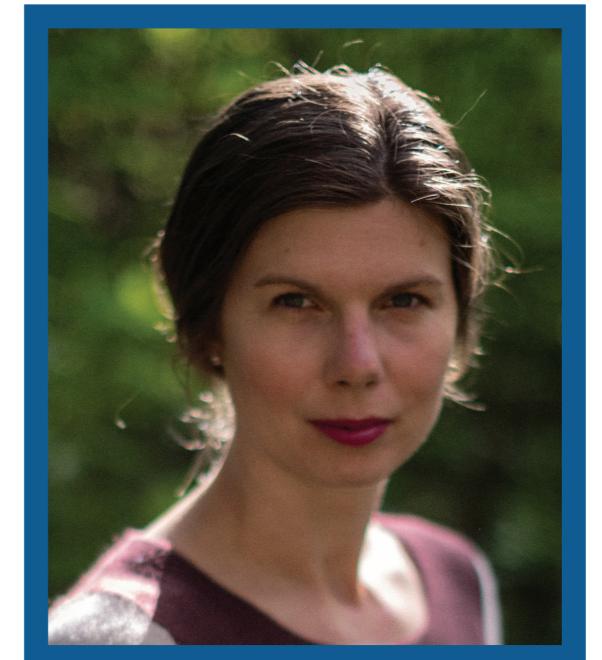


# Simple and reproducible visualization of virus-host co-occurrence networks using RCy3 and Cytoscape



Julia Gustavsen<sup>1</sup>, Chris Sander<sup>2</sup>, and Augustin Luna<sup>2</sup>

<sup>1</sup>University of British Columbia, Vancouver, BC, Canada

<sup>2</sup>Department of Biostatistics and Computational Biology, Dana-Farber Cancer Institute, Boston, MA, USA

## Introduction

- Network analysis and visualization have become popular exploratory and analytical tools in microbial and viral datasets (Lima-Mendez *et al* 2015; Weiss *et al* 2016)
- As scientists work with increasing amounts of data and the expectation of reproducible computational analyses increases, many users of network visualization programs are turning to scripted analyses instead of using a graphical user interface (GUI)
- Bioconductor package RCy3 (R for Cytoscape 3) (Shannon *et al* 2003; Ono *et al* 2015) provides way to create reproducible network analyses and visualisations

## Getting started



+



+



network file, containing meta-data for nodes and edges

## Visualizing

### In R script file:

Load the packages and network

```
library(RCy3)
library(RColorBrewer)
cy <- CytoscapeConnection()
load(file = "./data/network.gpl", verbose = TRUE)
cw <- CytoscapeWindow("Tara oceans", graph = ug, overwriteWindow = TRUE)
```

### Visualize prokaryotic nodes by phylum

```
families_to_colour <- unlist(unique(nodeData(ug, attr="prok_tax_phylum")))
node.colour <- brewer.pal(length(families_to_colour), "Set3")
setNodeColorRule(cw, "prok_tax_phylum", families_to_colour,
                 node.colour, "lookup", default.color='#ffffff')
```

### Modify: Which are the viral nodes? Change shape to diamonds

```
shapes_for_nodes <- c('DIAMOND')

phage_names <- grep("ph_", nodes(ug), value=TRUE)
setNodeShapeRule(cw, "label", phage_names, shapes_for_nodes)
```

### Modify: Which viral families have been identified?

```
setDefaultNodeBorderWidth (cw, 5)
families_to_colour <- c("Podoviridae", "Siphoviridae", "Myoviridae")
node.colour <- brewer.pal(length(families_to_colour), "Dark2")
setNodeBorderColorRule(cw, "Tax_subfamily", families_to_colour, node.colour,
                       "lookup", default.color = "#FFFFFF")
```

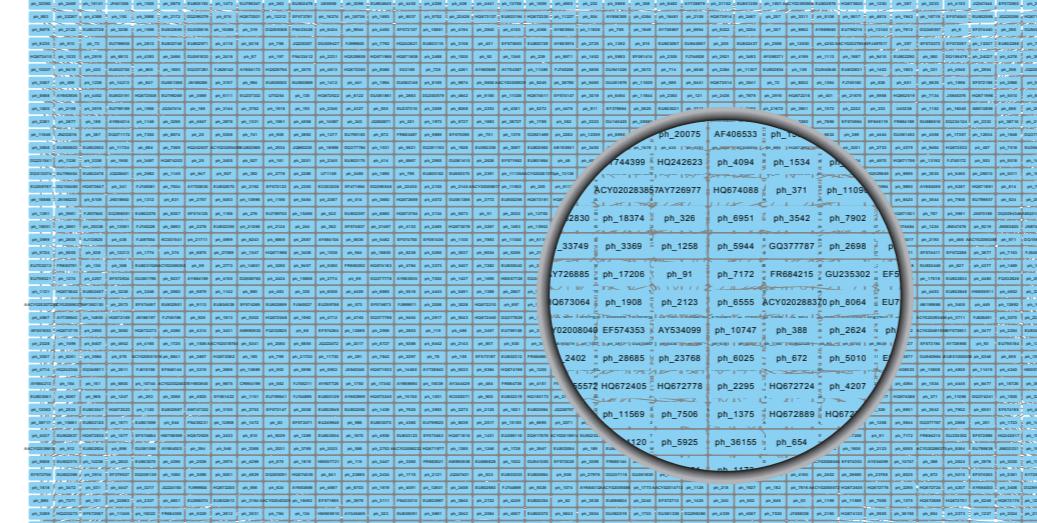
### Layout the network to visualize the connections

```
setLayoutProperties(cw, layout.name = 'allegro-spring-electric',
                   list(gravity = 100, scale = 6))
layoutNetwork(cw, layout.name = 'allegro-spring-electric')
```

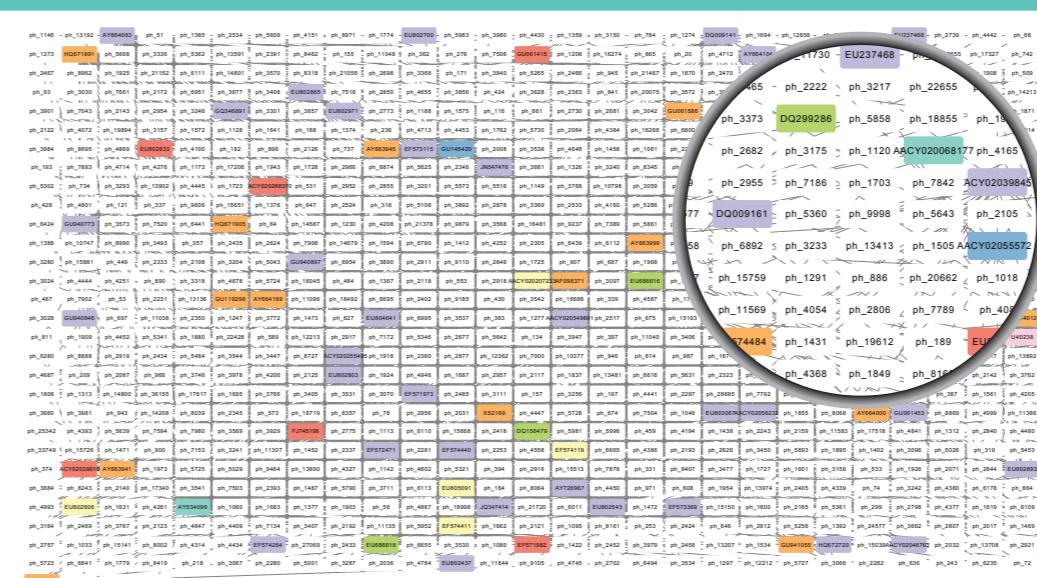
Working with pathways and other interactions? Find more networks and biological pathway tools using PaxtoolsR: <https://github.com/BioPAX/paxtoolsr>

Paxtools is a Bioconductor R package providing Paxtools and Pathway Commons functionality. This project provides users with the ability to read BioPAX files and access Pathway Commons web service functions.

### Results in Cytoscape window:

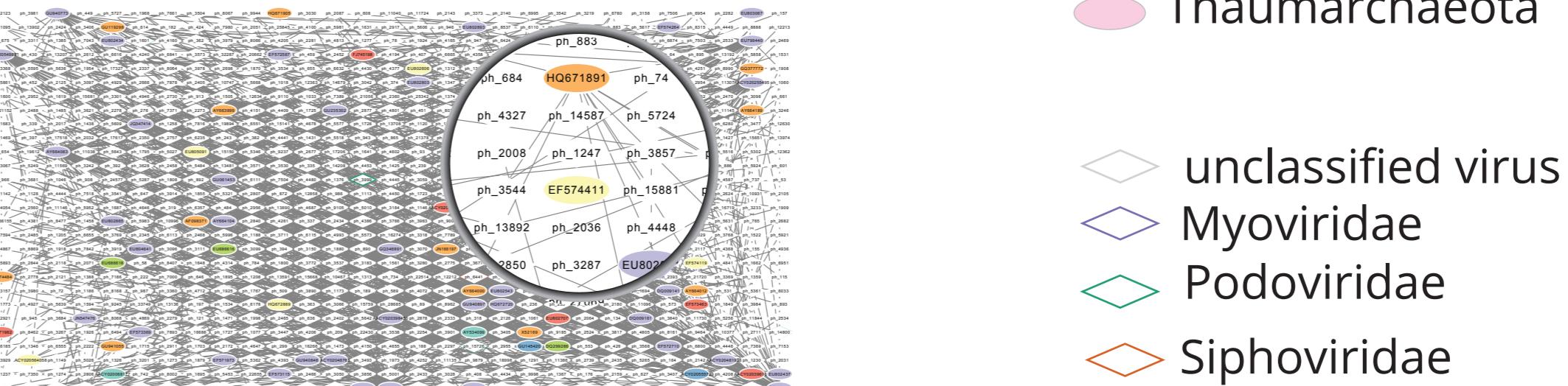


Displays all of the nodes (and edges - they are hidden behind the nodes)

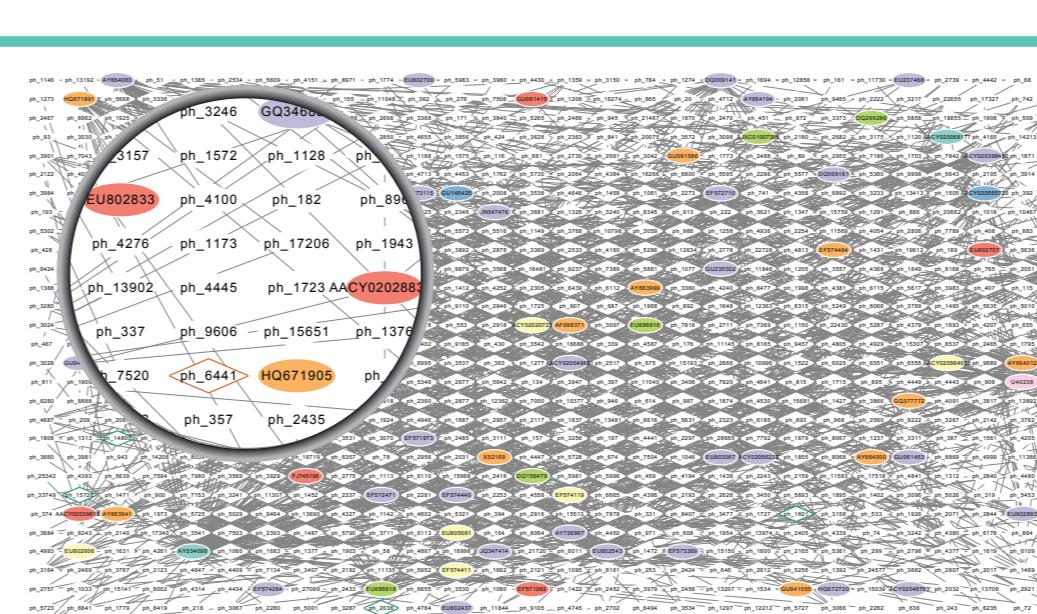


#### Legend:

Actinobacteria
Bacteroidetes
Chloroflexi
Cyanobacteria
Deferribacteres
Euryarchaeota
Proteobacteria
Thaumarchaeota

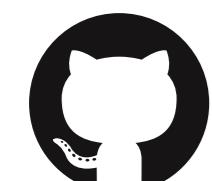
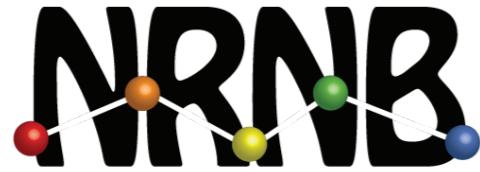


unclassified virus
Myoviridae
Podoviridae
Siphoviridae



## References

- Lima-Mendez G, Faust K, Henry N, Decelle J, Colin S, Carcillo F, et al. (2015). Determinants of community structure in the global plankton interactome. *Science* 348: 1262073.
- Ono K, Muetze T, Kolishovski G, Shannon P, Demchak B. (2015). CyREST: Turbocharging Cytoscape Access for External Tools via a RESTful API [version 1; referees: 2 approved]. *F1000Research* 4. e-pub ahead of print, doi: 10.12688/f1000research.6767.1.
- Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, et al. (2003). Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome research* 13: 2498-2504.
- Weiss S, Van Treuren W, Lozupone C, Faust K, Friedman J, Deng Y, et al. (2016). Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. *ISME J* 10: 1669-1681.



Run this code: [www.github.com/jooolia/RCy3\\_poster\\_VOM](https://github.com/jooolia/RCy3_poster_VOM)



@JuliaGustavsen