    "bottomroundrectangle", "cutrectangle", "barrel", "rhomboid", "diamond", "pentagon",
    "hexagon", "concavehexagon", "heptagon", "octagon", "star", "tag", "vee")
)
```

**Arguments**

obj	an RCyjs instance
newValue	a character string, one of "ellipse", "triangle", "rectangle", "roundrectangle", "bottomroundrectangle", "cutrectangle", "barrel", "rhomboid", "diamond", "pentagon", "hexagon", "concavehexagon", "heptagon", "octagon", "star", "tag", "vee"

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setDefaultNodeShape", graph=g)
  layout(rcy, "cose")
  setDefaultNodeShape(rcy, "barrel")
}
```

---

setDefaultNodeSize,RCyjs-method  
*setDefaultNodeSize*

---

**Description**

setDefaultNodeSize set all nodes to the same specified size, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'
setDefaultNodeSize(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	a numeric, in pixels

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodesSize", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeSize(rcy, 80)  
}
```

---

setDefaultNodeWidth,RCyjs-method  
*setDefaultNodeWidth*

---

**Description**

setDefaultNodeWidth set all nodes to the same specified width, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultNodeWidth(obj, newValue)
```

**Arguments**

obj	an RCyjs instance
newValue	a numeric, in pixels

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodesWidth", graph=g)  
  layout(rcy, "cose")  
  setDefaultNodeWidth(rcy, 80)  
}
```



---

setDefaultStyle,RCyjs-method  
*setDefaultStyle*

---

**Description**

setDefaultStyle use some sensible rendering options for all elements of the graph

**Usage**

```
## S4 method for signature 'RCyjs'  
setDefaultStyle(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setDefaultNodesSize", graph=g)  
  layout(rcy, "cose")  
  setDefaultStyle(rcy)  
}
```

---

setEdgeAttributes,RCyjs-method  
*setEdgeAttributes*

---

**Description**

setEdgeAttributes on the graph in the browse

**Usage**

```
## S4 method for signature 'RCyjs'  
setEdgeAttributes(obj, attribute, sourceNodes, targetNodes, edgeTypes, values)
```

**Arguments**

obj	an RCyjs instance
attribute	a character string
sourceNodes	vector of character strings
targetNodes	vector of character strings
edgeTypes	vector of character strings
values	vector of character strings

**Details**

Edges are specified by sourceNode/targetNode/edgeType triples.

**Value**

no return value

---

setEdgeStyle,RCyjs-method  
*setEdgeStyle*

---

**Description**

setEdgeStyle plain & fast (haystack) vs fancy & slower (bezier)

**Usage**

```
## S4 method for signature 'RCyjs'
setEdgeStyle(obj, mode = c("bezier", "haystack"))
```

**Arguments**

obj	an RCyjs instance
mode	a character string, either "bezier" or "haystack"

**Details**

cytoscape.js offers two kinds of edge rendering - a tradeoff in richness and speed edge target decorations (arrows, tee, etc) are only rendered with the "bezier" style

**Value**

no return value

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  layout(rcy, "cose")
  fit(rcy, 100)
  loadStyleFile(rcy, system.file(package="RCyjs", "extdata", "sampleStyle2.js"))
  setEdgeStyle(rcy, "bezier")
  redraw(rcy)
}
```

---

setGraph,RCyjs-method *setGraph*

---

**Description**

setGraph Establish a new graph in RCyjs, removing any previous graph

**Usage**

```
## S4 method for signature 'RCyjs'
setGraph(obj, graph)
```

**Arguments**

obj	RCyjs instance
graph	a graphNEL

**Details**

This method will remove any previous graph in the browser, adding a new one. Setting visual properties and performing layout must follow.

**Value**

nothing

**See Also**

[addGraph](#)

**Examples**

```
if(interactive()){
  sampleGraph <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo")
  setGraph(rcy, sampleGraph)
}
```

---

setNodeAttributes,RCyjs-method  
*setNodeAttributes*

---

### Description

setNodeAttributes put somewhat more detailed description here

### Usage

```
## S4 method for signature 'RCyjs'  
setNodeAttributes(obj, attribute, nodes, values)
```

### Arguments

obj	an RCyjs instance
attribute	a character string
nodes	character strings - node ids
values	scalar values, all of one type (all numeric, or all character, or all integer, ...)

### Details

multi-line description goes here with continuations on subsequent lines if you like

### Value

explain what the method returns

### Examples

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  layout(rcy, "cose")  
  fit(rcy, 100)  
  setNodeAttributes(rcy, "lfc", c("A", "B", "C"), c(0, 0, 0))  
  redraw(rcy)  
}
```

---

setNodeBorderColor,RCyjs-method  
*setNodeBorderColor*

---

**Description**

setNodeBorderColor set the specified nodes to the specified node border color

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeBorderColor(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	legal CSS color names (one or more)

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setNodeBorderColor", graph=g)  
  layout(rcy, "cose")  
  setNodeBorderColor(rcy, "green")  
}
```

---

setNodeBorderWidth,RCyjs-method  
*setNodeBorderWidth*

---

**Description**

setNodeBorderWidth set the specified nodes to the same specified node border width, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeBorderWidth(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	numeric, in pixels (one, or as many as there are nodeIDs)

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setNodeBorderWidth", graph=g)  
  layout(rcy, "cose")  
  setNodeBorderWidth(rcy, 3)  
}
```

---

setNodeColor,RCyjs-method  
*setNodeColor*

---

**Description**

setNodeColor set the specified nodes to the specified color

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeColor(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a character string, legal CSS color names (one or more)

**Value**

no value returned

## Examples

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setNodeColor", graph=g)  
  layout(rcy, "cose")  
  setNodeColor(rcy, 80)  
}
```

---

setNodeColorRule,RCyjs-method  
*setNodeColorRule*

---

## Description

setNodeColorRule control node color via values of the specified attribute

## Usage

```
## S4 method for signature 'RCyjs'  
setNodeColorRule(  
  obj,  
  attribute,  
  control.points,  
  colors,  
  mode = c("interpolate", "lookup")  
)
```

## Arguments

obj	an RCyjs instance
attribute	a character string, the node attribute category whose value controls color
control.points	a list of all possible values of the attribute
colors	the corresponding node color, one specified for each of the control.points
mode	a character string, either "interpolate" or "lookup"

## Details

for interpolate mode, in which the node attribute should be a continuously varying numerical quantity in-between colors are calculated for in-between values. for lookup mode, in which the node attribute is a discrete string variable, simple color lookup is performed.

## Value

no return value

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  layout(rcy, "cose")
  fit(rcy, 100)
  setNodeColorRule(rcy, "count", c(0, 100), c("green", "red"), mode="interpolate")
  redraw(rcy)
}
```

---

setNodeFontColor,RCyjs-method  
*setNodeFontColor*

---

**Description**

setNodeFontColor set the specified nodes to the same specified node font color

**Usage**

```
## S4 method for signature 'RCyjs'
setNodeFontColor(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a character string, a legal CSS color name (one or more)

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setNodeFontColor", graph=g)
  layout(rcy, "cose")
  setNodeFontColor(rcy, "red")
}
```



---

setNodeFontSize,RCyjs-method  
*setNodeFontSize*

---

**Description**

setNodeFontSize set the specified nodes to the same specified node font size

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeFontSize(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a numeric, in pixels (one, or as many as there are nodeIDs)

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setNodeFontSize", graph=g)  
  layout(rcy, "cose")  
  setNodeFontSize(rcy, 5)  
}
```

---

setNodeHeight,RCyjs-method  
*setNodeHeight*

---

**Description**

setNodeHeight set the specified nodes to the specified heights, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeHeight(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a numeric, in pixels (one, or as many as there are nodeIDs)

**Value**

no value returned

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setNodesHeight", graph=g)
  layout(rcy, "cose")
  setNodeHeight(rcy, 80)
}
```

---

setNodeLabelAlignment,RCyjs-method  
*setNodeLabelAlignment*

---

**Description**

setNodeLabelAlignment put somewhat more detailed description here

**Usage**

```
## S4 method for signature 'RCyjs'
setNodeLabelAlignment(obj, horizontal, vertical)
```

**Arguments**

obj	an RCyjs instance
horizontal	character string
vertical	character string

**Details**

multi-line description goes here with continuations on subsequent lines if you like

**Value**

explain what the method returns

---

setNodeLabelRule,RCyjs-method  
*setNodeLabelRule*

---

**Description**

setNodeLabelRule put somewhat more detailed description here

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeLabelRule(obj, attribute)
```

**Arguments**

obj                    an RCyjs instance  
attribute             a character string, the node attribute to display as label

**Details**

multi-line description goes here with continuations on subsequent lines if you like

**Value**

explain what the method returns

**Examples**

```
if(interactive()){  
  g <- createTestGraph(nodeCount=20, edgeCount=20)  
  rcy <- RCyjs(title="layouts", graph=g)  
  setNodeLabelRule(rcy, "label");  
}
```

---

setNodeShape,RCyjs-method  
*setNodeShape*

---

**Description**

setNodeShape set the specified nodes to specified shapes

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeShape(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a character string, one of the legitimate cytoscape.js node shapes

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setNodeShape", graph=g)  
  layout(rcy, "cose")  
  setNodeShape(rcy, 80)  
}
```

---

setNodeSize,RCyjs-method

*setNodeSize*

---

**Description**

setNodeSize set the specified nodes to the specified sizes, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeSize(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a numeric, in pixels (one, or as many as there are nodeIDs)

**Value**

no value returned

**Examples**

```

if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="setNodesSize", graph=g)
  layout(rcy, "cose")
  setNodeSize(rcy, 80)
}

```

---

setNodeSizeRule,RCyjs-method  
*setNodeSizeRule*

---

**Description**

setNodeSizeRule control node size via values of the specified attribute

**Usage**

```

## S4 method for signature 'RCyjs'
setNodeSizeRule(obj, attribute, control.points, node.sizes)

```

**Arguments**

obj	an RCyjs instance
attribute	a character string, the node attribute category whose value controls size
control.points	a list of values of the attribute
node.sizes	the corresponding node size, one specified for each of the control.points

**Details**

actual node sizes are interpolated via the specified relationship of control.points node.sizes

**Value**

no return value

**Examples**

```

if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  layout(rcy, "cose")
  fit(rcy, 100)
  setNodeSizeRule(rcy, "count", c(0, 30, 110), c(20, 50, 100));
  redraw(rcy)
}

```

---

setNodeWidth,RCyjs-method  
*setNodeWidth*

---

**Description**

setNodeWidth set the specified nodes to the specified widths, in pixels

**Usage**

```
## S4 method for signature 'RCyjs'  
setNodeWidth(obj, nodeIDs, newValues)
```

**Arguments**

obj	an RCyjs instance
nodeIDs	a character string (one or more)
newValues	a numeric, in pixels (one, or as many as there are nodeIDs)

**Value**

no value returned

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="setNodesWidth", graph=g)  
  layout(rcy, "cose")  
  setNodeWidth(rcy, 80)  
}
```

---

setPosition,RCyjs-method  
*setPosition*

---

**Description**

setPosition of nodes by their id

**Usage**

```
## S4 method for signature 'RCyjs'  
setPosition(obj, tbl.pos)
```

**Arguments**

obj                    an RCyjs instance  
tbl.pos                a data.frame with three columns: id, x, y

**Value**

no return value

**See Also**

[getPosition](#)

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="getPosition", graph=g)  
  layout(rcy, "cose")  
  tbl.pos <- getPosition(rcy)  
  # shift all the nodes to the right  
  tbl.pos$x <- tbl.pos$x + 50  
  setPosition(rcy, tbl.pos)  
}
```

---

setZoom,RCyjs-method    *setZoom*

---

**Description**

setZoom zoom in or out

**Usage**

```
## S4 method for signature 'RCyjs'  
setZoom(obj, newValue)
```

**Arguments**

obj                    an RCyjs instance  
newValue              numeric, typically be 0.1 (zoomed way out, nodes are small) and 10 (zoomed way in, nodes are large)

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  setZoom(rcy, 0.2)  
  Sys.sleep(1)  
  setZoom(rcy, 5)  
}
```

---

sfn,RCyjs-method      *sfn*

---

**Description**

sfn select first neighbors of the currently selected nodes

**Usage**

```
## S4 method for signature 'RCyjs'  
sfn(obj)
```

**Arguments**

obj                    an RCyjs instance

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  selectNodes(rcy, "A")  
  getSelectedNodes(rcy) # just one  
  sfn()  
  getSelectedNodes(rcy) # now three  
}
```



---

showAll,RCyjs-method    *showAll*

---

**Description**

showAll show any hidden objects: nodes, edges, or both

**Usage**

```
## S4 method for signature 'RCyjs'  
showAll(obj, which = c("both", "nodes", "edges"))
```

**Arguments**

obj                    an RCyjs instance  
which                 a character string, either "nodes", "edges" or "both"

**Value**

no return value

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  layout(rcy, "cose")  
  selectNodes(rcy, getNodes(rcy)$id)  
  hideSelectedNodes(rcy)  
  showAll(rcy, "nodes")  
}
```

---

showEdges,RCyjs-method  
                          *showEdges*

---

**Description**

showEdges if hidden, edges of the specified type will be made visible

**Usage**

```
## S4 method for signature 'RCyjs'  
showEdges(obj, edgeType)
```

**Arguments**

obj                    an RCyjs instance  
edgeType              a character string

**Details**

edgeType is a crucial feature for RCyjs. We assume it is an attribute found on every edge in every graph.

**Value**

no return value

**Examples**

```
if(interactive()){  
  rcy <- RCyjs(title="rcyjs demo", graph=simpleDemoGraph())  
  getNodes(rcy)  
  edaNames(rcy)            # includes "edgeType"  
  eda(rcy, "edgeType") # includes "phosphorylates"  
  hideEdges(rcy, edgeType="phosphorylates")  
  showEdges(rcy, edgeType="phosphorylates")  
}
```

---

showNodes,RCyjs-method

*showNodes*

---

**Description**

showNodes show the named nodes from view

**Usage**

```
## S4 method for signature 'RCyjs'  
showNodes(obj, nodeIDs)
```

**Arguments**

obj                    an RCyjs instance

**Value**

no return value

**See Also**

[showAll](#)

**Examples**

```
if(interactive()){
  g <- simpleDemoGraph()
  rcy <- RCyjs(title="rcyjs demo", graph=g)
  target <- nodes(g)[1]
  hideNodes(rcy, "A")
  getNodes(rcy, "hidden")
  getNodes(rcy, "visible")
  showNodes(rcy, "A")
  getNodes(rcy, "visible")
}
```

---

simpleDemoGraph	<i>simpleDemoGraph</i>
-----------------	------------------------

---

**Description**

simpleDemoGraph

**Usage**

```
simpleDemoGraph()
```

**Value**

a graphNEL with 3 nodes and 3 edges

**Examples**

```
g <- simpleDemoGraph()
```

---

vAlign,RCyjs-method	<i>vAlign</i>
---------------------	---------------

---

**Description**

vAlign vertically align selected nodes

**Usage**

```
## S4 method for signature 'RCyjs'
vAlign(obj)
```

**Arguments**

`obj` an RCyjs instance

**Details**

The shared x coordinate will be the mean of the x coordinates of selected nodes. The y coordinates are preserved.

**Value**

no return value

**Examples**

```
if(interactive()){  
  g <- simpleDemoGraph()  
  rcy <- RCyjs(title="rcyjs demo", graph=g)  
  layout(rcy, "cose")  
  selectNodes(rcy, nodes(g)[1:2])  
  vAlign(rcy)  
}
```

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