

Cytoscape User Tutorial

John “Scooter” Morris, Ph.D.

Resource for Biocomputing, Visualization, and Informatics,
UCSF



Today's Schedule



- 10:00- 10:15 Introductions/Installation
- 10:15- 10:45 Introduction to Cytoscape
- 10:45- 11:30 Hands-on Tutorial
- 11:30- 12:00 Q&A/Plugins



Installation



- USB Stick
 - Cytoscape 2.7 installers
 - A plugins folder with a variety of plugins
 - Several PDF's with tutorial exercises
 - We'll start with the “Introduction to Cytoscape”
 - Several sample data sets



Installation



- If you have not yet installed Cytoscape 2.7:
 - Install Cytoscape 2.7 by executing the appropriate installer
- If desired, copy plugins into your Cytoscape plugins folder
 - Linux: {Cytoscape install directory}/plugins
 - Windows: \Program Files\Cytoscape_v2.7.0\plugins
 - Mac OS X: /Applications/Cytoscape_v2.7.0/plugins



What is Cytoscape?



The screenshot displays the Cytoscape Version 2.5 interface. The main window shows a network graph with nodes of varying sizes and colors (yellow, green, red, grey) connected by edges. The interface includes several panels:

- Control Panel:** Contains tabs for Network, VizMapper™, and Editor. It shows the current visual style as 'Sample3' and a 'Visual Mapping Browser' with settings for Node Label (ID), Node Color (gal4RGexp), and Edge Color (interaction).
- Tool Panel:** Includes 'Rotate', 'Scale', and 'Align and Distribute' options.
- Data Panel:** A table showing node attributes.

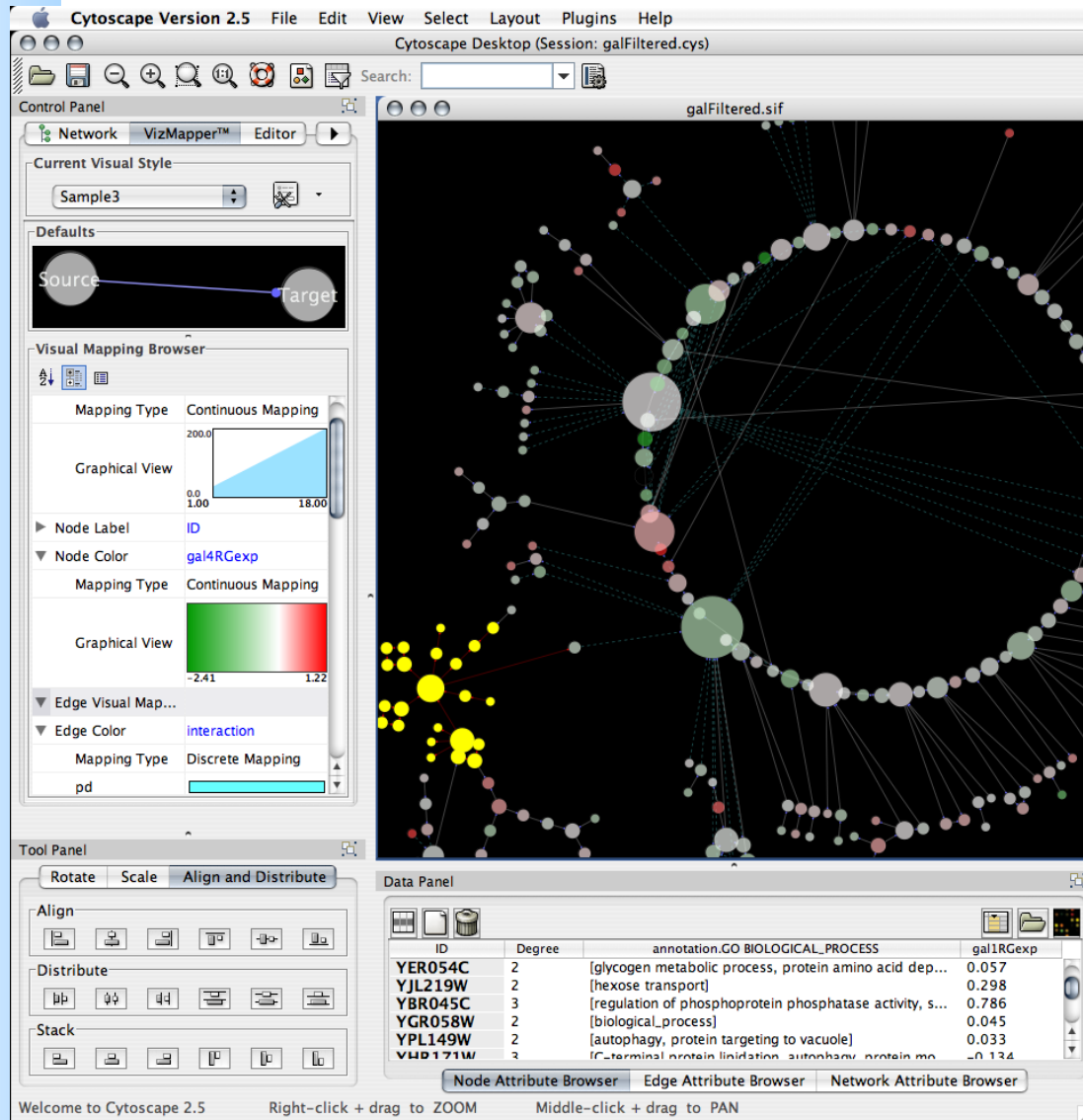
ID	Degree	annotation.GO BIOLOGICAL_PROCESS	gal1RGexp
YER054C	2	[glycogen metabolic process, protein amino acid dep...	0.057
YJL219W	2	[hexose transport]	0.298
YBR045C	3	[regulation of phosphoprotein phosphatase activity, s...	0.786
YGR058W	2	[biological_process]	0.045
YPL149W	2	[autophagy, protein targeting to vacuole]	0.033
VLD171W	2	[C-terminal protein ligation, autophagy, protein mo...	0.134

www.cytoscape.org

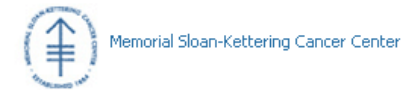
- Visualization
- Integration
- Analysis



What is Cytoscape?

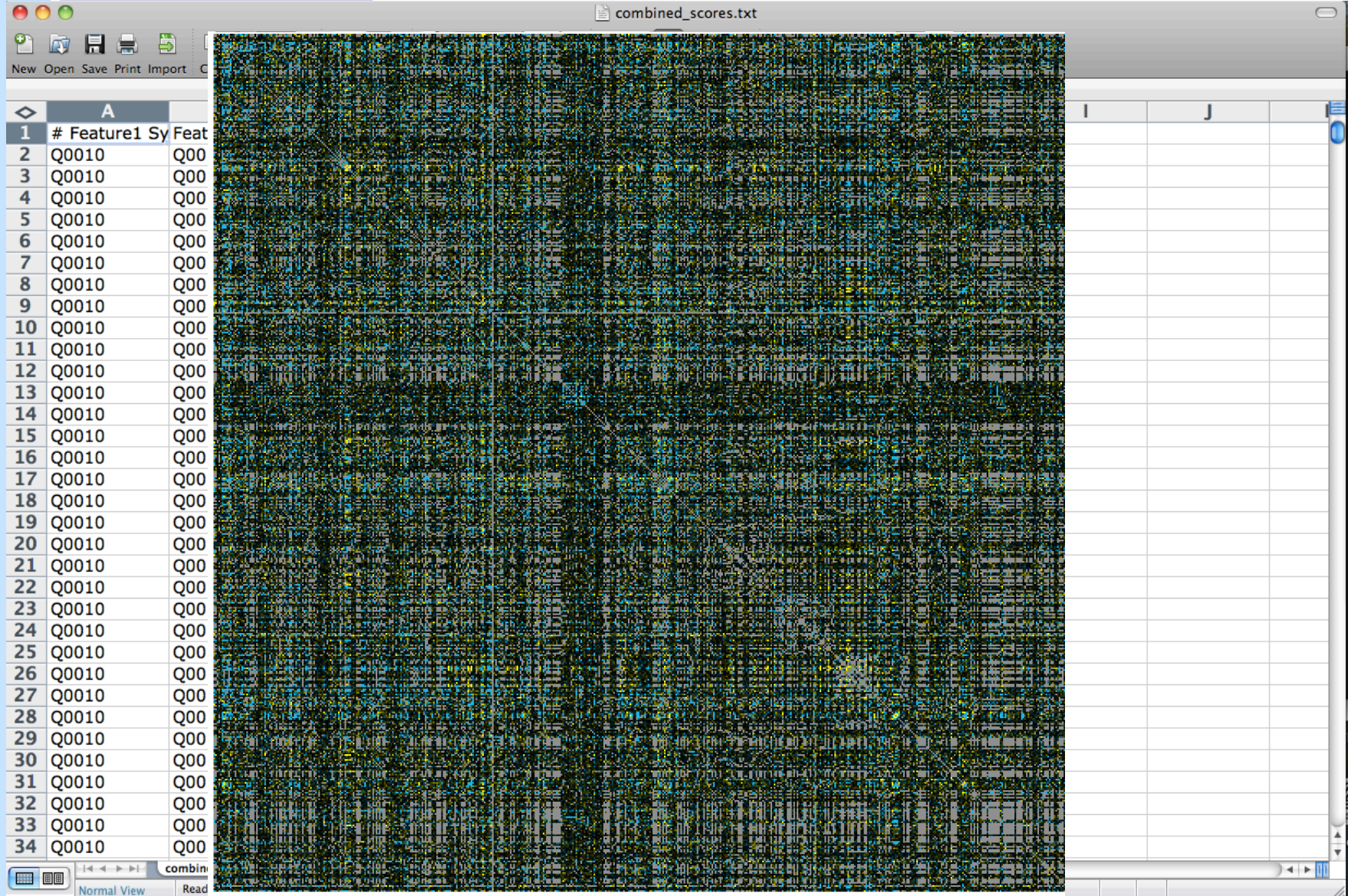


- Open source
- Cross platform
- A consortium





The Challenge





The Challenge



- Biological networks (nodes and edges)
 - Seldom tell us anything by themselves
 - Analysis involves:
 - Understanding the characteristics of the network
 - Modularity
 - Comparison with other networks (specifically random networks)
 - Visualization involves:
 - Placing nodes in a meaningful way (layouts)
 - Mapping biologically relevant data to the network
 - Node size
 - Node color
 - Edge weights



The Challenge



Cytoscape Desktop (Session: collins+Pombe.cys)

Search: **gim3**

Control Panel

Network	Nodes	Edges
combined_scores_good	2764(0)	16218(0)
combined_scores	2401(7)	11805(15)
DNA and Tran 07-21	743(10)	183728(46)
PombeChromosomeBi	524(9)	112125(36)

ClusterMaker TreeView : DNA and Tran 07-21--06b.csv

combined_scores_good.txt--clustered

Data Panel

ID	ORF	Other Orthologs	PombeORF	Sys. Name	Systematic Name	cluster
GIM3	SPAC227.05			YNL153C	SPAC227.05	164
PFD1	SPBC1D7.01			YJL179W	SPBC1D7.01	164
PAC10	SPAC3H8.07C			YGR078C	SPAC3H8.07C	164

Welcome to Cytoscape 2.6.2

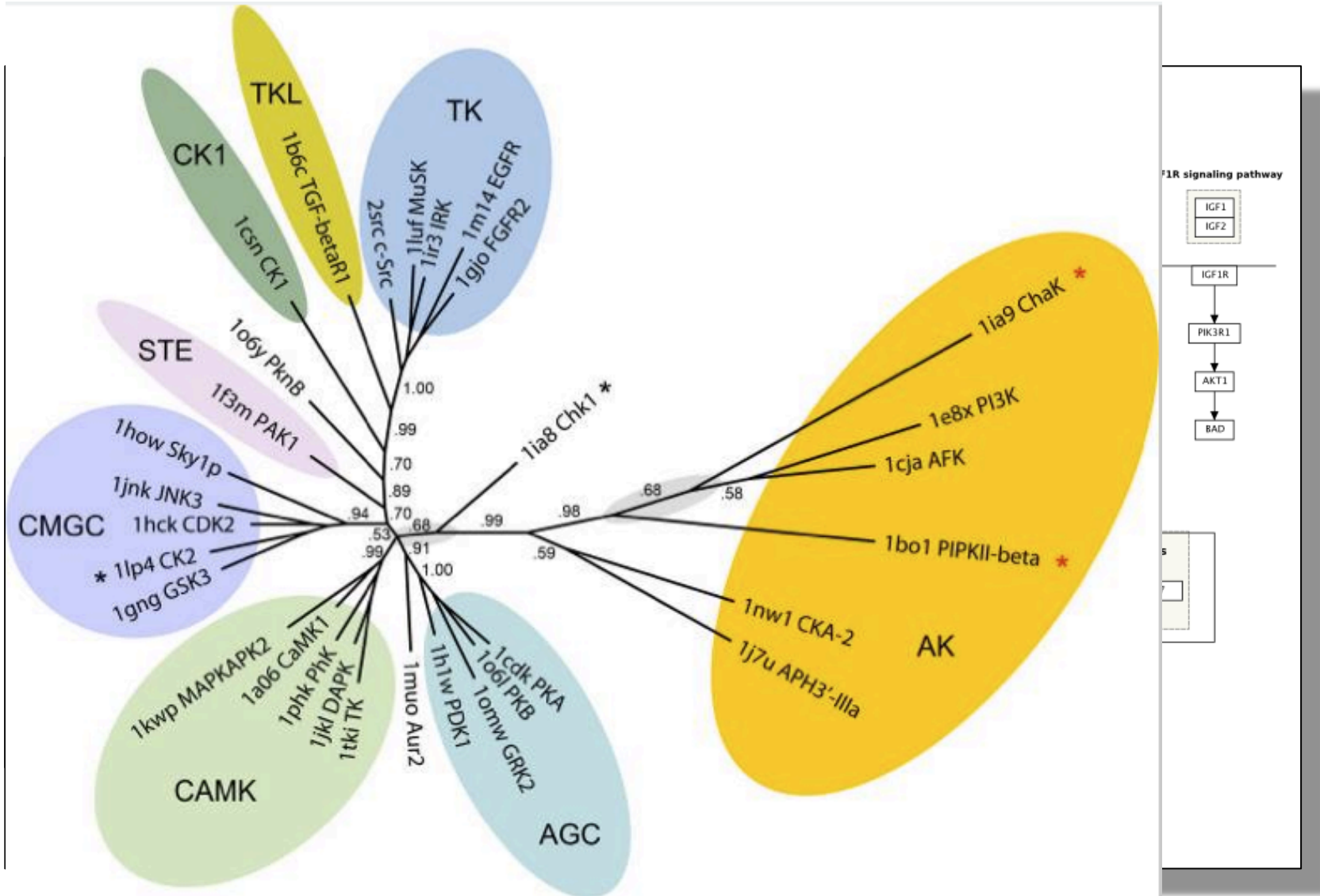
Right-click + drag to ZOOM

Middle-click + drag to PAN

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser



Biological Network Taxonomy

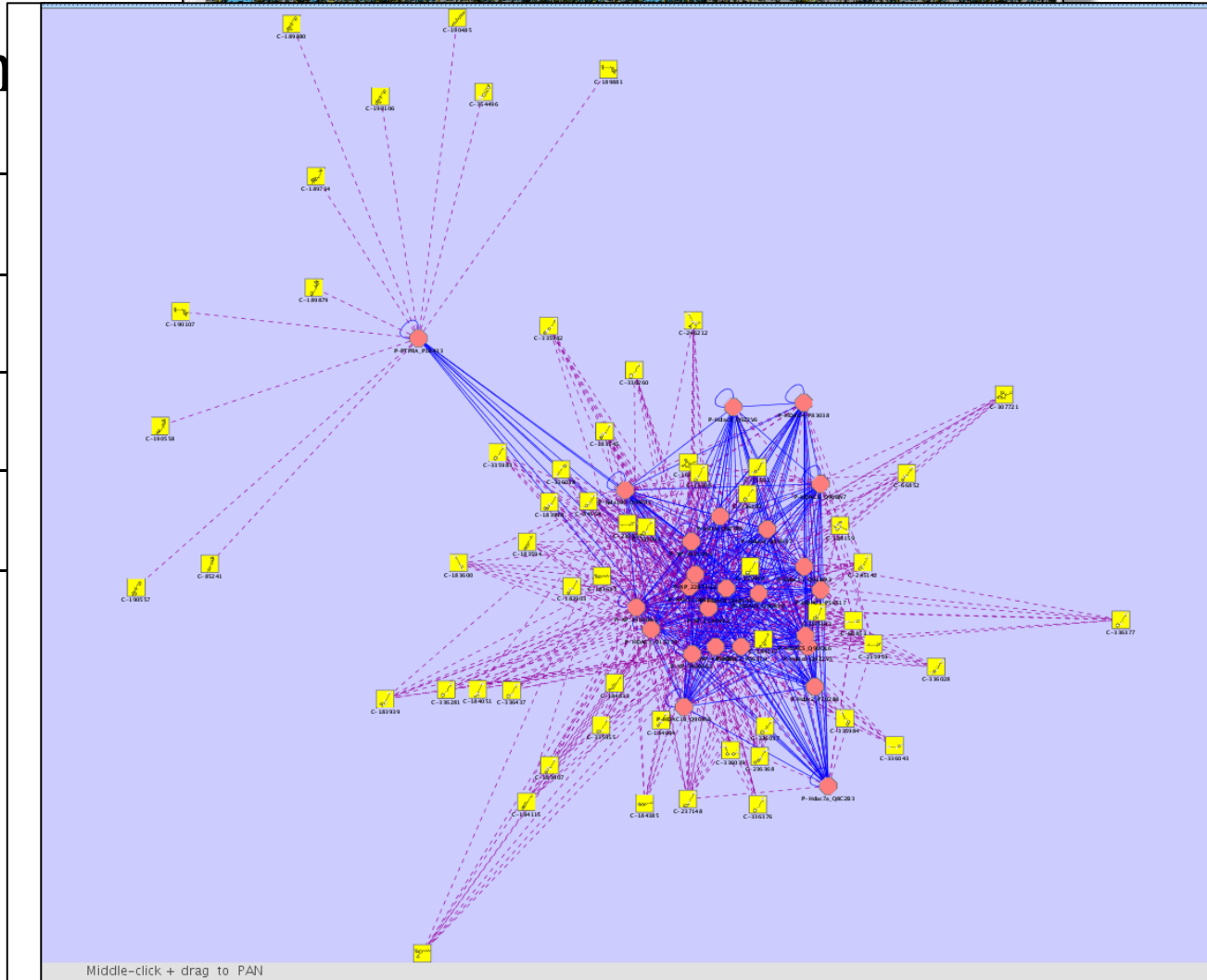




Biological Network Taxonomy



- In



Middle-click + drag to PAN

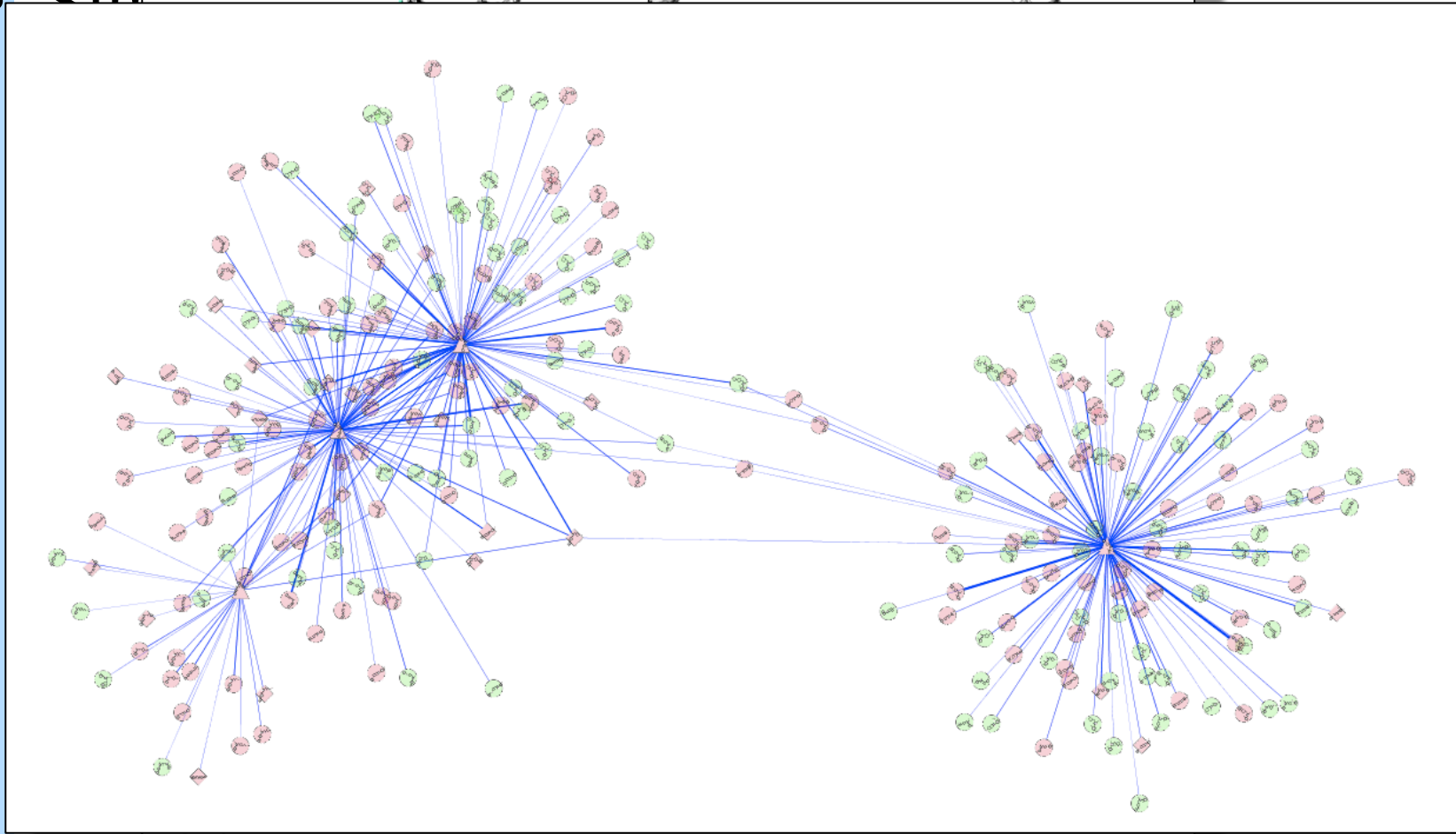
- SOC



Biological Network Taxonomy



Sim





Working with Data



- Loading Networks
- Loading and Manipulating Attributes



Loading Networks



The screenshot displays the Cytoscape Desktop interface. The main window shows a network graph with four nodes: node1, node0, node2, and node3. Node0 is centrally located and connected to all other nodes. Node1 is to the left, node2 is to the right, and node3 is at the bottom. The edges are blue lines.

The Control Panel on the left shows the 'VizMapper™' tab. Under 'Current Visual Style', 'default' is selected. The 'Visual Mapping Browser' shows 'Node Label' mapped to 'ID' using 'Passthrough Mapping'. A list of 'Unused Properties' includes Edge Color, Edge Font Face, Edge Font Size, Edge Label, Edge Label Color, Edge Label Opacity, Edge Label Width, Edge Line Style, and Edge Line Width.

The Data Panel at the bottom shows a table with one column labeled 'ID'. Below the table are tabs for 'Node Attribute Browser', 'Edge Attribute Browser', and 'Network Attribute Browser'. The 'Node Attribute Browser' tab is currently selected.

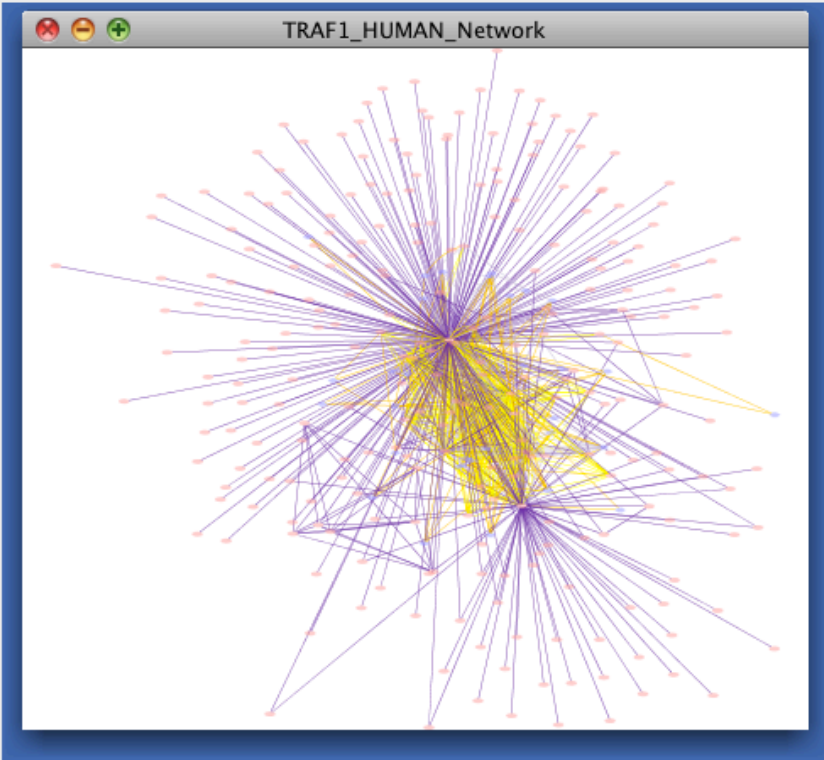
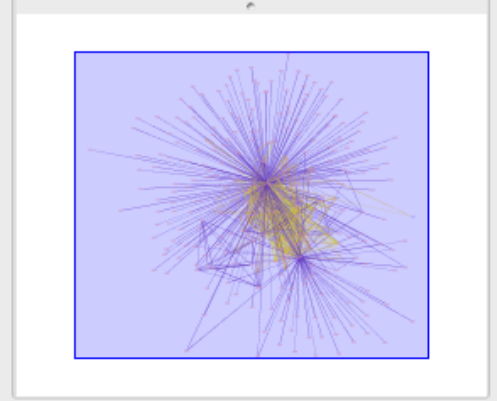
At the bottom of the window, the text reads: 'Welcome to Cytoscape 2.8.0 Right-click + drag to ZOOM Middle-click + drag to PAN'.



Control Panel

Network VizMapper™

Network	Nodes	Edges
TRAF1_HUMAN_Network	288(0)	952(0)



Results Panel

Node Details

Visual Legend [Filter Edges](#)

Edge Type

IN_SAME_COMPONENT

Edge is drawn if the first component of the second complex. This interaction sense that A COMPONENT COMPONENT_OF C implies COMPONENT_OF C. This is undirected.

COMPONENT_OF

Edge is drawn if two entities least one molecular complex necessarily mean they interact complex with n molecules create a clique composed

[View Details](#)

Tool Panel

Rotate Scale Align and Distribute

Scale:

1/8 1/4 1/2 1 2 4 8

Reset scale bar

Scale Selected Nodes Only

Data Panel

ID	Symbol



Import Annotation File

Import Attribute from Table

Data Sources

Attributes: Node Edge Network

Input File:

Advanced

Show Mapping Options Show Text File Import Options Import everything (Key is always ID) Case Sensitive

Annotation File to Attribute Mapping

Key Column in Annotation File

Primary Key: Key Attribute for Network

Alias?	Column (Attribute Name)	Data Type
<input type="checkbox"/>	Source	a_b String
<input type="checkbox"/>	Target	a_b String
<input type="checkbox"/>	Source Symbol	a_b String
<input type="checkbox"/>	Symbol	a_b String
<input type="checkbox"/>	Interaction	a_b String

Preview

Text File Left Click: Enable/Disable Column, Right Click: Edit Column

Legend: Key Alias

Network.txt

<input checked="" type="checkbox"/> Source	<input checked="" type="checkbox"/> Target	<input checked="" type="checkbox"/> Source Symbol	<input checked="" type="checkbox"/> Symbol	<input checked="" type="checkbox"/> Interaction
node0	node1	Node 0	Node 1	inhibits
node0	node3	Node 0	Node 3	activates
node0	node2	Node 0	Node 2	interacts
node2	node3	Node 2	Node 3	interacts

Key Attributes

node0
node1
node2
node3

Key Matched: 4 First 100 entries are loaded for preview. File Size: 213 Bytes



Cytoscape Desktop (Session Name: Network.cys)

Control Panel

Network	Nodes	Edges
Network.txt	4(4)	4(4)

Network.txt

```

graph TD
    node2 --- node0
    node2 --- node3
    node0 --- node1
    node3 --- node0
  
```

Data Panel

ID	Symbol
node2	Node 2
node0	Node 0
node1	Node 1
node3	Node 3

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

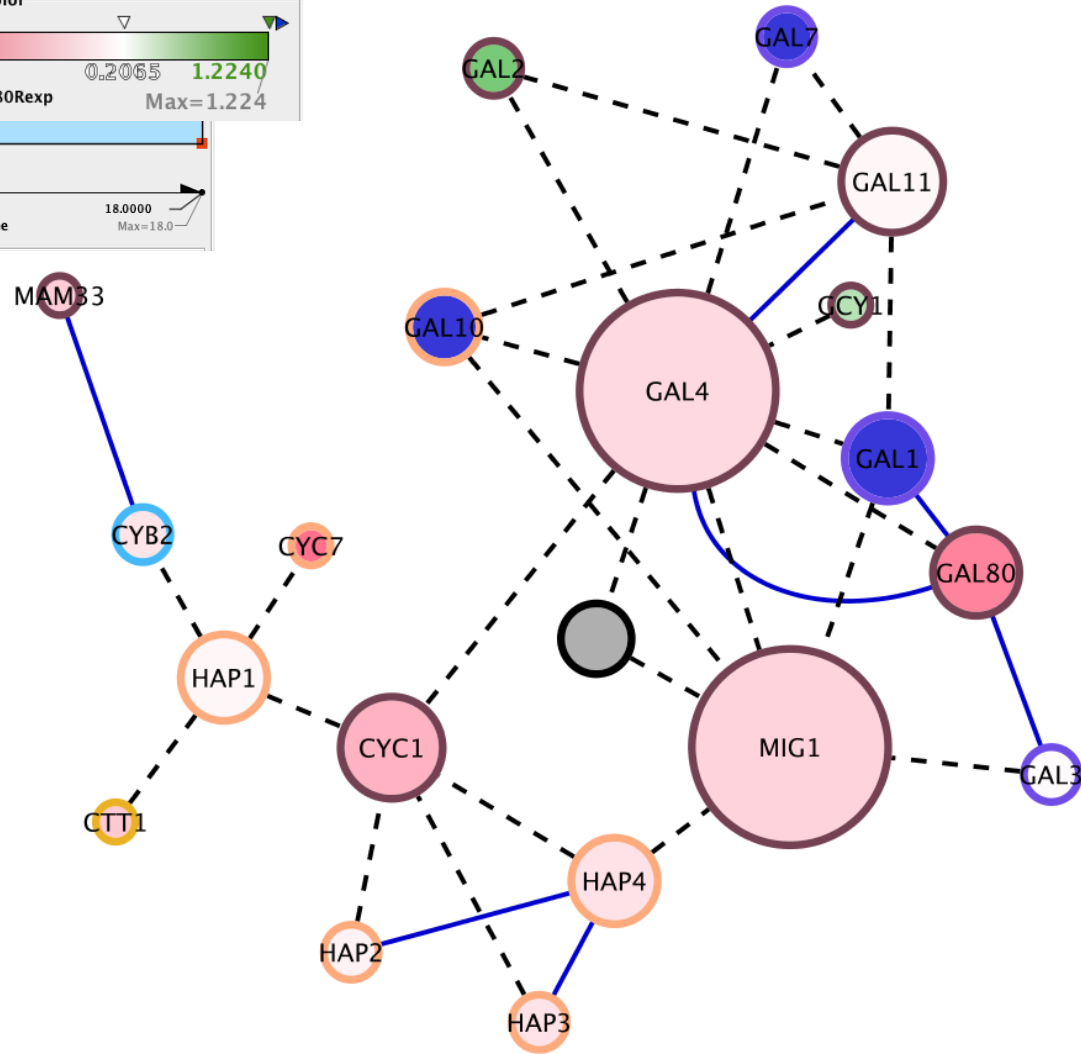
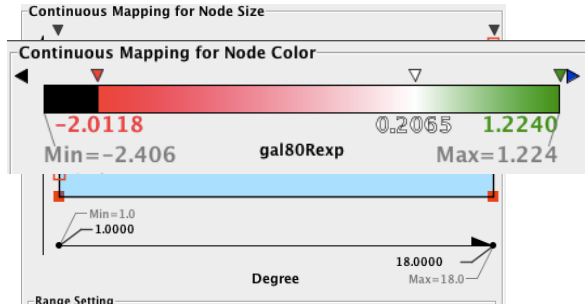
Welcome to Cytoscape 2.7.0 Right-click + drag to ZOOM Middle-click + drag to PAN



Visualizing data



- Data mapping
- Layouts
- Animation





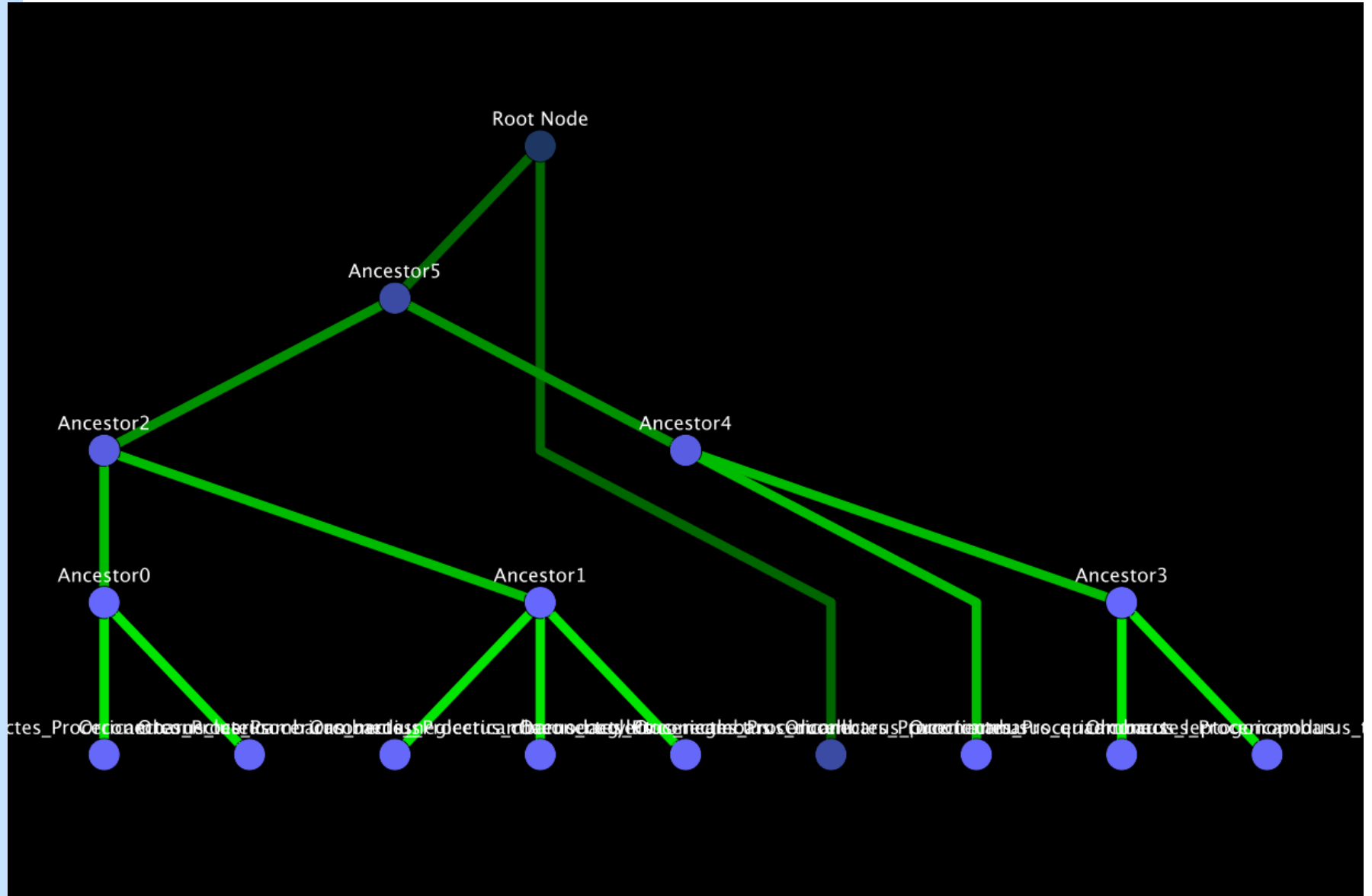
Data mapping

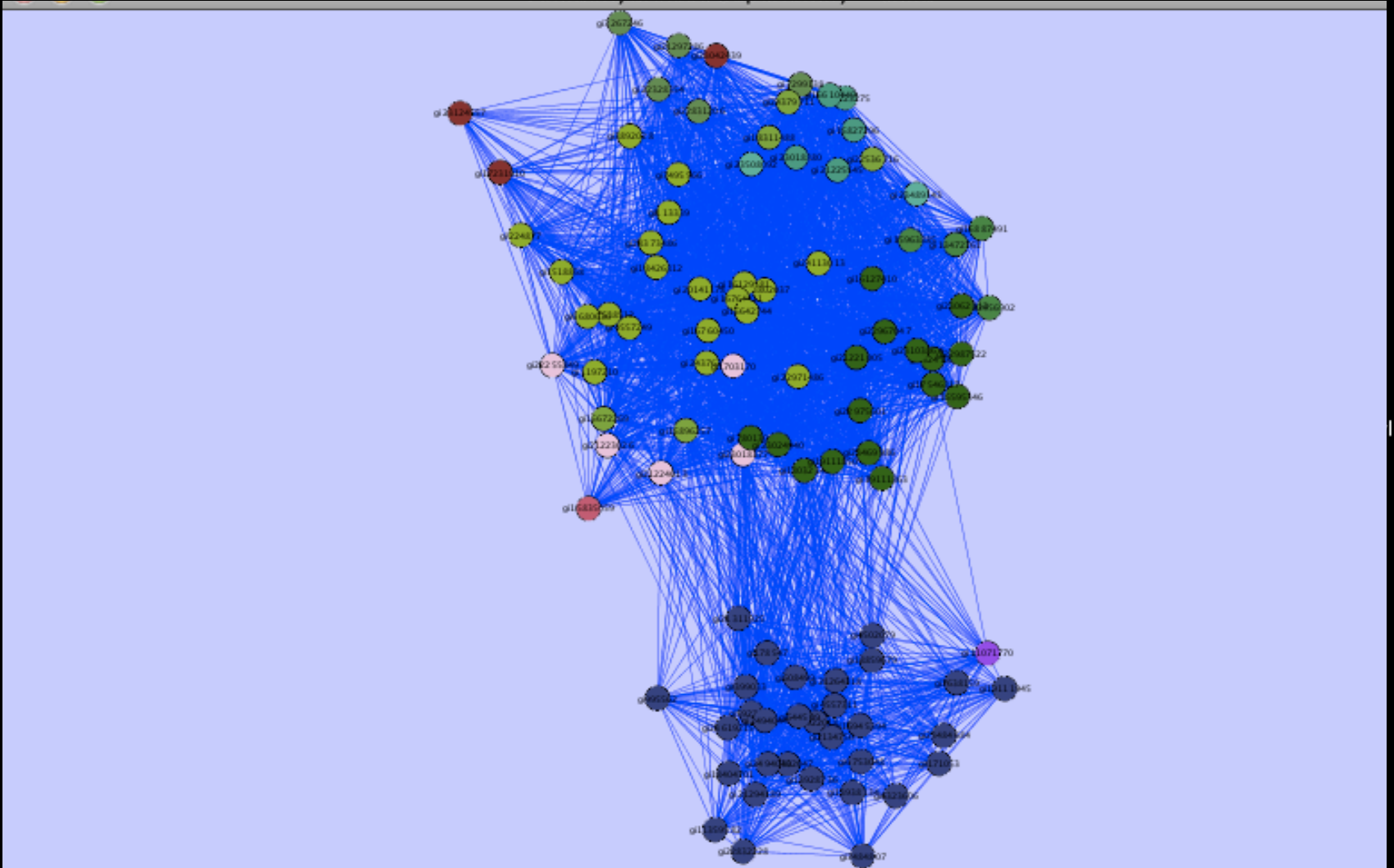


- Avoid cluttering your visualization with too much data
 - Map the data you are specifically interested in to call out meaningful differences
 - Mapping too much data to visual attributes may just confuse the viewer
 - Can always create multiple networks and map different values



Layouts





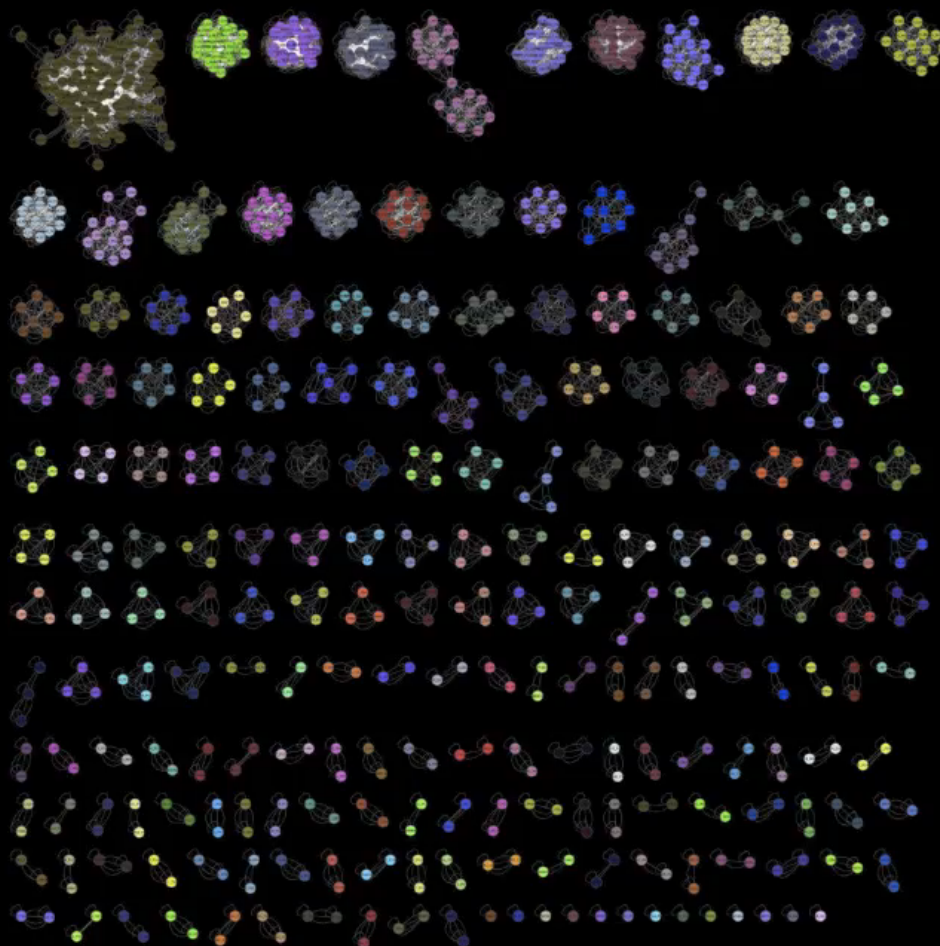
lus



Layouts



- Use layouts to convey the relationships between the nodes
- Layout algorithms may need to be “tuned” to fit your network
 - Layouts → Settings... menu
- Lots of parameters to change layout algorithm behavior
- Can also consider laying out portions of your network





Tips & Tricks



- “Root graph”
 - “There is one graph to rule them all....”
 - The networks in Cytoscape are all “views” on a single graph.
 - Changing the attribute for a node in one network *will* also change that attribute for a node with the same ID in all other loaded networks
 - There is no way to “copy” a node and keep the same ID
 - Make a copy of the session



Tips & Tricks



- Network views
 - When you open a large network, you will not get a view by default
 - To improve interactive performance, Cytoscape has the concept of “Levels of Detail”
 - Some visual attributes will only be apparent when you zoom in
 - The level of detail for various attributes can be changed in the preferences
 - To see what things will look like at full detail:
 - View → Show Graphics Details



- Sessions
 - Sessions save pretty much everything:
 - Networks
 - Properties
 - Visual styles
 - Screen sizes
 - Saving a session on a large screen may require some resizing when opened on your laptop



Tips & Tricks



- Logging
 - By default, Cytoscape writes it's logs to the Error Dialog: Help→Error Dialog
 - Can change a preference to write it to the console
 - Edit→Preferences→Properties...
 - Set `logger.console` to true
 - Don't forget to save your preferences
 - Restart Cytoscape
 - (can also turn on debugging: `cytoscape.debug`, but I don't recommend it)



Tips & Tricks



- Memory
 - Cytoscape uses lots of it
 - Doesn't like to let go of it
 - An occasional restart when working with large networks is a good thing
 - Destroy views when you don't need them
 - Java doesn't give us a good way to get the memory right at start time
 - Cytoscape 2.7 does a much better job at “guessing” good default memory sizes than previous versions



Tips & Tricks



- `.cytoscape` directory
 - Your defaults and any plugins downloaded from the plugin manager will go here
 - Sometimes, if things get really messed up, deleting (or renaming) this directory can give you a “clean slate”
- Plugin manager
 - “Outdated” doesn’t necessarily mean “won’t work”
 - Plugin authors don’t always update their plugins immediately after new releases
 - Click on “Show outdated plugins” to see the entire list of plugins.



Questions?



- Thanks for your attention!
- Fire up Cytoscape and follow the [Introduction_to_Cytoscape.pdf](#) tutorial

