

Office of Portfolio Analysis

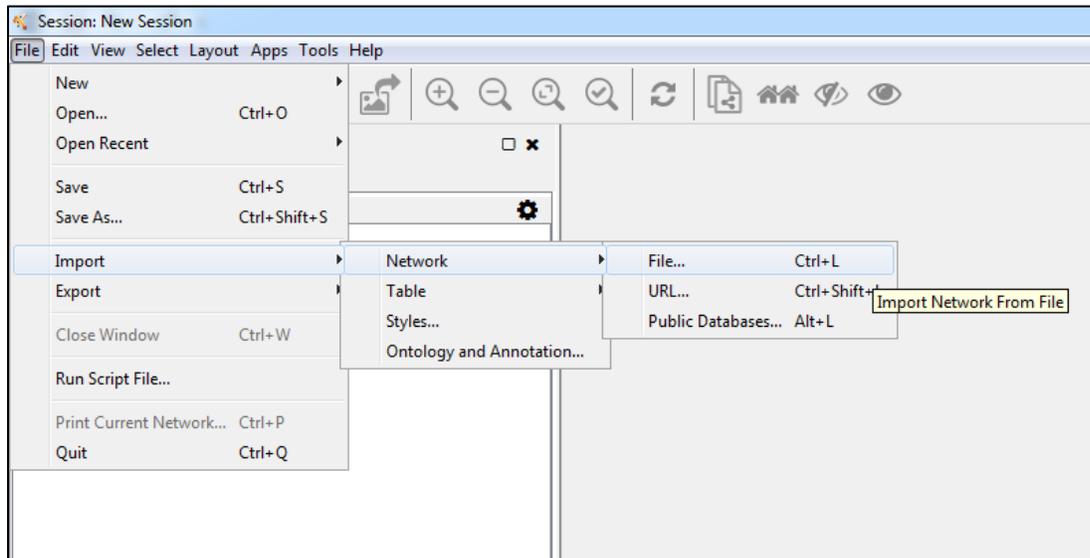
NETWORK ANALYSIS CLASS – CYTOSCAPE USER GUIDE-

OCTOBER 2017 V1.0

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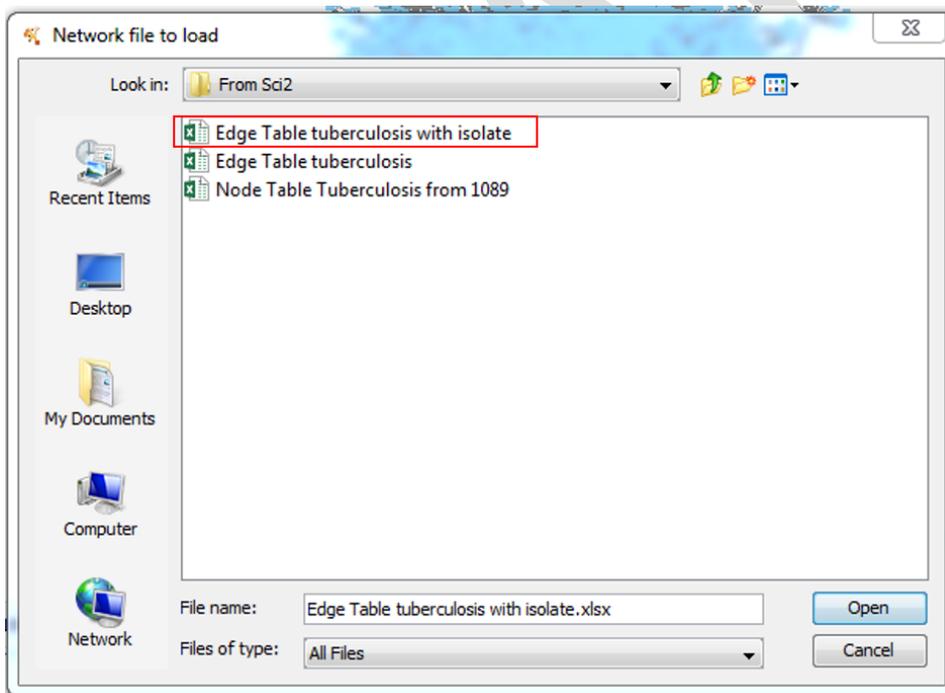
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Importing a co-author network data into Cytoscape



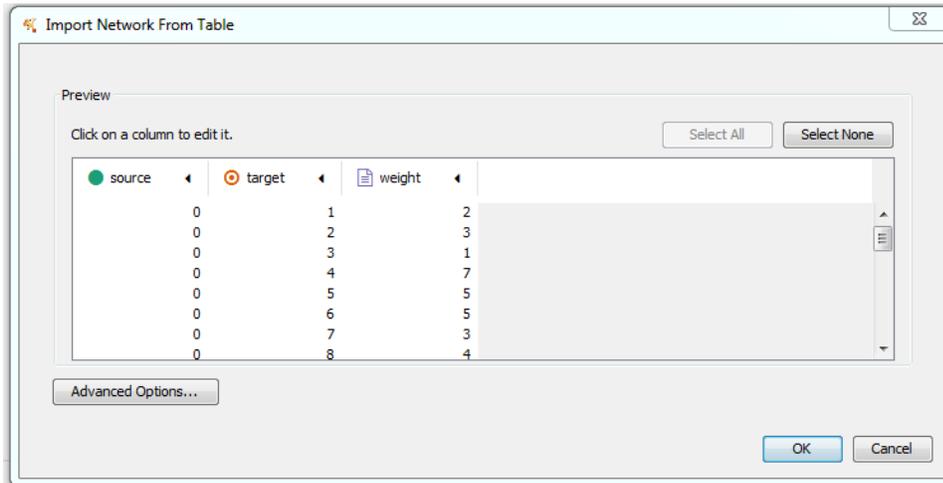
File → Import → Network → File.

Select the edges file with the isolated nodes added.

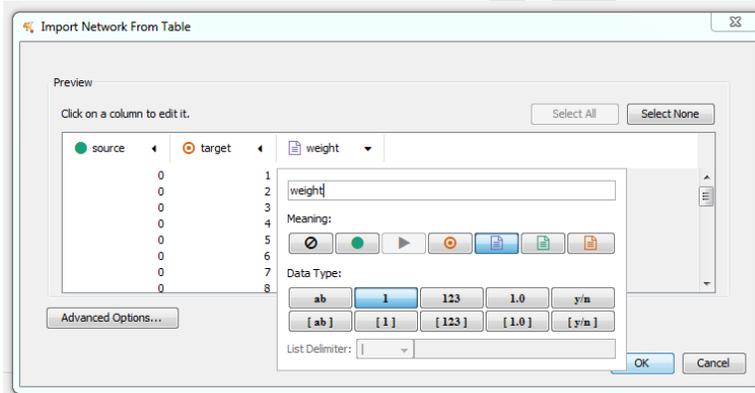


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A pop up window will prompt you to set up which column contains the source and target edges, as well as the edges attributes.

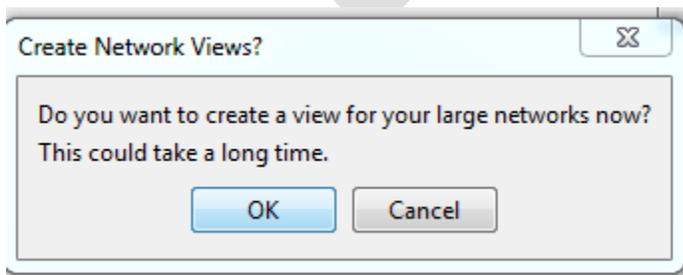


Because in co-author network edges don't have a direction, source and target are treated interchangeably. If any change needs to be done to the columns, right click on the column header and several options will appear:



Hover the mouse over each of the icons to learn about the different options.

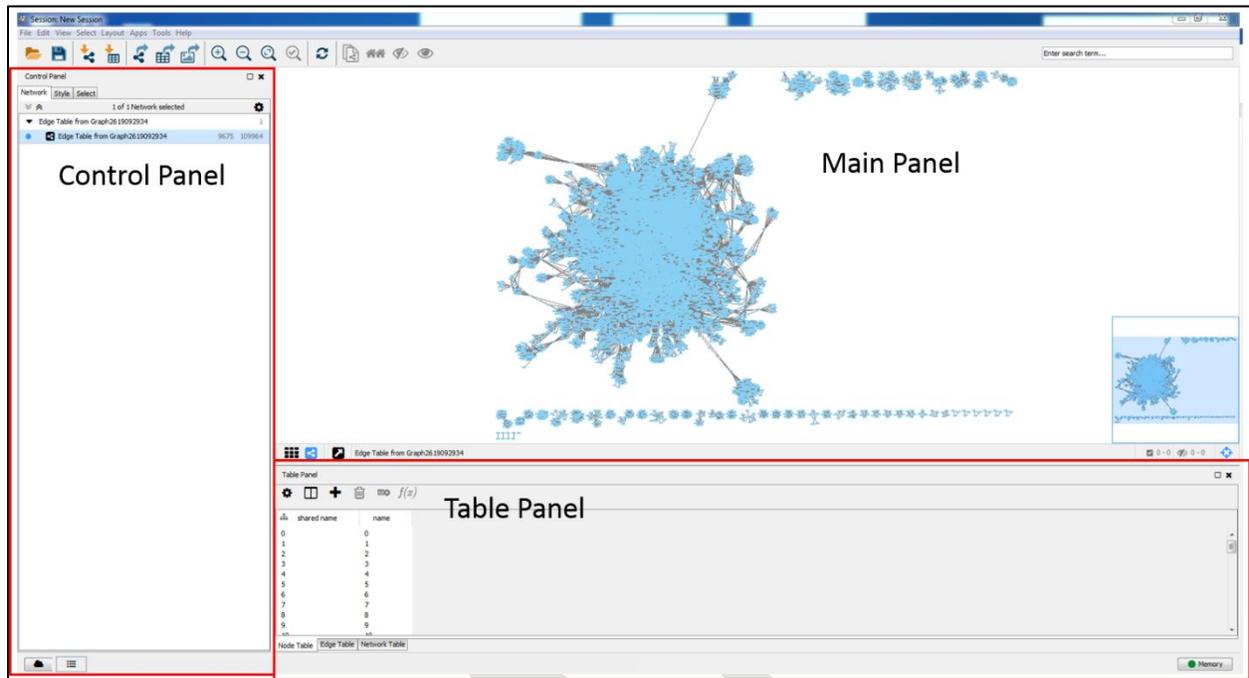
If a network is big, Cytoscape will ask you if you want to create the network visualization before moving forward.



If you select OK a network visualization will appear in the main panel.

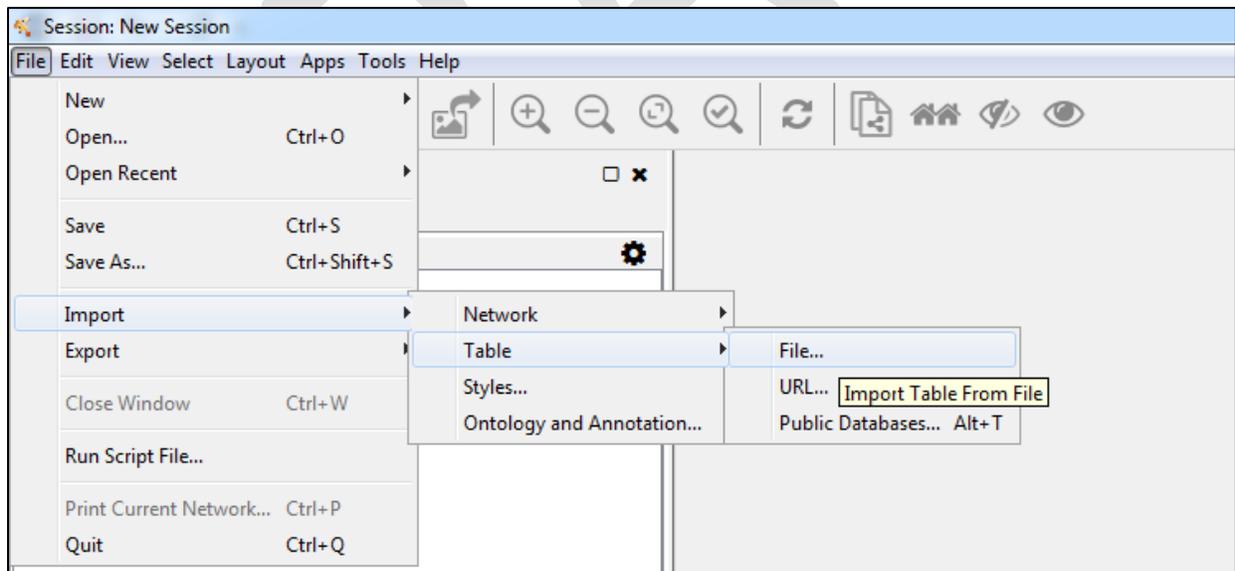
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Cytoscape panels



Importing nodes attributes

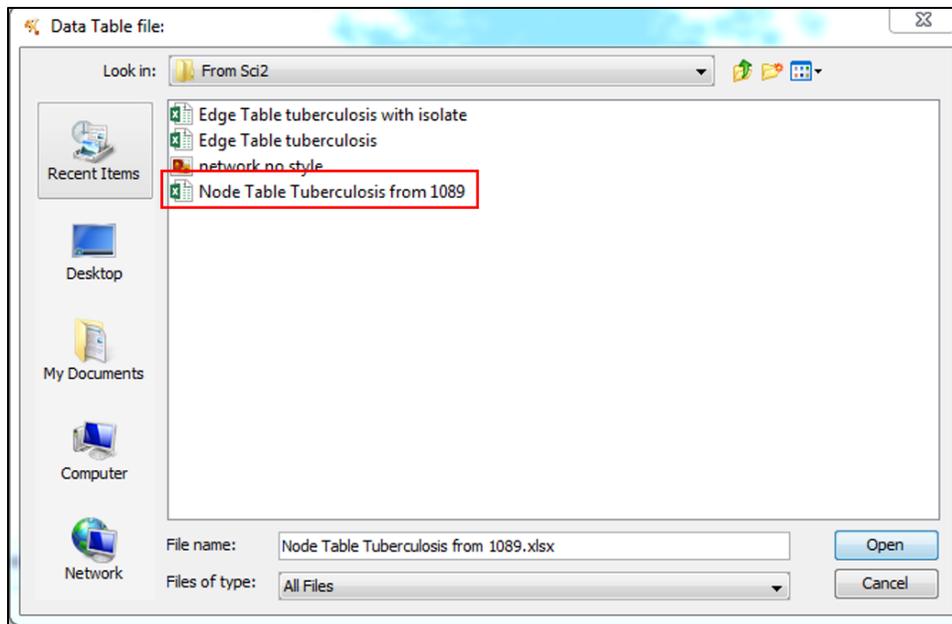
Before doing any changes to the network view, we will import the Nodes' file to match the authors' names to the Sci2 IDs (Sci2 IDs are the Key to link edges and nodes datasets).



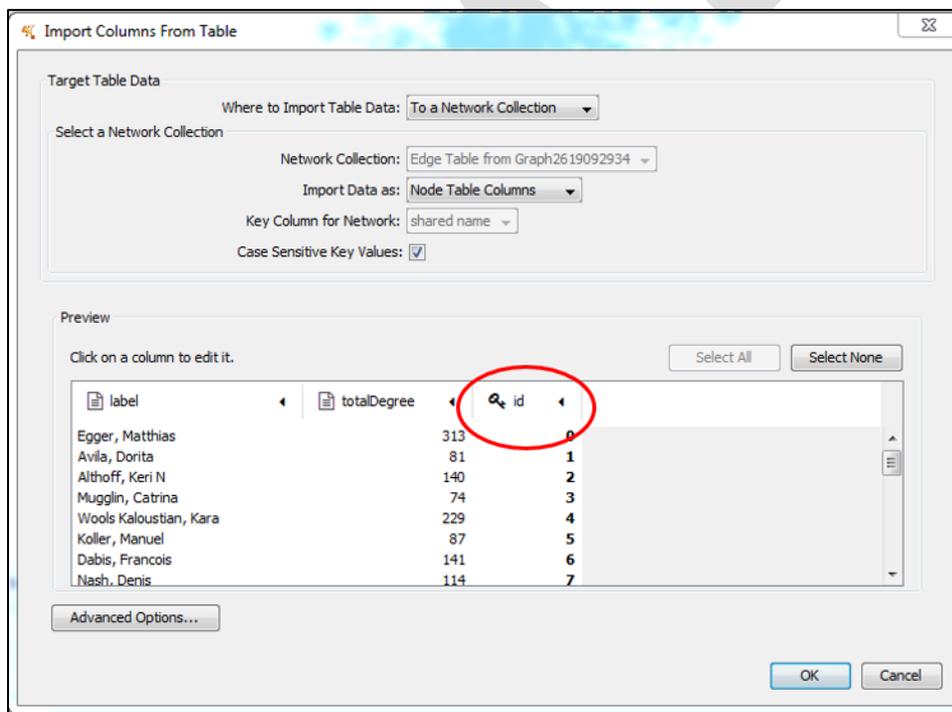
File → Import → Table → File.

Here we will select the nodes file.

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After opening the selected file the following window will appear:



Here the most important step is to set the "ID" column as the key to link the edges and nodes files. Label and total degree should be set as nodes' attributes.

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So now we have our network with the following information:

For the nodes:

shared name	name	label	totalDegree
0	0	Egger, M...	313
1	1	Avila, Do...	81
2	2	Althoff, K...	140
3	3	Mugglin, ...	74
4	4	Wools Kal...	229
5	5	Koller, M...	87
6	6	Dabis, Fr...	141
7	7	Nash, Denis	114
8	8	Gsponer, T	93
9	9	Sungkan...	74
10	10	Megowan	147

For the edges:

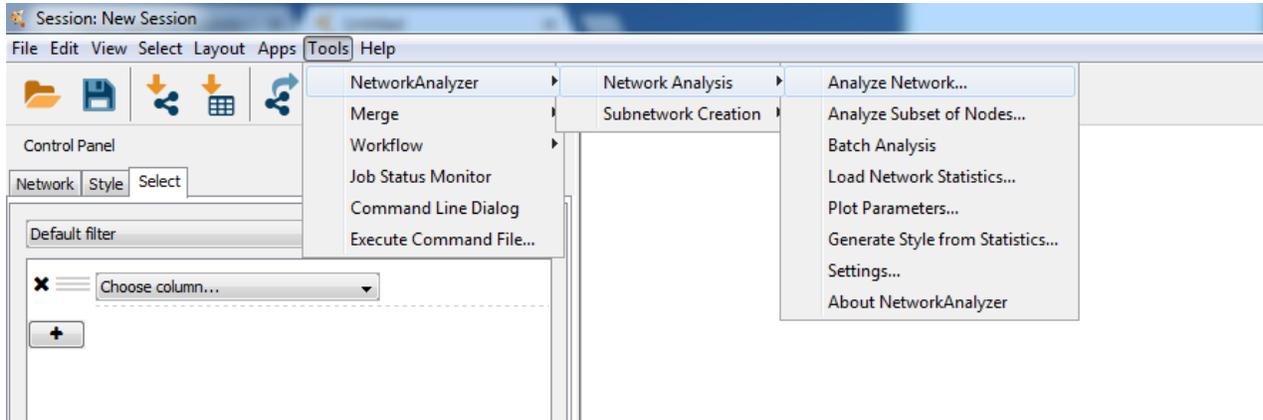
shared name	shared interaction	name	interaction	weight
0 (interacts with) 1	interacts with	0 (interact...	interacts with	2
0 (interacts with) 2	interacts with	0 (interact...	interacts with	3
0 (interacts with) 3	interacts with	0 (interact...	interacts with	1
0 (interacts with) 4	interacts with	0 (interact...	interacts with	7
0 (interacts with) 5	interacts with	0 (interact...	interacts with	5
0 (interacts with) 6	interacts with	0 (interact...	interacts with	5
0 (interacts with) 7	interacts with	0 (interact...	interacts with	3
0 (interacts with) 8	interacts with	0 (interact...	interacts with	4
0 (interacts with) 9	interacts with	0 (interact...	interacts with	1
0 (interacts with) 10	interacts with	0 (interact...	interacts with	4
0 (interacts with) 11	interacts with	0 (interact...	interacts with	2

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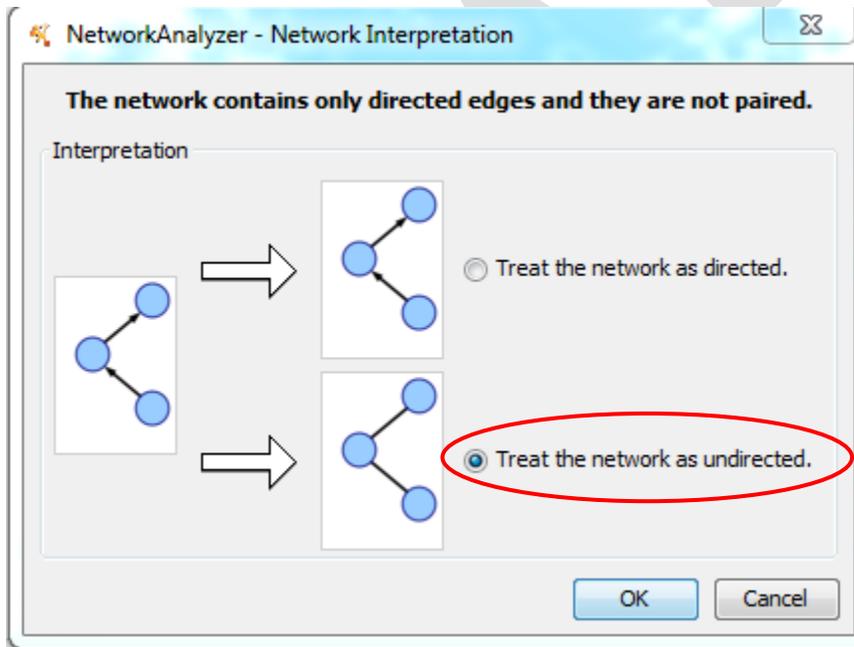
Running Cytoscape stats

Cytoscape can run the network stats at the network as well as the individual nodes and edges' level.

Tools → Network Analyzer → Network Analysis → Analyze Network

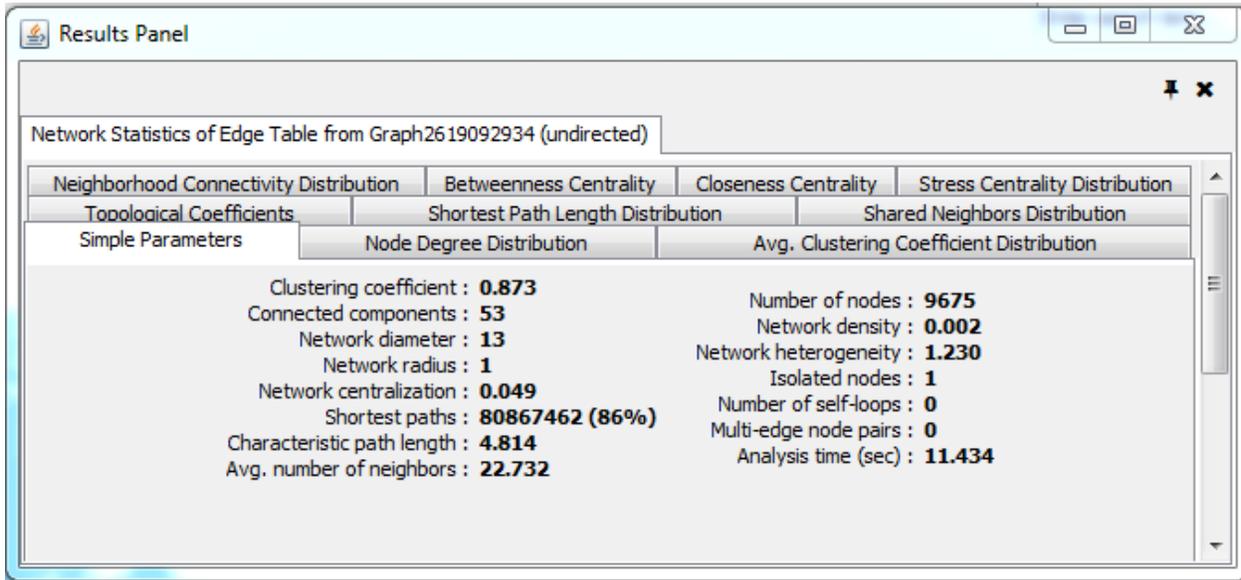


A window will ask you if the network you uploaded is undirected or not. Because we are building a co-author network, we will select “treat the network as undirected”



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The results panel will now pop up, showing the network stats.



Results Panel

Network Statistics of Edge Table from Graph2619092934 (undirected)

Neighborhood Connectivity Distribution	Betweenness Centrality	Closeness Centrality	Stress Centrality Distribution
Topological Coefficients	Shortest Path Length Distribution	Shared Neighbors Distribution	
Simple Parameters	Node Degree Distribution	Avg. Clustering Coefficient Distribution	

Clustering coefficient : **0.873**
Connected components : **53**
Network diameter : **13**
Network radius : **1**
Network centralization : **0.049**
Shortest paths : **80867462 (86%)**
Characteristic path length : **4.814**
Avg. number of neighbors : **22.732**

Number of nodes : **9675**
Network density : **0.002**
Network heterogeneity : **1.230**
Isolated nodes : **1**
Number of self-loops : **0**
Multi-edge node pairs : **0**
Analysis time (sec) : **11.434**

But at the table panel, we can see that individual stats are now available for nodes and edges as well.

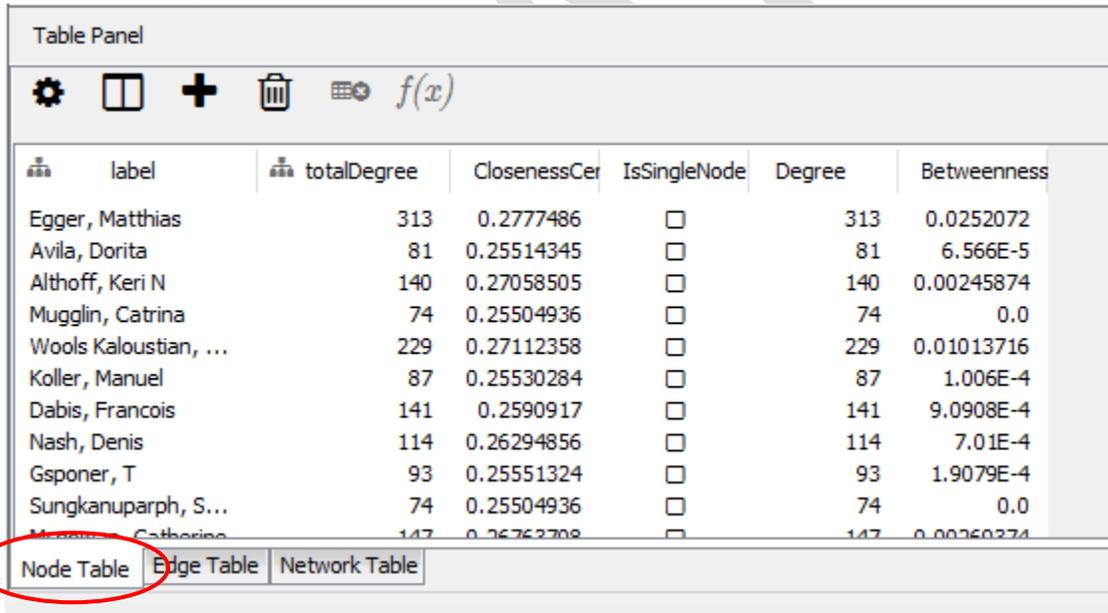


Table Panel

⚙️ 📄 + 🗑️ 📊 $f(x)$

label	totalDegree	ClosenessCer	IsSingleNode	Degree	Betweenness
Egger, Matthias	313	0.2777486	<input type="checkbox"/>	313	0.0252072
Avila, Dorita	81	0.25514345	<input type="checkbox"/>	81	6.566E-5
Althoff, Keri N	140	0.27058505	<input type="checkbox"/>	140	0.00245874
Mugglin, Catrina	74	0.25504936	<input type="checkbox"/>	74	0.0
Wools Kaloustian, ...	229	0.27112358	<input type="checkbox"/>	229	0.01013716
Koller, Manuel	87	0.25530284	<input type="checkbox"/>	87	1.006E-4
Dabis, Francois	141	0.2590917	<input type="checkbox"/>	141	9.0908E-4
Nash, Denis	114	0.26294856	<input type="checkbox"/>	114	7.01E-4
Gsponer, T	93	0.25551324	<input type="checkbox"/>	93	1.9079E-4
Sungkanuparph, S...	74	0.25504936	<input type="checkbox"/>	74	0.0
M...	147	0.26762708	<input type="checkbox"/>	147	0.00260274

Node Table Edge Table Network Table

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Table Panel






 $f(x)$

 shared name	 shared id	name	interaction	 weight	EdgeBetweenness
0 (interacts with) 1	interac...	0 (interacts with) 1	interacts...	2	1355.05246851
0 (interacts with) 2	interac...	0 (interacts with) 2	interacts...	3	8141.86575327
0 (interacts with) 3	interac...	0 (interacts with) 3	interacts...	1	1371.62388795
0 (interacts with) 4	interac...	0 (interacts with) 4	interacts...	7	21782.66790649
0 (interacts with) 5	interac...	0 (interacts with) 5	interacts...	5	1340.15411876
0 (interacts with) 6	interac...	0 (interacts with) 6	interacts...	5	2623.71686236
0 (interacts with) 7	interac...	0 (interacts with) 7	interacts...	3	1930.40583715
0 (interacts with) 8	interac...	0 (interacts with) 8	interacts...	4	1324.79581418
0 (interacts with) 9	interac...	0 (interacts with) 9	interacts...	1	1371.62388795
0 (interacts with) 10	interac...	0 (interacts with) 10	interacts...	4	7493.7983363
0 (interacts with) 11	interac...	0 (interacts with) 11	interacts...	2	1320.66128240

Node Table
 Edge Table
 Network Table

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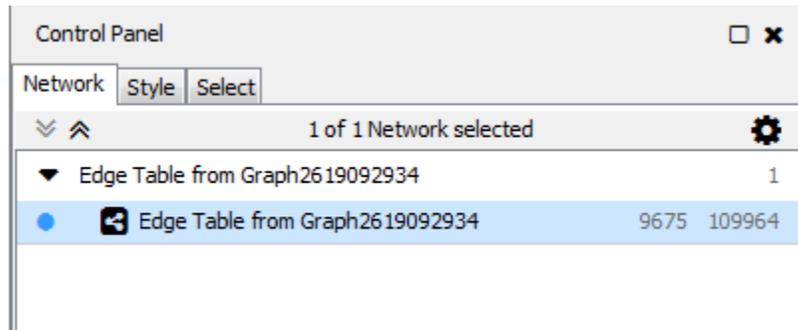
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Control Panel

The control panel has 3 tabs

Network tab

Here you can see which network you are working with as well as move from one network to another in case you have more than one network.

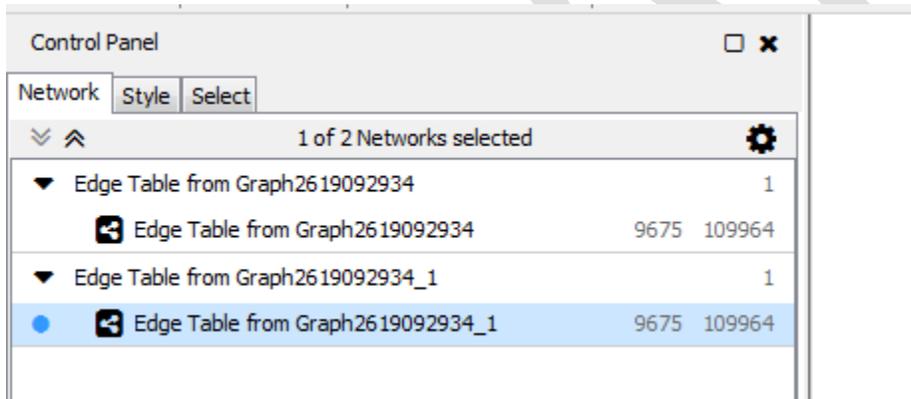


Cloning a network

To duplicate a network:

File → New → Network → Clone current network

Now you should be able to see this new network at the network's tab

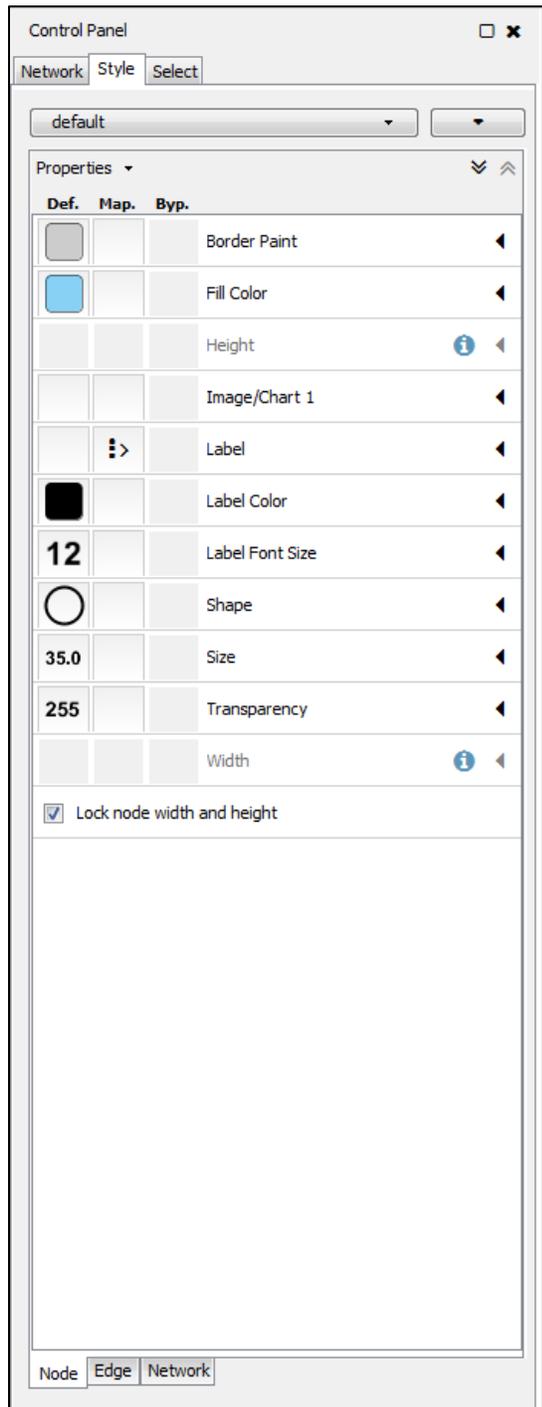


To rename the networks, right click on the network and select Rename network from the dropdown box.

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Now let's change some of the nodes and edges properties using the stats we have.

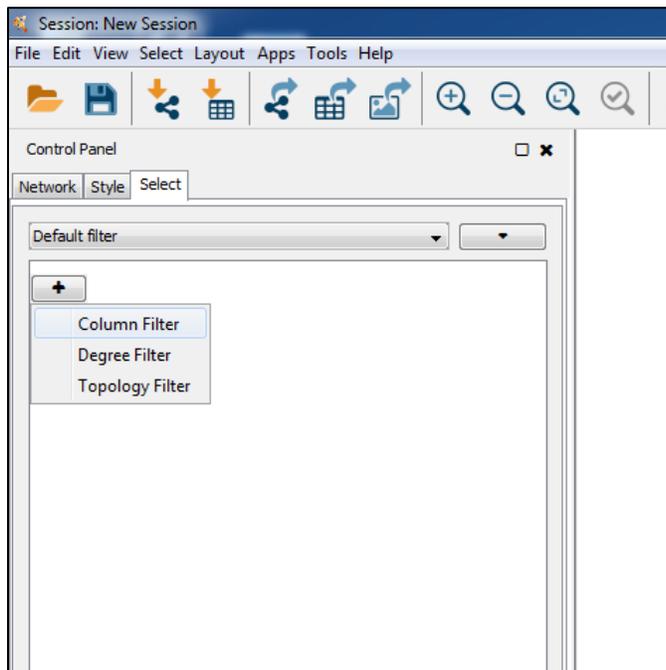
Style Tab



Each node/edge property has 3 options for changes:

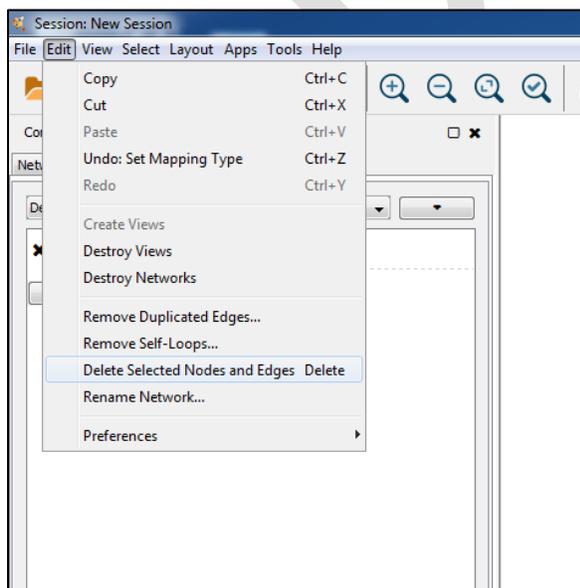
- *Def*: changes made using this box will target all nodes or edges in the network
- *Map*: changes using this option will target specific nodes/edges. Here you can use the nodes/edges stats that resulted from running the Tools -> Network Analyzer function (degree, betweenness, etc) to change the nodes properties. For example, you can size and color nodes based on degree centrality.
- *Byp (Bypass)*: this option allows you to change the attributes for only nodes/edges that are selected.

Select tab



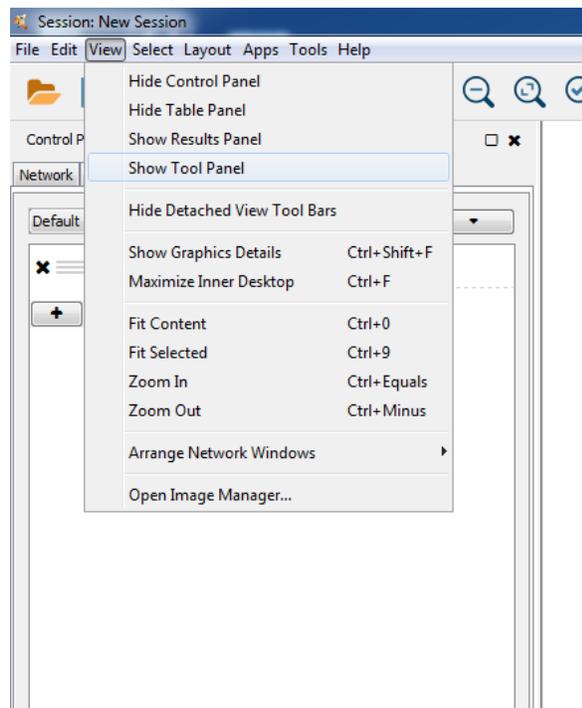
Here you will be able to select nodes and/or edges based on their properties. For example you can select nodes with degree between 50 and 500.

Main menu/Edit:



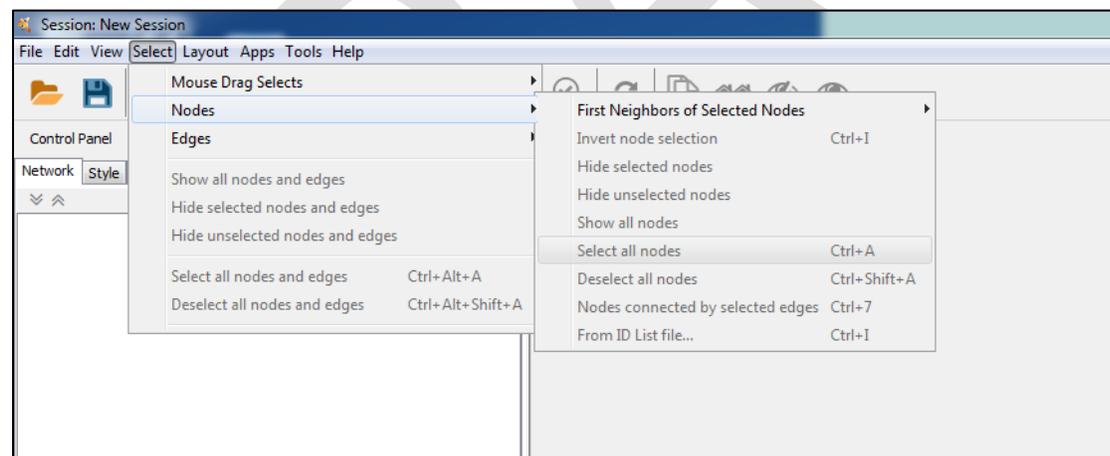
Here you can do things like removing selected edges and/or nodes.

Main Menu/View



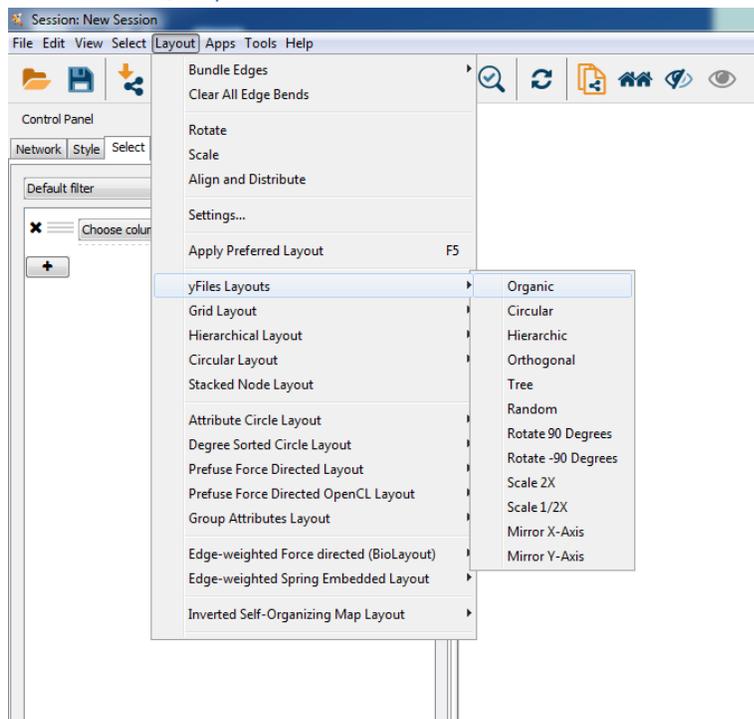
Here you can choose which panels you want to see or hide.

Main Menu/Select



Here you can select all nodes or edges, invert your selection of nodes/edges, and select a list of nodes from a list (nodes names should match exactly the name of the node in the network. Specially important when wanting to highlight PIs in a co-author network. The PI name might not be exactly the same as in the publication' author list).

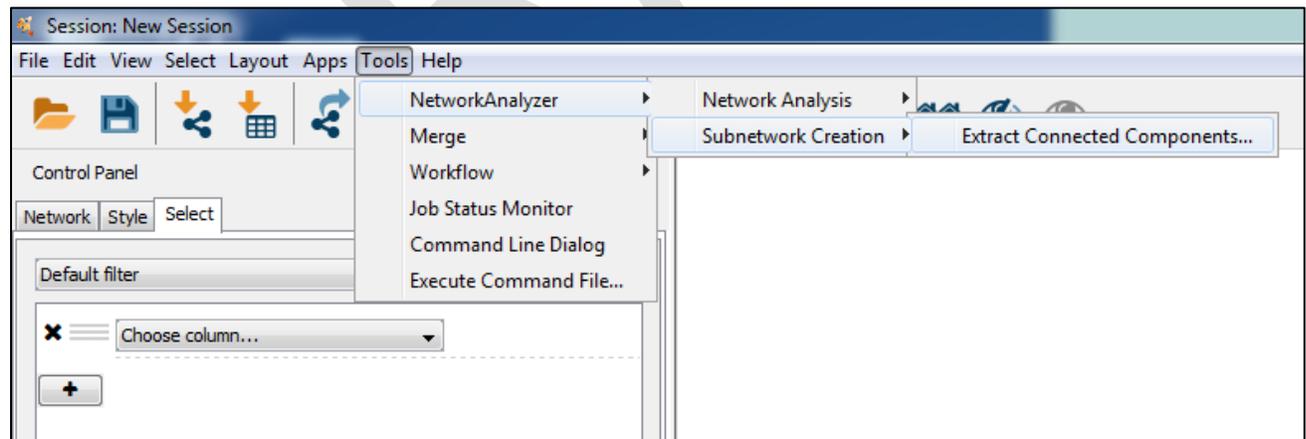
Main Menu/Layout



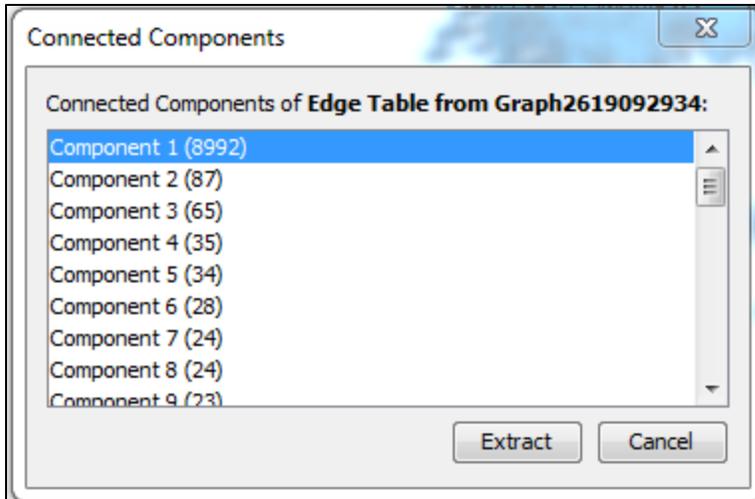
For co-author networks there are many possible layouts. The yFiles → Organic usually works well.

Main Menu/Tools

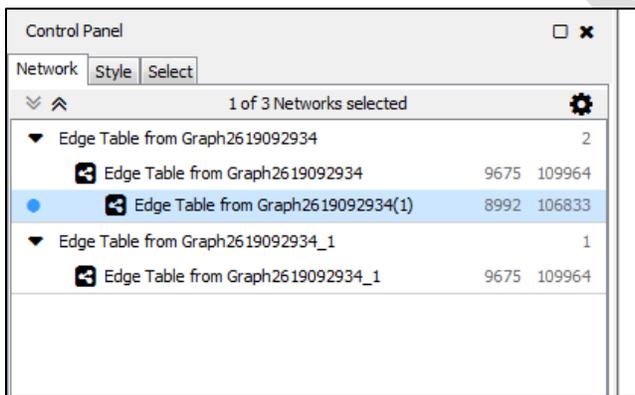
To extract the network components go to Tools → Network Analyzer → Subnetwork creation → Extract connected components



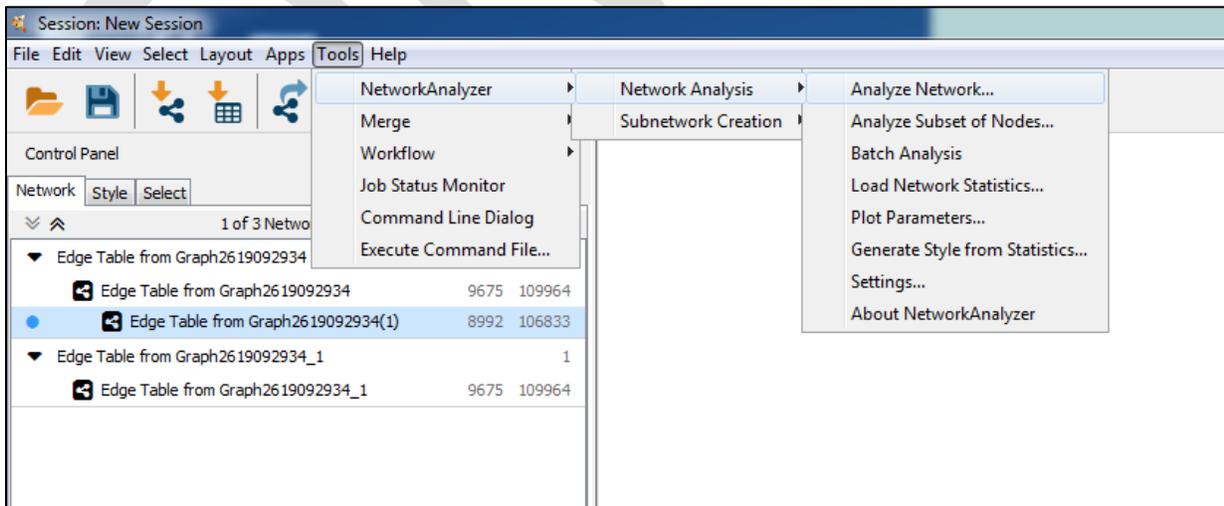
A window will pop up showing the network connected components. Here you can choose to extract one or more components which will then be able to be treated separately from the full network.



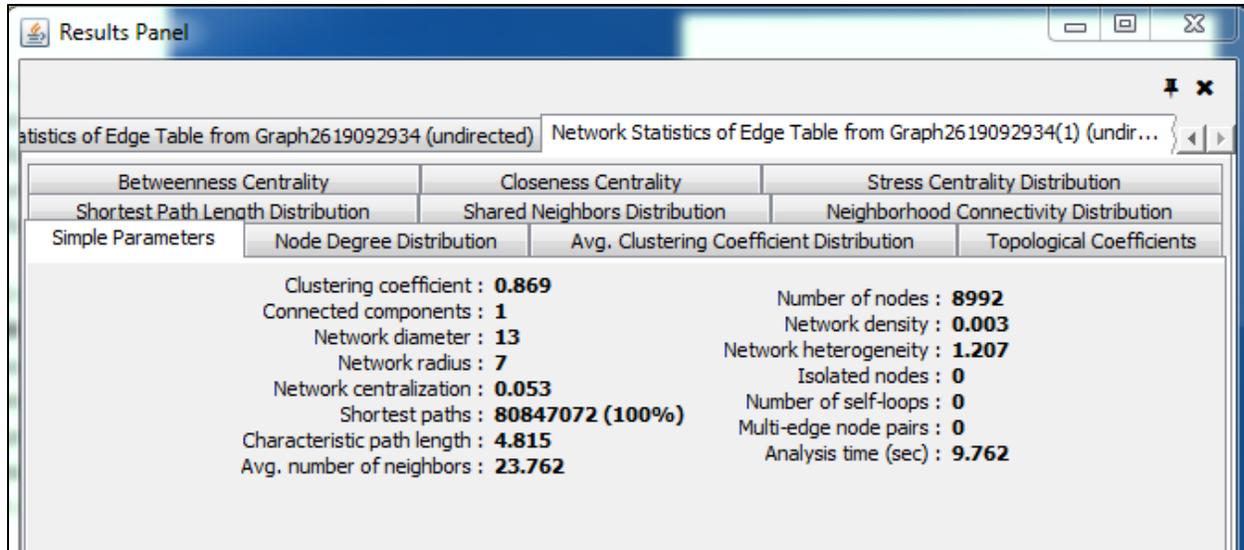
This new network will show up listed in the Network tab, below the network from where it came from



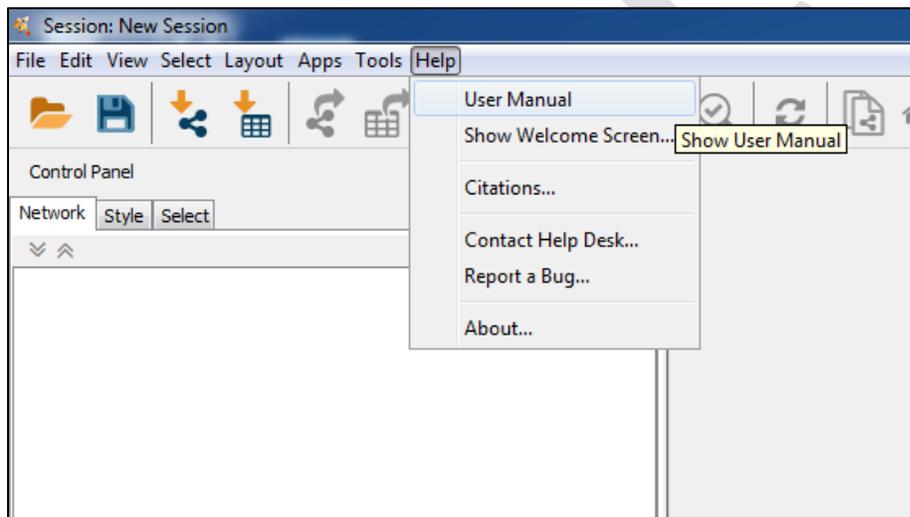
You can run the Network analyzer to obtain the stats for this specific component alone



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Main Menu/Help



Cytoscape user manual is available.

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Saving in Cytoscape

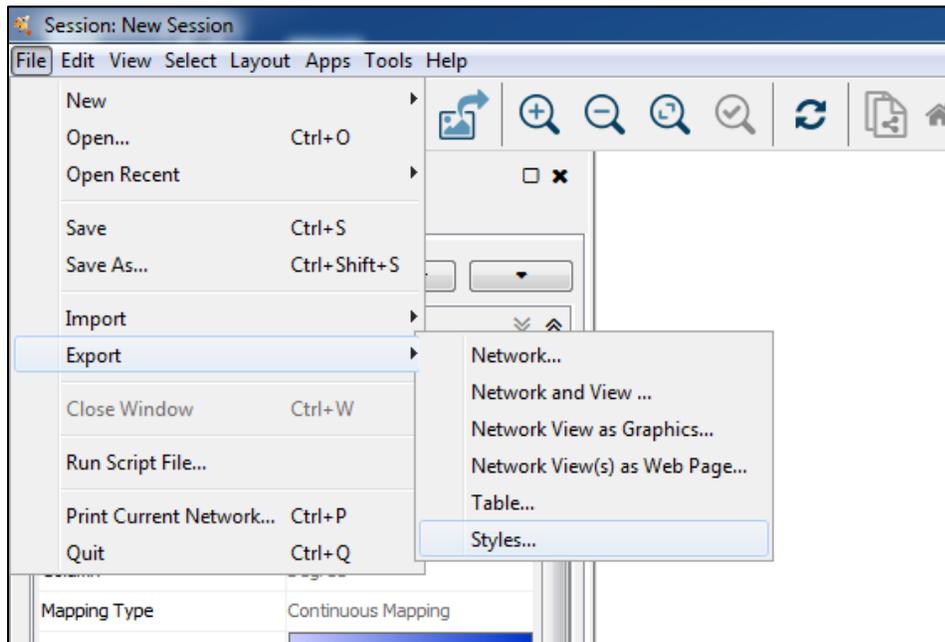
Saving a Cytoscape file

File → Save as. The default extension for Cytoscape files is .cys

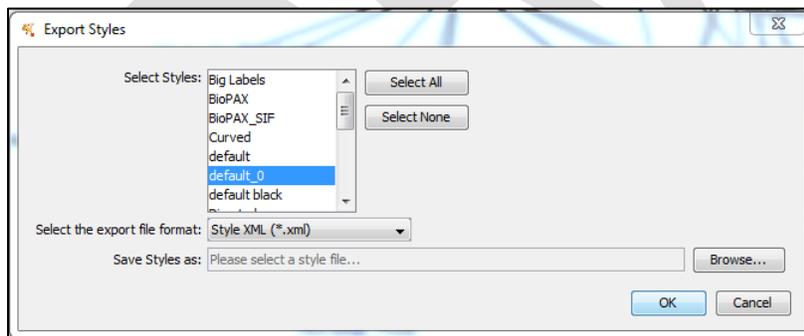
Saving a graph

File → Export → Network View as Graphics

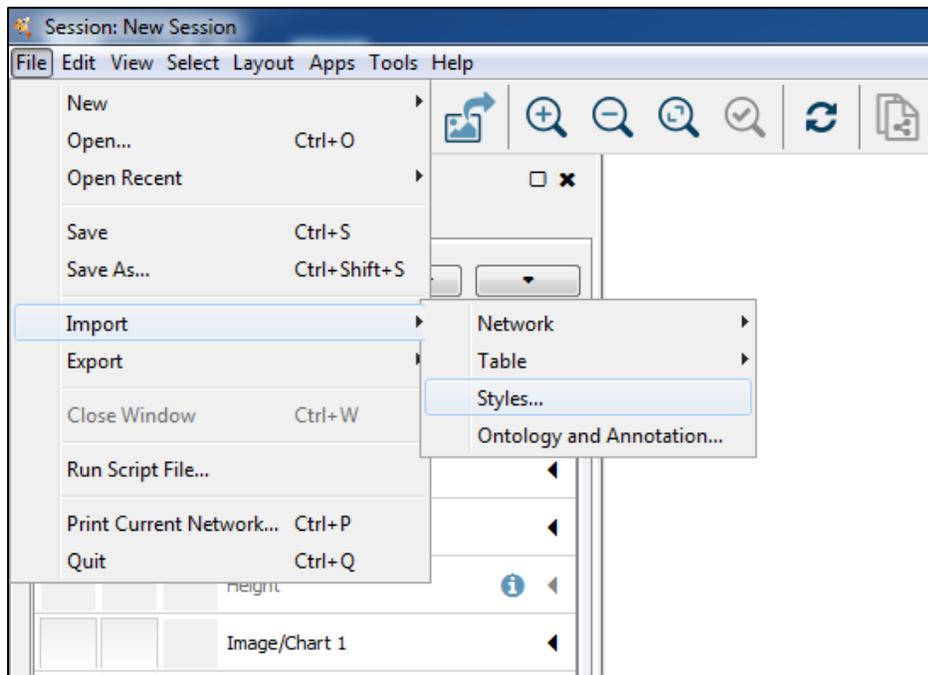
Saving style



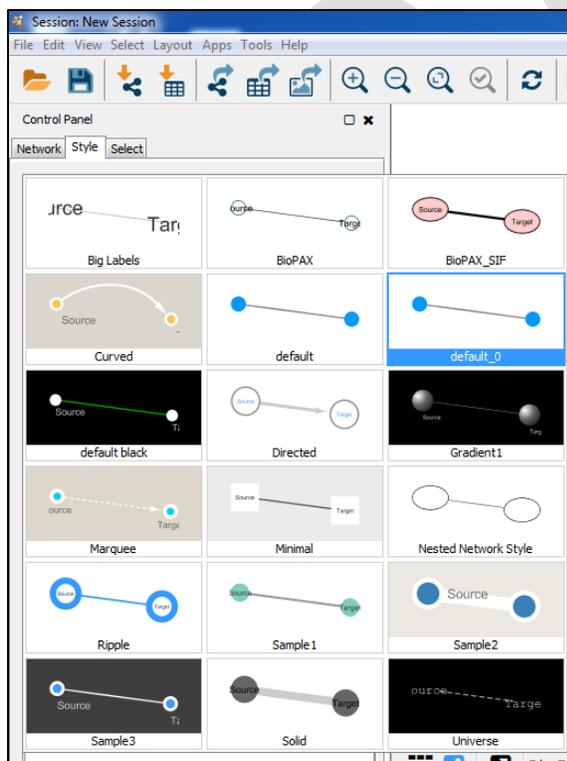
Leave the default style format



Importing a saved style



Important: when you import the style, it will not show immediately in the network. You have to look for it in the styles dropdown box. It is usually saved with the name "Default_0" or "Default_1"



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Cytoscape Manual & tutorials

There are many Cytoscape tutorials and manuals available online:

<http://manual.cytoscape.org/en/3.4.0/>

http://opentutorials.cgl.ucsf.edu/index.php/Tutorial:Introduction_to_Cytoscape#Navigating_Cytoscape

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