

# 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      *createTestGraph*

---

**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	<i>deleteGraph</i>
--------------------------	--------------------

---

**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)
}
```

---

getNodes,RCyjs-method *getNodes*

---

**Description**

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

**Usage**

```
## S4 method for signature 'RCyjs'
getNodes(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())
  getNodes(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

*noa*

---

### 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

*noaNames*

---

**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**

<code>obj</code>	an RCyjs instance
<code>nodeIDs</code>	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**

<code>obj</code>	an RCyjs instance
<code>newValue</code>	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")  
  setDefaultEdgeLineStyle(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", "pen-  
 tagon", "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            *simpleDemoGraph*

---

**Description**

simpleDemoGraph

**Usage**

```
simpleDemoGraph()
```

**Value**

a graphNEL with 3 nodes and 3 edges

**Examples**

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

---

vAlign,RCyjs-method    *vAlign*

---

**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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