Package 'RCy3'

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Type Package

Title Functions to Access and Control Cytoscape

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Imports httr, methods, RJSONIO, XML, utils, BiocGenerics, stats, graph, fs, uuid, stringi, glue, RCurl, base64url, base64enc, IRkernel, IRdisplay, RColorBrewer, gplots

Suggests BiocStyle, knitr, rmarkdown, igraph, grDevices

SystemRequirements Cytoscape (>= 3.7.1), CyREST (>= 3.8.0)

Description Vizualize, analyze and explore networks using Cytoscape via R. Anything you can do using the graphical user interface of Cytoscape, you can now do with a single RCy3 function.

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URL `https://github.com/cytoscape/RCy3`

BugReports `https://github.com/cytoscape/RCy3/issues`

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NeedsCompilation no

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Contents

`.exportShowImage` *.exportShowImage*

Description

Show network view in notebook output.

Usage

```
.exportShowImage(
  exportFirst,
  filename = "image",
  type = "PNG",
  resolution = NULL,
  units = NULL,
  height = NULL,
  width = NULL,
  zoom = NULL,
  sandboxName = NULL,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`exportFirst`	FALSE for notebookShowImage, TRUE for notebookExportShowImage.
`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`type`	(`character`) Type of image to export, e.g., PNG (default), JPEG, PDF, SVG.
`resolution`	(`numeric`) The resolution of the exported image, in DPI. Valid only for bitmap formats, when the selected width and height 'units' is inches. The possible values are: 72 (default), 100, 150, 300, 600.
`units`	(`character`) The units for the 'width' and 'height' values. Valid only for bitmap formats, such as PNG and JPEG. The possible values are: pixels (default), inches.
`height`	(`numeric`) The height of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`width`	(`numeric`) The width of the exported image. Valid only for bitmap formats, such as PNG and JPEG.

`zoom`	(`numeric`) The zoom value to proportionally scale the image. The default value is 100.0. Valid only for bitmap formats, such as PNG and JPEG
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Show network view in notebook output.

Value

display image

Examples

```
.exportShowImage()
```

`.getDefaultSandbox` *.getDefaultSandbox*

Description

.getDefaultSandbox

Usage

```
.getDefaultSandbox(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
.getDefaultSandbox()
```

`.getRequester` *.getRequester*

Description

.getRequester

Usage

```
.getRequester(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
.getRequester()
```

`addAnnotationBoundedText` *Add Bounded Text Annotation*

Description

Adds a bounded text annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
addAnnotationBoundedText(
  text = NULL,
  x.pos = NULL,
  y.pos = NULL,
  fontSize = NULL,
  fontFamily = NULL,
  fontStyle = NULL,
  color = NULL,
  angle = NULL,
  type = NULL,
  customShape = NULL,
  fillColor = NULL,
  opacity = NULL,
```

```
  borderThickness = NULL,
  borderColor = NULL,
  borderOpacity = NULL,
  height = NULL,
  width = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`text`	The text to be displayed
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`fontSize`	(optional) Numeric value; default is 12
`fontFamily`	(optional) Font family; default is Arial
`fontStyle`	(optional) Font style; default is
`color`	(optional) Hexidecimal color; default is #000000 (black)
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`type`	(optional) The type of the shape, default is RECTANGLE. See getNodeShapes() for valid options.
`customShape`	(optional) If a custom shape, this is the text of the shape
`fillColor`	(optional) Hexidecimal color; default is #000000 (black)
`opacity`	(optional) Opacity of fill color. Must be an integer between 0 and 100; default is 100.
`borderThickness`	(optional) Integer
`borderColor`	(optional) Hexidecimal color; default is #000000 (black)
`borderOpacity`	(optional) Integer between 0 and 100; default is 100.
`height`	(optional) Height of bounding shape; default is based on text height.
`width`	(optional) Width of bounding shape; default is based on text length.
`name`	(optional) Name of annotation object; default is "Text"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
addAnnotationBoundedText("test1")
addAnnotationBoundedText("test2", 1000, 1000, name="B2")
addAnnotationBoundedText("test3", 1200, 1000, 30, "Helvetica", "bold", "#990000",
    40,name="B3", canvas="foreground",z=4)
```

`addAnnotationImage` *Add Image Annotation*

Description

Adds a Image annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
addAnnotationImage(
  url = NULL,
  x.pos = NULL,
  y.pos = NULL,
  angle = NULL,
  opacity = NULL,
  brightness = NULL,
  contrast = NULL,
  borderThickness = NULL,
  borderColor = NULL,
  borderOpacity = NULL,
  height = NULL,
  width = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`url`	URL or path to image file. File paths can be absolute or relative to current working directory. URLs must start with http:// or https://.
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`opacity`	(optional) Opacity of fill color. Must be an integer between 0 and 100; default is 100.
`brightness`	(optional) Image brightness. Must be an integer between -100 and 100; default is 0
`contrast`	(optional) Image contrast. Must be an integer between -100 and 100; default is 0

`borderThickness`	(optional) Integer
`borderColor`	(optional) Hexidecimal color; default is #000000 (black)
`borderOpacity`	(optional) Integer between 0 and 100; default is 100.
`height`	(optional) Height of image; default is based on text height.
`width`	(optional) Width of image; default is based on text length.
`name`	(optional) Name of annotation object; default is "Image"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
addAnnotationImage("image.png")
addAnnotationImage("/Users/janedoe/Desktop/image.png", 1000, 1000, name="I2")
addAnnotationImage("https://www.example.com/image.png", 1200, 1000, 30,
    40, name="I3", canvas="background",z=4)
```

`addAnnotationShape` *Add Shape Annotation*

Description

Adds a shape annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
addAnnotationShape(
  type = NULL,
  customShape = NULL,
  x.pos = NULL,
  y.pos = NULL,
  angle = NULL,
  fillColor = NULL,
  opacity = NULL,
  borderThickness = NULL,
  borderColor = NULL,
  borderOpacity = NULL,
```

```
  height = NULL,
  width = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`type`	(optional) The type of the shape, default is RECTANGLE. See getNodeShapes() for valid options.
`customShape`	(optional) If a custom shape, this is the text of the shape
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`fillColor`	(optional) Hexidecimal color; default is #000000 (black)
`opacity`	(optional) Opacity of fill color. Must be an integer between 0 and 100; default is 100.
`borderThickness`	(optional) Integer
`borderColor`	(optional) Hexidecimal color; default is #000000 (black)
`borderOpacity`	(optional) Integer between 0 and 100; default is 100.
`height`	(optional) Height of shape; default is based on text height.
`width`	(optional) Width of shape; default is based on text length.
`name`	(optional) Name of annotation object; default is "Shape"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
addAnnotationShape("rectangle")
addAnnotationShape("rectangle", 1000, 1000, name="S2")
addAnnotationShape("rectangle", 1200, 1000, 30, "#990000",
    40,name="S3", canvas="background",z=4)
```

`addAnnotationText` *Add Text Annotation*

Description

Adds a text annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
addAnnotationText(
  text = NULL,
  x.pos = NULL,
  y.pos = NULL,
  fontSize = NULL,
  fontFamily = NULL,
  fontStyle = NULL,
  color = NULL,
  angle = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`text`	The text to be displayed
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`fontSize`	(optional) Numeric value; default is 12
`fontFamily`	(optional) Font family; default is Arial
`fontStyle`	(optional) Font style; default is
`color`	(optional) Hexidecimal color; default is #000000 (black)
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`name`	(optional) Name of annotation object; default is "Text"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
addAnnotationText("test1")
addAnnotationText("test2", 1000, 1000, name="T2")
addAnnotationText("test3", 1200, 1000, 30, "Helvetica", "bold", "#990000",
    40,name="T3", canvas="foreground",z=4)
```

`addCyEdges` *Add CyEdges*

Description

Add one or more edges to a Cytoscape network by listing source and target node pairs.

Usage

```
addCyEdges(
  source.target.list,
  edgeType = "interacts with",
  directed = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`source.target.list`	A `list` (or `list of lists`) of source and target node name or SUID pairs
`edgeType`	The type of interaction. Default is 'interacts with'.
`directed`	`boolean` for whether interactions are directed. Default is `FALSE`.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list` of `named lists` of SUID, source and target for each edge added.

Examples

```
addCyEdges(c('sourceNode','targetNode'))
addCyEdges(list(c('s1','t1'),c('s2','t2')))
```

`addCyNodes` *Add CyNodes*

Description

Add one or more nodes to a Cytoscape network.

Usage

```
addCyNodes(
  node.names,
  skip.duplicate.names = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	A `list` of node names
`skip.duplicate.names`	Skip adding a node if a node with the same name is already in the network. If `FALSE` then a duplicate node (with a unique SUID) will be added. Default is `TRUE`.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list` of `named lists` of name and SUID for each node added.

Examples

```
addCyNodes(c('Node A','Node B','Node C'))
```

`AddToGroup` *Add to Group*

Description

Adds the specified nodes and edges to the specified group.

Usage

```
AddToGroup(
  group.name,
  nodes = NULL,
  nodes.by.col = "SUID",
  edges = NULL,
  edges.by.col = "SUID",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`group.name`	Specifies the name used to identify the group
`nodes`	List of node SUIDs, names, other column values, or keyword: selected, unselected or all. Default is currently selected nodes.
`nodes.by.col`	name of node table column corresponding to provided nodes list. Default is 'SUID'.
`edges`	List of edge SUIDs, names, other column values, or keyword: selected, unselected or all. Default is currently selected edges.
`edges.by.col`	name of edge table column corresponding to provided edges list. Default is 'SUID'.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
AddToGroup('myGroup')
```

`analyzeNetwork` *Analyze Network*

Description

Calculate various network statistics.

Usage

```
analyzeNetwork(directed = FALSE, base.url = .defaultBaseUrl)
```

Arguments

`directed`	(optional) If TRUE, the network is considered a directed graph. Default is FALSE.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

The results are added to the Node and Edge tables and the Results Panel. The summary statistics in the Results Panel are also returned by the function as a list of named values.

Value

Named list of summary statistics

Examples

```
analyzeNetwork()
analyzeNetwork(TRUE)
```

`applyFilter` *Apply Filter*

Description

Run an existing filter by supplying the filter name.

Usage

```
applyFilter(
  filter.name = "Default filter",
  hide = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`filter.name`	Name of filter to apply. Default is "Default filter".
`hide`	Whether to hide filtered out nodes and edges. Default is FALSE. Ignored if all nodes or edges are filtered out. This is an alternative to filtering for node and edge selection.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Known bug: selection (or hiding) of edges using edge-based column filters does not work. As a workaround, simply repeat the createColumnFilter operation to perform selection (or hiding) of edges.

Value

List of selected nodes and edges.

See Also

unhideAll

Examples

```
applyFilter('myFilter')
applyFilter('myFilter', hide = TRUE)
```

`bundleEdges` *Bundle Edges*

Description

Apply edge bundling to the network specified. Edge bundling is executed with default parameters; optional parameters are not supported.

Usage

```
bundleEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
bundleEdges()
```

`checkNotebookIsRunning` *checkNotebookIsRunning*

Description

checkNotebookIsRunning

Usage

```
checkNotebookIsRunning()
```

Value

None

Examples

```
checkNotebookIsRunning()
```

`checkRunningRemote` *checkRunningRemote*

Description

Determine whether we're running locally or on a remote server. If locally (either via raw R or via a locally installed Notebook), we prefer to connect to Cytoscape over a local socket. If remote, we have to connect over Jupyter-Bridge. Either way, we can determine which by whether Cytoscape answers to a version check. If Cytoscape doesn't answer, we have no information ... and we have to wait until Cytoscape is started and becomes reachable before we can determine local vs remote.

Usage

```
checkRunningRemote(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
checkRunningRemote()
```

`clearEdgeBends` *Clear Edge Bends*

Description

Clear all edge bends, e.g., those created from edge bundling.

Usage

```
clearEdgeBends(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
clearEdgeBends()
```

`clearEdgePropertyBypass` *Clear Edge Property Bypass*

Description

Clear bypass values for any edge property of the specified edges, effectively restoring any previously defined style defaults or mappings.

Usage

```
clearEdgePropertyBypass(
  edge.names,
  visual.property,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs. Pending CyREST updates, if set to 'all', then the property is cleared for all edges.
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setEdgePropertyBypass

Examples

```
clearEdgePropertyBypass()
```

`clearNetworkCenterBypass`

Clear Network Center Bypass

Description

Clear the bypass value for center x and y for the network, effectively restoring prior default values.

Usage

```
clearNetworkCenterBypass(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
clearNetworkCenterBypass()
```

`clearNetworkPropertyBypass` *Clear Network Property Bypass*

Description

Clear bypass values for any network property, effectively restoring any previously defined style defaults or mappings.

Usage

```
clearNetworkPropertyBypass(
  visual.property,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`visual.property`	Name of a visual property. See getVisualPropertyNames.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodePropertyBypass

Examples

```
clearNetworkPropertyBypass()
```

`clearNetworkZoomBypass` *Clear Network Zoom Bypass*

Description

Clear the bypass value for the scale factor for the network, effectively restoring prior default values.

Usage

```
clearNetworkZoomBypass(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
clearNetworkZoomBypass()
```

`clearNodeOpacityBypass` *Clear Node Opacity Bypass*

Description

Clear the bypass value for node fill, label and border opacity for the specified node or nodes, effectively restoring any previously defined style defaults or mappings.

Usage

```
clearNodeOpacityBypass(node.names, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeOpacityBypass

Examples

```
clearNodeOpacityBypass(c('Node 1','Node 2'))
```

`clearNodePropertyBypass`

Clear Node Property Bypass

Description

Clear bypass values for any node property of the specified nodes, effectively restoring any previously defined style defaults or mappings.

Usage

```
clearNodePropertyBypass(
  node.names,
  visual.property,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs. Pending CyREST updates, if set to 'all', then the property is cleared for all nodes.
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodePropertyBypass

Examples

```
clearNodePropertyBypass()
```

`clearSelection` *Clear Selection*

Description

If any nodes are selected in the network, they will be unselected.

Usage

```
clearSelection(type = "both", network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`type`	'nodes', 'edges' or 'both' (default)
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
clearSelection()
```

`cloneNetwork` *Clone a Cytoscape Network*

Description

Makes a copy of a Cytoscape Network with all of its edges and nodes.

Usage

```
cloneNetwork(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network you want to clone; default is "current" network
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

The `suid` of the new network

Author(s)

Alexander Pico, Julia Gustavsen

Examples

```
cloneNetwork("cloned network")
```

`closeSession` *Close Session*

Description

Closes the current session in Cytoscape, destroying all unsaved work.

Usage

```
closeSession(save.before.closing, filename = NULL, base.url = .defaultBaseUrl)
```

Arguments

`save.before.closing`	`boolean` Whether to save before closing the current session. If FALSE, then all unsaved work will be lost.
`filename`	(optional) If `save.before.closing` is TRUE and the session has not previously been saved, then the path and name of the session file to save should be provided. Default is NULL.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

A boolean for whether to save before closing is required since you could lose data by closing without saving.

Value

None

Examples

```
closeSession(FALSE)
closeSession(TRUE, '/fullpath/mySession')
closeSession(TRUE)
```

`collapseGroup` *Collapse Group*

Description

Replaces the representation of all of the nodes and edges in a group with a single node.

Usage

```
collapseGroup(groups = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`groups`	(optional) List of group names or keywords: all, selected, unselected. Default is the currently selected group.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
collapseGroup()
```

`commandEcho` *Command Echo*

Description

The echo command will display the value of the variable specified by the variableName argument, or all variables if variableName is not provided.

Usage

```
commandEcho(variable.name = "*", base.url = .defaultBaseUrl)
```

Arguments

`variable.name`	(optional) The name of the variable to display. Default is to display all variable values using "*".
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Value of variable

Examples

```
commandEcho()
```

`commandOpenDialog` *Command Open Dialog*

Description

The command line dialog provides a field to enter commands and view results. It also provides the help command to display namespaces, commands, and arguments

Usage

```
commandOpenDialog(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
commandOpenDialog()
```

`commandPause` *Command Pause*

Description

The pause command displays a dialog with the text provided in the message argument and waits for the user to click OK.

Usage

```
commandPause(message = "", base.url = .defaultBaseUrl)
```

Arguments

`message`	(optional) Text to display in pause dialog
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
commandPause('Please click OK to continue.')
```

`commandQuit` *Command Quit*

Description

This command causes Cytoscape to exit. It is typically used at the end of a script file

Usage

```
commandQuit(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
commandQuit()
```

`commandRunFile` *Command Run File*

Description

The run command will execute a command script from the file pointed to by the file argument, which should contain Cytoscape commands, one per line. Arguments to the script are provided by the args argument

Usage

```
commandRunFile(file, args = NULL, base.url = .defaultBaseUrl)
```

Arguments

`file`	Path to command script file
`args`	The script arguments as key:value pairs separated by commas
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
commandRunFile('/path/to/my/file.txt')
```

`commandsAPI` *Open Swagger docs for CyREST Commands API*

Description

Opens swagger docs in default browser for a live instance of Commands available via CyREST.

Usage

```
commandsAPI(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Web page in browser

Examples

```
commandsAPI()
```

`commandsGET` *Commands GET*

Description

Using the same syntax as Cytoscape's Command Line Dialog, this function converts a command string into a CyREST query URL, executes a GET request, and parses the result content into an R list object. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
commandsGET(cmd.string, base.url = .defaultBaseUrl)
```

Arguments

`cmd.string`	(char) command
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list`, `status` or None.

Examples

```
commandsGET('layout get preferred network=current')
commandsGET('network list properties network=current')
commandsGET('layout force-directed defaultNodeMass=1')
```

`commandsHelp` *Commands Help*

Description

Using the same syntax as Cytoscape's Command Line Dialog, this function returns a list of available commands or args. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
commandsHelp(cmd.string = "help", base.url = .defaultBaseUrl)
```

Arguments

`cmd.string`	(char) command
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Works with or without 'help' command prefix. Note that if you ask about a command that doesn't have any arguments, this function will run the command!

Value

List of available commands or args

Examples

```
commandsHelp()
commandsHelp('node')
commandsHelp('node get attribute')
```

`commandSleep` *Command Sleep*

Description

The sleep command will pause processing for a period of time as specified by duration seconds. It is typically used as part of a command script.

Usage

```
commandSleep(duration = NULL, base.url = .defaultBaseUrl)
```

Arguments

`duration`	(optional) The time in seconds to sleep
`base.url`	(optional) Ignore unless you need to specify a custom domain, #' port or version to connect to the CyREST API. Default is http://localhost:1234 #' and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
commandSleep(5)
```

`commandsPOST` *Commands POST*

Description

Using the same syntax as Cytoscape's Command Line Dialog, this function converts a command string into a CyREST query URL, executes a POST request, and parses the result content into an R list object. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
commandsPOST(cmd.string, base.url = .defaultBaseUrl)
```

Arguments

`cmd.string`	(char) command
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list`, named `list`, `status` or None.

Examples

```
commandsPOST('layout get preferred')
commandsPOST('network list properties')
commandsPOST('layout force-directed defaultNodeMass=1')
```

`commandsRun` *Run a Command*

Description

Using the same syntax as Cytoscape's Command Line Dialog, this function converts a command string into a CyREST query URL, executes a GET request, and parses the result content into an R list object. Same as commandsGET.

Usage

```
commandsRun(cmd.string, base.url = .defaultBaseUrl)
```

Arguments

`cmd.string`	(char) command
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list`, `status` or None.

Examples

```
commandsRun('layout get preferred')
commandsRun('network list properties')
commandsRun('layout force-directed defaultNodeMass=1')
```

`copyVisualStyle` *Copy Visual Style*

Description

Create a new visual style by copying a specified style.

Usage

```
copyVisualStyle(from.style, to.style, base.url = .defaultBaseUrl)
```

Arguments

`from.style`	Name of visual style to copy
`to.style`	Name of new visual style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
copyVisualStyle()
```

`createColumnFilter` *Create Column Filter*

Description

Creates a filter to control node or edge selection. Works on columns of boolean, string, numeric and lists. Note the unique restrictions for criterion and predicate depending on the type of column being filtered.

Usage

```
createColumnFilter(
  filter.name,
  column,
  criterion,
  predicate,
  caseSensitive = FALSE,
  anyMatch = TRUE,
  type = "nodes",
  hide = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl,
  apply = TRUE
)
```

Arguments

`filter.name`	Name for filter.
`column`	Table column to base filter upon.
`criterion`	For boolean columns: TRUE or FALSE. For string columns: a string value, e.g., "hello". If the predicate is REGEX then this can be a regular expression as accepted by the Java Pattern class (https://docs.oracle.com/javase/7/docs/api/java/util/regex/Pattern.htm For numeric columns: If the predicate is BETWEEN or IS_NOT_BETWEEN then this is a two-element vector of numbers, example: c(1,5), otherwise a single number.
`predicate`	For boolean columns: IS, IS_NOT. For string columns: IS, IS_NOT, CONTAINS, DOES_NOT_CONTAIN, REGEX. For numeric columns: IS, IS_NOT, GREATER_THAN, GREATER_THAN_OR_EQUAL, LESS_THAN, LESS_THAN_OR_EQUAL, BETWEEN, IS_NOT_BETWEEN
`caseSensitive`	(optional) If string matching should be case sensitive. Default is FALSE.
`anyMatch`	(optional) Only applies to List columns. If true then at least one element in the list must pass the filter, if false then all the elements in the list must pass the filter. Default is TRUE.
`type`	(optional) Apply filter to "nodes" (default) or "edges".
`hide`	Whether to hide filtered out nodes and edges. Default is FALSE. Ignored if all nodes or edges are filtered out. This is an alternative to filtering for node and edge selection.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`apply`	(bool) True to execute filter immediately (default); False to define filter but not execute it (available in Cytoscape 3.9+).

Value

List of selected nodes and edges.

Examples

```
createColumnFilter('myFilter', 'log2FC', c(-1,1), "IS_NOT_BETWEEN")
createColumnFilter('myFilter', 'pValue', 0.05, "LESS_THAN")
createColumnFilter('myFilter', 'function', "kinase", "CONTAINS", FALSE)
createColumnFilter('myFilter', 'name', "^Y.*C$", "REGEX")
createColumnFilter('myFilter', 'isTarget', TRUE , "IS", apply=FALSE)
createColumnFilter('myFilter', 'isTarget', TRUE , "IS", hide=TRUE)
```

`createCompositeFilter` *Create Composite Filter*

Description

Combines filters to control node and edge selection based on previously created filters.

Usage

```
createCompositeFilter(
  filter.name,
  filter.list,
  type = "ALL",
  hide = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl,
  apply = TRUE
)
```

Arguments

`filter.name`	Name for filter.
`filter.list`	List of filters to combine.
`type`	(optional) Type of composition, requiring ALL (default) or ANY filters to pass for final node and edge selection.
`hide`	Whether to hide filtered out nodes and edges. Default is FALSE. Ignored if all nodes or edges are filtered out. This is an alternative to filtering for node and edge selection.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`apply`	(bool) True to execute filter immediately (default); False to define filter but not execute it (available in Cytoscape 3.9+).

Value

List of selected nodes and edges.

Examples

```
createCompositeFilter("comp1", c("filter1", "filter2"))
createCompositeFilter("comp2", c("filter1", "filter2"), "ANY")
createCompositeFilter("comp3", c("comp1", "filter3"), apply=FALSE)
```

`createCytoscapejsFromNetwork`
Create Cytoscapejs from Network

Description

Create a Cytoscape JS representation of a Cytoscape network

Usage

```
createCytoscapejsFromNetwork(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(SUID or str or NULL): Name or SUID of a network or view. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

(list) The Cytoscape JS object

Examples

```
createCytoscapejsFromNetwork()
```

`createDegreeFilter` *Create Degree Filter*

Description

Creates a filter to control node selection base on in/out degree.

Usage

```
createDegreeFilter(
  filter.name,
  criterion,
  predicate = "BETWEEN",
  edgeType = "ANY",
  hide = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl,
  apply = TRUE
)
```

Arguments

`filter.name`	Name for filter.
`criterion`	A two-element vector of numbers, example: c(1,5).
`predicate`	BETWEEN (default) or IS_NOT_BETWEEN
`edgeType`	(optional) Type of edges to consider in degree count: ANY (default), UNDIRECTED, INCOMING, OUTGOING, DIRECTED
`hide`	Whether to hide filtered out nodes and edges. Default is FALSE. Ignored if all nodes or edges are filtered out. This is an alternative to filtering for node and edge selection.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`apply`	(bool) True to execute filter immediately (default); False to define filter but not execute it (available in Cytoscape 3.9+).

Value

List of selected nodes and edges.

Examples

```
createDegreeFilter('myFilter', c(4,5))
createDegreeFilter('myFilter', c(2,5), apply=FALSE)
```

`createGraphFromNetwork` *createGraphFromNetwork*

Description

Returns the Cytoscape network as a Bioconductor graph.

Usage

```
createGraphFromNetwork(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A Bioconductor graph object.

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
cw <- CytoscapeWindow('network', graph=make_graphnel())
g <- createGraphFromNetwork()
g <- createGraphFromNetwork('myNetwork')
```

`createGroup` *Create Group*

Description

Create a group from the specified nodes.

Usage

```
createGroup(
  group.name,
  nodes = NULL,
  nodes.by.col = "SUID",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`group.name`	The name used to identify and optionaly label the group
`nodes`	List of node SUIDs, names, other column values, or keyword: selected, unselected or all. Default is currently selected nodes.
`nodes.by.col`	name of node table column corresponding to provided nodes list. Default is 'SUID'.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Group SUID

Examples

```
createGroup('myGroup')
```

`createGroupByColumn` *Create Group by Column*

Description

Create a group of nodes defined by a column value.

Usage

```
createGroupByColumn(
  group.name,
  column = NULL,
  value = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`group.name`	The name used to identify and optionaly label the group
`column`	The name or header of the Node Table column to use for selecting nodes to group
`value`	The value in the column to use for selecting nodes to group
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Group SUID

Examples

```
createGroupByColumn('myGroup','Cluster', 'A')
```

`createIgraphFromNetwork` *Create an igraph network from a Cytoscape network*

Description

Takes a Cytoscape network and generates data frames for vertices and edges to send to the graph_from_data_frame function. Returns the network.suid and applies the perferred layout set in Cytoscape preferences.

Usage

```
createIgraphFromNetwork(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Nodes and edges from the Cytoscape network will be translated into vertices and edges in igraph. Associated table columns will also be passed to igraph as vertiex and edge attributes. Note: all networks are implicitly modeled as directed in Cytoscape. Round-trip conversion of an undirected network in igraph via `createNetworkFromIgraph` to Cytoscape and back to igraph will result in a directed network.

Value

(igraph) an igraph network

See Also

createNetworkFromDataFrames, createNetworkFromIgraph

Examples

```
ig <- createIgraphFromNetwork()
ig <- createIgraphFromNetwork('myNetwork')
```

`createNetworkFromCytoscapejs`
Create a Network from Cytoscapejs

Description

Create a network from CytoscapeJS JSON

Usage

```
createNetworkFromCytoscapejs(
  cytoscapejs,
  title = NULL,
  collection = "My CytoscapeJS Network Collection",
  base.url = .defaultBaseUrl
)
```

Arguments

`cytoscapejs`	network (nodes, edges, attributes, node positions and metadata) in CytoscapeJS format
`title`	network name (NULL means use the name in cytoscapejs)
`collection`	collection name (NULL means create an unnamed collection)
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

The SUID of the new network

Examples

```
createNetworkFromCytoscapejs()
```

`createNetworkFromDataFrames`
Create a network from data frames

Description

Takes data frames for nodes and edges, as well as naming parameters to generate the JSON data format required by the "networks" POST operation via CyREST. Returns the network.suid and applies the perferred layout set in Cytoscape preferences.

Usage

```
createNetworkFromDataFrames(
  nodes = NULL,
  edges = NULL,
  title = "From dataframe",
  collection = "My Dataframe Network Collection",
  base.url = .defaultBaseUrl,
  ...
)
```

Arguments

`nodes`	(data.frame) see details and examples below; default NULL to derive nodes from edge sources and targets
`edges`	(data.frame) see details and examples below; default NULL for disconnected set of nodes
`title`	(char) network name
`collection`	(char) network collection name
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`...`	params for nodeSet2JSON() and edgeSet2JSON()

Details

NODES should contain a column of character strings named: id. This name can be overridden by the arg: node.id.list. Additional columns are loaded as node attributes. EDGES should contain columns of character strings named: source, target and interaction. These names can be overridden by args: source.id.list, target.id.list, interaction.type.list. Additional columns are loaded as edge attributes. The 'interaction' list can contain a single value to apply to all rows; and if excluded altogether, the interaction type wiil be set to "interacts with". NOTE: attribute values of types (num) will be imported as (Double); (int) as (Integer); (chr) as (String); and (logical) as (Boolean). (Lists) will be imported as (Lists) in CyREST v3.9+.

Value

(int) network SUID

Examples

```
nodes <- data.frame(id=c("node 0","node 1","node 2","node 3"),
           group=c("A","A","B","B"), # categorical strings
           score=as.integer(c(20,10,15,5))) # integers
edges <- data.frame(source=c("node 0","node 0","node 0","node 2"),
           target=c("node 1","node 2","node 3","node 3"),
           interaction=c("inhibits","interacts",
                         "activates","interacts"),  # optional
           weight=c(5.1,3.0,5.2,9.9)) # numeric

createNetworkFromDataFrames(nodes,edges)
```

`createNetworkFromGraph`

Create Network From Graph

Description

Creates a Cytoscape network from a Bioconductor graph.

Usage

```
createNetworkFromGraph(
  graph,
  title = "From graph",
  collection = "My GraphNEL Network Collection",
  base.url = .defaultBaseUrl
)
```

Arguments

`graph`	A GraphNEL object
`title`	(char) network name
`collection`	(char) network collection name
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Network SUID

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
library(graph)
g <- makeSimpleGraph()
createNetworkFromGraph(g)
```

`createNetworkFromIgraph` *Create a Cytoscape network from an igraph network*

Description

Takes an igraph network and generates data frames for nodes and edges to send to the createNetwork function. Returns the network.suid and applies the perferred layout set in Cytoscape preferences.

Usage

```
createNetworkFromIgraph(
  igraph,
  title = "From igraph",
  collection = "My Igraph Network Collection",
  base.url = .defaultBaseUrl,
  ...
)
```

Arguments

`igraph`	(igraph) igraph network object
`title`	(char) network name
`collection`	(char) network collection name
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`...`	params for nodeSet2JSON() and edgeSet2JSON(); see createNetwork

Details

Vertices and edges from the igraph network will be translated into nodes and edges in Cytoscape. Associated attributes will also be passed to Cytoscape as node and edge table columns. Note: undirected networks will be implicitly modeled as directed in Cytoscape. Conversion back via `createIgraphFromNetwork` will result in a directed network. Also note: igraph attributes of type "other" denoted by "x" are converted to "String" in Cytoscape.

Value

(int) network SUID

See Also

createNetworkFromDataFrames, createIgraphFromNetwork

Examples

```
library(igraph)
ig <- makeSimpleIgraph()
createNetworkFromIgraph(ig)
```

`createSubnetwork` *Create subnetwork from existing network*

Description

Copies a subset of nodes and edges into a newly created subnetwork.

Usage

```
createSubnetwork(
  nodes = NULL,
  nodes.by.col = "SUID",
  edges = NULL,
  edges.by.col = "SUID",
  exclude.edges = FALSE,
  subnetwork.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`nodes`	list of nodes by SUID, by specified nodes.by.col value (e.g., name) or by keyword: selected, unselected or all. Default is currently selected nodes.
`nodes.by.col`	name of node table column corresponding to provided nodes list; default is 'SUID'
`edges`	list of edges by SUID, by specified nodes.by.col value (e.g., name) or by keyword: selected, unselected or all. Default is currently selected edges.
`edges.by.col`	name of edge table column corresponding to provided edges list; default is 'SUID'
`exclude.edges`	(boolean) whether to exclude connecting edges; default is FALSE
`subnetwork.name`	name of new subnetwork to be created; default is to add a numbered suffix to source network name
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

If you specify both nodes and edges, the resulting subset will be the union of those sets. Typical usage only requires specifying either nodes or edges. Note that selected nodes will bring along their connecting edges by default (see exclude.edges arg) and selected edges will always bring along their source and target nodes.

Value

SUID of new subnetwork

Examples

```
createSubnetwork()
createSubnetwork("all")
createSubnetwork(subnetwork.name="mySubnetwork")
createSubnetwork(c("node 1","node 2","node 3"),"name")
createSubnetwork(c("AKT1","TP53","PIK3CA"),"display name")
createSubnetwork(edges="all") #subnetwork of all connected nodes
```

`createView` *Create Network View*

Description

Create a network view if one does not already exist

Usage

```
createView(layout = TRUE, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`layout`	(optional) If TRUE (default), the preferred layout will be applied to the new view. If FALSE, no layout will be applied.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

For networks larger than the view creation threshold, a network view is not created by default. This function creates a network view if one does not already exist.

Value

Network view SUID

Examples

```
getNetworkViews()
```

`createVisualStyle` *Create a visual style from components*

Description

Create a style from defaults and predefined mappings.

Usage

```
createVisualStyle(style.name, defaults, mappings, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	(char) name for style
`defaults`	(list) key-value pairs for default mappings.
`mappings`	(list) visual property mappings, see mapVisualProperty
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Requires attribute mappings to be previously created, see mapVisualProperty.

Value

None

See Also

applyStyle, mapVisualProperty

Examples

```
#first there has to be a network to apply style to
example(createNetworkFromDataFrames)

#then prepare style variables
style.name = "myStyle"
defaults <- list(NODE_SHAPE="diamond",
                 NODE_SIZE=30,
                 EDGE_TRANSPARENCY=120,
                 NODE_LABEL_POSITION="W,E,c,0.00,0.00")
nodeLabels <- mapVisualProperty('node label','id','p')
nodeFills <- mapVisualProperty('node fill color','group','d',c("A","B"), c("#FF9900","#66AAAA"))
arrowShapes <- mapVisualProperty('Edge Target Arrow Shape','interaction','d',
                            c("activates","inhibits","interacts"),c("Arrow","T","None"))
edgeWidth <- mapVisualProperty('edge width','weight','p')

#and then create the style
createVisualStyle(style.name, defaults, list(nodeLabels,nodeFills,arrowShapes,edgeWidth))
```

```
#finsh by applying the style
setVisualStyle(style.name)
```

`cybrowserClose` *Cybrowser Close*

Description

Close an internal web browser and remove all content. Provide an id for the browser you want to close.

Usage

```
cybrowserClose(id = NULL, base.url = .defaultBaseUrl)
```

Arguments

`id`	(optional) The identifier for the browser window to close
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
cybrowserClose('554')
```

`cybrowserDialog` *Cybrowser Dialog*

Description

Launch Cytoscape's internal web browser in a separate window. Provide an id for the window if you want subsequent control of the window e.g., via cybrowser hide.

Usage

```
cybrowserDialog(
  id = NULL,
  text = NULL,
  title = NULL,
  url = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`id`	(optional) The identifier for the browser window
`text`	(optional) HTML text to initially load into the browser
`title`	(optional) Text to be shown in the title bar of the browser window
`url`	(optional) The URL the browser should load
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

cybrowserShow

cybrowserHide

Examples

```
cybrowserDialog(url='http://cytoscape.org')
```

`cybrowserHide` *Cybrowser Hide*

Description

Hide an existing browser, whether it's in the Results panel or a separate window.

Usage

```
cybrowserHide(id = NULL, base.url = .defaultBaseUrl)
```

Arguments

`id`	(optional) The identifier for the browser window to hide
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

cybrowserShow

cybrowserDialog

Examples

```
cybrowserHide()
```

`cybrowserList` *Cybrowser List*

Description

List all browsers that are currently open, whether as a dialog or in the results panel.

Usage

```
cybrowserList(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of open cybrowser windows

Examples

```
cybrowserList()
```

`cybrowserSend` *Cybrowser Send*

Description

Send the text to the browser indicated by the id and return the response, if any. Note that the JSON result field could either be a bare string or JSON formatted text.

Usage

```
cybrowserSend(id = NULL, script, base.url = .defaultBaseUrl)
```

Arguments

`id`	(optional) The identifier for the browser window
`script`	(optional) A string that represents a JavaScript variable, script, or call to be executed in the browser. Note that only string results are returned.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

String result

Examples

```
cybrowserSend(id="Window 1", script="navigator.userAgent;")
```

`cybrowserShow` *Cybrowser Show*

Description

Launch Cytoscape's internal web browser in a pane in the Result Panel. Provide an id for the window if you want subsequent control of the window via cybrowser hide.

Usage

```
cybrowserShow(
  id = NULL,
  text = NULL,
  title = NULL,
  url = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`id`	(optional) The identifier for the browser window
`text`	(optional) HTML text to initially load into the browser
`title`	(optional) Text to be shown in the title bar of the browser window
`url`	(optional) The URL the browser should load
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

cybrowserDialog

cybrowserHide

Examples

```
cybrowserShow(url='http://cytoscape.org')
```

`cybrowserVersion` *Cybrowser Version*

Description

Display the version of the CyBrowser app.

Usage

```
cybrowserVersion(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Version number

Examples

```
cybrowserVersion()
```

`cyrestAPI` *Open Swagger docs for CyREST API*

Description

Opens swagger docs in default browser for a live instance of CyREST operations.

Usage

```
cyrestAPI(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Web page in browser

Examples

```
cyrestAPI()
```

`cyrestDELETE` *CyREST DELETE*

Description

Constructs the query, makes DELETE call and processes the result. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
cyrestDELETE(operation = NULL, parameters = NULL, base.url = .defaultBaseUrl)
```

Arguments

`operation`	A string to be converted to the REST query namespace
`parameters`	A named list of values to be converted to REST query parameters
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

CyREST result content

Examples

```
cyrestDELETE('session')
```

`cyrestGET` *CyREST GET*

Description

Constructs the query, makes GET call and processes the result. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
cyrestGET(operation = NULL, parameters = NULL, base.url = .defaultBaseUrl)
```

Arguments

`operation`	A string to be converted to the REST query namespace
`parameters`	A named list of values to be converted to REST query parameters
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

CyREST result content

Examples

```
cyrestGET('version')
```

`cyrestPOST` *CyREST POST*

Description

Constructs the query and body, makes POST call and processes the result. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
cyrestPOST(
  operation,
  parameters = NULL,
  body = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`operation`	A string to be converted to the REST query namespace
`parameters`	A named list of values to be converted to REST query parameters
`body`	A named list of values to be converted to JSON
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

CyREST result content

Examples

```
cyrestPOST('networks/51/views')
```

`cyrestPUT` *CyREST PUT*

Description

Constructs the query and body, makes PUT call and processes the result. The function check whether actual call is local or remote first. If remote, requests will go through Jupyter-Bridge.

Usage

```
cyrestPUT(
  operation,
  parameters = NULL,
  body = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`operation`	A string to be converted to the REST query namespace
`parameters`	A named list of values to be converted to REST query parameters
`body`	A named list of values to be converted to JSON
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

CyREST result content

Examples

```
cyrestPUT()
```

`cytoscapeApiVersions` *Available CyREST API Versions*

Description

Get the list of available CyREST API versions

Usage

```
cytoscapeApiVersions(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list` of API versions as `character` strings, e.g., "v1"

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
cytoscapeApiVersions()
# [1] "v1"
```

`cytoscapeFreeMemory` *Free Up Unused Memory for Cytoscape*

Description

Manually call Java's garbage collection `System.gc()` to free up unused memory. This process happens automatically, but may be useful to call explicitly for testing or evaluation purposes.

Usage

```
cytoscapeFreeMemory(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

status message

Author(s)

Alexander Pico

Examples

```
cytoscapeFreeMemory()
# [1] "Unused memory freed up."
```

`cytoscapeMemoryStatus` *Memory Available to Cytoscape*

Description

Returns the memory resources of the server running Cytoscape

Usage

```
cytoscapeMemoryStatus(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list` of `numeric` values

Author(s)

Alexander Pico

Examples

```
cytoscapeMemoryStatus()
#  usedMemory  freeMemory totalMemory   maxMemory
#         181        2624        2805       13653
```

`cytoscapeNumberOfCores` *Number of Processors Available to Cytoscape*

Description

Returns the processor resources of the server running Cytoscape

Usage

```
cytoscapeNumberOfCores(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `numeric` value

Author(s)

Alexander Pico

Examples

```
cytoscapeNumberOfCores()
# [1] 8
```

`cytoscapePing` *Ping Cytoscape*

Description

Tests the connection to Cytoscape via CyREST and verifies that supported versions of Cytoscape and CyREST API are loaded.

Usage

```
cytoscapePing(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

status message

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
cytoscapePing()
# [1] "You are connected to Cytoscape!"
```

`cytoscapeVersionInfo` *Cytoscape and CyREST API Versions*

Description

Returns the versions of the current Cytoscape and CyREST API

Usage

```
cytoscapeVersionInfo(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of versions

Author(s)

Alexander Pico

Examples

```
cytoscapeVersionInfo()
 # apiVersion cytoscapeVersion
 #       "v1" "3.7.0-SNAPSHOT"
```

`deleteAllNetworks` *Delete All Networks*

Description

Delete all networks from the current Cytoscape session.

Usage

```
deleteAllNetworks(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteAllNetworks()
```

`deleteAllVisualStyle` *Delete All Visual Style*

Description

Delete all visual styles from current Cytoscape session

Usage

```
deleteAllVisualStyle(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteAllVisualStyle()
```

`deleteAnnotation` *Delete Annotation*

Description

Remove an annotation from the current network view in Cytoscape

Usage

```
deleteAnnotation(names = NULL, base.url = .defaultBaseUrl)
```

Arguments

`names`	List of annotations by UUID or Name
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteAnnotation("016a4af1-69bc-4b99-8183-d6f118847f96")
deleteAnnotation(c("T2","T3"))
deleteAnnotation(sapply(getAnnotationList(), '[[', 'uuid'))
```

`deleteDuplicateEdges` *Delete Duplicate Edges*

Description

Removes edges with duplicate names. Only considers cases with identical source, target, interaction and directionality.

Usage

```
deleteDuplicateEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Duplicate edges are first selected and then deleted. Prior edge selections will be lost; node selections will not be affected.

Value

Lists of SUIDs for selected nodes and edges

Examples

```
deleteDuplicateEdges()
```

`deleteGroup` *Delete (or Ungroup) a Group*

Description

Deletes one or more groups, while leaving member nodes intact.

Usage

```
deleteGroup(
  groups = NULL,
  groups.by.col = "SUID",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`groups`	(optional) List of group SUIDs, names, other column values or keywords: all, selected, unselected. Default is the currently selected group.
`groups.by.col`	name of node table column corresponding to provided groups list. Default is 'SUID'.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Note: group nodes are ungrouped but not deleted in Cytoscape version 3.6.1

Value

None

Examples

```
deleteGroup()
```

`deleteNetwork` *Delete Network*

Description

Delete a network from the current Cytoscape session.

Usage

```
deleteNetwork(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteNetwork()
```

`deleteSelectedEdges` *Delete Selected Edges*

Description

Delete the currently selected edges in the network.

Usage

```
deleteSelectedEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of deleted edge SUIDs

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
deleteSelectedEdges()
```

`deleteSelectedNodes` *Delete Selected Nodes*

Description

Delete currently selected nodes from the network.

Usage

```
deleteSelectedNodes(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `named list` of deleted node suids ($nodes) as well as edge suids ($edges) deleted as a result of the node deletion

Examples

```
deleteSelectedNodes()
```

`deleteSelfLoops` *Delete Self Loops*

Description

Removes edges that connect to a single node as both source and target.

Usage

```
deleteSelfLoops(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Self loop edges are first selected and then deleted. Prior edge and node selections will be lost.

Value

Lists of SUIDs for selected nodes and edges

Examples

```
deleteSelfLoops()
```

`deleteStyleMapping` *Delete Style Mapping*

Description

Deletes a specified visual style mapping from specified style.

Usage

```
deleteStyleMapping(style.name, visual.prop, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	(char) name for style
`visual.prop`	(char) name of visual property to map. See getVisualPropertyNames().
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteStyleMapping()
```

`deleteTableColumn` *Delete a table column*

Description

Delete a column from node, edge or network tables.

Usage

```
deleteTableColumn(
  column,
  table = "node",
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`column`	Name of the column to delete
`table`	Name of table, e.g., node (default), edge, network
`namespace`	Namespace of table. Default is "default".
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `data.frame` of column values

Examples

```
deleteTableColumn('node','group')
```

`deleteVisualStyle` *Delete Visual Style*

Description

Deletes the specified visual style from current session.

Usage

```
deleteVisualStyle(style.name, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	(char) name of style to delete
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteVisualStyle("myStyle")
```

`diffusionAdvanced` *Diffusion Advanced*

Description

Diffusion will send the selected network view and its selected nodes to a web-based REST service to calculate network propagation. Results are returned and represented by columns in the node table. Advanced operation supports parameters.

Usage

```
diffusionAdvanced(
  heat.column.name = NULL,
  time = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`heat.column.name`	(optional) A node column name intended to override the default table column 'diffusion_input'. This represents the query vector and corresponds to h in the diffusion equation.
`time`	(optional) The extent of spread over the network. This corresponds to t in the diffusion equation.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Columns are created for each execution of Diffusion and their names are returned in the response. The nodes you would like to use as input should be selected. This will be used to generate the contents of the diffusion_input column, which represents the query vector and corresponds to h in the diffusion equation.

Value

Version number

Examples

```
diffusionAdvanced()
```

`diffusionBasic` *Diffusion Basic*

Description

Diffusion will send the selected network view and its selected nodes to a web-based REST service to calculate network propagation. Results are returned and represented by columns in the node table.

Usage

```
diffusionBasic(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Columns are created for each execution of Diffusion and their names are returned in the response. The nodes you would like to use as input should be selected. This will be used to generate the contents of the diffusion_input column, which represents the query vector and corresponds to h in the diffusion equation.

Value

Version number

Examples

```
diffusionBasic()
```

`disableApp` *Disable App*

Description

Disable an app to effectively remove it from your Cytoscape session without having to uninstall it.

Usage

```
disableApp(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
disableApp()
```

`dockPanel` *Dock Panel*

Description

Dock a panel back into the UI of Cytoscape.

Usage

```
dockPanel(panel.name, base.url = .defaultBaseUrl)
```

Arguments

`panel.name`	Name of the panel. Multiple ways of referencing panels is supported: WEST, control panel, control, c SOUTH, table panel, table, ta SOUTH_WEST, tool panel, tool, to EAST, results panel, results, r
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
dockPanel('table')
```

`doInitializeSandbox` *doInitializeSandbox*

Description

doInitializeSandbox

Usage

```
doInitializeSandbox(requester = NULL, base.url = .defaultBaseUrl)
```

Arguments

`requester`	requester
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
doInitializeSandbox()
```

`doRequestRemote` *doRequestRemote*

Description

Do requests remotely by connecting over Jupyter-Bridge.

Usage

```
doRequestRemote(method, qurl, qbody = NULL, headers = NULL)
```

Arguments

`method`	A string to be converted to the REST query namespace
`qurl`	A named list of values to be converted to REST query parameters
`qbody`	A named list of values to be converted to JSON
`headers`	httr headers

Value

httr response

Examples

```
doRequestRemote()
```

`doSetSandbox` *doSetSandbox*

Description

doSetSandbox

Usage

```
doSetSandbox(sandboxToSet, requester = NULL, base.url = .defaultBaseUrl)
```

Arguments

`sandboxToSet`	sandbox to set
`requester`	requester
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
doSetSandbox()
```

`enableApp` *Enable App*

Description

Enable a previously installed and disabled app in Cytoscape.

Usage

```
enableApp(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
enableApp()
```

`expandGroup` *Expand Group*

Description

Replaces the group node with member nodes for a set of groups.

Usage

```
expandGroup(groups = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`groups`	(optional) List of group names or keywords: all, selected, unselected. Default is the currently selected group.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
expandGroup()
```

`exportFilters` *Export Filters*

Description

Saves filters to file in JSON format.

Usage

```
exportFilters(
  filename = "filters.json",
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(char) Full path or path relative to current working directory, in addition to the name of the file. Default is "filters.json"
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows an error to be generated if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Unlike other export functions, Cytoscape will automatically overwrite files with the same name. You will not be prompted to confirm or reject overwrite. Use carefully!

Value

None

Examples

```
exportFilters()
```

`exportImage` *Export Image*

Description

Saves the current network view as an image file.

Usage

```
exportImage(
  filename = NULL,
  type = "PNG",
  resolution = NULL,
  units = NULL,
  height = NULL,
  width = NULL,
  zoom = NULL,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`type`	(`character`) Type of image to export, e.g., PNG (default), JPEG, PDF, SVG, PS (PostScript).
`resolution`	(`numeric`) The resolution of the exported image, in DPI. Valid only for bitmap formats, when the selected width and height 'units' is inches. The possible values are: 72 (default), 100, 150, 300, 600.
`units`	(`character`) The units for the 'width' and 'height' values. Valid only for bitmap formats, such as PNG and JPEG. The possible values are: pixels (default), inches.
`height`	(`numeric`) The height of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`width`	(`numeric`) The width of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`zoom`	(`numeric`) The zoom value to proportionally scale the image. The default value is 100.0. Valid only for bitmap formats, such as PNG and JPEG
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

The image is cropped per the current view in Cytoscape. Consider applying `fitContent` prior to export.

Value

server response

Examples

```
exportImage('/fullpath/myNetwork','PDF')
```

`exportJPG` *Export JPG*

Description

Saves the current network view as an jpg file.

Usage

```
exportJPG(
  filename = NULL,
  allGraphicsDetails = TRUE,
  hideLabels = FALSE,
  zoom = NULL,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`allGraphicsDetails`	(optional): TRUE results in image with highest detail; False allows faster image generation. The default is TRUE.
`hideLabels`	(optional): TRUE makes node and edge labels invisible in image. False allows them to be drawn. The default is False.
`zoom`	(`numeric`) The zoom value to proportionally scale the image. The default value is 100.0. Valid only for bitmap formats, such as PNG and JPEG
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Exports the current view to a graphics file and returns the path to the saved file. To speed up image export for large networks use the option 'allGraphicsDetails=FALSE'. Available for Cytoscape v3.10 or later.

Value

server response

Examples

```
exportJPG('/fullpath/myNetwork')
```

`exportNetwork` *Export Network*

Description

Export a network to one of mulitple file formats

Usage

```
exportNetwork(
  filename = NULL,
  type = "SIF",
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, then the current network name is used.
`type`	File type. SIF (default), CX, cyjs, graphML, NNF, xGMML.
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE. allows Cytoscape to overwrite it without asking. Default value is TRUE.

Value

None.

Examples

```
exportNetwork('/path/filename','SIF')
```

`exportNetworkToNDEx` *Export Network To NDEx*

Description

Send a copy of a Cytoscape network to NDEx as a new submission.

Usage

```
exportNetworkToNDEx(
  username,
  password,
  isPublic,
  network = NULL,
  metadata = NULL,
  ndex.url = "http://ndexbio.org",
  ndex.version = "v2",
  base.url = .defaultBaseUrl
)
```

Arguments

`username`	NDEx account username
`password`	NDEx account password
`isPublic`	(Boolean) Whether to make the network publicly accessible at NDEx.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`metadata`	(optional) A list of structured information describing the network
`ndex.url`	(optional) For alternative instances or deployments of NDEx; default is "http://ndexbio.org"
`ndex.version`	(optional) For alternative versions of the NDEx API; default is "v2"
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

NDEx identifier (`externalId`) for new submission

Examples

```
exportNetworkToNDEx("user", "pass", TRUE)
```

`exportPDF` *Export PDF*

Description

Saves the current network view as an pdf file.

Usage

```
exportPDF(
  filename = NULL,
  exportTextAsFont = TRUE,
  hideLabels = FALSE,
  pageSize = "Letter",
  orientation = "Portrait",
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`exportTextAsFont`	(optional): If TRUE (the default value), texts will be exported as fonts.
`hideLabels`	(optional): TRUE makes node and edge labels invisible in image. False allows them to be drawn. The default is False.
`pageSize`	(optional): (Auto|Letter|Legal|Tabloid|A0|A1|A2|A3|A4|A5) Predefined standard page size, or choose custom. Default is 'Letter'.
`orientation`	(optional): Page orientation, portrait or landscape.
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Exports the current view to a graphics file and returns the path to the saved file. To speed up image export for large networks use the option 'allGraphicsDetails=FALSE'. Available for Cytoscape v3.10 or later.

Value

server response

Examples

```
exportPDF('/fullpath/myNetwork')
```

`exportPNG` *Export PNG*

Description

Saves the current network view as an png file.

Usage

```
exportPNG(
  filename = NULL,
  allGraphicsDetails = TRUE,
  hideLabels = FALSE,
  transparentBackground = FALSE,
  zoom = NULL,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`allGraphicsDetails`	(optional): TRUE results in image with highest detail; False allows faster image generation. The default is TRUE.
`hideLabels`	(optional): TRUE makes node and edge labels invisible in image. False allows them to be drawn. The default is False.
`transparentBackground`	(optional): TRUE causes background to be transparent. The default is FALSE.
`zoom`	(`numeric`) The zoom value to proportionally scale the image. The default value is 100.0. Valid only for bitmap formats, such as PNG and JPEG
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Exports the current view to a graphics file and returns the path to the saved file. To speed up image export for large networks use the option 'allGraphicsDetails=FALSE'. Available for Cytoscape v3.10 or later.

Value

server response

Examples

```
exportPNG('/fullpath/myNetwork')
```

`exportPS` *Export PS*

Description

Saves the current network view as an ps file.

Usage

```
exportPS(
  filename = NULL,
  exportTextAsFont = TRUE,
  hideLabels = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`exportTextAsFont`	(optional): If TRUE (the default value), texts will be exported as fonts.
`hideLabels`	(optional): TRUE makes node and edge labels invisible in image. False allows them to be drawn. The default is False.
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Exports the current view to a graphics file and returns the path to the saved file. To speed up image export for large networks use the option 'allGraphicsDetails=FALSE'. Available for Cytoscape v3.10 or later.

Value

server response

Examples

```
exportPS('/fullpath/myNetwork')
```

`exportSVG` *Export SVG*

Description

Saves the current network view as an svg file.

Usage

```
exportSVG(
  filename = NULL,
  exportTextAsFont = TRUE,
  hideLabels = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`exportTextAsFont`	(optional): If TRUE (the default value), texts will be exported as fonts.
`hideLabels`	(optional): TRUE makes node and edge labels invisible in image. False allows them to be drawn. The default is False.
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Exports the current view to a graphics file and returns the path to the saved file. To speed up image export for large networks use the option 'allGraphicsDetails=FALSE'. Available for Cytoscape v3.10 or later.

Value

server response

Examples

```
exportSVG('/fullpath/myNetwork')
```

`exportVisualStyles` *Export Visual Styles*

Description

Save one or more visual styles to file.

Usage

```
exportVisualStyles(
  filename = NULL,
  type = "XML",
  styles = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(char) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. Default is "styles.xml"
`type`	(optional) Type of data file to export, e.g., XML, JSON (case sensitive). Default is XML. Note: Only XML can be read by importVisualStyles().
`styles`	(optional) The styles to be exported, listed as a comma-separated string. If no styles are specified, only the current one is exported.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE. allows Cytoscape to overwrite it without asking. Default value is TRUE.

Value

Path to saved file

See Also

importVisualStyles

Examples

```
exportVisualStyles('/fullpath/myStyle')
exportVisualStyles('/fullpath/myStyle', type = 'JSON')
exportVisualStyles('/fullpath/myStyle', style = 'Minimal,default,Directed')
```

`findRemoteCytoscape` *findRemoteCytoscape*

Description

Figure out whether CyREST is local or remote. If remote, we'll want to go through Jupyter-Bridge.

Usage

```
findRemoteCytoscape(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
findRemoteCytoscape()
```

`fitContent` *Fit Content*

Description

Zoom and pan network view to maximize either height or width of current network window.

Usage

```
fitContent(selected.only = FALSE, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`selected.only`	(Boolean) Whether to fit only current selection. Default is false, i.e., to fit the entire network.
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Takes first (presumably only) view associated with provided network

Value

None

Examples

```
fitContent()
```

`floatPanel` *Float Panel*

Description

Pop out a panel from the UI of Cytoscape. Other panels will expand into the space.

Usage

```
floatPanel(panel.name, base.url = .defaultBaseUrl)
```

Arguments

`panel.name`	Name of the panel. Multiple ways of referencing panels is supported: WEST, control panel, control, c SOUTH, table panel, table, ta SOUTH_WEST, tool panel, tool, to EAST, results panel, results, r
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
floatPanel('table')
```

`getAbsSandboxPath` *getAbsSandboxPath*

Description

Get absolute sandbox path.

Usage

```
getAbsSandboxPath(fileLocation)
```

Arguments

`fileLocation`	fileLocation

Value

file location

Examples

```
getAbsSandboxPath()
```

`getAllEdges` *Get All Edges*

Description

Retrieve the names of all the edges in the network.

Usage

```
getAllEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of node edges

Examples

```
getAllEdges()
```

`getAllNodes` *Get All Nodes*

Description

Retrieve the names of all the nodes in the network.

Usage

```
getAllNodes(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of node names

Examples

```
getAllNodes()
```

`getAllStyleMappings` *Get All Style Mappings*

Description

Retrieve the values the define all the mappings per visual property in a given style.

Usage

```
getAllStyleMappings(style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name for style; default is the ’default’ style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of lists with named values defining the visual property mappings

Examples

```
getStyleMapping()
```

`getAnnotationList` *Get Annotation List*

Description

A list of named lists with annotation information

Usage

```
getAnnotationList(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

You can obtain a list of UUIDs by applying a subset function like so: sapply(getAnnotationList(), '[[', 'uuid')

Value

RETURN_DESCRIPTION

Examples

```
getAnnotationList()
```

`getAppInformation` *Get App Information*

Description

Retrieve the name, brief description and version of a Cytoscape app.

Usage

```
getAppInformation(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

App name, brief description and version.

Examples

```
getAppInformation()
```

`getAppStatus` *App Status*

Description

Retrieve the current status of a Cytoscape app: Installed, Uninstalled or Disabled.

Usage

```
getAppStatus(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

App name and status

Examples

```
getAppStatus()
```

`getAppUpdates` *List Apps With Updates*

Description

Retrieve list of currently installed Cytoscape apps with updates available.

Usage

```
getAppUpdates(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of updatable app names, versions and statuses

Examples

```
getAppUpdates()
```

`getArrowShapes` *Get Arrow Shapes*

Description

Retrieve the names of the currently supported 'arrows' – the decorations can (optionally) appear at the ends of edges, adjacent to the nodes they connect, and conveying information about the nature of the nodes' relationship.

Usage

```
getArrowShapes(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of `character` strings, e.g., 'DIAMOND', 'T', 'ARROW'

Examples

```
getArrowShapes()
```

`getAvailableApps` *List Available Apps*

Description

Retrieve a list of apps available for installation in Cytoscape.

Usage

```
getAvailableApps(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of app names and latest versions

Examples

```
getAvailableApps()
```

`getBackgroundColorDefault` *Get Background Color Default*

Description

Retrieve the default background color.

Usage

```
getBackgroundColorDefault(style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
getBackgroundColorDefault()
```

`getBrowserClientChannel` *getBrowserClientChannel*

Description

Get the unique channel

Usage

```
getBrowserClientChannel()
```

Value

client channel

Examples

```
getBrowserClientChannel()
```

`getBrowserClientJs` *getBrowserClientJs*

Description

Prepend channel number of client Javascript so it can communicate with this process via Jupyter-bridge

Usage

```
getBrowserClientJs()
```

Value

Javascript inject code

Examples

```
getBrowserClientJs()
```

`getCollectionList` *Get Collection List*

Description

FUNCTION_DESCRIPTION

Usage

```
getCollectionList(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

RETURN_DESCRIPTION

Examples

```
getCollectionList()
```

`getCollectionName` *Get Collection Name*

Description

FUNCTION_DESCRIPTION

Usage

```
getCollectionName(collection.suid = NULL, base.url = .defaultBaseUrl)
```

Arguments

`collection.suid`	DESCRIPTION
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

RETURN_DESCRIPTION

Examples

```
getCollectionName()
```

`getCollectionNetworks` *Get Collection Networks*

Description

FUNCTION_DESCRIPTION

Usage

```
getCollectionNetworks(collection.suid = NULL, base.url = .defaultBaseUrl)
```

Arguments

`collection.suid`	DESCRIPTION
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

RETURN_DESCRIPTION

Examples

```
getCollectionNetworks()
```

`getCollectionSuid` *Get Collection Suid*

Description

FUNCTION_DESCRIPTION

Usage

```
getCollectionSuid(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	DESCRIPTION
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

RETURN_DESCRIPTION

Examples

```
getCollectionSuid()
```

`getCurrentSandbox` *getCurrentSandbox*

Description

Return both the current sandbox name and path.

Usage

```
getCurrentSandbox()
```

Value

current sandbox

Examples

```
getCurrentSandbox()
```

`getCurrentSandboxName` *getCurrentSandboxName*

Description

Return the current sandbox name.

Usage

```
getCurrentSandboxName()
```

Value

current sandbox name

Examples

```
getCurrentSandboxName()
```

`getCurrentSandboxPath` *getCurrentSandboxPath*

Description

Return the current sandbox path.

Usage

```
getCurrentSandboxPath()
```

Value

current sandbox path

Examples

```
getCurrentSandboxPath()
```

`getCurrentStyle` *Get Current Style*

Description

Get the current visual style applied to a network.

Usage

```
getCurrentStyle(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Name of style

Examples

```
getCurrentStyle()
getCurrentStyle('myNetwork')
```

`getDefaultSandbox` *getDefaultSandbox*

Description

Return whatever is the current default sandbox properties.

Usage

```
getDefaultSandbox()
```

Value

default sandbox

Examples

```
getDefaultSandbox()
```

`getDefaultSandboxPath` *getDefaultSandboxPath*

Description

Return the default path, which isn't one of the properties tracked in the default_sandbox.

Usage

```
getDefaultSandboxPath()
```

Value

default sandbox path

Examples

```
getDefaultSandboxPath()
```

`getDisabledApps` *List Disabled Apps*

Description

Retrieve list of currently disabled apps in Cytoscape.

Usage

```
getDisabledApps(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of disabled app names, versions and statuses

Examples

```
getDisabledApps()
```

`getEdgeColor` *Get Edge Color*

Description

Retrieve the actual line color of specified edges.

Usage

```
getEdgeColor(edge.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`edge.names`	List of edge names or SUIDs. Default is NULL for all edges.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getEdgeColor()
```

---

getEdgeCount *Get Edge Count*

Description

Reports the number of the edges in the network.

Usage

```
getEdgeCount(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`numeric`

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getEdgeCount()
```

---

getEdgeInfo *Get Edge Information*

Description

Returns source, target and edge table row values.

Usage

```
getEdgeInfo(edges, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`edges`	List of SUIDs or names of edges, i.e., values in the "name" column. Can also input a single edge.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This function is kinda slow. It takes approximately 70ms per edge to return a result, e.g., 850 edges will take a one minute.

Value

named `list` of `lists`

Author(s)

Alexander Pico

Examples

```
getEdgeInfo()
```

`getEdgeLineStyle` *Get Edge Line Style*

Description

Retrieve the actual line style of specified edges.

Usage

```
getEdgeLineStyle(edge.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`edge.names`	List of edge names or SUIDs. Default is NULL for all edges.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getEdgeLineStyle()
```

`getEdgeLineWidth` *Get Edge Line Width*

Description

Retrieve the actual line width of specified edges.

Usage

```
getEdgeLineWidth(edge.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`edge.names`	List of edge names or SUIDs. Default is NULL for all edges.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getEdgeLineWidth()
```

`getEdgeProperty` *Get Edge Property Values*

Description

Get values for any edge property of the specified edges.

Usage

```
getEdgeProperty(
  edge.names = NULL,
  visual.property,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs. Default is NULL for all edges.
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method retrieves the actual property of the node, given the current visual style, factoring together any default, mapping and bypass setting.

Value

Named list of property values

Examples

```
getEdgeProperty(c('node 0 (pp) node 1','node 0 (pp) node 2'),'EDGE_WIDTH')
```

---

getEdgeSelectionColorDefault

Get Edge Selection Color Default

Description

Retrieve the default selected edge color.

Usage

```
getEdgeSelectionColorDefault(style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
getEdgeSelectionColorDefault()
```

`getEdgeTargetArrowShape` *Get Edge Target Arrow Shape*

Description

Retrieve the actual target arrow shape of specified edges.

Usage

```
getEdgeTargetArrowShape(
  edge.names = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs. Default is NULL for all edges.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getEdgeTargetArrowShape()
```

`getFilterList` *Get Filter List*

Description

Retrieve list of named filters in current session.

Usage

```
getFilterList(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of filter names

Examples

```
getFilterList()
```

`getFirstNeighbors` *Get list of nodes neighboring provided list*

Description

Returns a non-redundant list of first neighbors of the supplied list of nodes or current node selection.

Usage

```
getFirstNeighbors(
  node.names = NULL,
  as.nested.list = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	A `list` of SUIDs or names from the `name` column of the `node table`. Default is currently selected nodes.
`as.nested.list`	`logical` Whether to return lists of neighbors per query node
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of unique node names, optionally nested per query node name.

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

See Also

selectNodes selectFirstNeighbors

Examples

```
getFirstNeighbors()
```

`getGroupInfo` *Get Group Information*

Description

Retrieve information about a group by name or identifier.

Usage

```
getGroupInfo(group, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`group`	Group name or SUID.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Group information

Examples

```
getGroupInfo('myGroup')
```

`getInstalledApps` *List Installed Apps*

Description

Retrieve list of currently installed apps in Cytoscape.

Usage

```
getInstalledApps(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of installed app names, versions and statuses

Examples

```
getInstalledApps()
```

`getJupyterBridgeURL` *getJupyterBridgeURL*

Description

Get the jupyter bridge server url

Usage

```
getJupyterBridgeURL()
```

Value

jupyter bridge server url

Examples

```
getJupyterBridgeURL()
```

`getLayoutNameMapping` *Get Layout Name Mapping*

Description

The Cytoscape 'Layout' menu lists many layout algorithms, but the names presented there are different from the names by which these algorithms are known to layout method. This method returns a named list in which the names are from the GUI, and the values identify the names you must use to choose an algorithms in the programmatic interface.

Usage

```
getLayoutNameMapping(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named `list` of `character` strings

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getLayoutNameMapping()
# Degree Sorted Circle Layout   Group Attributes Layout   Edge-weighted Spring Embedded Layout
#            "degree-circle"      "attributes-layout"                          "kamada-kawai"
```

`getLayoutNames` *Get Layout Names*

Description

Retrieve the names of the currently supported layout algorithms. These may be used in subsequent calls to the 'layoutNetwork' function.

Usage

```
getLayoutNames(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `list` of `character` strings, e.g., "force-directed" "circular" "grid"

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getLayoutNames()
# [1] "degree-circle"        "attributes-layout"      "kamada-kawai"
# [4] "force-directed"       "cose"                   "hierarchical"
# [7] "attribute-circle"     "stacked-node-layout"    "circular"
```

`getLayoutPropertyNames` *Get Layout Property Names*

Description

Returns a list of the tunable properties for the specified layout.

Usage

```
getLayoutPropertyNames(layout.name, base.url = .defaultBaseUrl)
```

Arguments

`layout.name`	(`character`) Name of the layout
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Run getLayoutNames to list available layouts.

Value

A `list` of `character` strings

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getLayoutPropertyNames('force-directed')
# [1] "numIterations"           "defaultSpringCoefficient" "defaultSpringLength"
# [4] "defaultNodeMass"         "isDeterministic"          "singlePartition"
```

`getLayoutPropertyType` *Get Layout Property Type*

Description

Returns the type of one of the tunable properties (property.name) for the specified layout.

Usage

```
getLayoutPropertyType(layout.name, property.name, base.url = .defaultBaseUrl)
```

Arguments

`layout.name`	(`character`) Name of the layout
`property.name`	(`character`) Name of the property
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Run getLayoutNames to list available layouts. Run getLayoutPropertyNames to list properties per layout.

Value

A `character` string specifying the type

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getLayoutPropertyType('force-directed','defaultSpringLength')
# "double"
```

---

getLayoutPropertyValue *Get Layout Property Value*

Description

Returns the appropriately typed value of the specified tunable property for the specified layout.

Usage

```
getLayoutPropertyValue(layout.name, property.name, base.url = .defaultBaseUrl)
```

Arguments

`layout.name`	(`character`) Name of the layout
`property.name`	(`character`) Name of the property
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Run getLayoutNames to list available layouts. Run getLayoutPropertyNames to list properties per layout.

Value

The current value set for this layout property. Typically an `integer`, `numeric` or `character` string value.

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getLayoutPropertyValue('force-directed','defaultSpringLength')
# 80
```

`getLineStyles` *Get Line Styles*

Description

Retrieve the names of the currently supported line types – values which can be used to render edges, and thus can be used in calls to 'setEdgeLineStyleRule'.

Usage

```
getLineStyles(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of `character` strings, e.g., 'SOLID', 'DOT'

Examples

```
getLineStyles()
```

`getNetworkCenter` *Get Network Center*

Description

Retrieve the center of specified network.

Usage

```
getNetworkCenter(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNetworkCenter()
```

`getNetworkCount` *Get the number of Cytoscape networks*

Description

Returns the number of Cytoscape networks in the current Cytoscape session

Usage

```
getNetworkCount(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`numeric`

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getNetworkCount()
# 3
```

`getNetworkList` *Get the list of Cytoscape networks*

Description

Returns the list of Cytoscape network names in the current Cytoscape session

Usage

```
getNetworkList(getSUIDs = FALSE, base.url = .defaultBaseUrl)
```

Arguments

`getSUIDs`	(optional) Whether to return SUIDs instead of titles; default is FALSE.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list`

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getNetworkList()
# 3
```

`getNetworkName` *Get the name of a network*

Description

Retrieve the title of a network

Usage

```
getNetworkName(suid = NULL, base.url = .defaultBaseUrl)
```

Arguments

`suid`	(optional) SUID of the network; default is current network. If a name is provided, then it is validated and returned.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

network name

Examples

```
getNetworkName()
getNetworkName(1111)
```

`getNetworkNDExId` *Get Network NDEx Id*

Description

Retrieve the NDEx externalId for a Cytoscape network, presuming it has already been exported to NDEx.

Usage

```
getNetworkNDExId(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

If the Cytoscape network is not associated with an NDEx network, the return value will be NULL.

Value

NDEx identifier (`externalId`) or NULL

Examples

```
getNetworkNDExId()
```

`getNetworkProperty` *Get Network Property Values*

Description

Get values for any network property.

Usage

```
getNetworkProperty(visual.property, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`visual.property`	Name of a visual property. See getVisualPropertyNames.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method retrieves the actual property of the node, given the current visual style, factoring together any default, mapping and bypass setting.

Value

Named list of property values

Examples

```
getNetworkProperty('NETWORK_SCALE_FACTOR')
```

`getNetworkSuid` *Get the SUID of a network*

Description

Retrieve the SUID of a network

Usage

```
getNetworkSuid(title = NULL, base.url = .defaultBaseUrl)
```

Arguments

`title`	(optional) Name of the network; default is "current" network. If an SUID is provided, then it is validated and returned.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

(`numeric`) Network suid

Author(s)

Alexander Pico

Examples

```
getNetworkSuid()
getNetworkSuid("myNetwork")
# 80
```

`getNetworkViews` *Get Network Views*

Description

Retrieve list of network view SUIDs

Usage

```
getNetworkViews(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of network view SUIDs

Examples

```
getNetworkViews()
```

`getNetworkViewSuid` *Get the SUID of a network view*

Description

Retrieve the SUID of a network view

Usage

```
getNetworkViewSuid(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape. If a network view SUID is provided, then it is validated and returned.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

(`numeric`) Network view suid. The first (presumably only) view associated a network is returned.

Author(s)

Alexander Pico

Examples

```
getNetworkViewSuid()
getNetworkViewSuid("myNetwork")
# 90
```

`getNetworkZoom` *Get Network Zoom*

Description

Retrieve the scale factor of specified network.

Usage

```
getNetworkZoom(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNetworkZoom()
```

`getNodeColor` *Get Node Color*

Description

Retrieve the actual fill color of specified nodes.

Usage

```
getNodeColor(node.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNodeColor()
```

`getNodeCount` *Get Node Count*

Description

Reports the number of nodes in the network.

Usage

```
getNodeCount(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`numeric`

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getNodeCount()
```

`getNodeHeight` *Get Node Height*

Description

Retrieve the actual height of specified nodes.

Usage

```
getNodeHeight(node.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNodeHeight()
```

`getNodeLabelPosition` *Get Node Label Position*

Description

Retrieve the actual label position of specified nodes.

Usage

```
getNodeLabelPosition(
  node.names = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNodeLabelPosition('Node 1')
```

`getNodeLabelPositionDefault` *Get Node Label Position Default*

Description

Retrieve the default selection node color.

Usage

```
getNodeLabelPositionDefault(style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
getNodeLabelPositionDefault()
```

`getNodePosition` *Get Node Position*

Description

Retrieve the actual x,y position of specified nodes.

Usage

```
getNodePosition(node.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Dataframe of x, y values

Examples

```
getNodePosition()
```

`getNodeProperty` *Get Node Property Values*

Description

Get values for any node property of the specified nodes.

Usage

```
getNodeProperty(
  node.names = NULL,
  visual.property,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method retrieves the actual property of the node, given the current visual style, factoring together any default, mapping and bypass setting.

Value

Named list of property values

Examples

```
getNodeProperty(c('node 0','node 1'),'NODE_SHAPE')
```

`getNodeSelectionColorDefault` *Get Node Selection Color Default*

Description

Retrieve the default selection node color.

Usage

```
getNodeSelectionColorDefault(style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
getNodeSelectionColorDefault()
```

`getNodeShapes` *Get Node Shapes*

Description

Retrieve the names of the currently supported node shapes, which can then be used in calls to setNodeShapeRule and setDefaultVizMapValue.

Usage

```
getNodeShapes(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of `character` strings, e.g. 'ELLIPSE', 'RECTANGLE'

Examples

```
getNodeShapes()
```

`getNodeSize` *Get Node Size*

Description

Retrieve the actual size of specified nodes.

Usage

```
getNodeSize(node.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNodeSize()
```

`getNodeWidth` *Get Node Width*

Description

Retrieve the actual width of specified nodes.

Usage

```
getNodeWidth(node.names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs. Default is NULL for all nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Named list of property values

Examples

```
getNodeWidth()
```

`getNotebookIsRunning` *getNotebookIsRunning*

Description

getNotebookIsRunning

Usage

```
getNotebookIsRunning()
```

Value

None

Examples

```
getNotebookIsRunning()
```

`getSandboxReinitialize` *getSandboxReinitialize*

Description

Return flag indicating that next command should reinitialize the sandbox according to the default_sandbox.

Usage

```
getSandboxReinitialize()
```

Value

sandbox reinitialize

Examples

```
getSandboxReinitialize()
```

`getSelectedEdgeCount` *Get Selected Edge Count*

Description

Returns the number of edges currently selected in the network.

Usage

```
getSelectedEdgeCount(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`numeric`

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getSelectedEdgeCount()
```

`getSelectedEdges` *Get Selected Edges*

Description

Retrieve the names of all the edges selected in the network.

Usage

```
getSelectedEdges(
  edge.suids = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.suids`	Whether to return edge SUIDs. Default is FALSE to return edge names.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of selected edge names

Examples

```
getSelectedEdges()
```

`getSelectedNodeCount` *Get Selected Node Count*

Description

Returns the number of nodes currently selected in the network.

Usage

```
getSelectedNodeCount(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`numeric`

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getSelectedNodeCount()
```

`getSelectedNodes` *Get Selected Nodes*

Description

Retrieve the names of all the nodes selected in the network.

Usage

```
getSelectedNodes(
  node.suids = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.suids`	Whether to return node SUIDs. Default is FALSE to return node names.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of selected node names

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
getSelectedNodes()
```

`getStyleDependencies` *Get the values of dependencies in a style*

Description

Retrieves style dependency settings.

Usage

```
getStyleDependencies(style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

server response

Available Dependencies

arrowColorMatchesEdge nodeCustomGraphicsSizeSync nodeSizeLocked

Examples

```
getStyleDependencies("myStyle")
```

`getStyleMapping` *Get Style Mapping*

Description

Retrieve the values the define the mappings for a given visual property in a style.

Usage

```
getStyleMapping(visual.prop, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`visual.prop`	Name of the visual property, e.g., NODE_FILL_COLOR
`style.name`	Name for style; default is the ’default’ style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of named values defining the visual property mappings

See Also

getVisualPropertyNames

Examples

```
getStyleMapping()
```

`getTableColumnNames` *Get Table Column Names*

Description

Retrieve the names of all columns in a table

Usage

```
getTableColumnNames(
  table = "node",
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table`	name of table, e.g., node, edge, network; default is "node"
`namespace`	namespace of table, e.g., default
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

list of column names

Examples

```
getTableColumnNames()
getTableColumnNames('edge')
getTableColumnNames('network')
```

`getTableColumns` *Get table column values*

Description

Retrieve one or more columns of data from node, edge or network tables.

Usage

```
getTableColumns(
  table = "node",
  columns = NULL,
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table`	name of table, e.g., node (default), edge, network
`columns`	names of columns to retrieve values from as list object or comma-separated list; default is all columns
`namespace`	namespace of table; default is "default"
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

The ’SUID’ column is always retrieved along with specified columns. The ’SUID’ values are used as `row.names` in the returned `data.frame`.

Value

A `data.frame` of column values

Examples

```
getTableColumns()
getTableColumns('node','group')
```

`getTableColumnTypes` *Get Table Column Types*

Description

Retrieve the types of all columns in a table

Usage

```
getTableColumnTypes(
  table = "node",
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table`	name of table, e.g., node, edge, network; default is "node"
`namespace`	namespace of table, e.g., default
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

a named list of column types

Examples

```
getTableColumnTypes()
getTableColumnTypes('edge')
getTableColumnTypes('network')
```

`getTableValue` *Get table cell value*

Description

Retrieve the value from a specific row and column from node, edge or network tables.

Usage

```
getTableValue(
  table,
  row.name,
  column,
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table`	name of table, e.g., node, edge, network
`row.name`	Node, edge or network name, i.e., the value in the "name" column
`column`	name of column to retrieve values from
`namespace`	namespace of table; default is "default"
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A `data.frame` of column values

Examples

```
getTableValue('node','node 1', 'score')
```

`getUninstalledApps` *List Uninstalled Apps*

Description

Retrieve list of apps not currently installed in Cytoscape.

Usage

```
getUninstalledApps(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of uninstalled app names, versions and statuses

Examples

```
getUninstalledApps()
```

`getVisualPropertyDefault` *Get Visual Property Default*

Description

Retrieve the default value for a visual property.

Usage

```
getVisualPropertyDefault(
  property,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`property`	Name of property, e.g., NODE_FILL_COLOR (see getVisualPropertyNames)
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
getVisualPropertyDefault('NODE_SIZE')
```

`getVisualPropertyNames` *Get Visual Property Names*

Description

Retrieve the names of all possible visual properties.

Usage

```
getVisualPropertyNames(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of names

Examples

```
getVisualPropertyNames()
```

`getVisualStyleJSON` *Get Visual Style JSON*

Description

Get all defaults and mappings for a visual style

Usage

```
getVisualStyleJSON(styleName, css = FALSE, base.url = .defaultBaseUrl)
```

Arguments

`styleName`	name of style
`css`	TRUE to create a CytoscapeJS CSS style, FALSE to create a generic JSON version. Default is FALSE.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of visual style properties

Examples

```
getVisualStyleJSON()
```

`getVisualStyleNames` *Get Visual Style Names*

Description

Retrieve a list of all visual style names.

Usage

```
getVisualStyleNames(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A list of names

Examples

```
getVisualStyleNames()
```

`groupAnnotation` *Group Annotation*

Description

Group annotation from the network view in Cytoscape

Usage

```
groupAnnotation(names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`names`	Name of annotation by UUID or Name
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

You can obtain a list of UUIDs by applying a subset function like so: sapply(getAnnotationList(), '[[', 'uuid')

Value

UUID of group annotation

Examples

```
groupAnnotation(c("29ac8349-7be4-404e-8363-9537cc39d1ad","3846e949-3130-4362-83de-d02f5368e3ad"))
groupAnnotation(c("annotation1","annotation2", "annotation3"))
groupAnnotation("annotation1")
groupAnnotation(sapply(getAnnotationList(), '[[', 'uuid'))
```

`hideAllPanels` *Hide All Panels*

Description

Hide control, table, tool and results panels.

Usage

```
hideAllPanels(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
hideAllPanels()
```

`hideEdges` *Hide Edges*

Description

Hide (but do not delete) the specified edge or edges, by setting the Visible property bypass value to false.

Usage

```
hideEdges(edge.names, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`edge.names`	List of edge names or SUIDs
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use unhideEdges or unhideAll.

Value

None

See Also

setEdgePropertyBypass, hideSelectedEdges, unhideEdges, unhideAll

Examples

```
hideEdges()
```

`hideNodes` *Hide Nodes*

Description

Hide (but do not delete) the specified node or nodes, by setting the Visible property bypass value to false.

Usage

```
hideNodes(node.names, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use unhideNodes or unhideAll.

Value

None

See Also

setNodePropertyBypass, hideSelectedNodes, unhideNodes, unhideAll

Examples

```
hideNodes()
```

`hidePanel` *Hide Panel*

Description

Hide a panel in the UI of Cytoscape. Other panels will expand into the space.

Usage

```
hidePanel(panel.name, base.url = .defaultBaseUrl)
```

Arguments

`panel.name`	Name of the panel. Multiple ways of referencing panels is supported: WEST, control panel, control, c SOUTH, table panel, table, ta SOUTH_WEST, tool panel, tool, to EAST, results panel, results, r
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
hidePanel('table')
```

`hideSelectedEdges` *Hide Selected Edges*

Description

Hide (but do not delete) the currently selected edges, by setting the Visible property bypass value to false.

Usage

```
hideSelectedEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use unhideEdges or unhideAll.

Value

None

See Also

setEdgePropertyBypass, hideEdges, unhideEdges, unhideAll

Examples

```
hideSelectedEdges()
```

`hideSelectedNodes` *Hide Selected Nodes*

Description

Hide (but do not delete) the currently selected nodes, by setting the Visible property bypass value to false.

Usage

```
hideSelectedNodes(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use unhideNodes or unhideAll.

Value

None

See Also

setNodePropertyBypass, hideNodes, unhideNodes, unhideAll

Examples

```
hideSelectedNodes()
```

`importFileFromUrl` *importFileFromUrl*

Description

The source URL identifies a file to be transferred from a cloud resource to either the to the current Cytoscape directory (if executing on the Cytoscape workstation) or sandbox (if executing on a remote server or a sandbox was explicitly created). If the destination file already exists, it is overwritten. The 'destFile' can be an absolute path if the workflow is executing on the local Cytoscape workstation. Supported URLs include: Raw URL: URL directly references the file to download (e.g., http://tpsoft.com/museum_images/IBM Dropbox: Use the standard Dropbox 'Get Link' feature to create the 'sourceUrl' link in the clipboard (e.g., https://www.dropbox.com/s/r15azh0xb53smu1/GDS112_full.soft?dl=0) GDrive: Use the standard Google Drive 'Get Link' feature to create the 'sourceUrl' link in the clipboard (e.g., https://drive.google.com/file/d/12sJaKQQbesF10xsrbgiNtUcqCQYY1YI3/view?usp=sharing) OneDrive: Use the OneDrive web site to right click on the file, choose the 'Embed' menu option, then copy the URL in the iframe's “src“ parameter into the clipboard (e.g., https://onedrive.live.com/embed?cid=C357475 GitHub: Use the GitHub web site to show the file or a link to it, and capture the URL in the clipboard (e.g., https://github.com/cytoscape/file-transfer-app/blob/master/test_data/GDS112_full.soft) Note that GitHub enforces a limit on the size of a file that can be stored there. We advise that you take this into account when choosing a cloud service for your files. When you capture a URL in the clipboard, you should copy it into your program for use with this function. This function is most useful for Notebooks running on the local Cytoscape workstation. For Notebooks that could run on a remote server, consider using sandboxUrlTo() and related sandbox functions.

Usage

```
importFileFromUrl(
  sourceURL,
  destFile,
  overwrite = TRUE,
  base.url = .defaultBaseUrl
)
```

Arguments

`sourceURL`	URL addressing cloud file to download
`destFile`	Name of file in the R workflow's file system ... if None, use file name in source_file
`overwrite`	Name of sandbox containing file. None means "the current sandbox".
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

dict: 'filePath': <new file's absolute path in Cytoscape workstation>, 'fileByteCount': number of bytes read

Examples

```
importFileFromUrl()
```

`importFilters` *Import Filters*

Description

Loads filters from a file in JSON format.

Usage

```
importFilters(filename, base.url = .defaultBaseUrl)
```

Arguments

`filename`	(char) Path and name of the filters file to load.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
importFilters()
```

`importNetworkFromFile` *Import Network From File*

Description

Loads a network from specified file

Usage

```
importNetworkFromFile(file = NULL, base.url = .defaultBaseUrl)
```

Arguments

`file`	Name of file in any of the supported formats (e.g., SIF, GML, xGMML, etc). If NULL, a demo network file in SIF format is loaded.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

(int) network SUID

Examples

```
importNetworkFromFile()
```

`importNetworkFromNDEx` *Import Network From NDEx*

Description

Import a network from the NDEx database into Cytoscape.

Usage

```
importNetworkFromNDEx(
  ndex.id,
  username = NULL,
  password = NULL,
  accessKey = NULL,
  ndex.url = "http://ndexbio.org",
  ndex.version = "v2",
  base.url = .defaultBaseUrl
)
```

Arguments

`ndex.id`	Network `externalId` provided by NDEx. This is not the same as a Cytoscape SUID.
`username`	(optional) NDEx account username; required for private content
`password`	(optional) NDEx account password; required for private content
`accessKey`	(optional) NDEx accessKey; alternate access to private content
`ndex.url`	(optional) For alternative instances or deployments of NDEx; default is "http://ndexbio.org"
`ndex.version`	(optional) For alternative versions of the NDEx API; default is "v2"
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

(integer) SUID of imported network

Examples

```
importNetworkFromNDEx(ndex.id)
```

`importVisualStyles` *Import Visual Styles*

Description

Loads styles from an XML file and returns the names of the loaded styles.

Usage

```
importVisualStyles(filename = "styles.xml", base.url = .defaultBaseUrl)
```

Arguments

`filename`	(char) Name of the style file to load. Only reads XML files. Default is "styles.xml".
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

(list) Names of styles loaded

See Also

exportVisualStyles

Examples

```
importVisualStyles()
```

`installApp` *Install App*

Description

Installs an app in Cytoscape.

Usage

```
installApp(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
installApp()
```

`invertEdgeSelection` *Invert Edge Selection*

Description

Select all edges that were not selected and deselect all edges that were selected.

Usage

```
invertEdgeSelection(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of newly selected edge SUIDs

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
invertEdgeSelection()
```

`invertNodeSelection` *Invert Node Selection*

Description

Select all nodes that were not selected and deselect all nodes that were selected.

Usage

```
invertNodeSelection(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of newly selected node SUIDs

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
invertNodeSelection()
```

`layoutCopycat` *Copy a layout from one network to another*

Description

Sets the coordinates for each node in the target network to the coordinates of a matching node in the source network.

Usage

```
layoutCopycat(
  sourceNetwork,
  targetNetwork,
  sourceColumn = "name",
  targetColumn = "name",
  gridUnmapped = TRUE,
  selectUnmapped = TRUE,
  base.url = .defaultBaseUrl
)
```

Arguments

`sourceNetwork`	(`character`) The name of network to get node coordinates from
`targetNetwork`	(`character`) The name of the network to apply coordinates to
`sourceColumn`	(optional `character`) The name of column in the sourceNetwork node table used to match nodes; default is 'name'
`targetColumn`	(optional `character`) The name of column in the targetNetwork node table used to match nodes; default is 'name'
`gridUnmapped`	(optional `character`) If this is set to true, any nodes in the target network that could not be matched to a node in the source network will be laid out in a grid; default is TRUE
`selectUnmapped`	optional `character`) If this is set to true, any nodes in the target network that could not be matched to a node in the source network will be selected in the target network; default is TRUE
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Optional parameters such as `gridUnmapped` and `selectUnmapped` determine the behavior of target network nodes that could not be matched.

Value

None

Examples

```
layoutCopycat('network1','network2')
```

`layoutNetwork` *Apply a layout to a network*

Description

Apply a layout to a network

Usage

```
layoutNetwork(layout.name = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`layout.name`	(`character`) Name of the layout (with optional parameters). If not specified, then the preferred layout set in the Cytoscape UI is applied.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Run getLayoutNames to list available layouts.

Value

None

Examples

```
layoutNetwork()
layoutNetwork('force-directed')
layoutNetwork('force-directed defaultSpringCoefficient=.00006 defaultSpringLength=80')
```

`listGroups` *List Groups*

Description

Retrieve a list of all group SUIDs in a network.

Usage

```
listGroups(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

List of group SUIDs

Examples

```
listGroups()
```

`loadTableData` *Loads data into Cytoscape tables keyed by row*

Description

This function loads data into Cytoscape node/edge/network tables provided a common key, e.g., name. Data.frame column names will be used to set Cytoscape table column names.

Usage

```
loadTableData(
  data,
  data.key.column = "row.names",
  table = "node",
  table.key.column = "name",
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`data`	(data.frame) each row is a node and columns contain node attributes
`data.key.column`	(char) name of data.frame column to use as key; default is "row.names"
`table`	(char) name of Cytoscape table to load data into, e.g., node, edge or network; default is "node"
`table.key.column`	(char) name of Cytoscape table column to use as key; default is "name"
`namespace`	namespace of table, e.g., default
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Numeric values will be stored as Doubles in Cytoscape tables. Integer values will be stored as Integers. Character or mixed values will be stored as Strings. Logical values will be stored as Boolean. Lists are stored as Lists by CyREST v3.9+. Existing columns with the same names will keep original type but values will be overwritten.

Value

server response

`lockNodeDimensions` *Lock Node Dimensions*

Description

Set a boolean value to have node width and height fixed to a single size value.

Usage

```
lockNodeDimensions(new.state, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.state`	(Boolean) Whether to lock node width and height
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
lockNodeDimensions(TRUE)
```

`makeSimpleGraph` *Make Simple Graph*

Description

This function creates a simple graphNEL object with various node and edge attribute types to help demonstrate round trip conversion with Cytoscape networks via RCy3.

Usage

```
makeSimpleGraph()
```

Value

A `graphNEL` object with a few nodes, edges and attributes

See Also

createNetworkFromGraph, createGraphFromNetwork, makeSimpleIgraph

Examples

```
{
makeSimpleGraph()
}
```

`makeSimpleIgraph` *Make Simple Igraph*

Description

This function creates a simple iGraph object with various node and edge attribute types to help demonstrate round trip conversion with Cytoscape networks via RCy3.

Usage

```
makeSimpleIgraph()
```

Value

A `igraph` object with a few nodes, edges and attributes

See Also

createNetworkFromIgraph, createIgraphFromNetwork, makeSimpleGraph

Examples

```
{
makeSimpleIgraph()
}
```

`mapTableColumn` *Map Table Column*

Description

Perform identifier mapping using an existing column of supported identifiers to populate a new column with identifiers mapped to the originals.

Usage

```
mapTableColumn(
  column,
  species,
  map.from,
  map.to,
  force.single = TRUE,
  table = "node",
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`column`	Name of column containing identifiers of type specified by `map.from`.
`species`	Common name for species associated with identifiers, e.g., Human. See details.
`map.from`	Type of identifier found in specified `column`. See details.
`map.to`	Type of identifier to populate in new column. See details.
`force.single`	(optional) Whether to return only first result in cases of one-to-many mappings; otherwise the new column will hold lists of identifiers. Default is TRUE.
`table`	(optional) Name of table, e.g., node (default), edge or network
`namespace`	(optional) Namespace of table, e.g., default (default), shared or hidden
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Supported species: Human, Mouse, Rat, Frog, Zebrafish, Fruit fly, Mosquito, Worm, Arabidopsis thaliana, Yeast, E. coli, Tuberculosis.

Supported identifier types (depending on species): Ensembl, Entrez Gene, Uniprot-TrEMBL, miRBase, UniGene, HGNC (symbols), MGI, RGD, SGD, ZFIN, FlyBase, WormBase, TAIR.

Value

dataframe with map.from and map.to columns. Beware: if map.to is not unique, it will be suffixed with an incrementing number in parentheses, e.g., if mapIdentifiers is repeated on the same network. However, the original map.to column will be returned regardless.

Examples

```
mapped.cols <- mapTableColumn('name','Yeast','Ensembl','SGD')
#          name        SGD
#17920  YER145C S000000947
#17921  YMR058W S000004662
#17922  YJL190C S000003726
#...
```

`mapVisualProperty` *Creates a mapping between an attribute and a visual property*

Description

Generates the appropriate data structure for the "mapping" parameter in updateStyleMapping.

Usage

```
mapVisualProperty(
  visual.prop,
  table.column,
  mapping.type,
  table.column.values,
  visual.prop.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`visual.prop`	(char) name of visual property to map
`table.column`	(char) name of table column to map
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p)
`table.column.values`	(list) list of values paired with visual.prop.values; skip for passthrough mapping
`visual.prop.values`	(list) list of values paired with table.column.values; skip for passthrough mapping
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

The paired list of values must be of the same length or mapping will fail. For gradient mapping, you may include two additional visual.prop.values in the first and last positions to map respectively to values less than and greater than those specified in table.column.values. Mapping will also fail if the data type of table.column.values does not match that of the existing table.column. Note that all imported numeric data are stored as Integers or Doubles in Cytosacpe tables; and character or mixed data are stored as Strings.

Value

(network=network, base.url=base.url) ready to convert into JSON by style mapping operations

List of visual properties

Node Border Stroke
Node Border Paint
Node Border Transparency
Node Border Width
Node CustomGraphics 1-9
Node CustomGraphics Position 1-9
Node CustomGraphics Size 1-9
Node CustomPaint 1-9
Node Depth
Node Fill Color
Node Height
Node Label
Node Label Color
Node Label Font Face
Node Label Font Size
Node Label Position
Node Label Transparency
Node Label Width
Node Network Image Visible
Node Paint
Node Selected
Node Selected Paint
Node Shape
Node Size
Node Tooltip
Node Transparency
Node Visible
Node Width
Node X Location
Node Y Location
Node Z Location

Edge Bend
Edge Curved
Edge Label
Edge Label Color
Edge Label Font Face
Edge Label Font Size
Edge Label Transparency
Edge Label Width
Edge Line Type
Edge Paint
Edge Selected
Edge Selected Paint
Edge Source Arrow Selected Paint
Edge Source Arrow Shape
Edge Source Arrow Size
Edge Source Arrow Unselected Paint
Edge Stroke Selected Paint
Edge Stroke Unselected Paint
Edge Target Arrow Selected Paint
Edge Target Arrow Shape
Edge Target Arrow Size
Edge Target Arrow Unselected Paint
Edge Tooltip
Edge Transparency
Edge Unselected Paint
Edge Visible
Edge Visual Property
Edge Width

Network Background Paint
Network Center X Location
Network Center Y Location
Network Center Z Location
Network Depth
Network Edge Selection
Network Height
Network Node Selection
Network Scale Factor
Network Size
Network Title
Network Width

See Also

updateStyleMapping getVisualPropertyNames

Examples

```
mapVisualProperty('node fill color','score','c',c(-4.0,0.0,9.0),c('#99CCFF','#FFFFFF','#FF7777'))
mapVisualProperty('node shape','type','d',c('protein','metabolite'),c('ellipse','rectangle'))
mapVisualProperty('node label','alias','p')
```

`matchArrowColorToEdge` *Match Arrow Color To Edge*

Description

Set a boolean value to have arrow shapes share the same color as the edge.

Usage

```
matchArrowColorToEdge(new.state, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.state`	(Boolean) Whether to match arrow color to edge.
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
matchArrowColorToEdge(TRUE)
```

`mergeNetworks` *Merge Networks*

Description

Combine networks via union, intersection, or difference operations. Lots of optional parameters choose from!

Usage

```
mergeNetworks(
  sources = NULL,
  title = NULL,
  operation = "union",
  nodeKeys = NULL,
  nodeMergeMap = NULL,
  nodesOnly = FALSE,
  edgeKeys = NULL,
  edgeMergeMap = NULL,
  networkMergeMap = NULL,
  inNetworkMerge = TRUE,
  base.url = .defaultBaseUrl
)
```

Arguments

`sources`	List of network names (max:2) to be merged.
`title`	(optional) Title of the resulting merged network. Default is a concatentation of operation and source network titles.
`operation`	(optional) Type of merge: union (default), intersection or difference.
`nodeKeys`	(optional) An order-dependent list of columns to match nodes across source networks. Default is "name" column for all sources.
`nodeMergeMap`	(optional) A list of column merge records specifying how to merge node table data. Each record should be of the form: c("network1 column", "network2 column", "merged column", "type"), where column names are provided and type is String, Integer, Double or List.
`nodesOnly`	(optional) If TRUE, this will merge the node tables and ignore edge and network table data. Default is FALSE.
`edgeKeys`	(optional) An order-dependent list of columns to match edges across source networks. Default is "name" column for all sources.
`edgeMergeMap`	(optional) A list of column merge records specifying how to merge edge table data. Each record should be of the form: c("network1 column", "network2 column", "merged column", "type"), where column names are provided and type is String, Integer, Double or List.
`networkMergeMap`	(optional) A list of column merge records specifying how to merge network table data. Each record should be of the form: c("network1 column", "network2 column", "merged column", "type"), where column names are provided and type is String, Integer, Double or List.
`inNetworkMerge`	(optional) If TRUE (default), nodes and edges with matching attributes in the same network will be merged.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

SUID of resulting merged network

Examples

```
mergeNetworks(c("Network 1", "Network 2"), "Merged Network")
mergeNetworks(c("my network","string network"), "Merged Network",
             nodeKeys=c("HGNC","query term"))
```

`notebookExportShowImage`

notebookExportShowImage

Description

Show network view in notebook output.

Usage

```
notebookExportShowImage(
  filename = "image",
  type = "PNG",
  resolution = NULL,
  units = NULL,
  height = NULL,
  width = NULL,
  zoom = NULL,
  sandboxName = NULL,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`type`	(`character`) Type of image to export, e.g., PNG (default), JPEG, PDF, SVG.
`resolution`	(`numeric`) The resolution of the exported image, in DPI. Valid only for bitmap formats, when the selected width and height 'units' is inches. The possible values are: 72 (default), 100, 150, 300, 600.
`units`	(`character`) The units for the 'width' and 'height' values. Valid only for bitmap formats, such as PNG and JPEG. The possible values are: pixels (default), inches.
`height`	(`numeric`) The height of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`width`	(`numeric`) The width of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`zoom`	(`numeric`) The zoom value to proportionally scale the image. The default value is 100.0. Valid only for bitmap formats, such as PNG and JPEG
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Show network view in notebook output.

Value

display image

Examples

```
notebookExportShowImage()
```

`notebookShowImage` *notebookShowImage*

Description

Show network view in notebook output.

Usage

```
notebookShowImage(
  filename = "image",
  type = "PNG",
  resolution = NULL,
  units = NULL,
  height = NULL,
  width = NULL,
  zoom = NULL,
  sandboxName = NULL,
  network = NULL,
  base.url = .defaultBaseUrl,
  overwriteFile = TRUE
)
```

Arguments

`filename`	(`character`) Full path or path relative to current working directory, in addition to the name of the file. Extension is automatically added based on the `type` argument. If blank, the current network name will be used.
`type`	(`character`) Type of image to export, e.g., PNG (default), JPEG, PDF, SVG.
`resolution`	(`numeric`) The resolution of the exported image, in DPI. Valid only for bitmap formats, when the selected width and height 'units' is inches. The possible values are: 72 (default), 100, 150, 300, 600.
`units`	(`character`) The units for the 'width' and 'height' values. Valid only for bitmap formats, such as PNG and JPEG. The possible values are: pixels (default), inches.
`height`	(`numeric`) The height of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`width`	(`numeric`) The width of the exported image. Valid only for bitmap formats, such as PNG and JPEG.
`zoom`	(`numeric`) The zoom value to proportionally scale the image. The default value is 100.0. Valid only for bitmap formats, such as PNG and JPEG
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`network`	(optional) Name or SUID of a network or view. Default is the "current" network active in Cytoscape. The first (presummably only) view associated a network is used if a specific view SUID is not provided.

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows Cytoscape show a message box before overwriting the file if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

Show network view in notebook output.

Value

display image

Examples

```
notebookShowImage()
```

`openAppStore` *Open App Store Page*

Description

Opens the Cytoscape App Store in a new tab in your default browser.

Usage

```
openAppStore(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
openAppStore()
```

`openSession` *Open Session File or URL*

Description

Open a session file or URL. This will clear all networks, tables and styles associated with current session. Be sure to saveSession first.

Usage

```
openSession(file.location = NULL, base.url = .defaultBaseUrl)
```

Arguments

`file.location`	File path or URL (with 'http' or 'https' prefix). Default is a sample session file.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

saveSession

Examples

```
openSession('/fullpath/mySession.CYS')
```

`paletteColorBrewerAccent` *paletteColorBrewerAccent Qualitative*

Description

Generate a qualitative Accent Brewer palette of a given size

Usage

```
paletteColorBrewerAccent(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 8 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerAccent()
```

`paletteColorBrewerBlues`

paletteColorBrewerBlues Sequential

Description

Generate a sequential Blues Brewer palette of a given size

Usage

```
paletteColorBrewerBlues(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerBlues()
```

`paletteColorBrewerBrBG`

paletteColorBrewerBrBG Divergent

Description

Generate a divergent BrBG Brewer palette of a given size

Usage

```
paletteColorBrewerBrBG(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerBrBG()
```

`paletteColorBrewerBuGn`

paletteColorBrewerBuGn Sequential

Description

Generate a sequential BuGn Brewer palette of a given size

Usage

```
paletteColorBrewerBuGn(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerBuGn()
```

`paletteColorBrewerBuPu`

paletteColorBrewerBuPu Sequential

Description

Generate a sequential BuPu Brewer palette of a given size

Usage

```
paletteColorBrewerBuPu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerBuPu()
```

`paletteColorBrewerDark2`

paletteColorBrewerDark2 Qualitative

Description

Generate a qualitative Dark2 Brewer palette of a given size

Usage

```
paletteColorBrewerDark2(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 8 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerDark2()
```

`paletteColorBrewerGnBu`

paletteColorBrewerGnBu Sequential

Description

Generate a sequential GnBu Brewer palette of a given size

Usage

```
paletteColorBrewerGnBu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerGnBu()
```

`paletteColorBrewerGreens`

paletteColorBrewerGreens Sequential

Description

Generate a sequential Greens Brewer palette of a given size

Usage

```
paletteColorBrewerGreens(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerGreens()
```

`paletteColorBrewerGreys`

paletteColorBrewerGreys Sequential

Description

Generate a sequential Greys Brewer palette of a given size

Usage

```
paletteColorBrewerGreys(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerGreys()
```

`paletteColorBrewerOranges`

paletteColorBrewerOranges Sequential

Description

Generate a sequential Oranges Brewer palette of a given size

Usage

```
paletteColorBrewerOranges(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerOranges()
```

`paletteColorBrewerOrRd`

paletteColorBrewerOrRd Sequential

Description

Generate a sequential OrRd Brewer palette of a given size

Usage

```
paletteColorBrewerOrRd(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerOrRd()
```

`paletteColorBrewerPaired`

paletteColorBrewerPaired Qualitative

Description

Generate a qualitative Paired Brewer palette of a given size

Usage

```
paletteColorBrewerPaired(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 12. See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPaired()
```

`paletteColorBrewerPastel1`

paletteColorBrewerPastel1 Qualitative

Description

Generate a qualitative Pastel1 Brewer palette of a given size

Usage

```
paletteColorBrewerPastel1(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPastel1()
```

`paletteColorBrewerPastel2`

paletteColorBrewerPastel2 Qualitative

Description

Generate a qualitative Pastel2 Brewer palette of a given size

Usage

```
paletteColorBrewerPastel2(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 8 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPastel2()
```

`paletteColorBrewerPiYG`

paletteColorBrewerPiYG Divergent

Description

Generate a divergent PiYG Brewer palette of a given size

Usage

```
paletteColorBrewerPiYG(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPiYG()
```

`paletteColorBrewerPRGn`

paletteColorBrewerPRGn Divergent

Description

Generate a divergent PRGn Brewer palette of a given size

Usage

```
paletteColorBrewerPRGn(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPRGn()
```

`paletteColorBrewerPuBu`

paletteColorBrewerPuBu Sequential

Description

Generate a sequential PuBu Brewer palette of a given size

Usage

```
paletteColorBrewerPuBu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPuBu()
```

`paletteColorBrewerPuBuGn`

paletteColorBrewerPuBuGn Sequential

Description

Generate a sequential PuBuGn Brewer palette of a given size

Usage

```
paletteColorBrewerPuBuGn(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPuBuGn()
```

`paletteColorBrewerPuOr`

paletteColorBrewerPuOr Divergent

Description

Generate a divergent PuOr Brewer palette of a given size

Usage

```
paletteColorBrewerPuOr(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPuOr()
```

`paletteColorBrewerPuRd` *paletteColorBrewerPuRd Sequential*

Description

Generate a sequential PuRd Brewer palette of a given size

Usage

```
paletteColorBrewerPuRd(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPuRd()
```

`paletteColorBrewerPurples` *paletteColorBrewerPurples Sequential*

Description

Generate a sequential Purples Brewer palette of a given size

Usage

```
paletteColorBrewerPurples(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerPurples()
```

`paletteColorBrewerRdBu`

paletteColorBrewerRdBu Divergent

Description

Generate a divergent RdBu Brewer palette of a given size

Usage

```
paletteColorBrewerRdBu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerRdBu()
```

`paletteColorBrewerRdPu`

paletteColorBrewerRdPu Sequential

Description

Generate a sequential RdPu Brewer palette of a given size

Usage

```
paletteColorBrewerRdPu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerRdPu()
```

`paletteColorBrewerRdYlBu` *paletteColorBrewerRdYlBu Divergent*

Description

Generate a divergent RdYlBu Brewer palette of a given size

Usage

```
paletteColorBrewerRdYlBu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerRdYlBu()
```

`paletteColorBrewerReds` *paletteColorBrewerReds Sequential*

Description

Generate a sequential Reds Brewer palette of a given size

Usage

```
paletteColorBrewerReds(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerReds()
```

`paletteColorBrewerSet1`

paletteColorBrewerSet1 Qualitative

Description

Generate a qualitative Set1 Brewer palette of a given size

Usage

```
paletteColorBrewerSet1(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerSet1()
```

`paletteColorBrewerSet2`

paletteColorBrewerSet2 Qualitative

Description

Generate a qualitative Set2 Brewer palette of a given size

Usage

```
paletteColorBrewerSet2(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 8 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerSet2()
```

`paletteColorBrewerSet3`

paletteColorBrewerSet3 Qualitative

Description

Generate a qualitative Set3 Brewer palette of a given size

Usage

```
paletteColorBrewerSet3(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 12. See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerSet3()
```

`paletteColorBrewerYlGn`

paletteColorBrewerYlGn Sequential

Description

Generate a sequential YlGn Brewer palette of a given size

Usage

```
paletteColorBrewerYlGn(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerYlGn()
```

`paletteColorBrewerYlGnBu` *paletteColorBrewerYlGnBu Sequential*

Description

Generate a sequential YlGnBu Brewer palette of a given size

Usage

```
paletteColorBrewerYlGnBu(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerYlGnBu()
```

`paletteColorBrewerYlOrBr` *paletteColorBrewerYlOrBr Sequential*

Description

Generate a sequential YlOrBr Brewer palette of a given size

Usage

```
paletteColorBrewerYlOrBr(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerYlOrBr()
```

`paletteColorBrewerYlOrRd` *paletteColorBrewerYlOrRd Sequential*

Description

Generate a sequential YlOrRd Brewer palette of a given size

Usage

```
paletteColorBrewerYlOrRd(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 . See RColorBrewer::display.brewer.all()

Value

List of palette colors

Examples

```
paletteColorBrewerYlOrRd()
```

`paletteColorRandom` *paletteColorRandom Qualitative*

Description

Generate a qualitative random color map of a given size

Usage

```
paletteColorRandom(value.count = 1)
```

Arguments

`value.count`	Number of colors to generate; default is 1

Value

List of random colors

See Also

genNodeColorMap genEdgeColorMap

Examples

```
paletteColorRandom()
```

`paletteColorVirdis` *paletteColorVirdis*

Description

Generate a Virdis Brewer palette of a given size

Usage

```
paletteColorVirdis(value.count = 3)
```

Arguments

`value.count`	Number of colors to generate; min is 3 (default); max is 9 Get colors from https://cran.r-project.org/web/packages/viridis/index.html . See virdis::virdis()

Value

List of palette colors

Examples

```
paletteColorVirdis()
```

`RCy3` *RCy3: Functions to Access and Control Cytoscape*

Description

Vizualize, analyze and explore networks using Cytoscape via R.

Details

To learn more about RCy3, start with the vignettes: `browseVignettes("RCy3")`

`RemoveFromGroup` *Remove from Group*

Description

Removes the specified nodes and edges from the specified group.

Usage

```
RemoveFromGroup(
  group.name,
  nodes = NULL,
  nodes.by.col = "SUID",
  edges = NULL,
  edges.by.col = "SUID",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`group.name`	Specifies the name used to identify the group
`nodes`	List of node SUIDs, names, other column values, or keyword: selected, unselected or all. Default is currently selected nodes.
`nodes.by.col`	name of node table column corresponding to provided nodes list. Default is 'SUID'.
`edges`	List of edge SUIDs, names, other column values, or keyword: selected, unselected or all. Default is currently selected edges.
`edges.by.col`	name of edge table column corresponding to provided edges list. Default is 'SUID'.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
RemoveFromGroup('myGroup')
```

`removeNodeCustomGraphics` *Remove Node Custom Graphics*

Description

Remove the default custom charts, images and gradients.

Usage

```
removeNodeCustomGraphics(
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
removeNodeCustomGraphics()
```

`renameNetwork` *Rename a network*

Description

Sets a new name for this network

Usage

```
renameNetwork(title, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`title`	New name for the network
`network`	(optional) Name or suid of the network that you want to rename; default is "current" network
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Duplicate network names are not allowed

Value

None

Author(s)

Alexander Pico, Julia Gustavsen

Examples

```
renameNetwork("renamed network")
```

`renameTableColumn` *Rename Table Column*

Description

Sets a new name for a column.

Usage

```
renameTableColumn(
  column,
  new.name,
  table = "node",
  namespace = "default",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`column`	Name of the column to rename
`new.name`	New name for the specified column
`table`	(optional) Name of table, e.g., node (default), edge or network
`namespace`	(optional) Namespace of table, e.g., default (default), shared or hidden

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
renameTableColumn('exp','log2FC')
```

`resetDefaultSandbox` *resetDefaultSandbox*

Description

Reset the entire state of the sandbox system.

Usage

```
resetDefaultSandbox()
```

Value

None

Examples

```
resetDefaultSandbox()
```

`rotateLayout` *Rotate Layout*

Description

Rotate the layout.

Usage

```
rotateLayout(
  angle,
  selected.only = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`angle`	The angle (in degrees) to rotate the network. From -180 to 180
`selected.only`	(Boolean) Whether to rotate only current selection. Default is false.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Author(s)

Yihang Xin

Examples

```
rotateLayout(90, 'current', selected.only=FALSE)
```

`runningRemoteCheck` *runningRmoteCheck*

Description

runningRmoteCheck

Usage

```
runningRemoteCheck(base.url = .defaultBaseUrl, newState = NULL)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`newState`	new state of running remote

Value

oldState

Examples

```
runningRmoteCheck()
```

`sandboxGetFileInfo` *sandboxGetFileInfo*

Description

Get metadata on file in sandbox (or entire sandbox). If the current sandbox is the entire file system on a Cytoscape workstation, trying to delete it is an error. Otherwise, deleting the current sandbox results in the default sandbox becoming the new current sandbox. When running standalone on the same workstation as Cytoscape, the default sandbox is the entire file system on the Cytoscape workstation. When running in a Notebook or remote server, the default sandbox is the 'default_sandbox' created automatically under the under the filetransfer directory in the CytoscapeConfiguration directory. If that sandbox is deleted, it will be re-created so that subsequent file operations can complete successfully. Note that this function can be used to query either a file or a directory.

Usage

```
sandboxGetFileInfo(fileName, sandboxName = NULL, base.url = .defaultBaseUrl)
```

Arguments

`fileName`	Name of file whose metadata to return ... can be sandbox-relative path ... "." returns metadata on sandbox itself
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

dict: 'filePath': <full path on Cytoscape workstation>, 'modifiedTime': <last changed time, " if file doesn't exist>, 'isFile': <True if file, False if directory>

Examples

```
sandboxGetFileInfo()
```

`sandboxGetFrom` *sandboxGetFrom*

Description

Transfer a file from a sandbox. The source file is transferred from the named (or current) sandbox to the R workflow's file system, overwriting an existing file if one already exists. The sourceFile can be an absolute path if the sandbox is the entire file system (i.e., for standalone R execution) or a path relative to the sandbox (i.e., for Notebook or remote execution or if a sandbox was explicitly created).

Usage

```
sandboxGetFrom(
  sourceFile,
  destFile = NULL,
  overwrite = TRUE,
  sandboxName = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`sourceFile`	Name of file to read (as absolute path or sandbox-relative path)
`destFile`	Name of file in the R workflow's file system ... if None, use file name in source_file
`overwrite`	Name of sandbox containing file. None means "the current sandbox".
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

sandboxGetFrom

Examples

```
sandboxGetFrom()
```

`sandboxInitializer` *sandboxInitializer*

Description

Start with a sandbox template and update properties using whatever is found in the new_sandbox.

Usage

```
sandboxInitializer(newSandbox = NULL, ...)
```

Arguments

`newSandbox`	newSandbox
`...`	...

Value

sandbox

Examples

```
sandboxInitializer()
```

`sandboxRemove` *sandboxRemove*

Description

Delete sandbox contents and remove its directory. If the current sandbox is the entire file system on a Cytoscape workstation, trying to delete it is an error. Otherwise, deleting the current sandbox results in the default sandbox becoming the new current sandbox. When running standalone on the same workstation as Cytoscape, the default sandbox is the entire file system on the Cytoscape workstation. When running in a Notebook or remote server, the default sandbox is the 'default_sandbox' created automatically under the under the filetransfer directory in the CytoscapeConfiguration directory. If that sandbox is deleted, it will be re-created so that subsequent file operations can complete successfully.

Usage

```
sandboxRemove(sandboxName = NULL, base.url = .defaultBaseUrl)
```

Arguments

`sandboxName`	Name of sandbox to delete. None means to delete the current sandbox. If that sandbox is the default sandbox, it is automatically re-created.
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

dict: 'sandboxPath': <directory on Cytoscape workstation>, 'existed': <True if sandbox existed>

Examples

```
sandboxRemove()
```

`sandboxRemoveFile` *sandboxRemoveFile*

Description

Remove a file from a sandbox. The named file is removed from the named sandbox. If the sandbox is the entire file system (i.e., for standalone R execution), the file name can be an absolute path. Otherwise, it is a path relative to the named sandbox. Note that there is no function that deletes a directory, except for sandboxRemove(), which deletes a sandbox and all of its contents.

Usage

```
sandboxRemoveFile(fileName, sandboxName = NULL, base.url = .defaultBaseUrl)
```

Arguments

`fileName`	Name of file to delete (as absolute path or sandbox-relative path)
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

dict: 'filePath': <file's absolute path in Cytoscape workstation>, 'existed': True if file existed before being deleted

Examples

```
sandboxRemoveFile()
```

`sandboxSendTo` *sandboxSendTo*

Description

Transfer a file to a sandbox. The source file is transferred to the named (or current) sandbox, overwriting an existing file if one already exists. The destFile can be an absolute path if the sandbox is the entire file system (i.e., for standalone R execution) or a path relative to the sandbox (i.e., for Notebook or remote execution or if a sandbox was explicitly created). Note that there is no function that transfers an entire directory. Note, though, that when using sandboxSet() to make a sandbox current, it is possible to copy the Cytoscape sample data directories into to the sandbox at the same time.

Usage

```
sandboxSendTo(
  sourceFile,
  destFile = NULL,
  overwrite = TRUE,
  sandboxName = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`sourceFile`	Name of file to read (as absolute path or sandbox-relative path)
`destFile`	Name of file in the R workflow's file system ... if None, use file name in source_file
`overwrite`	Name of sandbox containing file. None means "the current sandbox".
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

sandboxSendTo

Examples

```
sandboxSendTo()
```

---

sandboxSet *sandboxSet*

Description

Set a new default sandbox, creating it if necessary. A sandbox is the root for the file system used for all file operations. When running standalone on the same workstation as Cytoscape, the default sandbox is the directory that's current for the R kernel. When running in a Notebook or remote server, the default sandbox is the 'default_sandbox' created automatically under the under the filetransfer directory in the CytoscapeConfiguration directory. Naming a sandbox with this function creates a new sub-directory as a sibling to 'default_sandbox' and uses it for subsequent file operations. Setting a None sandbox uses the default sandbox instead. Sandboxes are highly recommended as an aid to creating workflows that can be shared with others.

Usage

```
sandboxSet(
  sandboxName,
  copySamples = TRUE,
  reinitialize = TRUE,
  base.url = .defaultBaseUrl
)
```

Arguments

`sandboxName`	Name of new default sandbox. None means to use the original default sandbox
`copySamples`	True to copy the Cytoscape sampleData into the sandbox
`reinitialize`	True to delete sandbox contents (if any) if sandbox already exists
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

sandbox path in Cytoscape workstation's file system

Examples

```
sandboxSet()
```

`sandboxUrlTo` *sandboxUrlTo*

Description

Transfer a cloud-based file to a sandbox. The source URL identifies a file to be transferred to the named (or current) sandbox, overwriting an existing file if one already exists. The destFile can be an absolute path if the sandbox is the entire file system (i.e., for standalone R execution), or it can be a path relative to the sandbox (i.e., for Notebook or remote execution or if a sandbox was explicitly created).

Usage

```
sandboxUrlTo(
  sourceURL,
  destFile,
  overwrite = TRUE,
  sandboxName = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`sourceURL`	URL addressing cloud file to download
`destFile`	Name of file in the R workflow's file system ... if None, use file name in source_file
`overwrite`	Name of sandbox containing file. None means "the current sandbox".
`sandboxName`	Name of sandbox containing file. None means "the current sandbox".
`base.url`	Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://127.0.0.1:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

dict: 'filePath': <new file's absolute path in Cytoscape workstation>, 'fileByteCount': number of bytes read

Examples

```
sandboxUrlTo()
```

`saveSession` *Save Session to File*

Description

Saves the current Cytoscape session as a CYS file.

Usage

```
saveSession(filename = NULL, base.url = .defaultBaseUrl, overwriteFile = TRUE)
```

Arguments

`filename`	Full path or path relative to current working directory, in addition to the name of the file. The `.cys` extension is automatically added. Leave blank to update previously saved session file.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.
`overwriteFile`	(optional) FALSE allows an error to be generated if the file already exists; TRUE allows Cytoscape to overwrite it without asking. Default value is TRUE.

Details

If no `filename` is provided, then it attempts to save to an existing CYS file associated with the session. If `filename` already exists, then it is overwritten.

Unlike most export functions in RCy3, Cytoscape will automatically overwrite CYS session files with the same name. You will not be prompted to confirm or reject overwrite. Use carefully!

Value

server response

Examples

```
saveSession('/fullpath/mySession')
saveSession()
```

`scaleLayout` *Scale Layout*

Description

Scale the layout in either the X, Y, or both directions.

Usage

```
scaleLayout(
  axis,
  scaleFactor,
  selected.only = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`axis`	The axis to scale. Options: "X Axis", "Y Axis", "Both Axes".
`scaleFactor`	The axis The scale factor to apply to the network.
`selected.only`	(Boolean) Whether to rotate only current selection. Default is false.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Author(s)

Yihang Xin

Examples

```
scaleLayout('X Axis', 2, 'current', selected.only=FALSE)
```

`selectAll` *Select all nodes and edges*

Description

Selects all nodes and edges in a Cytoscape Network

Usage

```
selectAll(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network into which you want to select; default is "current" network
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Selects all nodes and edges in a specified network.

Author(s)

Alexander Pico, Julia Gustavsen

See Also

`selectNodes`

Examples

```
selectAllNodes()
```

`selectAllEdges` *Select all edges*

Description

Selects all edges in a Cytoscape Network

Usage

```
selectAllEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Selects all edges in a specified network.

Author(s)

Alexander Pico, Julia Gustavsen

Examples

```
cw <- CytoscapeWindow('new.demo', new('graphNEL'))
selectAllEdges(cw)
```

`selectAllNodes` *Select all nodes*

Description

Selects all nodes in a Cytoscape Network

Usage

```
selectAllNodes(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network into which you want to select; default is "current" network
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Selects all nodes in a specified network.

Author(s)

Alexander Pico, Julia Gustavsen

See Also

`selectNodes`

Examples

```
selectAllNodes()
```

`selectEdges` *Select Edges*

Description

Select edges in the network by SUID, name or other column values.

Usage

```
selectEdges(
  edges,
  by.col = "SUID",
  preserve.current.selection = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edges`	List of edge SUIDs, names or other column values
`by.col`	Edge table column to lookup up provide edge values. Default is 'SUID'.
`preserve.current.selection`	`boolean` Whether to maintain previously selected edges.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of newly selected edge SUIDs

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
selectEdges()
```

`selectEdgesAdjacentToNodes`

Select Edges Adjacent To Nodes

Description

Takes list of node SUIDs, names or other column values and adds to the selection all edges connected to those nodes, regardless of directionality.

Usage

```
selectEdgesAdjacentToNodes(
  nodes,
  by.col = "name",
  selectNodes = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`nodes`	List of node SUIDs, names or other column values
`by.col`	Node table column to lookup up provide node values. Default is 'name'.
`selectNodes`	The default is TRUE. If TRUE, nodes will also be selected.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Lists of SUIDs for selected nodes and edges

Examples

```
selectEdgesAdjacentToNodes()
```

`selectEdgesAdjacentToSelectedNodes`
Select Edges Adjacent To Selected Nodes

Description

Takes currently selected nodes and adds to the selection all edges connected to those nodes, regardless of directionality.

Usage

```
selectEdgesAdjacentToSelectedNodes(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Lists of SUIDs for selected nodes and edges

Examples

```
selectEdgesAdjacentToSelectedNodes()
```

`selectEdgesConnectingSelectedNodes` *Select the edges connecting selected nodes in Cytoscape Network*

Description

Selects edges in a Cytoscape Network connecting the selected nodes, including self loops connecting single nodes.

Usage

```
selectEdgesConnectingSelectedNodes(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Lists of SUIDs for selected nodes and edges

Author(s)

Alexander Pico, Julia Gustavsen

Examples

```
selectEdgesConnectingSelectedNodes()
```

`selectFirstNeighbors` *Select first neighbor nodes*

Description

Select nodes directly connected to currently selected nodes. Can specify connection directionality using the direction param.

Usage

```
selectFirstNeighbors(
  direction = "any",
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`direction`	direction of connections to neighbors to follow, e.g., incoming, outgoing, undirected, or any (default)
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

list of suids of selected nodes, including original selection

Examples

```
selectFirstNeighbors()
selectFirstNeighors('outgoing')
selectFirstNeighors('incoming')
```

`selectNodes` *Select Nodes*

Description

Select nodes in the network by SUID, name or other column values.

Usage

```
selectNodes(
  nodes,
  by.col = "SUID",
  preserve.current.selection = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`nodes`	List of node SUIDs, names or other column values
`by.col`	Node table column to lookup up provide node values. Default is 'SUID'.
`preserve.current.selection`	`boolean` Whether to maintain previously selected nodes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

`list` of newly selected node SUIDs

Author(s)

AlexanderPico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
selectNodes()
```

`selectNodesConnectedBySelectedEdges` *Select Nodes Connected By Selected Edges*

Description

Takes currently selected edges and extends the selection to connected nodes, regardless of directionality.

Usage

```
selectNodesConnectedBySelectedEdges(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

Lists of SUIDs for currently selected nodes and edges

Examples

```
selectNodesConnectedBySelectedEdges()
```

`setBackgroundColorDefault` *Set Background Color Default*

Description

Set the default background color.

Usage

```
setBackgroundColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setBackgroundColorDefault('#888888')
```

`setCatchupFilterSecs` *Set Catchup Filter Delay*

Description

This function sets an internal delay variable that allows Cytoscape to "catchup" prior to subsequent functions. Call without specifying `secs` to restore default value.

Usage

```
setCatchupFilterSecs(secs = 1)
```

Arguments

`secs`	Number of seconds to delay.

Details

This delay is only necessary while concurrency bugs exist in the Cytoscape application. This delay may need to be increased from the default value in certain use cases, e.g., larger networks.

Value

None

See Also

setModelPropagationSecs, setCatchupNetworkSecs

Examples

```
{
setCatchupFilterSecs(2)
setCatchupFilterSecs() #restores default delay
}
```

`setCatchupNetworkSecs` *Set Catchup Network Delay*

Description

This function sets an internal delay variable that allows Cytoscape to "catchup" prior to subsequent functions. Call without specifying `secs` to restore default value.

Usage

```
setCatchupNetworkSecs(secs = 2)
```

Arguments

`secs`	Number of seconds to delay.

Details

This delay is only necessary while concurrency bugs exist in the Cytoscape application. This delay may need to be increased from the default value in certain use cases, e.g., larger networks.

Value

None

See Also

setModelPropagationSecs, setCatchupFilterSecs

Examples

```
{
setCatchupNetworkSecs(2)
setCatchupNetworkSecs() #restores default delay
}
```

`setCurrentNetwork` *Set current network*

Description

Selects the given network as "current"

Usage

```
setCurrentNetwork(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or suid of the network that you want set as current
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

server response

Examples

```
setCurrentNetwork('MyNetwork')
```

`setCurrentSandbox` *setCurrentSandbox*

Description

Set and return the current sandbox name and path.

Usage

```
setCurrentSandbox(sandboxName, sandboxPath)
```

Arguments

`sandboxName`	sandboxName
`sandboxPath`	sandboxPath

Value

current sandbox

Examples

```
setCurrentSandbox()
```

`setCurrentView` *Set Current View*

Description

Set which network view is "current".

Usage

```
setCurrentView(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of a network or view. The first (presummably only) view associated a network is used if a specific view SUID is not provided.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Takes first (presumably only) view associated with provided network

Value

None

Examples

```
setCurrentView()
```

`setDefaultSandbox` *setDefaultSandbox*

Description

Set and return the sandbox properties to be used as a default, probably based on whether running remote.

Usage

```
setDefaultSandbox(newSandbox = NULL, ...)
```

Arguments

`newSandbox`	newSandbox
`...`	...

Value

default sandbox

Examples

```
setDefaultSandbox()
```

`setDefaultSandboxPath` *setDefaultSandboxPath*

Description

Set and return the default path, which isn't one of the properties tracked in the default_sandbox.

Usage

```
setDefaultSandboxPath(newPath)
```

Arguments

`newPath`	new path of default sandbox

Value

default sandbox path

Examples

```
setDefaultSandboxPath()
```

`setEdgeColorBypass` *Set Edge Color Bypass*

Description

Override the color for particular edges.

Usage

```
setEdgeColorBypass(
  edge.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeColorBypass()
```

`setEdgeColorDefault` *Set Edge Color Default*

Description

Set the default edge color.

Usage

```
setEdgeColorDefault(new.color, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeColorDefault('#FD5903')
```

`setEdgeColorMapping` *Set Edge Color Mapping*

Description

Map table column values to colors to set the edge color.

Usage

```
setEdgeColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeColorMapping('score', c(0,5), c('#FFFFFF','#FF7755'))
setEdgeColorMapping('score', colors=paletteColorBrewerRdBu)
setEdgeColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

`setEdgeFontFaceBypass` *Set Edge Font Face Bypass*

Description

Override the font face for particular edges.

Usage

```
setEdgeFontFaceBypass(
  edge.names,
  new.fonts,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.fonts`	List of font faces, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeFontFaceBypass()
```

---

setEdgeFontFaceDefault

Set Edge Font Face Default

Description

Set the default edge font.

Usage

```
setEdgeFontFaceDefault(new.font, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.font`	String specification of font face, style and size, e.g., "SansSerif,plain,12" or "Dialog,plain,10"
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeFontFaceDefault("Dialog,plain,10")
```

---

setEdgeFontFaceMapping

Set Edge Font Face Mapping

Description

Sets font face for edge labels.

Usage

```
setEdgeFontFaceMapping(
  table.column,
  table.column.values,
  fonts,
  mapping.type = "d",
  default.font = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping
`fonts`	List of string specifications of font face, style and size, e.g., c("SansSerif,plain,12", "Dialog,plain,10")
`mapping.type`	(char) discrete or passthrough (d,p); default is discrete
`default.font`	String specification of font face, style and size, e.g., "SansSerif,plain,12" or "Dialog,plain,10"
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeFontFaceMapping("myfonts", c("normal","small"),
c("SansSerif,plain,12", "Dialog,plain,10"))
```

`setEdgeFontSizeBypass` *Set Edge Font Size Bypass*

Description

Override the font size for particular edges.

Usage

```
setEdgeFontSizeBypass(
  edge.names,
  new.sizes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.sizes`	List of size values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeFontSizeBypass()
```

---

setEdgeFontSizeDefault

Set Edge Font Size Default

Description

Set the default edge font size.

Usage

```
setEdgeFontSizeDefault(new.size, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.size`	Numeric value for size
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeFontSizeDefault(12)
```

`setEdgeFontSizeMapping` *Set Edge Font Size Mapping*

Description

Map table column values to sizes to set the edge size.

Usage

```
setEdgeFontSizeMapping(
  table.column,
  table.column.values = NULL,
  sizes = NULL,
  mapping.type = "c",
  default.size = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`sizes`	List of sizes to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.size`	Size value to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeFontSizeMapping('score')
setEdgeFontSizeMapping('score', sizes=c(6,24))
setEdgeFontSizeMapping('score', c(0,30), c(35,55))
```

`setEdgeLabelBypass` *Set Edge Label Bypass*

Description

Override the label for particular edges.

Usage

```
setEdgeLabelBypass(
  edge.names,
  new.labels,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.labels`	List of labels, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeLabelBypass()
```

`setEdgeLabelColorBypass`

Set Edge Label Color Bypass

Description

Override the label color for particular edges.

Usage

```
setEdgeLabelColorBypass(
  edge.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeLabelColorBypass()
```

`setEdgeLabelColorDefault`

Set Edge Label Color Default

Description

Set the default edge label color.

Usage

```
setEdgeLabelColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLabelColorDefault("#FD5903")
```

`setEdgeLabelColorMapping`

Set Edge Label Color Mapping

Description

Map table column values to colors to set the edge border color.

Usage

```
setEdgeLabelColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLabelColorMapping('score', c(0,5), c('#FFFFFF','#FF7755'))
setEdgeLabelColorMapping('score', colors=paletteColorBrewerRdBu)
setEdgeLabelColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

`setEdgeLabelDefault` *Set Edge Label Default*

Description

Set the default edge label.

Usage

```
setEdgeLabelDefault(new.label, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.label`	String label for unmapped edges.
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLabelDefault('unknown')
```

`setEdgeLabelMapping` *Set Edge Label Mapping*

Description

Pass the values from a table column to display as edge labels.

Usage

```
setEdgeLabelMapping(
  table.column,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLabelMapping('label')
```

`setEdgeLabelOpacityBypass` *Set Edge Label Opacity Bypass*

Description

Override the label opacity for particular edges.

Usage

```
setEdgeLabelOpacityBypass(
  edge.names,
  new.value,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.value`	List of opacity values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeLabelOpacityBypass()
```

`setEdgeLabelOpacityDefault`

Set Edge Label Opacity Default

Description

Set default opacity value for all unmapped edge labels.

Usage

```
setEdgeLabelOpacityDefault(
  new.opacity,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.opacity`	Numeric values between 0 and 255; 0 is invisible.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLabelOpacityDefault(50)
```

`setEdgeLabelOpacityMapping`

Set Edge Label Opacity Mapping

Description

Sets opacity for edge label only.

Usage

```
setEdgeLabelOpacityMapping(
  table.column,
  table.column.values = NULL,
  opacities = NULL,
  mapping.type = "c",
  default.opacity = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`opacities`	(integer) values between 0 and 255; 0 is invisible. A range of 50 to 255 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.opacity`	Opacity value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLabelOpacityMapping('weight')
setEdgeLabelOpacityMapping('weight', opacities=c(0,100))
setEdgeLabelOpacityMapping('weight', c(1,10), c(50,255))
```

`setEdgeLineStyleBypass`

Set Edge Line Style Bypass

Description

Override the style for particular edges.

Usage

```
setEdgeLineStyleBypass(
  edge.names,
  new.styles,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.styles`	List of style values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeLineStyleBypass()
```

`setEdgeLineStyleDefault`

Set Edge Line Style Default

Description

Set the default edge style.

Usage

```
setEdgeLineStyleDefault(
  new.line.style,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.line.style`	Name of line style, e.g., SOLID, LONG_DASH, etc (see getLineStyles)
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLineStyleDefault('LONG_DASH')
```

`setEdgeLineStyleMapping`

Set Edge Line Style Mapping

Description

Map table column values to styles to set the edge style.

Usage

```
setEdgeLineStyleMapping(
  table.column,
  table.column.values = NULL,
  line.styles = NULL,
  default.line.style = "SOLID",
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.

`line.styles`	List of line styles. Leave NULL to perform an automatic mapping to available line styles. See getLineStyles.
`default.line.style`	Style to set as default. See getLineStyles.
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLineStyleMapping('type')
setEdgeLineStyleMapping('type',c('pp','pd'),c('SOLID','LONG_DASH'))
```

`setEdgeLineWidthBypass` *Set Edge Line Width Bypass*

Description

Override the width for particular edges.

Usage

```
setEdgeLineWidthBypass(
  edge.names,
  new.widths,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.widths`	List of width values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeLineWidthBypass()
```

`setEdgeLineWidthDefault`

Set Edge Line Width Default

Description

Set the default edge width.

Usage

```
setEdgeLineWidthDefault(
  new.width,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.width`	Numeric value for width
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLineWidthDefault(3)
```

`setEdgeLineWidthMapping` *Set Edge Line Width Mapping*

Description

Map table column values to widths to set the edge line width.

Usage

```
setEdgeLineWidthMapping(
  table.column,
  table.column.values = NULL,
  widths = NULL,
  mapping.type = "c",
  default.width = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`widths`	List of width values to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.width`	Width value to set as default for all unmapped values for all unmapped values.
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeLineWidthMapping('score')
setEdgeLineWidthMapping('score', widths=c(1,10))
setEdgeLineWidthMapping('score', c(0,30), c(1,5))
```

`setEdgeOpacityBypass` *Set Edge Opacity Bypass*

Description

Override the opacity for particular edges.

Usage

```
setEdgeOpacityBypass(
  edge.names,
  new.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.values`	List of values to set, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeOpacityBypass()
```

`setEdgeOpacityDefault` *Set Edge Opacity Default*

Description

Set default opacity value for all unmapped edges.

Usage

```
setEdgeOpacityDefault(
  new.opacity,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.opacity`	Numeric values between 0 and 255; 0 is invisible.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeOpacityDefault(50)
```

`setEdgeOpacityMapping` *Set Edge Opacity Mapping*

Description

Map table column values to opacities to set the edge opacity.

Usage

```
setEdgeOpacityMapping(
  table.column,
  table.column.values = NULL,
  opacities = NULL,
  mapping.type = "c",
  default.opacity = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`opacities`	(integer) values between 0 and 255; 0 is invisible. A range of 50 to 255 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.opacity`	Opacity value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeOpacityMapping('weight')
setEdgeOpacityMapping('weight', opacities=c(0,100))
setEdgeOpacityMapping('weight', c(1,10), c(50,255))
```

`setEdgePropertyBypass` *Set Edge Property Bypass*

Description

Set bypass values for any edge property of the specified edges, overriding default values and mappings defined by any visual style.

Usage

```
setEdgePropertyBypass(
  edge.names,
  new.values,
  visual.property,
  bypass = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.values`	List of values to set, or single value
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`bypass`	Whether to set permanent bypass value. Default is `TRUE`.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for the visual properties of the edge or edges specified. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

clearEdgePropertyBypass

Examples

```
setEdgePropertyBypass()
```

`setEdgeSelectionColorDefault`

Set Edge Selection Color Default

Description

Set the default selected edge color.

Usage

```
setEdgeSelectionColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeSelectionColorDefault('#FD5903')
```

`setEdgeSourceArrowColorBypass`

Set Edge Source Arrow Color Bypass

Description

Override the source arrow color for particular edges.

Usage

```
setEdgeSourceArrowColorBypass(
  edge.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeSourceArrowColorBypass()
```

`setEdgeSourceArrowColorDefault`

Set Edge Source Arrow Color Default

Description

Set the default edge source arrow color.

Usage

```
setEdgeSourceArrowColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeSourceArrowColorDefault('#FD5903')
```

`setEdgeSourceArrowColorMapping` *Set Edge Source Arrow Color Mapping*

Description

Map table column values to colors to set the source arrow color.

Usage

```
setEdgeSourceArrowColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeSourceArrowColorMapping('score', c(0,5), c('#FFFFFF','#FF7755'))
setEdgeSourceArrowColorMapping('score', colors=paletteColorBrewerRdBu)
setEdgeSourceArrowColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

`setEdgeSourceArrowMapping` *Set Edge Source Arrow Mapping*

Description

Map table column values to shapes to set the source arrow shape.

Usage

```
setEdgeSourceArrowMapping(
  table.column,
  table.column.values = NULL,
  shapes = NULL,
  default.shape = "ARROW",
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`shapes`	List of shapes to map to table.column.values. Leave NULL to perform an automatic mapping to available shapes. See getArrowShapes
`default.shape`	Shape to set as default. See getArrowShapes
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeSourceArrowMapping('type')
setEdgeSourceArrowMapping('type',c('activation','inhibition'),c('ARROW','T'))
```

`setEdgeSourceArrowShapeBypass`

Set Edge Source Arrow Shape Bypass

Description

Override the source arrow shape for particular edges.

Usage

```
setEdgeSourceArrowShapeBypass(
  edge.names,
  new.shapes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.shapes`	List of shapes, or single value. See getArrowShapes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeSourceArrowShapeBypass()
```

`setEdgeSourceArrowShapeDefault`

Set Edge Source Arrow Shape Default

Description

Set the default edge source arrow shape.

Usage

```
setEdgeSourceArrowShapeDefault(
  new.shape,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.shape`	Name of shape, e.g., ARROW, T, etc (see getArrowShapes)
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeSourceArrowShapeDefault('ARROW')
```

`setEdgeSourceArrowShapeMapping`

Set Edge Source Arrow Shape Mapping

Description

Map table column values to shapes to set the source arrow shape.

Usage

```
setEdgeSourceArrowShapeMapping(
  table.column,
  table.column.values = NULL,
  shapes = NULL,
  default.shape = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`shapes`	List of shapes to map to table.column.values. Leave NULL to perform an automatic mapping to available shapes. See getArrowShapes
`default.shape`	Shape to set as default. See getArrowShapes
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeSourceArrowShapeMapping('type')
setEdgeSourceArrowShapeMapping('type',c('activation','inhibition'),
  c('ARROW','T'))
```

`setEdgeTargetArrowColorBypass`

Set Edge Target Arrow Color Bypass

Description

Override the target arrow color for particular edges.

Usage

```
setEdgeTargetArrowColorBypass(
  edge.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeTargetArrowColorBypass()
```

`setEdgeTargetArrowColorDefault`

Set Edge Target Arrow Color Default

Description

Set the default edge target arrow color.

Usage

```
setEdgeTargetArrowColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTargetArrowColorDefault('#FD5903')
```

---

setEdgeTargetArrowColorMapping

Set Edge Target Arrow Color Mapping

Description

Map table column values to colors to set the target arrow color.

Usage

```
setEdgeTargetArrowColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTargetArrowColorMapping('score', c(0,5), c('#FFFFFF','#FF7755'))
setEdgeTargetArrowColorMapping('score', colors=paletteColorBrewerRdBu)
setEdgeTargetArrowColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

`setEdgeTargetArrowMapping`

Set Edge Target Arrow Mapping

Description

Map table column values to shapes to set the target arrow shape.

Usage

```
setEdgeTargetArrowMapping(
  table.column,
  table.column.values = NULL,
  shapes = NULL,
  default.shape = "ARROW",
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`shapes`	List of shapes to map to table.column.values. Leave NULL to perform an automatic mapping to available shapes. See getArrowShapes
`default.shape`	Shape to set as default. See getArrowShapes
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTargetArrowMapping('type')
setEdgeTargetArrowMapping('type',c('activation','inhibition'),c('ARROW','T'))
```

`setEdgeTargetArrowShapeBypass`

Set Edge Target Arrow Shape Bypass

Description

Override the target arrow shape for particular edges.

Usage

```
setEdgeTargetArrowShapeBypass(
  edge.names,
  new.shapes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.shapes`	List of values to set, or single value. See getArrowShapes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeTargetArrowShapeBypass()
```

`setEdgeTargetArrowShapeDefault`

Set Edge Target Arrow Shape Default

Description

Set the default edge target arrow shape.

Usage

```
setEdgeTargetArrowShapeDefault(
  new.shape,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.shape`	Name of shape, e.g., ARROW, T, etc (see getArrowShapes)
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTargetArrowShapeDefault('ARROW')
```

`setEdgeTargetArrowShapeMapping`

Set Edge Target Arrow Shape Mapping

Description

Map table column values to shapes to set the target arrow shape.

Usage

```
setEdgeTargetArrowShapeMapping(
  table.column,
  table.column.values = NULL,
  shapes = NULL,
  default.shape = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`shapes`	List of shapes to map to table.column.values. Leave NULL to perform an automatic mapping to available shapes. See getArrowShapes
`default.shape`	Shape to set as default. See getArrowShapes
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTargetArrowShapeMapping('type')
setEdgeTargetArrowShapeMapping('type',c('activation','inhibition'),
  c('ARROW','T'))
```

`setEdgeTooltipBypass` *Set Edge Tooltip Bypass*

Description

Override the tooltip for particular edges.

Usage

```
setEdgeTooltipBypass(
  edge.names,
  new.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`edge.names`	List of edge names or SUIDs
`new.values`	List of tooltip values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the edge or edges specified. This method ultimately calls the generic function, setEdgePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearEdgePropertyBypass.

Value

None

See Also

setEdgePropertyBypass, clearEdgePropertyBypass

Examples

```
setEdgeTooltipBypass()
```

`setEdgeTooltipDefault` *Set Edge Tooltip Default*

Description

Set the default edge tooltip

Usage

```
setEdgeTooltipDefault(
  new.tooltip,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.tooltip`	String tooltip for unmapped edges.
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTooltipDefault('unknown')
```

`setEdgeTooltipMapping` *Set Edge Tooltip Mapping*

Description

Pass the values from a table column to display as edge tooltips.

Usage

```
setEdgeTooltipMapping(
  table.column,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setEdgeTooltipMapping('description')
```

`setLayoutProperties` *Set Layout Properties*

Description

Sets the specified properties for the specified layout. Unmentioned properties are left unchanged.

Usage

```
setLayoutProperties(layout.name, properties.list, base.url = .defaultBaseUrl)
```

Arguments

`layout.name`	(`character`) Name of the layout
`properties.list`	(`list`) List of one or more `property=value` pairs
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Run getLayoutNames to list available layouts. Run getLayoutPropertyNames to list properties per layout.

Value

None

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
setLayoutProperties('force-directed', list(defaultSpringLength=50, defaultSpringCoefficient=6E-04))
# Successfully updated the property 'defaultSpringLength'.
# Successfully updated the property 'defaultSpringCoefficient'.
```

`setModelPropagationSecs`

Set Model Propagation Delay

Description

This function sets an internal delay variable that allows Cytoscape to "catchup" prior to subsequent functions. Call without specifying `secs` to restore default value.

Usage

```
setModelPropagationSecs(secs = 5)
```

Arguments

`secs`	Number of seconds to delay.

Details

This delay is only necessary while concurrency bugs exist in the Cytoscape application. This delay may need to be increased from the default value in certain use cases, e.g., larger networks.

Value

None

See Also

setCatchupFilterSecs, setCatchupNetworkSecs

Examples

```
{
setModelPropagationSecs(2)
setModelPropagationSecs() #restores default delay
}
```

`setNetworkCenterBypass`

Set Network Center Bypass

Description

Set the bypass value for center x and y for the network. This function could be used to pan and scroll the Cytoscape canvas.

Usage

```
setNetworkCenterBypass(
  x,
  y,
  bypass = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`x`	Coordinate value, increases going to the right.
`y`	Coordinate value, increase going down.
`bypass`	Whether to set permanent bypass value. Default is `FALSE` per common use of temporary center settings.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values for this visual property. This method ultimately calls the generic function, setNetworkPropertyBypass, which can be used to set any visual property. To restore defaults, use clearNetworkPropertyBypass.

Value

None

See Also

setNetworkPropertyBypass, clearNetworkPropertyBypass

Examples

```
setNetworkCenterBypass()
```

`setNetworkPropertyBypass` *Set Network Property Bypass*

Description

Set bypass values for any network property, overriding default values defined by any visual style.

Usage

```
setNetworkPropertyBypass(
  new.value,
  visual.property,
  bypass = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.value`	Value to set
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`bypass`	Whether to set permanent bypass value. Default is `TRUE`.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for the visual properties of the node or nodes specified. To restore defaults and mappings, use clearNodePropertyBypass.

Value

None

See Also

clearNetworkPropertyBypass

Examples

```
setNetworkPropertyBypass()
```

`setNetworkZoomBypass` *Set Network Zoom Bypass*

Description

Set the bypass value for scale factor for the network.

Usage

```
setNetworkZoomBypass(
  new.value,
  bypass = FALSE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.value`	Zoom factor
`bypass`	Whether to set permanent bypass value. Default is `FALSE` per common use of temporary zoom settings.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values for this visual property. This method ultimately calls the generic function, setNetworkPropertyBypass, which can be used to set any visual property. To restore defaults, use clearNetworkPropertyBypass.

Value

None

See Also

setNetworkPropertyBypass, clearNetworkPropertyBypass

Examples

```
setNetworkZoomBypass()
```

`setNodeBorderColorBypass` *Set Node Border Color Bypass*

Description

Override the border color for particular nodes.

Usage

```
setNodeBorderColorBypass(
  node.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeBorderColorBypass('Node 1', '#FF55AA')
setNodeBorderColorBypass(c('Node 1','Node 2'), '#FF55AA')
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_BORDER_PAINT')
```

---

setNodeBorderColorDefault

Set Node Border Color Default

Description

Set the default node border color.

Usage

```
setNodeBorderColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeBorderColorDefault('#FD5903')
```

---

setNodeBorderColorMapping

Set Node Border Color Mapping

Description

Map table column values to colors to set the node border color.

Usage

```
setNodeBorderColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeBorderColorMapping('score', c(0,5), c('#FFFFFF','#FF7755'))
setNodeBorderColorMapping('score', colors=paletteColorBrewerRdBu)
setNodeBorderColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

`setNodeBorderOpacityBypass`

Set Node Border Opacity Bypass

Description

Override the border opacity for particular nodes.

Usage

```
setNodeBorderOpacityBypass(
  node.names,
  new.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.values`	List of values to set, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeBorderOpacityBypass()
```

`setNodeBorderOpacityDefault`

Set Node Border Opacity Default

Description

Set defaults opacity value for all unmapped node borders.

Usage

```
setNodeBorderOpacityDefault(
  new.opacity,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.opacity`	Numeric values between 0 and 255; 0 is invisible.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeBorderOpacityDefault(50)
```

`setNodeBorderOpacityMapping`
Set Node Border Opacity Mapping

Description

Sets opacity for node border only.

Usage

```
setNodeBorderOpacityMapping(
  table.column,
  table.column.values = NULL,
  opacities = NULL,
  mapping.type = "c",
  default.opacity = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`opacities`	(integer) values between 0 and 255; 0 is invisible. A range of 50 to 255 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.opacity`	Opacity value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeBorderOpacityMapping('score')
setNodeBorderOpacityMapping('score', opacities=c(0,100))
setNodeBorderOpacityMapping('score', c(-5,5), c(50,255))
```

`setNodeBorderWidthBypass`

Set Node Border Width Bypass

Description

Override the border width for particular nodes.

Usage

```
setNodeBorderWidthBypass(
  node.names,
  new.sizes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.sizes`	List of size values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeBorderWidthBypass('Node 1', 5)
setNodeBorderWidthBypass(c('Node 1','Node 2'), 5)
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_BORDER_WIDTH')
```

`setNodeBorderWidthDefault`

Set Node Border Width Default

Description

Set the default node border width.

Usage

```
setNodeBorderWidthDefault(
  new.width,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.width`	Numeric value for width
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeBorderWidthDefault(2)
```

`setNodeBorderWidthMapping` *Set Node Border Width Mapping*

Description

Map table column values to widths to set the node border width.

Usage

```
setNodeBorderWidthMapping(
  table.column,
  table.column.values = NULL,
  widths = NULL,
  mapping.type = "c",
  default.width = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`widths`	List of width values to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.width`	Width value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeBorderWidthMapping('score')
setNodeBorderWidthMapping('score', widths=c(1,10))
setNodeBorderWidthMapping('score', c(0,30), c(1,5))
```

`setNodeColorBypass` *Set Node Color Bypass*

Description

Set the bypass value for fill color for the specified node or nodes.

Usage

```
setNodeColorBypass(
  node.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeColorBypass ('node1', '#FF0088')
setNodeColorBypass (c('node1', 'node2'), c('#88FF88', '#FF0088'))
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_FILL_COLOR')
```

`setNodeColorDefault` *Set Node Color Default*

Description

Set the default node color.

Usage

```
setNodeColorDefault(new.color, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeColorDefault('#FD5903')
```

`setNodeColorMapping` *Set Node Color Mapping*

Description

Map table column values to colors to set the node fill color.

Usage

```
setNodeColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeColorMapping('score', c(-5,0,5), c('#5577FF','#FFFFFF','#FF7755'))
setNodeColorMapping('score', colors=paletteColorBrewerRdBu)
setNodeColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

---

setNodeComboOpacityMapping

Set Node Combo Opacity Mapping

Description

Sets opacity for node fill, border and label all together.

Usage

```
setNodeComboOpacityMapping(
  table.column,
  table.column.values = NULL,
  opacities = NULL,
  mapping.type = "c",
  default.opacity = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`opacities`	(integer) values between 0 and 255; 0 is invisible. A range of 50 to 255 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.opacity`	Opacity value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeComboOpacityMapping('score')
setNodeComboOpacityMapping('score', opacities=c(0,100))
setNodeComboOpacityMapping('score', c(-5,5), c(50,255))
```

`setNodeCustomBarChart` *Set Node Custom Bar Chart*

Description

Makes a bar chart per node using specified node table columns by setting a default custom graphic style.

Usage

```
setNodeCustomBarChart(
  columns,
  type = "GROUPED",
  colors = NULL,
  range = NULL,
  orientation = "VERTICAL",
  colAxis = FALSE,
  rangeAxis = FALSE,
  zeroLine = FALSE,
  axisWidth = 0.25,
  axisColor = "#000000",
  axisFontSize = 1,
  separation = 0,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`columns`	List of node column names to be displayed, in order.
`type`	Type of bar chart: GROUPED (default), STACKED, HEAT_STRIPS, or UP_DOWN
`colors`	(optional) List of colors to be matched with columns or with range, depending on type. Default is a set of colors from an appropriate Brewer palette.
`range`	(optional) Min and max values of chart. Default is to use min and max from specified data columns.
`orientation`	(optional) HORIZONTAL or VERTICAL (default).
`colAxis`	(optional) Show axis with column labels. Default is FALSE.
`rangeAxis`	(optional) Show axis with range of values. Default is FALSE.
`zeroLine`	(optional) Show a line at zero. Default is FALSE.
`axisWidth`	(optional) Width of axis lines, if shown. Default is 0.25.
`axisColor`	(optional) Color of axis lines, if shown. Default is black.
`axisFontSize`	(optional) Font size of axis labels, if shown. Default is 1.
`separation`	(optional) Distance between bars. Default is 0.0.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeCustomPosition, removeNodeCustomGraphics

Examples

```
setNodeCustomBarChart(c("data1","data2","data3"))
```

`setNodeCustomBoxChart` *Set Node Custom Box Chart*

Description

Makes a box chart per node using specified node table columns by setting a default custom graphic style.

Usage

```
setNodeCustomBoxChart(
  columns,
  colors = NULL,
  range = NULL,
  orientation = "VERTICAL",
  rangeAxis = FALSE,
  zeroLine = FALSE,
  axisWidth = 0.25,
  axisColor = "#000000",
  axisFontSize = 1,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`columns`	List of node column names to be displayed.
`colors`	(optional) List of colors to be matched with columns or with range, depending on type. Default is a set of colors from an appropriate Brewer palette.
`range`	(optional) Min and max values of chart. Default is to use min and max from specified data columns.
`orientation`	(optional) HORIZONTAL or VERTICAL (default).
`rangeAxis`	(optional) Show axis with range of values. Default is FALSE.

`zeroLine`	(optional) Show a line at zero. Default is FALSE.
`axisWidth`	(optional) Width of axis lines, if shown. Default is 0.25.
`axisColor`	(optional) Color of axis lines, if shown. Default is black.
`axisFontSize`	(optional) Font size of axis labels, if shown. Default is 1.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeCustomPosition, removeNodeCustomGraphics

Examples

```
setNodeCustomBoxChart(c("data1","data2","data3"))
```

`setNodeCustomHeatMapChart`

Set Node Custom HeatMap Chart

Description

Makes a heatmap chart per node using specified node table columns by setting a default custom graphic style.

Usage

```
setNodeCustomHeatMapChart(
  columns,
  colors = NULL,
  range = NULL,
  orientation = "HORIZONTAL",
  rangeAxis = FALSE,
  zeroLine = FALSE,
  axisWidth = 0.25,
  axisColor = "#000000",
  axisFontSize = 1,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`columns`	List of node column names to be displayed.
`colors`	(optional) List of colors to be matched with columns or with range, depending on type. Default is a set of colors from an appropriate Brewer palette.
`range`	(optional) Min and max values of chart. Default is to use min and max from specified data columns.
`orientation`	(optional) VERTICAL or HORIZONTAL (default).
`rangeAxis`	(optional) Show axis with range of values. Default is FALSE.
`zeroLine`	(optional) Show a line at zero. Default is FALSE.
`axisWidth`	(optional) Width of axis lines, if shown. Default is 0.25.
`axisColor`	(optional) Color of axis lines, if shown. Default is black.
`axisFontSize`	(optional) Font size of axis labels, if shown. Default is 1.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeCustomPosition, removeNodeCustomGraphics

Examples

```
setNodeCustomHeatMapChart(c("data1","data2","data3"))
```

`setNodeCustomLinearGradient`

Set Node Custom Linear Gradient

Description

Makes a gradient fill per node by setting a default custom graphic style.

Usage

```
setNodeCustomLinearGradient(
  colors = c("#DDDDDD", "#888888"),
  anchors = c(0, 1),
  angle = 0,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`colors`	(optional) List of colors to define gradient
`anchors`	(optional) Position of colors from 0.0 to 1.0.
`angle`	(optional) Angle of gradient. Default is 0 (left-to-right).
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeCustomLinearGradient()
```

`setNodeCustomLineChart`

Set Node Custom Line Chart

Description

Makes a line chart per node using specified node table columns by setting a default custom graphic style.

Usage

```
setNodeCustomLineChart(
  columns,
  colors = NULL,
  range = NULL,
  lineWidth = 1,
  rangeAxis = FALSE,
  zeroLine = FALSE,
  axisWidth = 0.25,
  axisColor = "#000000",
  axisFontSize = 1,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`columns`	List of node column names to be displayed.
`colors`	(optional) List of colors to be matched with columns or with range, depending on type. Default is a set of colors from an appropriate Brewer palette.
`range`	(optional) Min and max values of chart. Default is to use min and max from specified data columns.
`lineWidth`	(optional) Width of chart line. Default is 1.0.
`rangeAxis`	(optional) Show axis with range of values. Default is FALSE.
`zeroLine`	(optional) Show a line at zero. Default is FALSE.
`axisWidth`	(optional) Width of axis lines, if shown. Default is 0.25.
`axisColor`	(optional) Color of axis lines, if shown. Default is black.
`axisFontSize`	(optional) Font size of axis labels, if shown. Default is 1.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeCustomPosition, removeNodeCustomGraphics

Examples

```
setNodeCustomLineChart(c("data1","data2","data3"))
```

`setNodeCustomPieChart` *Set Node Custom Pie Chart*

Description

Makes a pie chart per node using specified node table columns by setting a default custom graphic style.

Usage

```
setNodeCustomPieChart(
  columns,
  colors = NULL,
  startAngle = 0,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`columns`	List of node column names to be displayed.
`colors`	(optional) List of colors to be matched with columns or with range, depending on type. Default is a set of colors from an appropriate Brewer palette.
`startAngle`	(optional) Angle to start filling pie. Default is 0.0.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeCustomPosition, removeNodeCustomGraphics

Examples

```
setNodeCustomPieChart(c("data1","data2","data3"))
```

`setNodeCustomPosition` *Set Node Custom Position*

Description

Adjust the position of a custom graphic relative to its node.

Usage

```
setNodeCustomPosition(
  nodeAnchor = "C",
  graphicAnchor = "C",
  justification = "c",
  xOffset = 0,
  yOffset = 0,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`nodeAnchor`	Position on node to place the graphic: NW,N,NE,E,SE,S,SW,W or C for center (default)
`graphicAnchor`	Position on graphic to place on node: NW,N,NE,E,SE,S,SW,W or C for center (default)
`justification`	Positioning of content within graphic: l,r,c (default)
`xOffset`	Additional offset in the x direction
`yOffset`	Additional offset in the y direction
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeCustomPosition()
```

`setNodeCustomRadialGradient` *Set Node Custom Radial Gradient*

Description

Makes a gradient fill per node by setting a default custom graphic style.

Usage

```
setNodeCustomRadialGradient(
  colors = c("#DDDDDD", "#888888"),
  anchors = c(0, 1),
  xCenter = 0.5,
  yCenter = 0.5,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`colors`	(optional) List of colors to define gradient
`anchors`	(optional) Position of colors from 0.0 to 1.0.
`xCenter`	(optional) X position for center of radial effect from 0.0 to 1.0. Default is 0.5.
`yCenter`	(optional) Y position for center of radial effect from 0.0 to 1.0. Default is 0.5.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeCustomRadialGradient()
```

---

setNodeCustomRingChart

Set Node Custom Ring Chart

Description

Makes a ring chart per node using specified node table columns by setting a default custom graphic style.

Usage

```
setNodeCustomRingChart(
  columns,
  colors = NULL,
  startAngle = 0,
  holeSize = 0.5,
  slot = 1,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`columns`	List of node column names to be displayed.
`colors`	(optional) List of colors to be matched with columns or with range, depending on type. Default is a set of colors from an appropriate Brewer palette.
`startAngle`	(optional) Angle to start filling ring Default is 0.0.

`holeSize`	(optional) Size of hole in ring. Ranges 0-1. Default is 0.5.
`slot`	(optional) Which custom graphics slot to modify. Slots 1-9 are available for independent charts, gradients and images. Default is 1.
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

See Also

setNodeCustomPosition, removeNodeCustomGraphics

Examples

```
setNodeCustomRingChart(c("data1","data2","data3"))
```

`setNodeFillOpacityBypass`

Set Node Fill Opacity Bypass

Description

Override the fill opacity for particular nodes.

Usage

```
setNodeFillOpacityBypass(
  node.names,
  new.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.values`	List of values to set, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeFillOpacityBypass('Node 1', 100)
setNodeFillOpacityBypass(c('Node 1','Node 2'), 100)
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_TRANSPARENCY')
```

`setNodeFillOpacityDefault`

Set Node Fill Opacity Default

Description

Set default opacity value for all unmapped nodes.

Usage

```
setNodeFillOpacityDefault(
  new.opacity,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.opacity`	Numeric values between 0 and 255; 0 is invisible.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeFillOpacityDefault(50)
```

`setNodeFillOpacityMapping`

Set Node Fill Opacity Mapping

Description

Sets opacity for node fill only.

Usage

```
setNodeFillOpacityMapping(
  table.column,
  table.column.values = NULL,
  opacities = NULL,
  mapping.type = "c",
  default.opacity = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`opacities`	(integer) values between 0 and 255; 0 is invisible. A range of 50 to 255 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.opacity`	Opacity value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeFillOpacityMapping('score')
setNodeFillOpacityMapping('score', opacities=c(0,100))
setNodeFillOpacityMapping('score', c(-5,5), c(50,255))
```

`setNodeFontFaceBypass` *Set Node Font Face Bypass*

Description

Override the font face for particular nodes.

Usage

```
setNodeFontFaceBypass(
  node.names,
  new.fonts,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.fonts`	List of font faces, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeFontFaceBypass()
```

`setNodeFontFaceDefault` *Set Node Font Face Default*

Description

Set the default node font.

Usage

```
setNodeFontFaceDefault(new.font, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.font`	String specification of font face, style and size, e.g., "SansSerif,plain,12" or "Dialog,plain,10"
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeFontFaceDefault("Dialog,plain,10")
```

`setNodeFontFaceMapping` *Set Node Font Face Mapping*

Description

Sets font face for node labels.

Usage

```
setNodeFontFaceMapping(
  table.column,
  table.column.values,
  fonts,
  mapping.type = "d",
  default.font = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping
`fonts`	List of string specifications of font face, style and size, e.g., c("SansSerif,plain,12", "Dialog,plain,10")
`mapping.type`	(char) discrete or passthrough (d,p); default is discrete
`default.font`	String specification of font face, style and size, e.g., "SansSerif,plain,12" or "Dialog,plain,10"
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeFontFaceMapping("myfonts", c("normal","small"),
c("SansSerif,plain,12", "Dialog,plain,10"))
```

`setNodeFontSizeBypass` *Set Node Font Size Bypass*

Description

Override the font size for particular nodes.

Usage

```
setNodeFontSizeBypass(
  node.names,
  new.sizes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.sizes`	List of size values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeFontSizeBypass('Node 1', 5)
setNodeFontSizeBypass(c('Node 1','Node 2'), 5)
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_LABEL_FONT_SIZE')
```

`setNodeFontSizeDefault`

Set Node Font Size Default

Description

Set the default node font size.

Usage

```
setNodeFontSizeDefault(new.size, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.size`	Numeric value for size
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeFontSizeDefault(12)
```

`setNodeFontSizeMapping` *Set Node Font Size Mapping*

Description

Map table column values to sizes to set the node size.

Usage

```
setNodeFontSizeMapping(
  table.column,
  table.column.values = NULL,
  sizes = NULL,
  mapping.type = "c",
  default.size = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`sizes`	List of sizes to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.size`	Size value to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeFontSizeMapping('score')
setNodeFontSizeMapping('score', sizes=c(6,24))
setNodeFontSizeMapping('score', c(0,30), c(35,55))
```

`setNodeHeightBypass` *Set Node Height Bypass*

Description

Override the height for particular nodes.

Usage

```
setNodeHeightBypass(
  node.names,
  new.heights,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.heights`	List of height values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeHeightBypass('Node 1', 35)
setNodeHeightBypass(c('Node 1','Node 2'), 35)
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_HEIGHT')
```

`setNodeHeightDefault` *Set Node Height Default*

Description

Set the default node height.

Usage

```
setNodeHeightDefault(new.height, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.height`	Numeric value for height.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeHeightDefault(35)
```

`setNodeHeightMapping` *Set Node Height Mapping*

Description

Map table column values to the node heights.

Usage

```
setNodeHeightMapping(
  table.column,
  table.column.values = NULL,
  heights = NULL,
  mapping.type = "c",
  default.height = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`heights`	List of height values to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.height`	Size value to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Using this function will unlock node width and height to use separate values.

Value

None

Examples

```
setNodeHeightMapping('score')
setNodeHeightMapping('score', heights=c(30,80))
setNodeHeightMapping('score', c(0,30), c(35,55))
```

`setNodeLabelBypass` *Set Node Label Bypass*

Description

Override the label for particular nodes.

Usage

```
setNodeLabelBypass(
  node.names,
  new.labels,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.labels`	List of labels, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeLabelBypass('Node 1', 'Custom Label')
setNodeLabelBypass(c('Node 1','Node 2'), 'Custom Label')
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_LABEL')
```

`setNodeLabelColorBypass`

Set Node Label Color Bypass

Description

Override the label color for particular nodes.

Usage

```
setNodeLabelColorBypass(
  node.names,
  new.colors,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.colors`	List of hex colors, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeLabelColorBypass('Node 1', '#FF55AA')
setNodeLabelColorBypass(c('Node 1','Node 2'), '#FF55AA')
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_LABEL_COLOR')
```

`setNodeLabelColorDefault` *Set Node Label Color Default*

Description

Set the default node label color.

Usage

```
setNodeLabelColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelColorDefault('#FD5903')
```

`setNodeLabelColorMapping` *Set Node Label Color Mapping*

Description

Map table column values to colors to set the node border color.

Usage

```
setNodeLabelColorMapping(
  table.column,
  table.column.values = NULL,
  colors = NULL,
  mapping.type = "c",
  default.color = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`colors`	List of hex colors to map to table.column.values or a color palette function, e.g., paletteColorBrewerSet3 (without quotes). See RColorBrewer::display.brewer.all()
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.color`	Hex color to set as default
`style.name`	Name of style; default is "default" style

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelColorMapping('score', c(0,5), c('#FFFFFF','#FF7755'))
setNodeLabelColorMapping('score', colors=paletteColorBrewerRdBu)
setNodeLabelColorMapping('score', colors=paletteColorBrewerSet3, mapping.type='d')
```

`setNodeLabelDefault` *Set Node Label Default*

Description

Set the default node label.

Usage

```
setNodeLabelDefault(new.label, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.label`	String label for unmapped nodes.
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelDefault('unknown')
```

`setNodeLabelMapping` *Set Node Label Mapping*

Description

Pass the values from a table column to display as node labels.

Usage

```
setNodeLabelMapping(
  table.column,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelMapping('name')
```

`setNodeLabelOpacityBypass` *Set Node Label Opacity Bypass*

Description

Override the label opacity for particular nodes.

Usage

```
setNodeLabelOpacityBypass(
  node.names,
  new.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.values`	List of values to set, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeLabelOpacityBypass()
```

`setNodeLabelOpacityDefault`

Set Node Label Opacity Default

Description

Set default opacity value for all unmapped node labels.

Usage

```
setNodeLabelOpacityDefault(
  new.opacity,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.opacity`	Numeric values between 0 and 255; 0 is invisible.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelOpacityDefault(50)
```

`setNodeLabelOpacityMapping`

Set Node Label Opacity Mapping

Description

Sets opacity for node label only.

Usage

```
setNodeLabelOpacityMapping(
  table.column,
  table.column.values = NULL,
  opacities = NULL,
  mapping.type = "c",
  default.opacity = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`opacities`	(integer) values between 0 and 255; 0 is invisible. A range of 50 to 255 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.opacity`	Opacity value to set as default for all unmapped values
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelOpacityMapping('score')
setNodeLabelOpacityMapping('score', opacities=c(0,100))
setNodeLabelOpacityMapping('score', c(-5,5), c(50,255))
```

---

setNodeLabelPositionBypass

Set Node Label Position Bypass

Description

Override the label position for particular nodes.

Usage

```
setNodeLabelPositionBypass(
  node.names,
  new.positions,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.positions`	List of label positions, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeLabelPositionBypass('Node 1','E,S,c,0.00,0.00')
```

`setNodeLabelPositionDefault` *Set Node Label Position Default*

Description

Set the default node label position

Usage

```
setNodeLabelPositionDefault(
  new.nodeAnchor,
  new.graphicAnchor,
  new.justification,
  new.xOffset,
  new.yOffset,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.nodeAnchor`	New position on node to place the graphic: C,NW,N,NE,E,SE,S,SW,W
`new.graphicAnchor`	New position on graphic to place on node: C,NW,N,NE,E,SE,S,SW,W
`new.justification`	New positioning of content within graphic: l,r,c
`new.xOffset`	New additional offset in the x direction
`new.yOffset`	New additional offset in the y direction
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeLabelPositionDefault("S","C","c",0.00,0.00)
```

`setNodeOpacityBypass` *Set Node Opacity Bypass*

Description

Set the bypass value for node fill, label and border opacity for the specified node or nodes.

Usage

```
setNodeOpacityBypass(
  node.names,
  new.values,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.values`	List of values to set, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodeOpacityBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodeOpacityBypass

Examples

```
setNodeOpacityBypass('Node 1', 100)
setNodeOpacityBypass(c('Node 1','Node 2'), 100)
clearNodeOpacityBypass(c('Node 1','Node 2'))
```

`setNodePositionBypass` *Set Node Position Bypass*

Description

Sets the bypass value of node position for one or more nodes. Only applicable if node dimensions are locked. See `lockNodeDimensions`.

Usage

```
setNodePositionBypass(
  node.names,
  new.x.locations = NULL,
  new.y.locations = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.x.locations`	List of x position values, or single value, default is current x position
`new.y.locations`	List of y position values, or single value, default is current y position
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodePositionBypass('Node 1', 35)
```

`setNodePropertyBypass` *Set Node Property Bypass*

Description

Set bypass values for any node property of the specified nodes, overriding default values and mappings defined by any visual style.

Usage

```
setNodePropertyBypass(
  node.names,
  new.values,
  visual.property,
  bypass = TRUE,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.values`	List of values to set, or single value
`visual.property`	Name of a visual property. See getVisualPropertyNames.
`bypass`	Whether to set permanent bypass value. Default is `TRUE`.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for the visual properties of the node or nodes specified. To restore defaults and mappings, use clearNodePropertyBypass.

Value

None

See Also

clearNodePropertyBypass

Examples

```
setNodePropertyBypass()
```

`setNodeSelectionColorDefault` *Set Node Selection Color Default*

Description

Set the default selection node color.

Usage

```
setNodeSelectionColorDefault(
  new.color,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.color`	Color as hex code, e.g., #FD5903
`style.name`	(optional) Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeSelectionColorDefault('#FD5903')
```

`setNodeShapeBypass` *Set Node Shape Bypass*

Description

Override the shape for particular nodes.

Usage

```
setNodeShapeBypass(
  node.names,
  new.shapes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.shapes`	List of shapes, or single value. See getNodeShapes.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeShapeBypass('Node 1', 'ROUND_RECTANGLE')
setNodeShapeBypass(c('Node 1','Node 2'), 'ROUND_RECTANGLE')
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_SHAPE')
```

`setNodeShapeDefault` *Set Node Shape Default*

Description

Set the default node shape.

Usage

```
setNodeShapeDefault(new.shape, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.shape`	Name of shape, e.g., ELLIPSE, RECTANGLE, etc (see getNodeShapes)
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeShapeDefault('ELLIPSE')
```

`setNodeShapeMapping` *Set Node Shape Mapping*

Description

Map table column values to shapes to set the node shape.

Usage

```
setNodeShapeMapping(
  table.column,
  table.column.values = NULL,
  shapes = NULL,
  default.shape = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`shapes`	List of shapes to map to table.column.values. Leave NULL to perform an automatic mapping to available shapes. See getNodeShapes
`default.shape`	Shape to set as default. See getNodeShapes
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeShapeMapping('type')
setNodeShapeMapping('type',c('protein','dna'),c('ELLIPSE','RECTANGLE'))
```

`setNodeSizeBypass` *Set Node Size Bypass*

Description

Sets the bypass value of node size for one or more nodes. Only applicable if node dimensions are locked. See `lockNodeDimensions`.

Usage

```
setNodeSizeBypass(
  node.names,
  new.sizes,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.sizes`	List of size values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeSizeBypass('Node 1', 35)
setNodeSizeBypass(c('Node 1','Node 2'), 35)
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_SIZE')
```

`setNodeSizeDefault` *Set Node Size Default*

Description

Set the default node size.

Usage

```
setNodeSizeDefault(new.size, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.size`	Numeric value for size
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeSizeDefault(35)
```

`setNodeSizeMapping` *Set Node Size Mapping*

Description

Map table column values to node font sizes.

Usage

```
setNodeSizeMapping(
  table.column,
  table.column.values = NULL,
  sizes = NULL,
  mapping.type = "c",
  default.size = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`sizes`	List of sizes to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.size`	Size value to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Using this function will lock node width and height to use a singular "size" value.

Value

None

Examples

```
setNodeSizeMapping('score')
setNodeSizeMapping('score', sizes=c(30,80))
setNodeSizeMapping('score', c(0,30), c(35,55))
```

`setNodeTooltipBypass` *Set Node Tooltip Bypass*

Description

Sets a bypass tooltip for one or more nodes

Usage

```
setNodeTooltipBypass(
  node.names,
  new.tooltip,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.tooltip`	List of tooltips, or a single tooltip
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeTooltipBypass('Node 1', 'This is an important node.')
```

`setNodeTooltipDefault` *Set Node Tooltip Default*

Description

Set the default node tooltip

Usage

```
setNodeTooltipDefault(
  new.tooltip,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.tooltip`	String tooltip for unmapped nodes.
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeTooltipDefault('unknown')
```

`setNodeTooltipMapping` *Set Node Tooltip Mapping*

Description

Pass the values from a table column to display as node tooltips.

Usage

```
setNodeTooltipMapping(
  table.column,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeTooltipMapping('description')
```

`setNodeWidthBypass` *Set Node Width Bypass*

Description

Override the width for particular nodes.

Usage

```
setNodeWidthBypass(
  node.names,
  new.widths,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`node.names`	List of node names or SUIDs
`new.widths`	List of width values, or single value
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method permanently overrides any default values or mappings defined for this visual property of the node or nodes specified. This method ultimately calls the generic function, setNodePropertyBypass, which can be used to set any visual property. To restore defaults and mappings, use clearNodePropertyBypass, see examples.

Value

None

See Also

setNodePropertyBypass, clearNodePropertyBypass

Examples

```
setNodeWidthBypass('Node 1', 35)
setNodeWidthBypass(c('Node 1','Node 2'), 35)
clearNodePropertyBypass(c('Node 1','Node 2'), 'NODE_WIDTH')
```

`setNodeWidthDefault` *Set Node Width Default*

Description

Set the default node width.

Usage

```
setNodeWidthDefault(new.width, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

`new.width`	Numeric value for width.
`style.name`	Name of style; default is "default" style.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeWidthDefault(35)
```

`setNodeWidthMapping` *Set Node Width Mapping*

Description

Map table column values to the node widths.

Usage

```
setNodeWidthMapping(
  table.column,
  table.column.values = NULL,
  widths = NULL,
  mapping.type = "c",
  default.width = NULL,
  style.name = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`table.column`	Name of Cytoscape table column to map values from
`table.column.values`	List of values from Cytoscape table to be used in mapping. Leave NULL to perform an automatic mapping to all column values.
`widths`	List of width values to map to table.column.values. A range of 10 to 100 is used by default for automatic mapping.
`mapping.type`	(char) continuous, discrete or passthrough (c,d,p); default is continuous
`default.width`	Size value to set as default
`style.name`	Name of style; default is "default" style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None #' @details Using this function will unlock node width and height to use separate values.

Examples

```
setNodeWidthMapping('score')
setNodeWidthMapping('score', widths=c(30,80))
setNodeWidthMapping('score', c(0,30), c(35,55))
```

`setNotebookIsRunning` *setNotebookIsRunning*

Description

setNotebookIsRunning

Usage

```
setNotebookIsRunning(newState = NULL)
```

Arguments

`newState`	new state of running remote

Value

oldState

Examples

```
setNotebookIsRunning()
```

`setSandboxReinitialize` *setSandboxReinitialize*

Description

Set and return flag indicating that next command should reinitialize the sandbox according to the default_sandbox.

Usage

```
setSandboxReinitialize(doReinitialize = TRUE)
```

Arguments

`doReinitialize`	default is TRUE

Value

sandbox reinitialize

Examples

```
setCurrentSandbox()
```

`setStyleDependencies` *Set Style Dependencies*

Description

Sets the values of dependencies in a style, overriding any prior settings.

Usage

```
setStyleDependencies(
  style.name = NULL,
  dependencies,
  base.url = .defaultBaseUrl
)
```

Arguments

`style.name`	Name of style; default is "default" style
`dependencies`	A `list` of style dependencies, see Available Dependencies below. Note: each dependency is set by a boolean, TRUE or FALSE (T or F)
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

server response

Available Dependencies

arrowColorMatchesEdge nodeCustomGraphicsSizeSync nodeSizeLocked

Examples

```
setStyleDependencies("myStyle",list(nodeSizeLocked=TRUE))
```

`setVisualPropertyDefault` *Set Visual Property Default*

Description

Set the default value for a visual property.

Usage

```
setVisualPropertyDefault(
  style.string,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`style.string`	A named list including "visualProperty" and "value"
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setVisualPropertyDefault(list(visualProperty = "NODE_SIZE", value = 35))
```

`setVisualStyle` *Set Visual Style*

Description

Apply a visual style to a network.

Usage

```
setVisualStyle(style.name, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	Name of a visual style
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setVisualStyle()
```

`spoofResponse-class` *spoofResponse*

Description

Call CyREST as a remote service via Jupyter-bridge

`syncNodeCustomGraphicsSize` *Sync Node Custom Graphics Size*

Description

Set a boolean value to have the size of custom graphics match that of the node.

Usage

```
syncNodeCustomGraphicsSize(
  new.state,
  style.name = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`new.state`	(Boolean) Whether to sync node custom graphics size
`style.name`	Name of style; default is "default" style
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
syncNodeCustomGraphicsSize(TRUE)
```

`toggleGraphicsDetails` *Toggle Graphics Details*

Description

Regardless of the current zoom level and network size, show (or hide) graphics details, e.g., node labels.

Usage

```
toggleGraphicsDetails(base.url = .defaultBaseUrl)
```

Arguments

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Displaying graphics details on a very large network will affect pan and zoom performance, depending on your available RAM. See cytoscapeMemoryStatus.

Value

None

Examples

```
showGraphicsDetails(TRUE)
```

`ungroupAnnotation` *Ungroup Annotation Group*

Description

Ungroup annotation group from the network view in Cytoscape

Usage

```
ungroupAnnotation(names = NULL, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`names`	Name of annotation group by UUID or Name
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

You can obtain a list of UUIDs by applying a subset function like so: sapply(getAnnotationList(), '[[', 'uuid')

Value

None

Examples

```
ungroupAnnotation("016a4af1-69bc-4b99-8183-d6f118847f96")
ungroupAnnotation(c("316869a4-39fc-4731-8f45-199dec9af10d","c3621eb4-4687-490f-9396-b829dd8767d5"))
ungroupAnnotation("Group 1")
ungroupAnnotation(c("Group1","Group2", "Group3"))
```

`unhideAll` *Unhide All*

Description

Unhide all previously hidden nodes and edges, by clearing the Visible property bypass value.

Usage

```
unhideAll(network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method sets node and edge visibility bypass to true, overriding any defaults or mappings. Pending CyREST updates, this method will ultimately call the generic function, clearEdgePropertyBypass, which can be used to clear any visual property.

Value

None

See Also

clearEdgePropertyBypass, unhideNodes unhideEdges

Examples

```
unhideAll()
```

`unhideEdges` *Unhide Edges*

Description

Unhide specified edges that were previously hidden, by clearing the Visible property bypass value.

Usage

```
unhideEdges(edge.names, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`edge.names`	List of edge names or SUIDs
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method ultimately calls the generic function, clearEdgePropertyBypass, which can be used to clear any visual property.

Value

None

See Also

clearEdgePropertyBypass, unhideAll

Examples

```
unhideEdges()
```

`unhideNodes` *Unhide Nodes*

Description

Unhide specified nodes that were previously hidden, by clearing the Node Visible property bypass value.

Usage

```
unhideNodes(node.names, network = NULL, base.url = .defaultBaseUrl)
```

Arguments

`node.names`	List of node names or SUIDs
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

This method ultimately calls the generic function, clearNodePropertyBypass, which can be used to clear any visual property.

Value

None

See Also

clearNodePropertyBypass, unhideAll

Examples

```
unhideNodes()
```

`uninstallApp` *Uninstall App*

Description

Uninstall an app from Cytoscape.

Usage

```
uninstallApp(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
uninstallApp()
```

`UpdateAnnotationBoundedText`

Update Bounded Text Annotation

Description

Adds a bounded text annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
UpdateAnnotationBoundedText(
  text = NULL,
  annotationName = NULL,
  x.pos = NULL,
  y.pos = NULL,
  fontSize = NULL,
  fontFamily = NULL,
  fontStyle = NULL,
  color = NULL,
  angle = NULL,
  type = NULL,
  customShape = NULL,
  fillColor = NULL,
  opacity = NULL,
  borderThickness = NULL,
  borderColor = NULL,
  borderOpacity = NULL,
  height = NULL,
  width = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`text`	The text to be displayed
`annotationName`	Name of annotation by UUID or Name
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`fontSize`	(optional) Numeric value; default is 12
`fontFamily`	(optional) Font family; default is Arial
`fontStyle`	(optional) Font style; default is
`color`	(optional) Hexidecimal color; default is #000000 (black)
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)

`type`	(optional) The type of the shape, default is RECTANGLE. See getNodeShapes() for valid options.
`customShape`	(optional) If a custom shape, this is the text of the shape
`fillColor`	(optional) Hexidecimal color; default is #000000 (black)
`opacity`	(optional) Opacity of fill color. Must be an integer between 0 and 100; default is 100.
`borderThickness`	(optional) Integer
`borderColor`	(optional) Hexidecimal color; default is #000000 (black)
`borderOpacity`	(optional) Integer between 0 and 100; default is 100.
`height`	(optional) Height of bounding shape; default is based on text height.
`width`	(optional) Width of bounding shape; default is based on text length.
`name`	(optional) Name of annotation object; default is "Text"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
UpdateAnnotationBoundedText("test1", "annotationName")
UpdateAnnotationBoundedText("test2", "annotationName", 1000, 1000, name="B2")
UpdateAnnotationBoundedText("test3", "annotationName", 1200, 1000, 30, "Helvetica",
"bold", "#990000", 40, name="B3", canvas="foreground",z=4)
```

`updateAnnotationImage` *Update Image Annotation*

Description

Updates a Image annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
updateAnnotationImage(
  url = NULL,
  annotationName = NULL,
  x.pos = NULL,
  y.pos = NULL,
  angle = NULL,
  opacity = NULL,
  brightness = NULL,
  contrast = NULL,
  borderThickness = NULL,
  borderColor = NULL,
  borderOpacity = NULL,
  height = NULL,
  width = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`url`	URL or path to image file. File paths can be absolute or relative to current working directory. URLs must start with http:// or https://.
`annotationName`	Name of annotation by UUID or Name
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`opacity`	(optional) Opacity of fill color. Must be an integer between 0 and 100; default is 100.
`brightness`	(optional) Image brightness. Must be an integer between -100 and 100; default is 0
`contrast`	(optional) Image contrast. Must be an integer between -100 and 100; default is 0
`borderThickness`	(optional) Integer
`borderColor`	(optional) Hexidecimal color; default is #000000 (black)
`borderOpacity`	(optional) Integer between 0 and 100; default is 100.
`height`	(optional) Height of image; default is based on text height.
`width`	(optional) Width of image; default is based on text length.
`name`	(optional) Name of annotation object; default is "Image"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.

`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
updateAnnotationImage("image.png")
updateAnnotationImage("/Users/janedoe/Desktop/image.png", 1000, 1000, name="I2")
updateAnnotationImage("https://www.example.com/image.png", 1200, 1000, 30,
    40, name="I3", canvas="background",z=4)
```

`updateAnnotationShape` *Update Shape Annotation*

Description

Updates a shape annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
updateAnnotationShape(
  type = NULL,
  customShape = NULL,
  annotationName = NULL,
  x.pos = NULL,
  y.pos = NULL,
  angle = NULL,
  fillColor = NULL,
  opacity = NULL,
  borderThickness = NULL,
  borderColor = NULL,
  borderOpacity = NULL,
  height = NULL,
  width = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`type`	(optional) The type of the shape, default is RECTANGLE. See getNodeShapes() for valid options.
`customShape`	(optional) If a custom shape, this is the text of the shape

`annotationName`	Name of annotation by UUID or Name
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`fillColor`	(optional) Hexidecimal color; default is #000000 (black)
`opacity`	(optional) Opacity of fill color. Must be an integer between 0 and 100; default is 100.
`borderThickness`	(optional) Integer
`borderColor`	(optional) Hexidecimal color; default is #000000 (black)
`borderOpacity`	(optional) Integer between 0 and 100; default is 100.
`height`	(optional) Height of shape; default is based on text height.
`width`	(optional) Width of shape; default is based on text length.
`name`	(optional) Name of annotation object; default is "Shape"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
updateAnnotationShape("rectangle", "annotationName")
updateAnnotationShape("rectangle", "annotationName", 1000, 1000, name="S2")
updateAnnotationShape("rectangle", "annotationName", 1200, 1000, 30, "#990000",
    40,name="S3", canvas="background",z=4)
```

`updateAnnotationText` *Update Text Annotation*

Description

Updates a text annotation to a Cytoscape network view. The object will also be added to the Annotation Panel in the GUI.

Usage

```
updateAnnotationText(
  text = NULL,
  annotationName = NULL,
  x.pos = NULL,
  y.pos = NULL,
  fontSize = NULL,
  fontFamily = NULL,
  fontStyle = NULL,
  color = NULL,
  angle = NULL,
  name = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`text`	The text to be displayed
`annotationName`	Name of annotation by UUID or Name
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`fontSize`	(optional) Numeric value; default is 12
`fontFamily`	(optional) Font family; default is Arial
`fontStyle`	(optional) Font style; default is
`color`	(optional) Hexidecimal color; default is #000000 (black)
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`name`	(optional) Name of annotation object; default is "Text"
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
updateAnnotationText("test1", "annotationName")
updateAnnotationText("test2", "annotationName", 1000, 1000, name="T2")
updateAnnotationText("test3", "annotationName", 1200, 1000, 30, "Helvetica", "bold", "#990000",
    40,name="T3", canvas="foreground",z=4)
```

`updateApp` *Update App*

Description

Update a Cytoscape app to the latest available version.

Usage

```
updateApp(app, base.url = .defaultBaseUrl)
```

Arguments

`app`	Name of app
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
updateApp()
```

`updateGroupAnnotation` *Update Group Annotation*

Description

Updates a group annotation, changing the given properties.

Usage

```
updateGroupAnnotation(
  name = NULL,
  annotationName = NULL,
  x.pos = NULL,
  y.pos = NULL,
  angle = NULL,
  canvas = NULL,
  z.order = NULL,
  network = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`name`	(optional) Name of annotation object
`annotationName`	Name of annotation by UUID or Name
`x.pos`	(optional) X position in pixels from left; default is center of current view
`y.pos`	(optional) Y position in pixels from top; default is center of current view
`angle`	(optional) Angle of text orientation; default is 0.0 (horizontal)
`canvas`	(optional) Canvas to display annotation, i.e., foreground (default) or background
`z.order`	(optional) Arrangement order specified by number (larger values are in front of smaller values); default is 0
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

A named list of annotation properties, including UUID

Examples

```
updateGroupAnnotation("test1", "annotationName")
```

`updateNetworkInNDEx` *Update Network In NDEx*

Description

Update an existing network in NDEx, given a previously assoicaiated Cytoscape network, e.g., previously exported to NDEx or imported from NDEx.

Usage

```
updateNetworkInNDEx(
  username,
  password,
  isPublic,
  network = NULL,
  metadata = NULL,
  base.url = .defaultBaseUrl
)
```

Arguments

`username`	NDEx account username
`password`	NDEx account password
`isPublic`	(Boolean) Whether to make the network publicly accessible at NDEx.
`network`	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
`metadata`	(optional) A list of structured information describing the network
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

NDEx identifier (`externalId`) for the updated submission

Examples

```
updateNetworkInNDEx("user", "pass", TRUE)
```

`updateStyleDefaults` *Updates the default values of visual properties in a style*

Description

Updates visual property defaults, overriding any prior settings. See mapVisualProperty for the list of visual properties.

Usage

```
updateStyleDefaults(style.name, defaults, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	(char) name for style
`defaults`	(list) a list of visual property default settings
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Value

server response

See Also

mapVisualProperty

Examples

```
updateStyleDefaults('myStyle',list('node fill color'='#0000FF','node size'=50))
```

`updateStyleMapping` *Updates a visual property mapping in a style*

Description

Updates the visual property mapping, overriding any prior mapping. Creates a visual property mapping if it doesn't already exist in the style.

Usage

```
updateStyleMapping(style.name, mapping, base.url = .defaultBaseUrl)
```

Arguments

`style.name`	(char) name for style
`mapping`	a single visual property mapping, see mapVisualProperty
`base.url`	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is http://localhost:1234 and the latest version of the CyREST API supported by this version of RCy3.

Details

Requires visual property mappings to be previously created, see mapVisualProperty.

Value

server response

See Also

mapVisualProperty

Examples

```
updateStyleMapping('myStyle',mapVisualProperty('node label','name','p'))
```

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