Package 'RCyjs'

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Type Package

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Contents

addGraph,RCyjs-method 3
addGraphFromFile,RCyjs-method 4
clearSelection,RCyjs-method 5
createTestGraph 6

dataFramesToJSON . . . 6
deleteGraph,RCyjs-method . . . 7
deleteSelectedNodes,RCyjs-method . . . 8
eda . . . 8
edaNames . . . 9
fit,RCyjs-method . . . 10
fitSelection,RCyjs-method . . . 10
getEdgeCount,RCyjs-method . . . 11
getJSON,RCyjs-method . . . 12
getLayoutStrategies,RCyjs-method . . . 12
getNodeCount,RCyjs-method . . . 13
getNodes,RCyjs-method . . . 14
getPosition,RCyjs-method . . . 14
getSelectedNodes,RCyjs-method . . . 15
getSupportedEdgeDecoratorShapes,RCyjs-method . . . 16
getSupportedNodeShapes,RCyjs-method . . . 16
getZoom,RCyjs-method . . . 17
graphNELtoJSON.string . . . 18
hAlign,RCyjs-method . . . 18
hideAllEdges,RCyjs-method . . . 19
hideEdges,RCyjs-method . . . 20
hideNodes,RCyjs-method . . . 21
hideSelectedNodes,RCyjs-method . . . 22
invertNodeSelection,RCyjs-method . . . 23
layout,RCyjs-method . . . 23
layoutSelectionInGrid,RCyjs-method . . . 24
layoutSelectionInGridInferAnchor,RCyjs-method . . . 25
loadStyleFile,RCyjs-method . . . 26
noa . . . 27
noaNames . . . 27
RCyjs-class . . . 28
readAndStandardizeJSONNetworkFile . . . 29
readAndStandardizeJSONStyleFile . . . 29
redraw,RCyjs-method . . . 30
restoreLayout,RCyjs-method . . . 30
saveJPG,RCyjs-method . . . 31
saveLayout,RCyjs-method . . . 32
savePNG,RCyjs-method . . . 33
selectFirstNeighborsOfSelectedNodes,RCyjs-method . . . 34
selectNodes,RCyjs-method . . . 34
setBackgroundColor,RCyjs-method . . . 35
setDefaultEdgeColor,RCyjs-method . . . 36
setDefaultEdgeLineColor,RCyjs-method . . . 36
setDefaultEdgeLineStyle,RCyjs-method . . . 37
setDefaultEdgeSourceArrowColor,RCyjs-method . . . 38
setDefaultEdgeSourceArrowShape,RCyjs-method . . . 39
setDefaultEdgeTargetArrowColor,RCyjs-method . . . 40
setDefaultEdgeTargetArrowShape,RCyjs-method . . . 40

setDefaultEdgeWidth,RCyjs-method . . . 41
setDefaultNodeBorderColor,RCyjs-method . . . 42
setDefaultNodeBorderWidth,RCyjs-method . . . 43
setDefaultNodeColor,RCyjs-method . . . 43
setDefaultNodeFontColor,RCyjs-method . . . 44
setDefaultNodeFontSize,RCyjs-method . . . 45
setDefaultNodeHeight,RCyjs-method . . . 46
setDefaultNodeShape,RCyjs-method . . . 46
setDefaultNodeSize,RCyjs-method . . . 47
setDefaultNodeWidth,RCyjs-method . . . 48
setDefaultStyle,RCyjs-method . . . 49
setEdgeAttributes,RCyjs-method . . . 49
setEdgeStyle,RCyjs-method . . . 50
setGraph,RCyjs-method . . . 51
setNodeAttributes,RCyjs-method . . . 52
setNodeBorderColor,RCyjs-method . . . 53
setNodeBorderWidth,RCyjs-method . . . 53
setNodeColor,RCyjs-method . . . 54
setNodeColorRule,RCyjs-method . . . 55
setNodeFontColor,RCyjs-method . . . 56
setNodeFontSize,RCyjs-method . . . 57
setNodeHeight,RCyjs-method . . . 57
setNodeLabelAlignment,RCyjs-method . . . 58
setNodeLabelRule,RCyjs-method . . . 59
setNodeShape,RCyjs-method . . . 59
setNodeSize,RCyjs-method . . . 60
setNodeSizeRule,RCyjs-method . . . 61
setNodeWidth,RCyjs-method . . . 62
setPosition,RCyjs-method . . . 62
setZoom,RCyjs-method . . . 63
sfn,RCyjs-method . . . 64
showAll,RCyjs-method . . . 65
showEdges,RCyjs-method . . . 65
showNodes,RCyjs-method . . . 66
simpleDemoGraph . . . 67
vAlign,RCyjs-method . . . 67

Index **69**

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

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)
  deletetGraph(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 toa
   }
```

---

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. Becuase "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 and "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 stategies){
     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 Biocondcutor 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 assignements

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 specifed 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 specifed 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 specifed 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 richess 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 specifed 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 specifed 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 specifed 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 continusously 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 specifed 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 specifed 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 specifed 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

setNodelLabelAlignment

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 specifed 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 specifed 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 specifed 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)
  }
```

Index

.RCyjs *(RCyjs-class)*, 28

addGraph, *7*, *51*
addGraph *(addGraph,RCyjs-method)*, 3
addGraph,RCyjs-method, 3
addGraphFromFile
(addGraphFromFile,RCyjs-method), 4
addGraphFromFile,RCyjs-method, 4

clearSelection
(clearSelection,RCyjs-method), 5
clearSelection,RCyjs-method, 5
createTestGraph, 6

dataFramesToJSON, 6
deleteGraph *(deleteGraph,RCyjs-method)*, 7
deleteGraph,RCyjs-method, 7
deleteSelectedNodes
(deleteSelectedNodes,RCyjs-method), 8
deleteSelectedNodes,RCyjs-method, 8

eda, 8
edaNames, 9

fit *(fit,RCyjs-method)*, 10
fit,RCyjs-method, 10
fitSelection
(fitSelection,RCyjs-method), 10
fitSelection,RCyjs-method, 10

getEdgeCount
(getEdgeCount,RCyjs-method), 11
getEdgeCount,RCyjs-method, 11
getJSON *(getJSON,RCyjs-method)*, 12
getJSON,RCyjs-method, 12
getLayoutStrategies, *24*
getLayoutStrategies
(getLayoutStrategies,RCyjs-method), 12
getLayoutStrategies,RCyjs-method, 12
getNodeCount
(getNodeCount,RCyjs-method), 13
getNodeCount,RCyjs-method, 13
getNodes *(getNodes,RCyjs-method)*, 14
getNodes,RCyjs-method, 14
getPosition, *63*
getPosition *(getPosition,RCyjs-method)*, 14
getPosition,RCyjs-method, 14
getSelectedNodes
(getSelectedNodes,RCyjs-method), 15
getSelectedNodes,RCyjs-method, 15
getSupportedEdgeDecoratorShapes
(getSupportedEdgeDecoratorShapes,RCyjs-method), 16
getSupportedEdgeDecoratorShapes,RCyjs-method, 16
getSupportedNodeShapes
(getSupportedNodeShapes,RCyjs-method), 16
getSupportedNodeShapes,RCyjs-method, 16
getZoom *(getZoom,RCyjs-method)*, 17
getZoom,RCyjs-method, 17
graphNELtoJSON.string, 18

hAlign *(hAlign,RCyjs-method)*, 18
hAlign,RCyjs-method, 18
hideAllEdges
(hideAllEdges,RCyjs-method), 19
hideAllEdges,RCyjs-method, 19
hideEdges *(hideEdges,RCyjs-method)*, 20
hideEdges,RCyjs-method, 20
hideNodes *(hideNodes,RCyjs-method)*, 21
hideNodes,RCyjs-method, 21

hideSelectedNodes
(hideSelectedNodes,RCyjs-method), 22
hideSelectedNodes,RCyjs-method, 22

invertNodeSelection
(invertNodeSelection,RCyjs-method), 23
invertNodeSelection,RCyjs-method, 23

layout (layout,RCyjs-method), 23
layout,RCyjs-method, 23
layoutSelectionInGrid
(layoutSelectionInGrid,RCyjs-method), 24
layoutSelectionInGrid,RCyjs-method, 24
layoutSelectionInGridInferAnchor
(layoutSelectionInGridInferAnchor,RCyjs-method), 25
layoutSelectionInGridInferAnchor,RCyjs-method, 25
loadStyleFile
(loadStyleFile,RCyjs-method), 26
loadStyleFile,RCyjs-method, 26

noa, 27
noaNames, 27

RCyjs (RCyjs-class), 28
RCyjs-class, 28
readAndStandardizeJSONNetworkFile, 29
readAndStandardizeJSONStyleFile, 29
redraw (redraw,RCyjs-method), 30
redraw,RCyjs-method, 30
restoreLayout, *32*
restoreLayout
(restoreLayout,RCyjs-method), 30
restoreLayout,RCyjs-method, 30

saveJPG (saveJPG,RCyjs-method), 31
saveJPG,RCyjs-method, 31
saveLayout, *31*
saveLayout (saveLayout,RCyjs-method), 32
saveLayout,RCyjs-method, 32
savePNG (savePNG,RCyjs-method), 33
savePNG,RCyjs-method, 33

selectFirstNeighborsOfSelectedNodes
(selectFirstNeighborsOfSelectedNodes,RCyjs-method), 34
selectFirstNeighborsOfSelectedNodes,RCyjs-method, 34
selectNodes (selectNodes,RCyjs-method), 34
selectNodes,RCyjs-method, 34
setBackgroundColor
(setBackgroundColor,RCyjs-method), 35
setBackgroundColor,RCyjs-method, 35
setDefaultEdgeColor
(setDefaultEdgeColor,RCyjs-method), 36
setDefaultEdgeColor,RCyjs-method, 36
setDefaultEdgeLineColor
(setDefaultEdgeLineColor,RCyjs-method), 36
setDefaultEdgeLineColor,RCyjs-method, 36
setDefaultEdgeLineStyle
(setDefaultEdgeLineStyle,RCyjs-method), 37
setDefaultEdgeLineStyle,RCyjs-method, 37
setDefaultEdgeSourceArrowColor
(setDefaultEdgeSourceArrowColor,RCyjs-method), 38
setDefaultEdgeSourceArrowColor,RCyjs-method, 38
setDefaultEdgeSourceArrowShape
(setDefaultEdgeSourceArrowShape,RCyjs-method), 39
setDefaultEdgeSourceArrowShape,RCyjs-method, 39
setDefaultEdgeTargetArrowColor
(setDefaultEdgeTargetArrowColor,RCyjs-method), 40
setDefaultEdgeTargetArrowColor,RCyjs-method, 40
setDefaultEdgeTargetArrowShape
(setDefaultEdgeTargetArrowShape,RCyjs-method), 40
setDefaultEdgeTargetArrowShape,RCyjs-method, 40
setDefaultEdgeWidth
(setDefaultEdgeWidth,RCyjs-method),

41
setDefaultEdgeWidth,RCyjs-method, 41
setDefaultNodeBorderColor
(setDefaultNodeBorderColor,RCyjs-method), 42
setDefaultNodeBorderColor,RCyjs-method, 42
setDefaultNodeBorderWidth
(setDefaultNodeBorderWidth,RCyjs-method), 43
setDefaultNodeBorderWidth,RCyjs-method, 43
setDefaultNodeColor
(setDefaultNodeColor,RCyjs-method), 43
setDefaultNodeColor,RCyjs-method, 43
setDefaultNodeFontColor
(setDefaultNodeFontColor,RCyjs-method), 44
setDefaultNodeFontColor,RCyjs-method, 44
setDefaultNodeFontSize
(setDefaultNodeFontSize,RCyjs-method), 45
setDefaultNodeFontSize,RCyjs-method, 45
setDefaultNodeHeight
(setDefaultNodeHeight,RCyjs-method), 46
setDefaultNodeHeight,RCyjs-method, 46
setDefaultNodeShape
(setDefaultNodeShape,RCyjs-method), 46
setDefaultNodeShape,RCyjs-method, 46
setDefaultNodeSize
(setDefaultNodeSize,RCyjs-method), 47
setDefaultNodeSize,RCyjs-method, 47
setDefaultNodeWidth
(setDefaultNodeWidth,RCyjs-method), 48
setDefaultNodeWidth,RCyjs-method, 48
setDefaultStyle
(setDefaultStyle,RCyjs-method), 49
setDefaultStyle,RCyjs-method, 49
setEdgeAttributes
(setEdgeAttributes,RCyjs-method), 49
setEdgeAttributes,RCyjs-method, 49
setEdgeStyle
(setEdgeStyle,RCyjs-method), 50
setEdgeStyle,RCyjs-method, 50
setGraph, 7
setGraph (setGraph,RCyjs-method), 51
setGraph,RCyjs-method, 51
setNodeAttributes
(setNodeAttributes,RCyjs-method), 52
setNodeAttributes,RCyjs-method, 52
setNodeBorderColor
(setNodeBorderColor,RCyjs-method), 53
setNodeBorderColor,RCyjs-method, 53
setNodeBorderWidth
(setNodeBorderWidth,RCyjs-method), 53
setNodeBorderWidth,RCyjs-method, 53
setNodeColor
(setNodeColor,RCyjs-method), 54
setNodeColor,RCyjs-method, 54
setNodeColorRule
(setNodeColorRule,RCyjs-method), 55
setNodeColorRule,RCyjs-method, 55
setNodeFontColor
(setNodeFontColor,RCyjs-method), 56
setNodeFontColor,RCyjs-method, 56
setNodeFontSize
(setNodeFontSize,RCyjs-method), 57
setNodeFontSize,RCyjs-method, 57
setNodeHeight
(setNodeHeight,RCyjs-method), 57
setNodeHeight,RCyjs-method, 57
setNodeLabelAlignment
(setNodeLabelAlignment,RCyjs-method), 58
setNodeLabelAlignment,RCyjs-method, 58
setNodeLabelRule
(setNodeLabelRule,RCyjs-method), 59
setNodeLabelRule,RCyjs-method, 59
setNodeShape

(setNodeShape,RCyjs-method), 59
setNodeShape,RCyjs-method, 59
setNodeSize (setNodeSize,RCyjs-method), 60
setNodeSize,RCyjs-method, 60
setNodeSizeRule (setNodeSizeRule,RCyjs-method), 61
setNodeSizeRule,RCyjs-method, 61
setNodeWidth (setNodeWidth,RCyjs-method), 62
setNodeWidth,RCyjs-method, 62
setPosition (setPosition,RCyjs-method), 62
setPosition,RCyjs-method, 62
setZoom (setZoom,RCyjs-method), 63
setZoom,RCyjs-method, 63
sfn (sfn,RCyjs-method), 64
sfn,RCyjs-method, 64
showAll, *21*, *22*, *66*
showAll (showAll,RCyjs-method), 65
showAll,RCyjs-method, 65
showEdges (showEdges,RCyjs-method), 65
showEdges,RCyjs-method, 65
showNodes (showNodes,RCyjs-method), 66
showNodes,RCyjs-method, 66
simpleDemoGraph, 67

vAlign (vAlign,RCyjs-method), 67
vAlign,RCyjs-method, 67