Cytoscape and iGraph

by Alexander Pico

2018-03-18

This vignette will show you how to convert networks between iGraph and Cytoscape.

Installation

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

```
library(igraph)
```

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

From igraph to Cytoscape

The igraph package is a popular network tool among R users. With RCy3, you can easily translate igraph networks to Cytoscape networks!

Here is a basic igraph network construction from the graph_from_data_frame docs, http://igraph.org /r/doc/graph_from_data_frame.html:

```
actors <- data.frame(name=c("Alice", "Bob", "Cecil", "David",
                            "Esmeralda"),
                     age=c(48,33,45,34,21),
                     gender=c("F","M","F","M","F"))
relations <- data.frame(from=c("Bob", "Cecil", "Cecil", "David",
                               "David", "Esmeralda"),
                        to=c("Alice", "Bob", "Alice", "Alice", "Bob", "Alice"),
                        same.dept=c(FALSE,FALSE,TRUE,FALSE,FALSE,TRUE),
                        friendship=c(4,5,5,2,1,1), advice=c(4,5,5,4,2,3))
ig <- graph_from_data_frame(relations, directed=TRUE, vertices=actors)

# if function not found, then you need to install igraph. Try library(igraph)
```

You now have an igraph network, g. In order to translate the network together with all vertex (node) and edge attributes over to Cytoscape, simply use:

```
createNetworkFromIgraph(ig,"myIgraph")
```

From Cytoscape to igraph

Inversely, you can use createIgraphFromNetwork() in RCy3 to retreive vertex (node) and edge data.frames to construct an igraph network.

```
ig2 <- createIgraphFromNetwork("myIgraph")
```

Compare the round-trip result for yourself…

```
ig
ig2
```