

Introduction to RCy3

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This vignette will show you how to connect to Cytoscape from R using CyREST. It will cover the installation of required packages and demonstrate some basic functionality of CyREST, commands and RCy3

It is recommended that you run this vignette *prior* to Cytoscape Automation workshops to mitigate troubleshooting time.

Installation

```
source("https://bioconductor.org/biocLite.R")
biocLite("RCy3")
```

Required Software

The whole point of RCy3 is to connect with Cytoscape. You will need to install and launch Cytoscape:

- Download the latest Cytoscape from <http://www.cytoscape.org/download.php>
- Complete installation wizard
- Launch Cytoscape

First Contact

These functions are a convenient way to verify a connection to Cytoscape and for logging the versions of CyREST and Cytoscape in your scripts.

```
cytoscapePing()
cytoscapeVersionInfo()
```

My First Network

Let's create a Cytoscape network from some basic R objects

```
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
```

```
stringsAsFactors=FALSE)
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
  stringsAsFactors=FALSE)

createNetworkFromDataFrames(nodes,edges)
```

Switch Styles

Check out the marquee style!

```
setVisualStyle('Marquee')
```

My Own Style

Create your own style with node attribute fill mappings and some defaults

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

createVisualStyle(style.name, defaults,
  list(nodeLabels,nodeFills,arrowShapes,edgeWidth))
setVisualStyle(style.name)
```

Browse Available Functions, Commands and Arguments

RCy3 functions

```
help(package=RCy3)
```

Open swagger docs for live instances of CyREST API and Commands API:

```
cyrestAPI() # CyREST API
```

```
commandsAPI() # Commands API
```

List available commands and arguments in R. Use “help” to list top level:

```
commandsHelp("help")
```

List **network** commands. Note that “help” is optional:

```
commandsHelp("help network")
```

List arguments for the **network select** command:

```
commandsHelp("help network select")
```

Those are the basics. You are now ready to work with some real data! See other basic and advanced R tutorials, <https://github.com/cytoscape/cytoscape-automation/tree/master/for-scripters/R>.