

# Package ‘RCyjs’

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**Type** Package

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

**Version** 1.0.0

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**Depends** R (>= 3.1.0), BrowserViz, graph (>= 1.44.0)

**Imports** methods, httpuv (>= 1.3.2), Rcpp (>= 0.11.5), jsonlite (>= 0.9.15), igraph, BiocGenerics

**Suggests** RUnit, BiocStyle, RefNet

**Description** Interactive viewing and exploration of graphs, connecting R to Cytoscape.js

**License** GPL-2

**URL** <http://rcytoscape.systemsbiology.net>

**LazyLoad** yes

**biocViews** Visualization, GraphAndNetwork, ThirdPartyClient

**NeedsCompilation** no

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 RCyjsClass

*RCyjs: Interactive R/browser network visualization, using cytoscape.js*


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## Description

A "Cytoscape ecosystem" exists, with the desktop Cytoscape 3.x as the heavyweight tool, and the browser-based cytoscape.js a very nice and somewhat compatible alternative. The current package, RCyjs, provides programmatic control of cytoscape.js from an R session using the BrowserViz base class. This ensures that both R and the cytoscape.js sessions retain full interactivity. A large portion of the RCyjs API is taken from the RCytoscape package.

## Usage

```

RCyjs(portRange, host="localhost", title="RCyjs", graph=graphNEL(), quiet=TRUE)
simpleDemoGraph()
createTestGraph(nodeCount, edgeCount)
biocGraphToCytoscapeJSON(graph)
noa(graph, node.attribute.name)
eda(graph, edge.attribute.name)
noaNames(graph)
edaNames(graph)

## S4 method for signature 'RCyjsClass'
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## S4 method for signature 'RCyjsClass'
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## S4 method for signature 'RCyjsClass'
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setNodeColorRule(obj, attribute, control.points, colors, mode)
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## S4 method for signature 'RCyjsClass'
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getPosition(obj, nodeIDs=NA)
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getLayout(obj)
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saveLayout(obj, filename)
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setZoom(obj, newValue)
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fitContent(obj)
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selectNodes(obj, nodeIDs)
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setDefaultNodeSize(obj, newValue)
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setDefaultNodeHeight(obj, newValue)
## S4 method for signature 'RCyjsClass'
setDefaultNodeShape(obj, newValue)
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setDefaultNodeFontSize(obj, newValue)
## S4 method for signature 'RCyjsClass'
setDefaultNodeBorderColor(obj, newValue)
## S4 method for signature 'RCyjsClass'
setDefaultEdgeTargetArrowShape(obj, newValue)
```

```

## S4 method for signature 'RCyjsClass'
setDefaultEdgeColor(obj, newValue)
## S4 method for signature 'RCyjsClass'
setDefaultEdgeTargetArrowColor(obj, newValue)
## S4 method for signature 'RCyjsClass'
setDefaultEdgeFontSize(obj, newValue)
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setDefaultEdgeSourceArrowColor(obj, newValue)
## S4 method for signature 'RCyjsClass'
setDefaultEdgeSourceArrowShape(obj, newValue)

```

### Arguments

portRange	One or more consecutive integers in the range 1025-65535. A typical choice is 9000:9024. The BrowserViz class constructor will try these one at a time in succession until a free port is found and the connection to your web browser is established. If no open ports are found in the supplied range, an error is reported.
host	Nearly always left to its default value, "localhost" but included as a parameter supporting remote computers for future flexibility.
title	The constructor creates a new window (or a new tab, depending on how you web browser is configured). This title is displayed at the top of the window or tab.
graph	A graphNEL object.
quiet	Trace and tracking messages are written to the R console if this variable is set to FALSE.
obj	The RCyjsClass object returned by the class constructor.
newValue	A new size, color, shape (etc.) value to be used in rendering the network.
horizontal	"left", "right", "center": specifies node label position.
vertical	"top", "bottom", "center": specifies node label position.
attribute	Many network rendering rules are controlled by the value of a node or edge attribute. This character string is the name of that controlling attribute.
control.points	Values (2 or more) of an edge or node attribute at which color, size (etc) rendering changes.

<code>node.sizes</code>	A list of pixel values.
<code>colors</code>	A list of colors. Well-known names (e.g., "red") can be used. An RGB triplet (red, green blue) will always work, and provides more specificity: "rgb(0, 255, 128)"
<code>mode</code>	either "lookup" for when the controlling node or edge attribute is categorical, or "interpolate" when the attribute is continuous.
<code>node.shapes</code>	One of "ellipse", "triangle", "pentagon", "hexagon", "heptagon", "octagon", "star", "rectangle", "roundrectangle".
<code>widths</code>	The width, in pixels, for edges.
<code>shapes</code>	For edge "decorations" – the arrow (and etcetera) that decorates the ends of edges, as they connect to nodes. Currently supported values are "arrow", "tee" and "none" (the default).
<code>strategy</code>	A character string, this names a network layout strategy. Currently supported: "breadthfirst", "circle", "concentric", "cose", "grid", "random".
<code>nodeIDs</code>	Nodes as identified by the "id" field in their cytoscape.js data.
<code>tbl.pos</code>	A 3-column data.frame describing node positions: "id", "x", "y"
<code>filename</code>	A character string representing a valid path in your filesystem.
<code>nodeCount</code>	An integer value for the requested graph.
<code>edgeCount</code>	An integer value for the requested graph.
<code>node.attribute.name</code>	a character string.
<code>edge.attribute.name</code>	a character string.

**Author(s)**

Paul Shannon

**Examples**

```

library(RCyjs)

g <- simpleDemoGraph() # a 3-node, 3-edge graph with some node and edge attributes
noaNames(g)
edaNames(g)

rcy <- RCyjs(portRange=9047:9057, quiet=TRUE, graph=g);

title <- "demo"
setBrowserWindowTitle(rcy, title)

tbl.nodes <- getNodes(rcy)

setNodeLabelRule(rcy, "label");
setNodeSizeRule(rcy, "count", c(0, 30, 110), c(20, 50, 100));
setNodeColorRule(rcy, "count", c(0, 100), c("rgb(0,255,0)", "rgb(255,0,0)"), mode="interpolate")

```

```
redraw(rcy)
layout(rcy, "cose")
closeWebSocket(rcy)
```

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