

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

<code>nodeCount</code>	1 or more
<code>edgeCount</code>	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

<code>tbl.edges</code>	data.frame, with source, target and interaction columns, others option for edge attributes
<code>tbl.nodes</code>	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 to a  
}
```

getLayoutStrategies,RCyjs-method
getLayoutStrategies

Description

`getLayoutStrategies` return a list of those currently offered

Usage

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

Arguments

`obj` an RCyjs instance

Value

a list of character strings

Examples

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

getNodeCount,RCyjs-method
getNodeCount

Description

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

Usage

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

Arguments

`obj` RCyjs instance

Value

numeric count

Examples

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

getNode,RCyjs-method *getNode*

Description

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

Usage

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

Arguments

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

Details

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

Value

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

Examples

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

getPosition,RCyjs-method
getPosition

Description

getPosition for all or specified nodes

Usage

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

Arguments

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

Value

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

Examples

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

getSelectedNodes,RCyjs-method
getSelectedNodes

Description

getSelectedNodes get the selected nodes

Usage

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

Arguments

obj an RCyjs instance

Value

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

Examples

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

getSupportedEdgeDecoratorShapes,RCyjs-method
getSupportedEdgeDecoratorShapes

Description

`getSupportedEdgeDecoratorShapes` return a list of those currently offered

Usage

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

Arguments

`obj` an `RCyjs` instance

Value

a list of character strings

Examples

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

getSupportedNodeShapes,RCyjs-method
getSupportedNodeShapes

Description

`getSupportedNodeShapes` return a list of those currently offered

Usage

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


Arguments

obj an RCyjs instance

Value

a list of character strings

Examples

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

getZoom,RCyjs-method *getZoom*

Description

getZoom learn the zoom level of the current display

Usage

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

Arguments

obj an RCyjs instance

Value

no return value

Examples

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

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

Description

Convert R graphNEL object to cytoscape.js JSON.

Usage

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

Arguments

`g` a graphNEL

Examples

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

`hAlign,RCyjs-method` *hAlign*

Description

`hAlign` horizontally align selected nodes

Usage

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

Arguments

`obj` an RCyjs instance

Details

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

Value

no return value

Examples

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

hideAllEdges,RCyjs-method

hideAllEdges

Description

hideAllEdges

Usage

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

Arguments

obj an RCyjs instance

Value

no return value

Examples

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

hideEdges,RCyjs-method
hideEdges

Description

hideEdges hide all edges of the specified type

Usage

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

Arguments

obj	an RCyjs instance
edgeType	a character string

Details

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

Value

no return value

Examples

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

hideNodes,RCyjs-method

hideNodes

Description

hideNodes hide the named nodes from view

Usage

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

Arguments

obj an RCyjs instance

Details

The hidden nodes are not deleted from the graph

Value

no return value

See Also

[showAll](#)

Examples

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

hideSelectedNodes,RCyjs-method
hideSelectedNodes

Description

hideSelectedNodes hide selected nodes from view

Usage

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

Arguments

obj an RCyjs instance

Details

The hidden nodes are not deleted from the graph

Value

no return value

See Also

[showAll](#)

Examples

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

invertNodeSelection,RCyjs-method
invertNodeSelection

Description

invertNodeSelection deselect all selected nodes, select all previously unselected nodes

Usage

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

Arguments

obj an RCyjs instance

Value

no return value

Examples

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

layout,RCyjs-method *layout*

Description

layout apply a layout algorithm to the current grap

Usage

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

Arguments

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

Value

explain what the method returns

See Also

[getLayoutStrategies](#)

Examples

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

layoutSelectionInGrid,RCyjs-method
layoutSelectionInGrid

Description

layoutSelectionInGrid arrange selected nodes in this region

Usage

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

Arguments

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

Value

no return value

Examples

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

layoutSelectionInGridInferAnchor,RCyjs-method
layoutSelectionInGridInferAnchor

Description

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

Usage

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

Arguments

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

Details

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

Value

explain what the method returns

Examples

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

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

loadStyleFile,RCyjs-method

loadStyleFile

Description

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

Usage

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

Arguments

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

Value

nothing

References

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

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

Examples

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

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

Description

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

Usage

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

Arguments

graph	a graphNEL
node.attribute.name	a character string

Value

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

Examples

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

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

Description

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

Usage

```
noaNames(graph)
```

Arguments

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

Value

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

Examples

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

 RCyjs-class

Create an RCyjs object

Description

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

Usage

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

Arguments

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

Value

An object of the RCyjs class

Examples

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

readAndStandardizeJSONNetworkFile

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

Description

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

Usage

readAndStandardizeJSONNetworkFile(filename)

Arguments

file a json file

readAndStandardizeJSONStyleFile

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

Description

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

Usage

readAndStandardizeJSONStyleFile(filename)

Arguments

file a json file

redraw,RCyjs-method *redraw*

Description

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

Usage

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

Arguments

obj an RCyjs instance

Value

explain what the method returns

Examples

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

restoreLayout,RCyjs-method
 restoreLayout

Description

restoreLayout restore a previously-saved layout

Usage

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

Arguments

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

Value

no return value

See Also

[saveLayout](#)

Examples

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

saveJPG,RCyjs-method *saveJPG*

Description

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

Usage

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

Arguments

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

Value

no return value

Examples

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

saveLayout,RCyjs-method

saveLayout

Description

saveLayout to a named file

Usage

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

Arguments

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

Details

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

Value

no return value

See Also

[restoreLayout](#)

Examples

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

savePNG,RCyjs-method *savePNG*

Description

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

Usage

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

Arguments

obj	an RCyjs instance
filename	a character string

Value

no return value

Examples

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

`selectFirstNeighborsOfSelectedNodes,RCyjs-method`
selectFirstNeighborsOfSelectedNodes

Description

`selectFirstNeighborsOfSelectedNodes`

Usage

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

Arguments

`obj` an RCyjs instance

Value

no return value

Examples

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

`selectNodes,RCyjs-method`
selectNodes

Description

`selectNodes` by node id

Usage

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

Arguments

obj an RCyjs instance
nodeIDs character strings

Value

no return value

Examples

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

setBackgroundColor,RCyjs-method
setBackgroundColor

Description

setBackgroundColor of the entire cytoscape.js div

Usage

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

Arguments

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

Value

no return value

Examples

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

setDefaultEdgeColor,RCyjs-method
setDefaultEdgeColor

Description

setDefaultEdgeColor

Usage

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

Arguments

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

Value

no value returned

Examples

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

setDefaultEdgeLineColor,RCyjs-method
setDefaultEdgeLineColor

Description

setDefaultEdgeLineColor

Usage

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

Arguments

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

Value

no value returned

Examples

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

setDefaultEdgeLineStyle,RCyjs-method
setDefaultEdgeLineStyle

Description

setDefaultEdgeLineStyle put somewhat more detailed description here

Usage

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

Arguments

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

Details

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

Value

no value returned

Examples

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

setDefaultEdgeSourceArrowColor,RCyjs-method
setDefaultEdgeSourceArrowColor

Description

setDefaultEdgeSourceArrowColor

Usage

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

Arguments

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

Value

no value returned

Examples

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

setDefaultEdgeSourceArrowShape,RCyjs-method
setDefaultEdgeSourceArrowShape

Description

setDefaultEdgeSourceArrowShape put somewhat more detailed description here

Usage

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

Arguments

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

Details

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

Value

no value returned

Examples

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

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

Description

```
setDefaultEdgeTargetArrowColor
```

Usage

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

Arguments

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

Value

```
no value returned
```

Examples

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

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

Description

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

Usage

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


Arguments

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

Details

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

Value

no value returned

Examples

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

setDefaultEdgeWidth,RCyjs-method
setDefaultEdgeWidth

Description

setDefaultEdgeWidth in pixels

Usage

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

Arguments

obj	an RCyjs instance
newValue	a numeric

Value

no value returned

Examples

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

setDefaultNodeBorderColor,RCyjs-method
setDefaultNodeBorderColor

Description

setDefaultNodeBorderColor put somewhat more detailed description here

Usage

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

Arguments

obj	an RCyjs instance
newValue	any CSS color

Value

no value returned

Examples

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

setDefaultNodeBorderWidth,RCyjs-method
setDefaultNodeBorderWidth

Description

setDefaultNodeBorderWidth in pixels

Usage

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

Arguments

obj	an RCyjs instance
newValue	numeric, in pixels

Value

no value returned

Examples

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

setDefaultNodeColor,RCyjs-method
setDefaultNodeColor

Description

setDefaultNodeColor put somewhat more detailed description here

Usage

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

Arguments

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

Details

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

Value

no value returned

Examples

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

setDefaultNodeFontColor,RCyjs-method
setDefaultNodeFontColor

Description

setDefaultNodeFontColor

Usage

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

Arguments

obj an RCyjs instance
newValue any CSS color

Value

no value returned

Examples

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

setDefaultNodeFontSize,RCyjs-method
setDefaultNodeFontSize

Description

setDefaultNodeFontSize put somewhat more detailed description here

Usage

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

Arguments

obj	an RCyjs instance
newValue	numeric, in points

Details

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

Value

no value returned

Examples

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

setDefaultNodeHeight,RCyjs-method
setDefaultNodeHeight

Description

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

Usage

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

Arguments

obj	an RCyjs instance
newValue	a numeric, in pixels

Value

no value returned

Examples

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

setDefaultNodeShape,RCyjs-method
setDefaultNodeShape

Description

setDefaultNodeShape change the shape of all nodes

Usage

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

Arguments

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

Value

no value returned

Examples

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

setDefaultNodeSize,RCyjs-method
setDefaultNodeSize

Description

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

Usage

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

Arguments

obj	an RCyjs instance
newValue	a numeric, in pixels

Value

no value returned

Examples

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

setDefaultNodeWidth,RCyjs-method
setDefaultNodeWidth

Description

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

Usage

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

Arguments

obj	an RCyjs instance
newValue	a numeric, in pixels

Value

no value returned

Examples

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

setDefaultStyle,RCyjs-method
setDefaultStyle

Description

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

Usage

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

Arguments

obj an RCyjs instance

Value

no value returned

Examples

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

setEdgeAttributes,RCyjs-method
setEdgeAttributes

Description

setEdgeAttributes on the graph in the browse

Usage

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

Arguments

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

Details

Edges are specified by sourceNode/targetNode/edgeType triples.

Value

no return value

setEdgeStyle,RCyjs-method
setEdgeStyle

Description

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

Usage

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

Arguments

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

Details

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

Value

no return value

Examples

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

setGraph,RCyjs-method *setGraph*

Description

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

Usage

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

Arguments

obj	RCyjs instance
graph	a graphNEL

Details

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

Value

nothing

See Also

[addGraph](#)

Examples

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

setNodeAttributes,RCyjs-method
setNodeAttributes

Description

setNodeAttributes put somewhat more detailed description here

Usage

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

Arguments

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

Details

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

Value

explain what the method returns

Examples

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

setNodeBorderColor,RCyjs-method
setNodeBorderColor

Description

setNodeBorderColor set the specified nodes to the specified node border color

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeBorderWidth,RCyjs-method
setNodeBorderWidth

Description

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

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeColor,RCyjs-method
setNodeColor

Description

setNodeColor set the specified nodes to the specified color

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeColorRule,RCyjs-method
setNodeColorRule

Description

setNodeColorRule control node color via values of the specified attribute

Usage

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

Arguments

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

Details

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

Value

no return value

Examples

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

setNodeFontColor,RCyjs-method
setNodeFontColor

Description

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

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeFontSize,RCyjs-method
setNodeFontSize

Description

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

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeHeight,RCyjs-method
setNodeHeight

Description

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

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeLabelAlignment,RCyjs-method
setNodeLabelAlignment

Description

setNodeLabelAlignment put somewhat more detailed description here

Usage

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

Arguments

obj	an RCyjs instance
horizontal	character string
vertical	character string

Details

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

Value

explain what the method returns

setNodeLabelRule,RCyjs-method
setNodeLabelRule

Description

setNodeLabelRule put somewhat more detailed description here

Usage

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

Arguments

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

Details

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

Value

explain what the method returns

Examples

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

setNodeShape,RCyjs-method
setNodeShape

Description

setNodeShape set the specified nodes to specified shapes

Usage

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

Arguments

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

Value

no value returned

Examples

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

setNodeSize,RCyjs-method

setNodeSize

Description

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

Usage

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

Arguments

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

Value

no value returned

Examples

```

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

```

```

setNodeSizeRule,RCyjs-method
setNodeSizeRule

```

Description

setNodeSizeRule control node size via values of the specified attribute

Usage

```

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

```

Arguments

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

Details

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

Value

no return value

Examples

```

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

```

setNodeWidth,RCyjs-method
setNodeWidth

Description

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

Usage

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

Arguments

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

Value

no value returned

Examples

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

setPosition,RCyjs-method
setPosition

Description

setPosition of nodes by their id

Usage

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

Arguments

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

Value

no return value

See Also

[getPosition](#)

Examples

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

setZoom,RCyjs-method *setZoom*

Description

setZoom zoom in or out

Usage

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

Arguments

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

Value

no return value

Examples

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

sfn,RCyjs-method *sfn*

Description

sfn select first neighbors of the currently selected nodes

Usage

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

Arguments

obj an RCyjs instance

Value

no return value

Examples

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

showAll,RCyjs-method *showAll*

Description

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

Usage

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

Arguments

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

Value

no return value

Examples

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

showEdges,RCyjs-method
 showEdges

Description

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

Usage

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

Arguments

obj an RCyjs instance
edgeType a character string

Details

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

Value

no return value

Examples

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

showNodes,RCyjs-method

showNodes

Description

showNodes show the named nodes from view

Usage

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

Arguments

obj an RCyjs instance

Value

no return value

See Also

[showAll](#)

Examples

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

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

Description

simpleDemoGraph

Usage

```
simpleDemoGraph()
```

Value

a graphNEL with 3 nodes and 3 edges

Examples

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

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

Description

vAlign vertically align selected nodes

Usage

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

Arguments

`obj` an RCyjs instance

Details

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

Value

no return value

Examples

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

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