

Package ‘RCy3’

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Author Alex Pico [aut, cre] (<<https://orcid.org/0000-0001-5706-2163>>),
Tanja Muetze [aut],
Paul Shannon [aut],
Ruth Isserlin [ctb],
Shraddha Pai [ctb],
Julia Gustavsen [ctb],
Georgi Kolishovski [ctb]

Maintainer Alex Pico <alex.pico@gladstone.ucsf.edu>

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addCyEdges	<i>Add CyEdges</i>
------------	--------------------

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 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	<i>Add to Group</i>
------------	---------------------

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

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

Value

None

Examples

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

analyzeNetwork	<i>Analyze Network</i>
----------------	------------------------

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

<code>filter.name</code>	Name of filter to apply. Default is "Default filter".
<code>hide</code>	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.
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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	<i>Bundle Edges</i>
-------------	---------------------

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
bundleEdges()
```

clearEdgeBends	<i>Clear Edge Bends</i>
----------------	-------------------------

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 <code>http://localhost:1234</code> 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

<code>edge.names</code>	List of edge names. Pending CyREST updates, if set to 'all', then the property is cleared for all edges.
<code>visual.property</code>	Name of a visual property. See getVisualPropertyNames .
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
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. 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	<i>Clear Selection</i>
----------------	------------------------

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 <code>http://localhost:1234</code> 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	<i>Clone a Cytoscape Network</i>
--------------	----------------------------------

Description

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

Usage

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

Arguments

network	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

```
## Not run:
cloneNetwork("cloned network")

## End(Not run)
```

closeSession	<i>Close Session</i>
--------------	----------------------

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	<i>Collapse Group</i>
---------------	-----------------------

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	<i>Command Echo</i>
-------------	---------------------

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	<i>Command Open Dialog</i>
-------------------	----------------------------

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	<i>Command Pause</i>
--------------	----------------------

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	<i>Command Quit</i>
-------------	---------------------

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	<i>Command Run File</i>
----------------	-------------------------

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	<i>Open Swagger docs for CyREST Commands API</i>
-------------	--

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	<i>Commands GET</i>
-------------	---------------------

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.

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.

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	<i>Command Sleep</i>
--------------	----------------------

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	<i>Commands POST</i>
--------------	----------------------

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.

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	<i>Copy Visual Style</i>
-----------------	--------------------------

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
copyVisualStyle()
```

createColumnFilter	<i>Create Column Filter</i>
--------------------	-----------------------------

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
  )

```

Arguments

<code>filter.name</code>	Name for filter.
<code>column</code>	Table column to base filter upon.
<code>criterion</code>	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.html). 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.
<code>predicate</code>	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
<code>caseSensitive</code>	(optional) If string matching should be case sensitive. Default is FALSE.
<code>anyMatch</code>	(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.
<code>type</code>	(optional) Apply filter to "nodes" (default) or "edges".
<code>hide</code>	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.
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to 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 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")
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  
)
```

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.

Value

List of selected nodes and edges.

Examples

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

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  
)
```

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.

Value

List of selected nodes and edges.

Examples

```
createDegreeFilter('myFilter', c(2,5))
```

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 optionally 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 optionally 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 preferred 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 vertex 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')
```

```
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 preferred 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 will 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 <code>http://localhost:1234</code> 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(igraph)
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 preferred layout set in Cytoscape preferences.

Usage

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

Arguments

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

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)
```

<code>createSubnetwork</code>	<i>Create subnetwork from existing network</i>
-------------------------------	--

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

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

Details

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

```

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 mapVisualStyleProperty
base.url	(optional) Ignore unless you need to specify a custom domain, port or version to 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 mapVisualStyleProperty.

Value

None

See Also

applyStyle, mapVisualStyleProperty

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 <- mapVisualStyleProperty('node label','id','p')
nodeFills <- mapVisualStyleProperty('node fill color','group','d',c("A","B"), c("#FF9900","#66AAAA"))
arrowShapes <- mapVisualStyleProperty('Edge Target Arrow Shape','interaction','d',
                                     c("activates","inhibits","interacts"),c("Arrow","T","None"))
edgeWidth <- mapVisualStyleProperty('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 <code>http://localhost:1234</code> 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	<i>Cybrowser Send</i>
---------------	-----------------------

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 <code>http://localhost:1234</code> 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	<i>Cybrowser Show</i>
---------------	-----------------------

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	<i>Cybrowser Version</i>
------------------	--------------------------

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

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()
```

cyrestGET

CyREST GET

Description

Constructs the query, makes GET call and processes the result

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

CyREST result content

Examples

```
cyrestGET()
```

`cyrestPOST`*CyREST POST*

Description

Constructs the query and body, makes POST call and processes the result

Usage

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

Arguments

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

Value

CyREST result content

Examples

```
cyrestPOST()
```

`cyrestPUT`*CyREST PUT*

Description

Constructs the query and body, makes PUT call and processes the result

Usage

```

cyrestPUT(
  operation,
  parameters = NULL,
  body = FALSE,
  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.
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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	<i>Ping Cytoscape</i>
---------------	-----------------------

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()
```

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	<i>Delete (or Ungroup) a Group</i>
-------------	------------------------------------

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	<i>Delete Network</i>
---------------	-----------------------

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
deleteNetwork()
```

deleteSelectedEdges	<i>Delete Selected Edges</i>
---------------------	------------------------------

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 <code>http://localhost:1234</code> 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

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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	<i>Delete Self Loops</i>
-----------------	--------------------------

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	<i>Delete Style Mapping</i>
--------------------	-----------------------------

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 getVisualStyleNames().
base.url	(optional) Ignore unless you need to specify a custom domain, port or version to 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	<i>Delete a table column</i>
-------------------	------------------------------

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

<code>style.name</code>	(char) name of style to delete
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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')
```

 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)
```

Arguments

<code>filename</code>	(char) Full path or path relative to current working directory, in addition to the name of the file. Default is "filters.json"
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

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
)
```

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 (presumably 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

The image is cropped per the current view in Cytoscape. Consider applying [fitContent](#) prior to export.

Value

server response

Examples

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

exportNetwork

Export Network

Description

Export a network to one of multiple file formats

Usage

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

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, xGMLL.
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.

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)
```

exportVisualStyles *Export Visual Styles*

Description

Save one or more visual styles to file.

Usage

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

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.

Value

Path to saved file

See Also

importVisualStyles

Examples

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

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 (presumably 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

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

Value

None

Examples

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

`getAllEdges`
Get All Edges

Description

Retrieve the names of all the edges in the network.

Usage

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

Arguments

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

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

Value

list of node names

Examples

```
getAllNodes()
```

`getAppInformation`*Get App Information*

Description

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

Usage

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

Arguments

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

Value

App name, brief description and version.

Examples

```
getAppInformation()
```

getAppStatus	<i>App Status</i>
--------------	-------------------

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	<i>List Apps With Updates</i>
---------------	-------------------------------

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 <code>http://localhost:1234</code> 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	<i>Get Arrow Shapes</i>
----------------	-------------------------

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 <code>http://localhost:1234</code> 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()
```

<code>getAvailableApps</code>	<i>List Available Apps</i>
-------------------------------	----------------------------

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()
```

<code>getBackgroundColorDefault</code>	<i>Get Background Color Default</i>
--	-------------------------------------

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()
```

`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	<i>Get Collection Suid</i>
-------------------	----------------------------

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()
```

getCurrentStyle	<i>Get Current Style</i>
-----------------	--------------------------

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')
```

getDisabledApps	<i>List Disabled Apps</i>
-----------------	---------------------------

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	<i>Get Edge Color</i>
--------------	-----------------------

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. 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

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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	<i>Get Edge Line Style</i>
------------------	----------------------------

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. 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()
```

<code>getEdgeLineWidth</code>	<i>Get Edge Line Width</i>
-------------------------------	----------------------------

Description

Retrieve the actual line width of specified edges.

Usage

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

Arguments

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

<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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. 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	<i>Get Filter List</i>
---------------	------------------------

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 node 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	<i>Get Group Information</i>
--------------	------------------------------

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	<i>List Installed Apps</i>
------------------	----------------------------

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()
```

```
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"
```

<code>getLayoutNames</code>	<i>Get Layout Names</i>
-----------------------------	-------------------------

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

<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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"
```

<code>getLayoutPropertyName</code>	<i>Get Layout Property Names</i>
------------------------------------	----------------------------------

Description

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

Usage

```
getLayoutPropertyName(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
```

getLineStyle	<i>Get Line Styles</i>
--------------	------------------------

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

```
getLineStyle(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

```
getLineStyle()
```

getNetworkCenter	<i>Get Network Center</i>
------------------	---------------------------

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	<i>Get the number of Cytoscape networks</i>
-----------------	---

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

```
## Not run:
getNetworkCount()
# 3

## End(Not run)
```

getNetworkList *Get the list of Cytoscape networks*

Description

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

Usage

```
getNetworkList(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

Author(s)

Alexander Pico, Tanja Muetze, Georgi Kolishovski, Paul Shannon

Examples

```
## Not run:  
getNetworkList()  
# 3  
  
## End(Not run)
```

getNetworkName *Get the name of a network*

Description

Retrieve the title of a network

Usage

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


Arguments

suid	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	<i>Get Network NDEx Id</i>
------------------	----------------------------

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 <code>http://localhost:1234</code> 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	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	<i>Get Network Views</i>
-----------------	--------------------------

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	<i>Get Node Color</i>
--------------	-----------------------

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. 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

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

getNodePosition	<i>Get Node Position</i>
-----------------	--------------------------

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. 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. 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 <code>http://localhost:1234</code> 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

<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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. 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	<i>Get Node Width</i>
--------------	-----------------------

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. 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()
```

getSelectedEdgeCount	<i>Get Selected Edge Count</i>
----------------------	--------------------------------

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()
```

<code>getSelectedEdges</code>	<i>Get Selected Edges</i>
-------------------------------	---------------------------

Description

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

Usage

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

Arguments

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

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

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

getTableColumnNames	<i>Get Table Column Names</i>
---------------------	-------------------------------

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	<i>Get table column values</i>
-----------------	--------------------------------

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	<i>Get table cell value</i>
---------------	-----------------------------

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

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

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

Value

List of names

Examples

```
getVisualPropertyNames()
```

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()
```

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
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	<i>Hide Nodes</i>
-----------	-------------------

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
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

<code>panel.name</code>	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
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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	<i>Hide Selected Nodes</i>
-------------------	----------------------------

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()
```

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()
```

<code>installApp</code>	<i>Install App</i>
-------------------------	--------------------

Description

Installs an app in Cytoscape.

Usage

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

Arguments

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

Value

None

Examples

```
installApp()
```

<code>invertEdgeSelection</code>	<i>Invert Edge Selection</i>
----------------------------------	------------------------------

Description

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

Usage

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

Arguments

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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	<i>List Groups</i>
------------	--------------------

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

List of group SUIDs

Examples

```
listGroups()
```

loadTableData	<i>Loads data into Cytoscape tables keyed by row</i>
---------------	--

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	<i>Make Simple Graph</i>
-----------------	--------------------------

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	<i>Make Simple Igraph</i>
------------------	---------------------------

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, miR-Base, 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	<i>Creates a mapping between an attribute and a visual property</i>
-------------------	---

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 Cytoscape 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	Edge Bend	Network Background Paint
Node Border Paint	Edge Curved	Network Center X Location
Node Border Transparency	Edge Label	Network Center Y Location
Node Border Width	Edge Label Color	Network Center Z Location
Node CustomGraphics 1-9	Edge Label Font Face	Network Depth
Node CustomGraphics Position 1-9	Edge Label Font Size	Network Edge Selection
Node CustomGraphics Size 1-9	Edge Label Transparency	Network Height
Node CustomPaint 1-9	Edge Label Width	Network Node Selection
Node Depth	Edge Line Type	Network Scale Factor
Node Fill Color	Edge Paint	Network Size
Node Height	Edge Selected	Network Title
Node Label	Edge Selected Paint	Network Width
Node Label Color	Edge Source Arrow Selected Paint	
Node Label Font Face	Edge Source Arrow Shape	
Node Label Font Size	Edge Source Arrow Size	
Node Label Position	Edge Source Arrow Unselected Paint	

Node Label Transparency	Edge Stroke Selected Paint
Node Label Width	Edge Stroke Unselected Paint
Node Network Image Visible	Edge Target Arrow Selected Paint
Node Paint	Edge Target Arrow Shape
Node Selected	Edge Target Arrow Size
Node Selected Paint	Edge Target Arrow Unselected Paint
Node Shape	Edge Tooltip
Node Size	Edge Transparency
Node Tooltip	Edge Unselected Paint
Node Transparency	Edge Visible
Node Visible	Edge Visual Property
Node Width	Edge Width
Node X Location	
Node Y Location	
Node Z Location	

See Also

updateStyleMapping getVisualStylePropertyNames

Examples

```
mapVisualStyleProperty('node fill color', 'score', 'c', c(-4.0, 0.0, 9.0), c('#99CCFF', '#FFFFFF', '#FF7777'))
mapVisualStyleProperty('node shape', 'type', 'd', c('protein', 'metabolite'), c('ellipse', 'rectangle'))
mapVisualStyleProperty('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 to be merged.
title	(optional) Title of the resulting merged network. Default is a concatenation 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"))
```

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')
```

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

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

Description

Sets a new name for this network

Usage

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

Arguments

title	New name for the network
network	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

```
## Not run:  
renameNetwork("renamed network")  
  
## End(Not run)
```

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

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

saveSession	<i>Save Session to File</i>
-------------	-----------------------------

Description

Saves the current Cytoscape session as a CYS file.

Usage

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

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

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()
```

selectAllEdges	<i>Select all edges</i>
----------------	-------------------------

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

```
## Not run:
cw <- CytoscapeWindow('new.demo', new('graphNEL'))
selectAllEdges(cw)

## End(Not run)
```

selectAllNodes	<i>Select all nodes</i>
----------------	-------------------------

Description

Selects all nodes in a Cytoscape Network

Usage

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


Arguments

network	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

<code>edges</code>	List of edge SUIDs, names or other column values
<code>by.col</code>	Edge table column to lookup up provide edge values. Default is 'SUID'.
<code>preserve.current.selection</code>	boolean Whether to maintain previously selected edges.
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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()
```

```
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

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

```
## Not run:  
selectEdgesConnectingSelectedNodes()  
  
## End(Not run)
```

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()
selectFirstNeighbors('outgoing')
selectFirstNeighbors('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

<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>new.color</code>	Color as hex code, e.g., <code>#FD5903</code>
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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 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')
```

setCurrentView	<i>Set Current View</i>
----------------	-------------------------

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 (presumably 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()
```

setEdgeColorBypass	<i>Set Edge Color Bypass</i>
--------------------	------------------------------

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
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
colors	List of hex colors to map to table.column.values
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(0,5), c('#FFFFFF', '#FF7755'))
```

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
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

<code>new.font</code>	String specification of font face, style and size, e.g., "SansSerif,plain,12" or "Dialog,plain,10"
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>fonts</code>	List of string specifications of font face, style and size, e.g., <code>c("SansSerif,plain,12", "Dialog,plain,10")</code>
<code>mapping.type</code>	(char) discrete or passthrough (d,p); default is discrete
<code>default.font</code>	String specification of font face, style and size, e.g., <code>"SansSerif,plain,12"</code> or <code>"Dialog,plain,10"</code>
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
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

<code>new.size</code>	Numeric value for size
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
sizes	List of size values to map to table.column.values
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', 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
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 <code>http://localhost:1234</code> 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
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 <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>colors</code>	(integer) values between 0 and 255; 0 is invisible
<code>mapping.type</code>	(char) continuous, discrete or passthrough (c,d,p); default is continuous
<code>default.color</code>	Hex color to set as default
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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'))
```

```
setEdgeLabelDefault     Set Edge Label Default
```

Description

Set the default edge label.

Usage

```
setEdgeLabelDefault(new.label, style.name = NULL, base.url = .defaultBaseUrl)
```

Arguments

<code>new.label</code>	String label for unmapped edges.
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
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

<code>new.opacity</code>	Numeric values between 0 and 255; 0 is invisible.
<code>style.name</code>	Name of style; default is "default" style.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>opacities</code>	(integer) values between 0 and 255; 0 is invisible
<code>mapping.type</code>	(char) continuous, discrete or passthrough (c,d,p); default is continuous
<code>default.opacity</code>	Opacity value to set as default for all unmapped values
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape. port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
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

<code>edge.names</code>	List of edge names
<code>new.styles</code>	List of style values, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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 [getLineStylees](#))

`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,
  line.styles,
  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
line.styles	List of 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',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
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
widths	List of width values to map to table.column.values
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', 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
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

<code>new.opacity</code>	Numeric values between 0 and 255; 0 is invisible.
<code>style.name</code>	Name of style; default is "default" style.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>opacities</code>	(integer) values between 0 and 255; 0 is invisible
<code>mapping.type</code>	(char) continuous, discrete or passthrough (c,d,p); default is continuous
<code>default.opacity</code>	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', 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
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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to 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

<code>edge.names</code>	List of edge names
<code>new.colors</code>	List of hex colors, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
colors	List of hex colors to map to table.column.values
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'))
```

```
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,  
  shapes,  
  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
shapes	List of shapes to map to table.column.values. 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',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
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,  
    shapes,  
    default.shape = NULL,  
    style.name = NULL,  
    network = NULL,  
    base.url = .defaultBaseUrl  
)
```

Arguments

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>shapes</code>	List of arrow shapes to map to <code>table.column.values</code> . See getArrowShapes
<code>default.shape</code>	Shape to set as default. See getArrowShapes
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
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
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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>colors</code>	List of hex colors to map to <code>table.column.values</code>
<code>mapping.type</code>	(char) continuous, discrete or passthrough (c,d,p); default is continuous
<code>default.color</code>	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'))
```

```
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,
  shapes,
  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
shapes	List of shapes to map to table.column.values. 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',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

<code>edge.names</code>	List of edge names
<code>new.shapes</code>	List of values to set, or single value. See getArrowShapes .
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>new.shape</code>	Name of shape, e.g., ARROW, T, etc (see getArrowShapes)
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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,  
  shapes,  
  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
shapes	List of arrow shapes to map to table.column.values. 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',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
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 <code>http://localhost:1234</code> 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

<code>new.value</code>	Value to set
<code>visual.property</code>	Name of a visual property. See getVisualPropertyNames .
<code>bypass</code>	Whether to set permanent bypass value. Default is TRUE.
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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 <code>http://localhost:1234</code> 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
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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>colors</code>	(integer) values between 0 and 255; 0 is invisible
<code>mapping.type</code>	(char) continuous, discrete or passthrough (c,d,p); default is continuous
<code>default.color</code>	Hex color to set as default
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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'))
```

```
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
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

<code>new.opacity</code>	Numeric values between 0 and 255; 0 is invisible.
<code>style.name</code>	Name of style; default is "default" style.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
opacities	(integer) values between 0 and 255; 0 is invisible
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', 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
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 <code>http://localhost:1234</code> 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
widths	List of width values to map to table.column.values
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', 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
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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
colors	List of hex colors to map to table.column.values
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'))
```

```
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
opacities	(integer) values between 0 and 255; 0 is invisible
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', 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

<code>node.names</code>	List of node names
<code>new.values</code>	List of values to set, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
opacities	(integer) values between 0 and 255; 0 is invisible
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', 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
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

<code>new.font</code>	String specification of font face, style and size, e.g., "SansSerif,plain,12" or "Dialog,plain,10"
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>fonts</code>	List of string specifications of font face, style and size, e.g., <code>c("SansSerif,plain,12", "Dialog,plain,10")</code>
<code>mapping.type</code>	(char) discrete or passthrough (d,p); default is discrete
<code>default.font</code>	String specification of font face, style and size, e.g., <code>"SansSerif,plain,12"</code> or <code>"Dialog,plain,10"</code>
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
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

<code>new.size</code>	Numeric value for size
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
sizes	List of size values to mape to table.column.values
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', 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

<code>node.names</code>	List of node names
<code>new.heights</code>	List of height values, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
heights	List of height values to map to table.column.values
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.

Value

None

Examples

```
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

<code>node.names</code>	List of node names
<code>new.labels</code>	List of labels, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
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 <code>http://localhost:1234</code> 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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>table.column.values</code>	List of values from Cytoscape table to be used in mapping
<code>colors</code>	(integer) values between 0 and 255; 0 is invisible
<code>mapping.type</code>	(char) continuous, discrete or passthrough (c,d,p); default is continuous
<code>default.color</code>	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'))
```

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
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

<code>new.opacity</code>	Numeric values between 0 and 255; 0 is invisible.
<code>style.name</code>	Name of style; default is "default" style.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
opacities	(integer) values between 0 and 255; 0 is invisible
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', c(-5,5), c(50,255))
```

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

<code>node.names</code>	List of node names
<code>new.values</code>	List of values to set, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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'))
```

`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
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

<code>new.color</code>	Color as hex code, e.g., #FD5903
<code>style.name</code>	(optional) Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>node.names</code>	List of node names
<code>new.shapes</code>	List of shapes, or single value. See getNodeShapes .
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>new.shape</code>	Name of shape, e.g., ELLIPSE, RECTANGLE, etc (see getNodeShapes)
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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,  
  shapes,  
  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
shapes	List of shapes to map to table.column.values. 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',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

<code>node.names</code>	List of node names
<code>new.sizes</code>	List of size values, or single value
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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
sizes	List of font size values to map to table.column.values
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

```
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

<code>node.names</code>	List of node names
<code>new.tooltip</code>	List of tooltips, or a single tooltip
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>new.tooltip</code>	String tooltip for unmapped nodes.
<code>style.name</code>	Name of style; default is "default" style
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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

<code>table.column</code>	Name of Cytoscape table column to map values from
<code>style.name</code>	Name of style; default is "default" style
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
setNodeTooltipMapping('description')
```

setNodeWidthBypass	<i>Set Node Width Bypass</i>
--------------------	------------------------------

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
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
widths	List of width values to map to table.column.values
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

Examples

```
setNodeWidthMapping('score', c(0,30), c(35,55))
```

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

```
setVisualStyleDefault(list(visualProperty = "NODE_SIZE", value = 35))
```

setVisualStyle	<i>Set Visual Style</i>
----------------	-------------------------

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()
```

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)
```

`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
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

<code>node.names</code>	List of node names
<code>network</code>	(optional) Name or SUID of the network. Default is the "current" network active in Cytoscape.
<code>base.url</code>	(optional) Ignore unless you need to specify a custom domain, port or version to connect to the CyREST API. Default is <code>http://localhost:1234</code> 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	<i>Uninstall App</i>
--------------	----------------------

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

```
uninstallApp()
```

updateApp	<i>Update App</i>
-----------	-------------------

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 <code>http://localhost:1234</code> and the latest version of the CyREST API supported by this version of RCy3.

Value

None

Examples

updateApp()

 updateNetworkInNDEx *Update Network In NDEx*

Description

Update an existing network in NDEx, given a previously associated Cytoscape network, e.g., previously exported to NDEx or imported from NDEx.

Usage

```
updateNetworkInNDEx(
  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 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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