Tutorial:Filtering and Editing in Cytoscape 3

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This tutorial will introduce you to some techniques for filtering and editing a network in Cytoscape:

- Apply filters to remove low-confidence edges.
- Perform basic network edits.

Prerequisites

This tutorial features the following data:

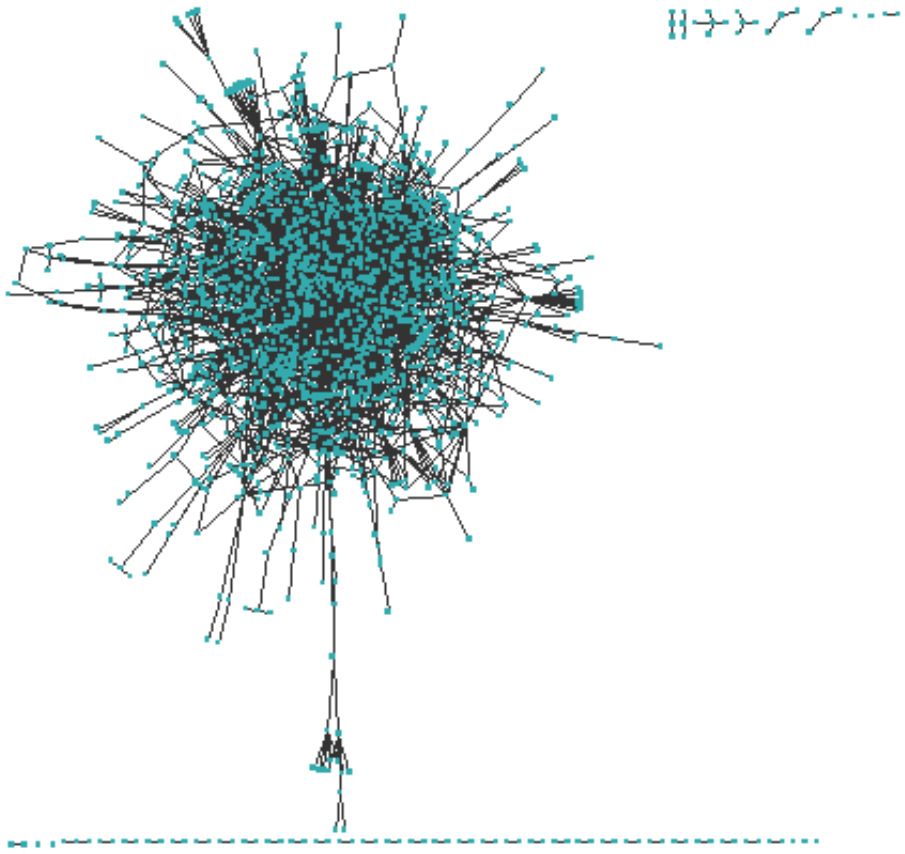
- STELZL.sif (http://opentutorials.rbvi.ucsf.edu/index.php/File:STELZL.sif) , a portion of a human interaction data set published 2005 Oct 20 in Stelzl et al., Cell. 2005 Sep 23;122(6):957-68 and available from Cytoscape (http://www.cytoscape.org/cgi-bin/moin.cgi/Data_Sets/) .
- The corresponding attribute set STELZL.txt (http://opentutorials.rbvi.ucsf.edu/index.php/File:STELZL.txt) , available at the same site.

Before starting, please download these data sets to your computer by right-clicking on the links to the files and saving them.

Loading a network and attributes

- Launch Cytoscape.
- Load the STELZ.sif network file by going to the **File** menu on the Cytoscape desktop, then select **Import → Network → File**, and specifying the location you have downloaded the file to.
- Load the node attribute file STELZ.txt by going to **File → Import → Table → File...**. Remember to **Transfer first line as column names** under **Show text File import options**.
- Generate a yFiles organic layout for your network.

Your network should now look like this:

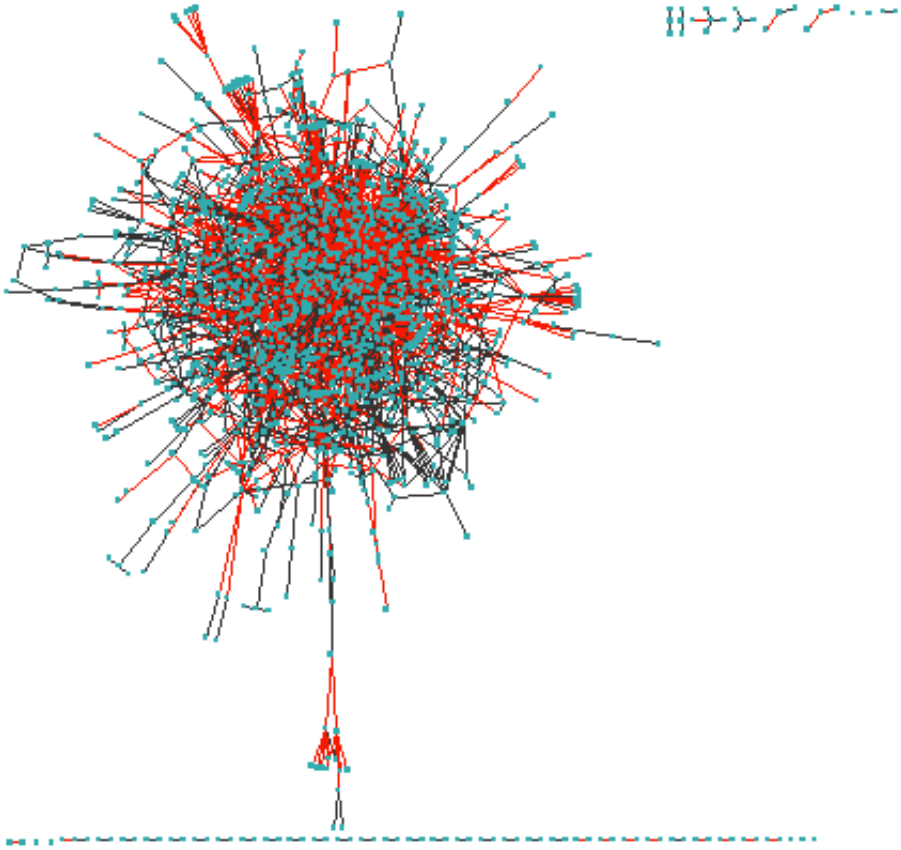


- In the **Node Table** tab of the **Table Panel**, click on the **Show Columns**  button.
- Notice the attribute named **Official HUGO Symbol**, which should be selected by default. If it is not, select this attribute by clicking on it with the left mouse button. Exit the menu with the right mouse button.
- Select some nodes on the Cytoscape canvas. You should now see their IDs (Entrez gene IDs, in this case), and their official HUGO gene names.

Using Filters

Your interactions in your network has evidence from varying sources: high-confidence yeast two-hybrid interactions(lacz4) and low-confidence yeast two-hybrid interactions(sd4), coAP and GST pull-down interactions, and supporting evidence of interaction reported in literature. Verify this by examining the edge types under the **Edge Table**. We will now use Cytoscape's filters to remove some lower-confidence edges.

- Go to **Select → Use Filters** from the Cytoscape desktop menu, or click on the **Filters** tab of the **Control Panel**. This should open the Filters window in the Control Panel.
- In the **Filters** window, click on the **Option** drop-down and select **Create new filter**. Enter a name for your filter, for example **high-confidence**.
- In the **Filter Definition** field, select edge.interaction in the drop-down. Click the **Add** button.
- In the **Advanced** field, in the **interaction** field, check the box for **Not** and select **sd4** in the drop-down. Click **Apply** to apply the filter. This will select all interactions, except those with the lower-confidence **sd4** evidence.
- A set of 2307 edges have been selected in your network. Your network should now look like this:



- At this point, only the relevant edges are selected. To also select the connected nodes, go to **Select → Nodes → Nodes connected by selected edges**.
- Create a new network from the selection under **File → New → Network → From selected nodes, selected edges**.
- Your Cytoscape window should now appear as shown:



Compared to the network you started with, the network you have now has fewer edges, but all the edges are determined through by higher-confidence experimentation or by literature-based methods. For some types of analysis, this is a more appropriate set of edges. Note that this will not filter out nodes that only have self-edges. But at this point, such nodes are easy to select with the mouse and delete.

Editing

At times, it can be very useful to modify a network slightly: to add or remove nodes or edges. For instance, if you have prior knowledge of some biological process, you might want to add some nodes for proteins that you know are involved in the process, but that don't appear in your data set.

All network editing functions are available in a right-click context menu in the **Network View Window**.

- To add a node, right-click anywhere in the **Network View Window** ***and select*** *Node*'.
- Select the node with your mouse. In the **Node Table**, you should see a node with the **shared name** Node 1.
- Give your new node a name by clicking on the entry in the **Node Table**, and entering a name under the column labeled **Official HUGO Symbol**.
- To add an edge to the node, right-click on the node and choose **Edit → Add Edge**. Drag the end of the newly created edge to another node in the network, and click to attach it.

It is also possible to add nodes and interactions in a sif format.

- Locate the CPNE6 gene using the **Search** interface. Note the gene ID, 9362.
- We are going to add a known interaction between CPNE6 and GRB7, Entrez ID 2886. With the CPNE6 gene in focus (not selected), right-click anywhere in the **Network View Window** and select

Add → Edge (and possibly Nodes) using SIF....
- In the **SIF Interpreter** dialog, enter **2886 interacts 9362** and click **OK**. You should see the new node with id 2886 connected to CPNE6.

Congratulations! You are now finished the advanced course in Cytoscape menu operation.

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