Tutorial:Introduction to Cytoscape 3-part2

From OpenTutorials

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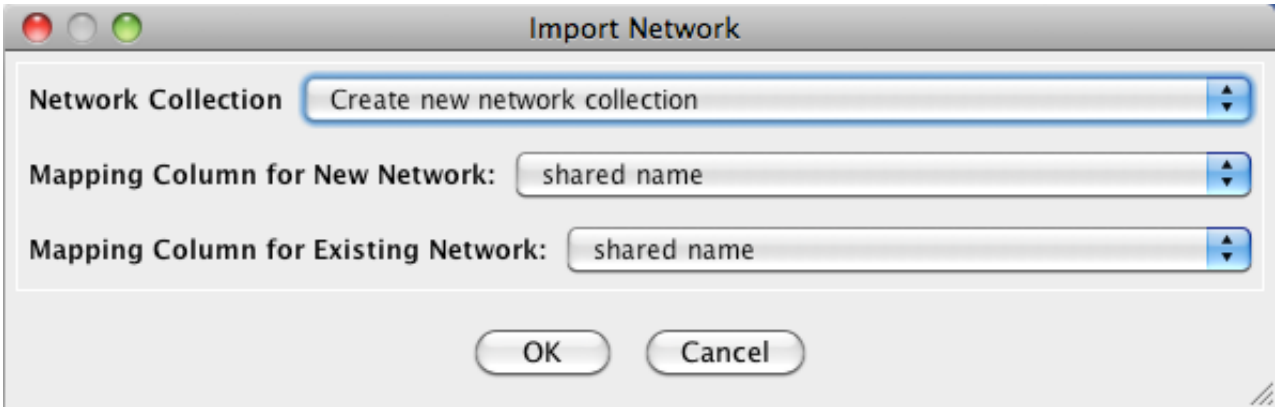
Cytoscape is an open source software tool for *integrating*, *visualizing*, and *analyzing* data in the context of networks. This tutorial is part two of the Introduction to Cytoscape 3 tutorial and covers:

- Network loading
- Importing data
- Visualizing data with VizMapper
- Layouts
- App manager

Loading a Simple Network

- Go to **File → Import → Network → File...**
- You should see a file chooser dialog.
- In the Cytoscape 3 directory, open the **sampleData** folder and select **galFiltered.sif** and then click on **Open**.

You should see the following dialog:



In the dialog, you can select to add the new network to an existing network collection or to create a new one. You can also select which column should be used for mapping between networks.

Manipulating Your Network

Now that you have a network loaded, you can interact with it in a number of ways:

- Start by clicking on the node at the upper left corner of the network. The node with turn yellow. If you hold your mouse down over the node and drag it around the node will move on the screen.
- Now add another node to the selection by holding down the Shift key and clicking on a node. Note that both nodes are now selected (yellow). Again, move the nodes around. Node that both nodes will move.
- To select a group of nodes, hold the mouse down in the upper left-hand corner and drag your mouse over a region of the network. Again, a group of nodes will be selected and can be moved around on the screen.
- To zoom in on the selected nodes, click on the  icon.
- To move the window around the network, you can either use the middle mouse button, or drag the small window outlined in blue around in the Network Overview Pane.
- Finally, zoom your network out by clicking on the  icon.

While useful, hand selecting nodes in dense networks can be error-prone and difficult. However, you can specifically search for a node by name or attribute:

- In the **Search** input field on the toolbar, type in *ynr050c*. This will select that node and zoom the display to focus on it.

The search interface will also allow you to select nodes by other attributes, but first, we need to import more attributes...

Visualizing Data on Networks

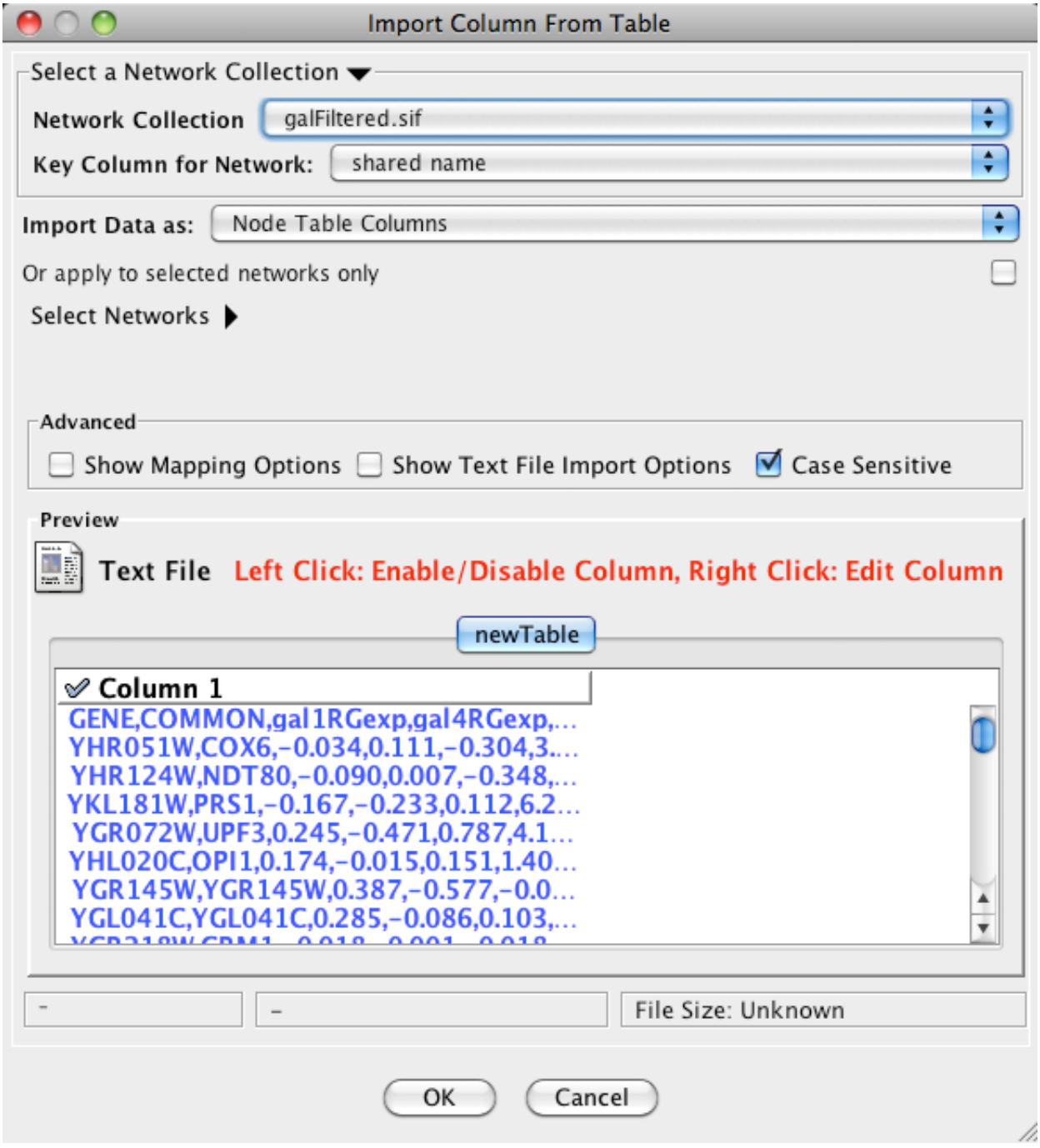
Cytoscape provides a number of features to load arbitrary data and visualize that data by mapping the attribute values to visual styles.

Importing Your Data

Cytoscape can read file structures that are delimited Text or Excel files.

- Go to **File → Import → Table → File...**
- You will see a file chooser dialog. Select the **galExpData.csv** from the **sampleData** folder and then click on **Open**.

You should see the following dialog:



- In the **Select a Network Collection** section, choose the network to import the attributes to, and the column used as key to map to.
- Next, under **Import Data As**, select **Node Table Columns**.

Notice that the data preview shows data from all columns as one field. To correct this, we need to change which delimiter is used:

- In the **Advanced** section, select **Show Text File Import Options**
- In the **Delimiter** field, deselect **Tab** and instead select **Comma**.
- In the **Attribute Names** section, select **Transfer first line attribute names**
- Click **OK** to import.

You've successfully loaded data! Now explore the **Table Panel** to confirm the mapping of the data to the network.

- Locate the **Show Column** button  in the **Table Panel**.
- Select the data attributes: gal1RG, gal4RG, and gal80R.
- Return to the **Table Panel** by clicking away from the attribute list
- Select some nodes in the network (ctrl-A selects all nodes) and see the associated data in the **Table Panel**

Note that the default setting is to only show data from selected nodes in the **Table Panel**. To instead display data from the entire network, click the  button in the **Table Panel** and select **Show all**. You now have access to your networked data and can begin playing with visualization.

- Go to **Layout → Prefuse Force Directed Layout**.
- Go to the **VizMapper** tab in the **Control Panel** and select **Sample1**.

The **VizMapper** lists a set of default visual styles. In the next section you will customize a visual style to highlight your data values.

Viewing Attributes

In the previous section, you were able to select a couple of attributes to display in the Data Panel. In this section, we will explore a little more about attributes and the Data Panel.

- Type *mcm1* in the **Search:** box. This will select the node:*YMR043W*, and display the attributes for that node in the **Data Panel**.
- We're going add a new attribute for *MCM1*. Click on the **Create New Column** icon  and select **New Single Column → String**.
- Type in **pdb** for the name of the attribute -- this will define a new string attribute for nodes, and add it to the **Table Panel**.
- Now click into the empty cell for newly-created **pdb** attribute for **YMR043W** and type *1mnm*, which is the PDB ID for the yeast protein *mcm1*. You need to hit Return or Tab to enter that data.
- Move the **pdb** attribute to be the second column by dragging the column header to be behind the **name** column.
- Finally, select a number of nodes and note that the attributes for all of the nodes are shown in the **Table Panel**.
- By clicking on the column header, you can sort the columns. Clicking again changes the order of the sort.

Visualizing Data with VizMapper

- Go to **File → Open** (click 'Yes' to losing current session).
- You should see the Open a Session File Dialog.
- Open the **sampleData** folder and select **galFiltered.cys** and then click on **Open**.

Notice how the galFiltered visual style maps multiple data and annotation values to:

- Edge Stroke Color
- Edge Width
- Node Fill Color
- Node Label

Modifying a Visual Style

Customizing the way you visualize and manipulate networks is a key function of Cytoscape. This is achieved through the use of the **VizMapper** tool.

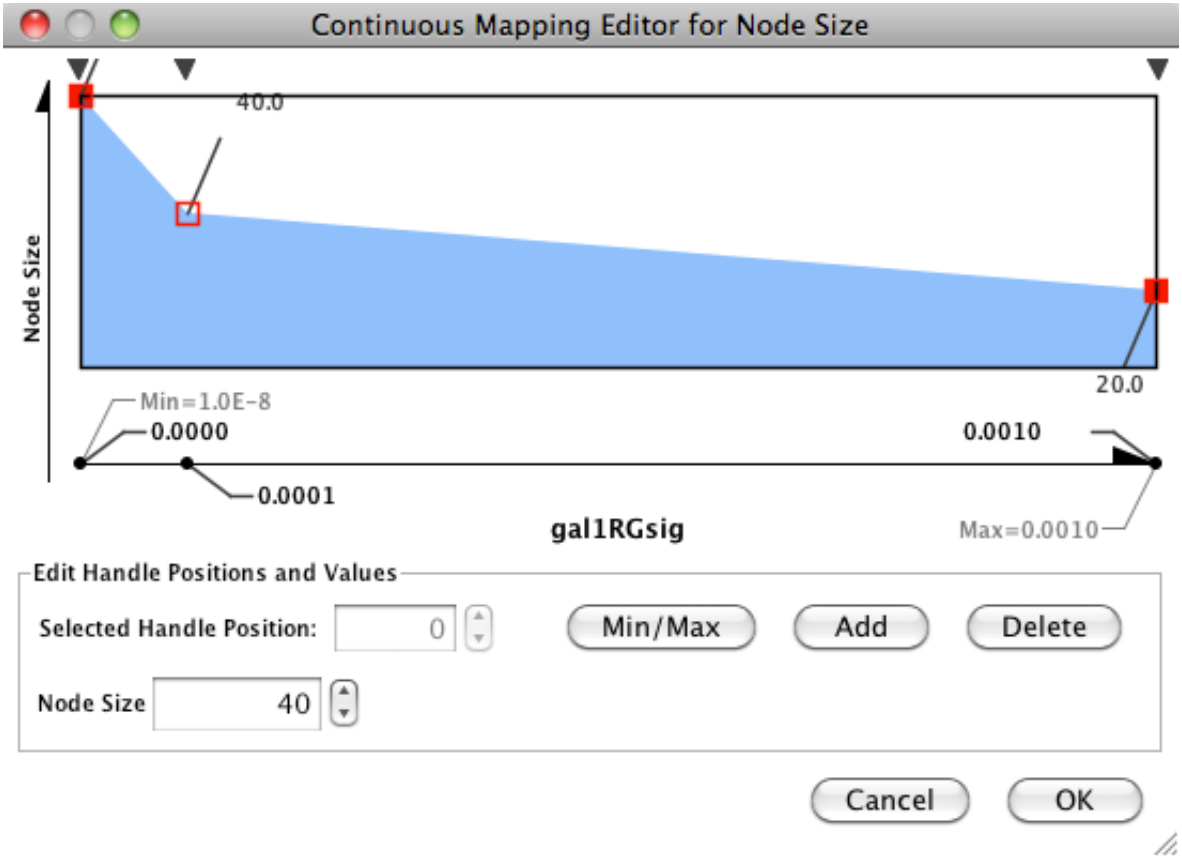
- To launch the **VizMapper**, either select the **VizMapper** tab on the Control Panel.
- Find **Node Fill Color** in the **Visual Mapping Browser** and expand it by clicking on the triangle icon for expand/collapse.
- Click on the value 'gal4RGexp' to select an alternative data value to map to node color: select 'gal80Rexp'. Notice the changes in the network display.
- Click on the gradient color mapping to open the **Gradient Editor**.
- Control the values and colors of the mapping by means of triangular handles and endpoint markers.
- Double-click on any handle or marker to change it's color: change green to blue and change red to yellow. Notice the immediate changes to the network.
- Click-and-drag any handle to slide its value between the min and max.
- To save your changes, close the editor.
- Find **Edge Stroke Color** in the **Visual Mapping Browser** and expand it by clicking on the triangle icon.
- Notice the discrete mapping of colors to values. Click on any color mapping to change the color.
- Close the editor to save your changes.

Creating a Visual Style (Advanced)

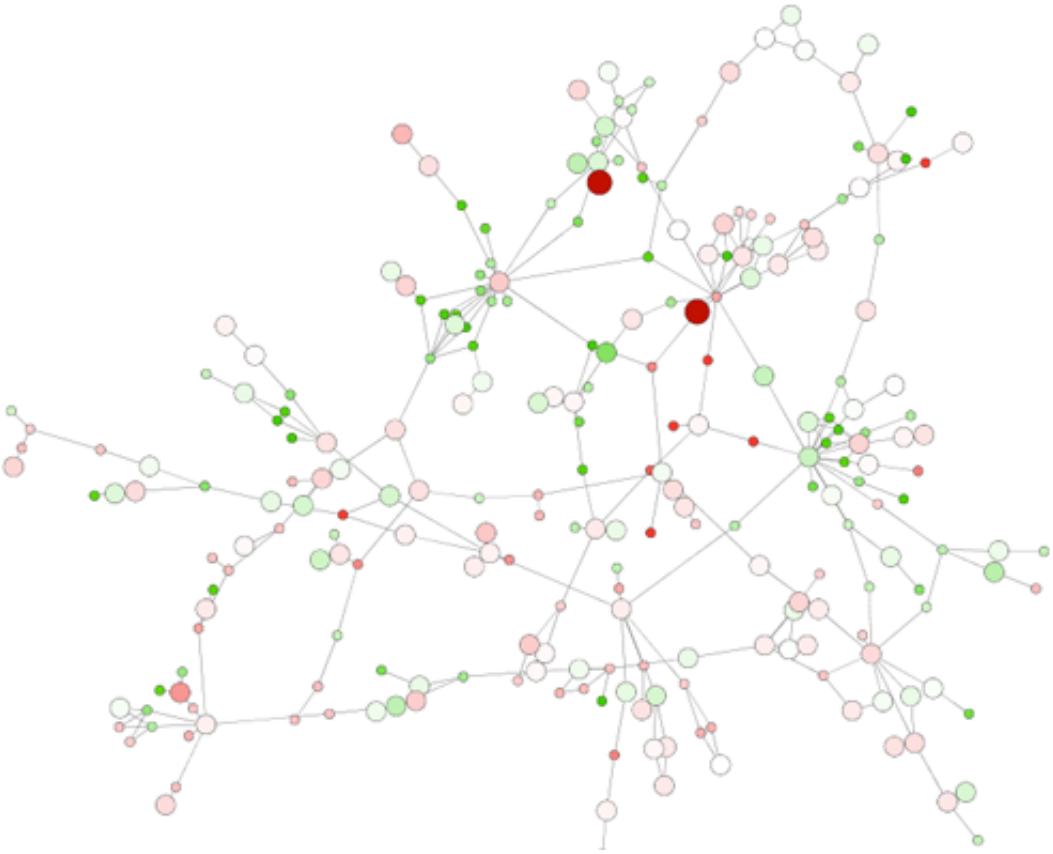
- In the **Current Visual Style** section, start a new visual style by clicking the **Options** button  and selecting **"Create new Visual Style"**.
- Enter a name for your custom visual style when prompted, click on **OK**.
- Find **Node Color** in the list of **Unused Properties** and double-click to activate.
- For **Node Color** select the value 'gal1RGexp' to map expression fold values. For **Mapping Type** select 'Continuous'. Click on the gradient to open the dialog:
  - Click on **Min/Max** button and set to -1 and 1, respectively.
  - Double-click on gradient handles to set colors, e.g.
    - below -1.0 = green
    - -0.8 = green
    - 0.8 = red
    - above 1.0 = red

    - Click **Add** to add another gradient handle (added to max by default). Drag to center at 0.0. Leave as white color.
    - Close gradient dialog.
- Next, we want to edit the visual properties for Node Size. This property is not part of the default list of properties in the **VizMapper**, so click **Show All** at the top of the **Visual Mapping Browser** in the **VizMapper**.
- Activate **Node Size**. Select 'gal1RGsig' to map p-values. For **Mapping Type** select 'Continuous'. Click on gradient to open dialog:
    - Note: We want smaller p-values (more significant) to show as larger nodes
    - Click **Min/Max** and set the values accordingly: 1.0E-8 and 1.0E-3.
    - Double-click on solid red box for p-values *below the minimum* (far left) to set the *maximum* node size. Set to 70.0.
    - Double-click on solid red box for p-values *below the maximum* (far right) to set the *minimum* node size. Set to 20.0.
    - Select handles along the top border to drag the x-position (p-value) of the gradient points. When selected, you can also set the Attribute and Node Size value by editing the **Handle Settings** field. You can also drag (or double-click) the open red boxes to set the y-position (Node Size).
    - Set the left open box to Node Size 70.0 and the right open box to 20.0. This defines the range of the gradient.
    - Click 'Add' to add a new gradient handle. Set it to Attribute Value = 1E-4 and Node Size = 40.0.

This creates a pseudo-exponential gradient mapping:



- Click 'OK' in the gradient dialog and explore the visualization you have created!



- Zoom by selecting an area and clicking 
- Use the bird's-eye-view panel (bottom-left) to pan around network
- Return to **VizMapper** and switch mappings to another column of data:
  - For **Node Color** select 'gal4RG'.
  - For **Node Size** select 'gal4RGsig'.

Notice the change in the view of the network! You can reuse the mappings across multiple data sets. Now is a good time to save your Cytoscape session, to save the visual style you've created.

Laying Out Your Network

A network layout is a process that positions the nodes and edges for the network. There are a large variety of layouts in Cytoscape and plugins might add new layouts. All of the layouts will appear under the **Layouts** menu. In this section, we will explore some of the layouts which are the core layouts supported by the Cytoscape team. Most layouts support the ability to only layout a portion of the network, and most expose parameters that can be used to tune the layout algorithm.

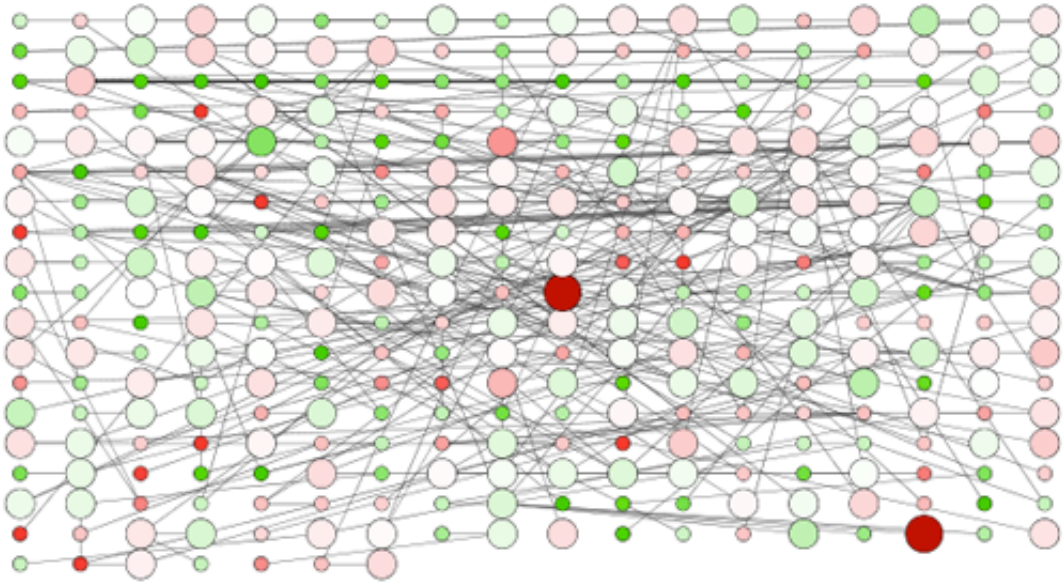
Simple Layouts

Grid Layout

The simplest layout that Cytoscape provides is the **Grid Layout**, which simply places all of the nodes in a grid arrangement.

- Using the network you loaded before, select **Layout → Grid Layout**. You should see the image

below:

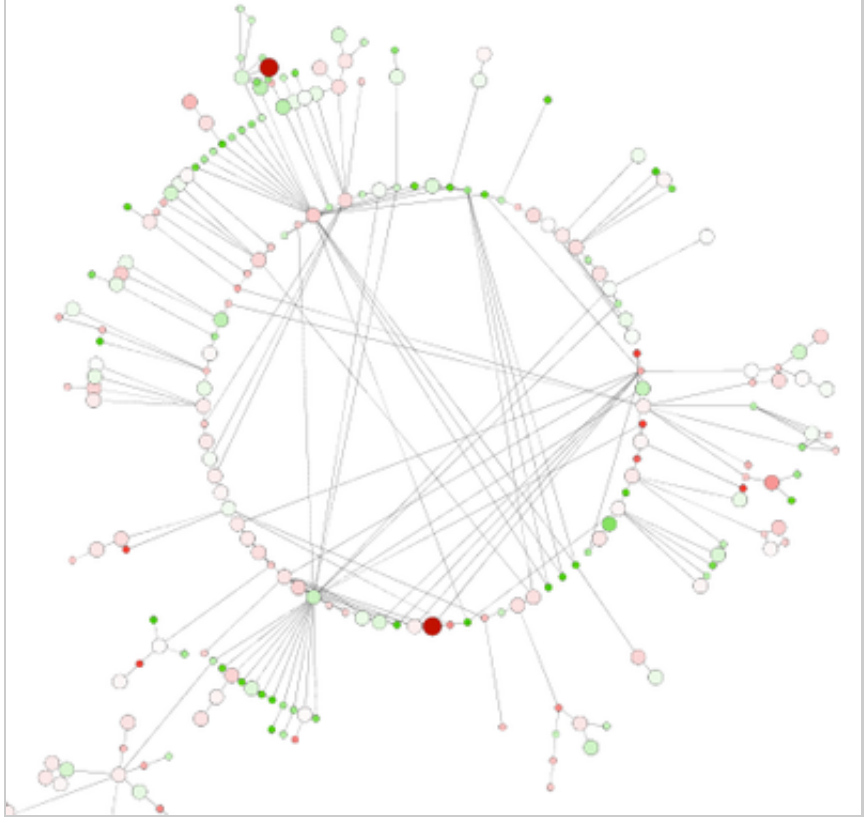


- Now, select **Edit → Undo: Grid Layout** and notice how your network reverts to the previous condition. Many (but not all) of Cytoscape's actions may be undone.
- Select a group of nodes in your network and again select **Layout → Grid Layout**. Notice that this now has a sub-menu with two options: **All Nodes** and **Selected Nodes Only**.
- Choose **Selected Nodes Only**. Note that only the nodes you selected are changed.

Circular Layout

Grid is very fast, but it's of limited usefulness. Alternatives:

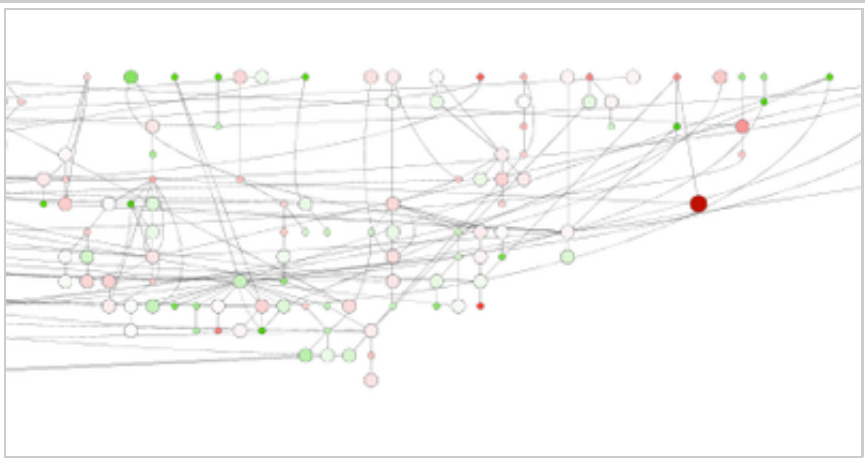
- **Circular Layout** places all of the nodes in a circular arrangement.
  - Very quick
  - *Partitions* the network into disconnected parts and independently lays out those parts.



Circular Layout

Hierarchical Layout

- **Hierarchical Layout** forces the nodes into a tree structure.
  - Works best when the network is naturally tree-structured
  - Also works reasonably well when the network is mostly hierarchical.



Hierarchical Layout

Data-Driven Simple Layouts

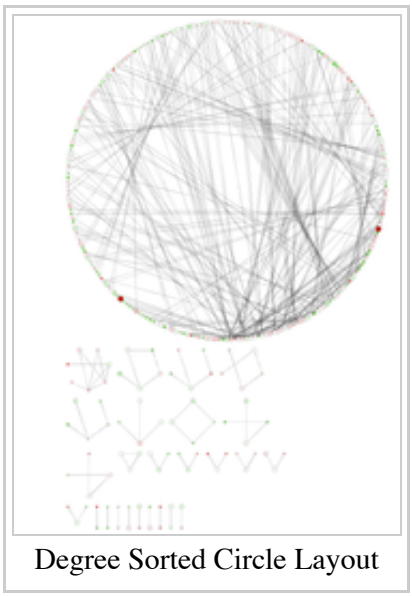
Often what is desired is to organize the nodes in space to reflect some data property of the nodes themselves. We'll look at three of the simple ones:

- **Degree Sorted Circle**: Orders the node around a circle based on node degree (number of edges)
- **Attribute Circule Layout**: Orders the node around a circle based on the value of some attribute
- **Group Attributes Layout**: Groups the nodes based on the value of some attribute

Degree Sorted Circle Layout

For example, assume you are interested in hubs (nodes with high degree):

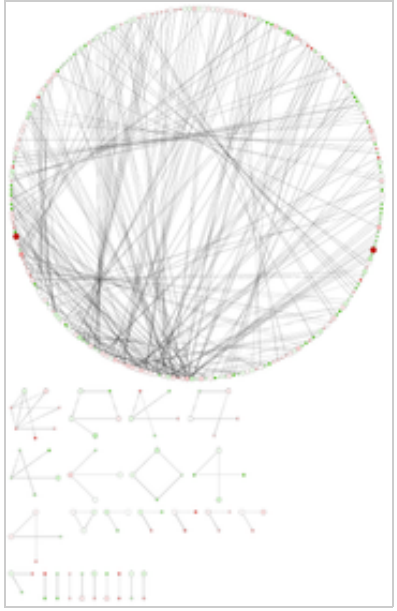
- Select **Layout → Degree Sorted Circle Layout**.
  - Note the highest degree nodes are in the same region of the circle and the degree decreases as you proceed counter-clockwise around the circle.
  - Also note that this layout supports partitioning of the network into disconnected components.
  - This layout algorithm adds the attribute **degree** to every node, which is very useful for coloring nodes.



Degree Sorted Circle Layout

Attribute Circle Layout

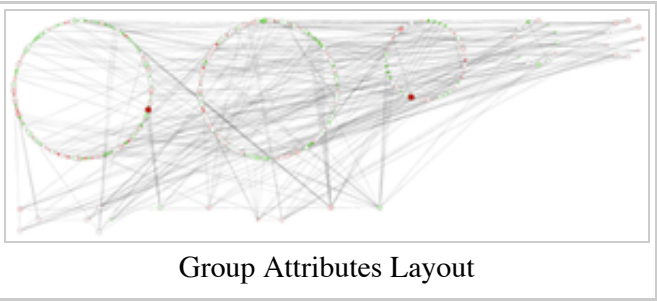
- Now try **Layout → Attribute Circle Layout → Degree**.
  - This should give you a very similar layout to the Degree sorted circle layout.
  - You should also try using other attributes to layout.



Attribute Circle Layout

Group Attributes Layout

- Finally, select **Layout → Group Attributes Layout → Degree**.
  - Note that this layout organizes all of the nodes with the same degree into a circle and then positions the circles into a grid.
  - Partitions the graph before layouts.



Group Attributes Layout

These layouts are useful to represent data attributes associated with the nodes of a network, however, they don't provide much information about the network structure itself. For that, using more complicated layouts are required.

Force-Directed Layouts

The force-directed methods for laying out graphs all use some kind of physical simulation that models the nodes as physical objects and the edges as springs connecting those objects together.

- Cytoscape provides 3 force-directed layouts:
  - Edge-weighted Force directed (BioLayout)
  - Edge-weighted Spring Embedded
  - Prefuse Force Directed

In this exercise, we'll use the **Prefuse Force-Directed Layout** (see prefuse.org (http://prefuse.org)).

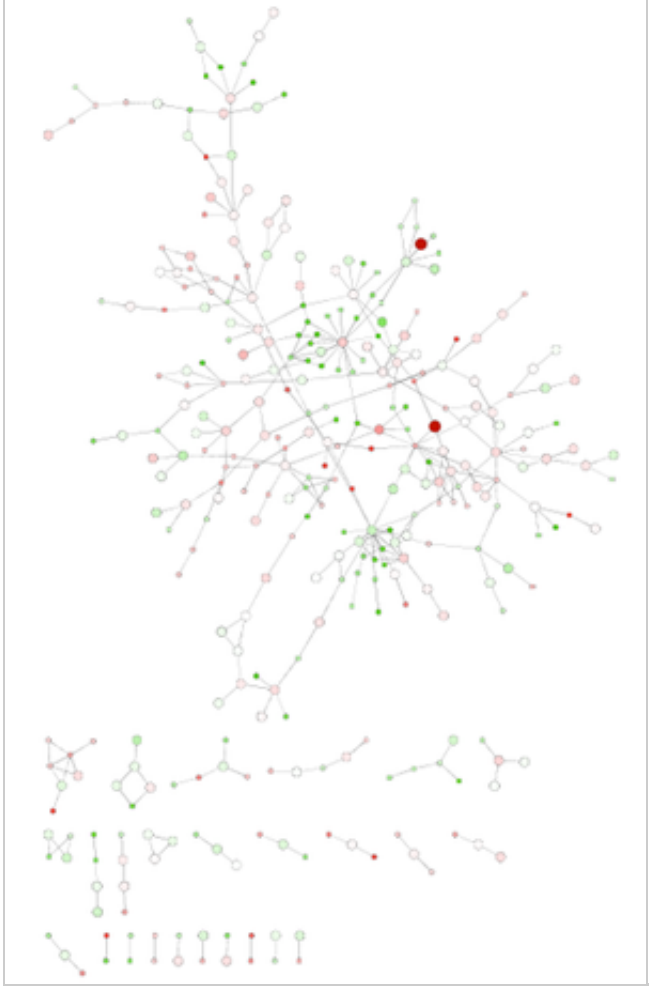
Force-Directed Layout

- We'll do all of our work from the Layout settings dialog, so bring up the dialog by **Layout → Settings...**
- In the **Layout Settings** dialog:
  - Select **Prefuse Force Directed Layout** under **Layout Algorithm**.
  - The result should look like this:



Force Directed Settings Dialog

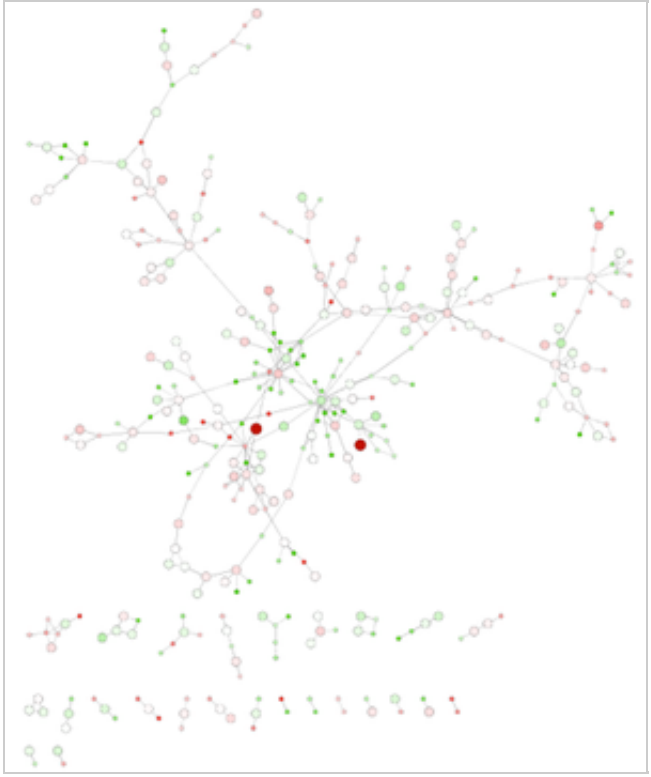
- Lets start by creating a layout using the default parameters.
  - Select **Execute Layout**.
  - Note how this exposes more of the structure of the network than any of the previous layouts.



Prefuse Force Directed Layout

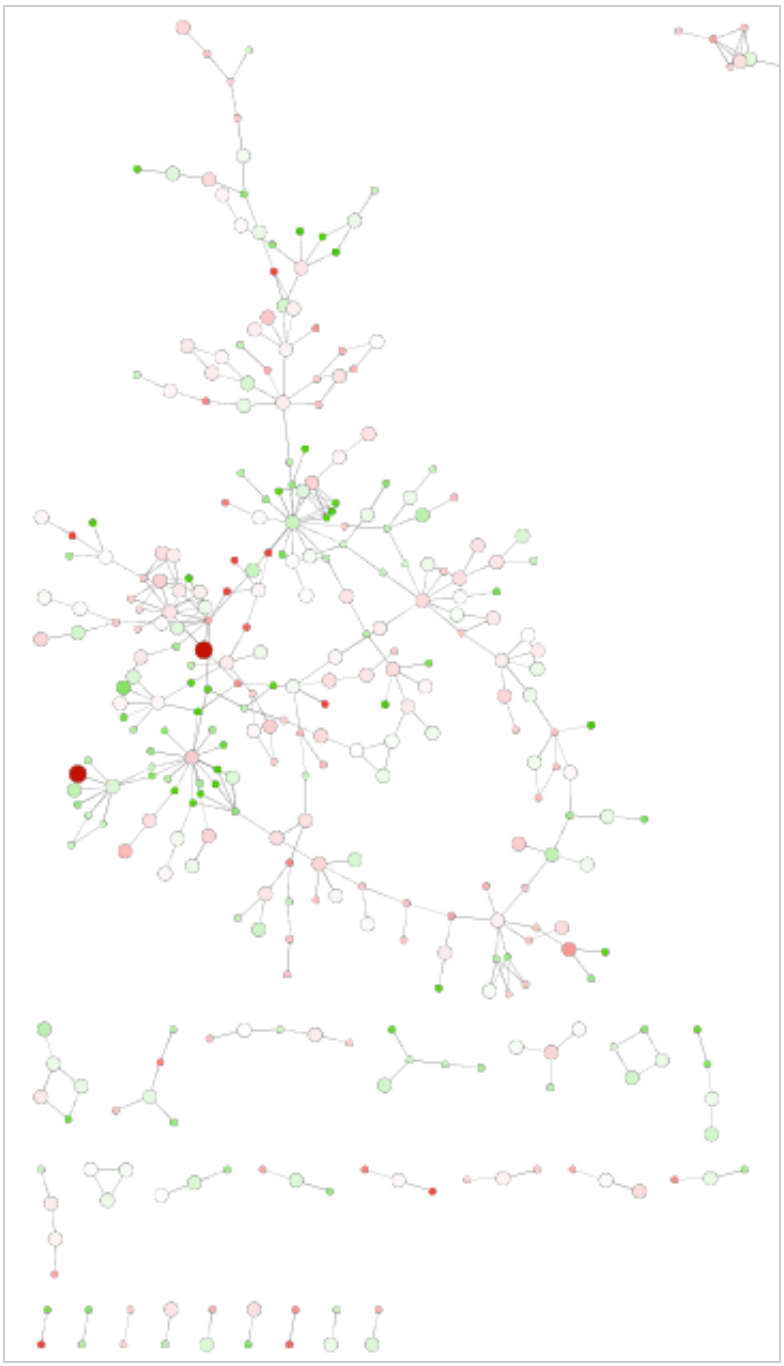
Now, let's see what the parameters do.

- Start by changing the **Default Spring Length** to **20**, and select **Execute Layout**. The default spring length is the length of a spring (edge) with no forces exerted upon it. Essentially, it's the length of an edge connecting two nodes with no other connections.
- Note how the layout has changed. The resulting network tends to be more closely packed in the denser regions.



Prefuse Force Directed Layout (spring length 20)

- Finally, lets change **Default Spring Length** back to **50** and the **Default Spring Coefficient** to **1E-3**. The spring coefficient is a measure of the strength of the spring.
- Now click **Execute Layout**. Note that the network remains pretty compact, even though we've reset the default spring length back to 50.



Prefuse Force Directed Layout (spring coefficient 1E-3)

Prefuse Force Directed Layout is also a good layout to use for circumstances when you want to have the length of your edges reflect some numeric weight on each edge.

- Select the attribute containing your edge weights from the drop-down menu **Weight using**.
- This often requires some tuning of the spring coefficient and the spring length to get an aesthetically pleasing layout.

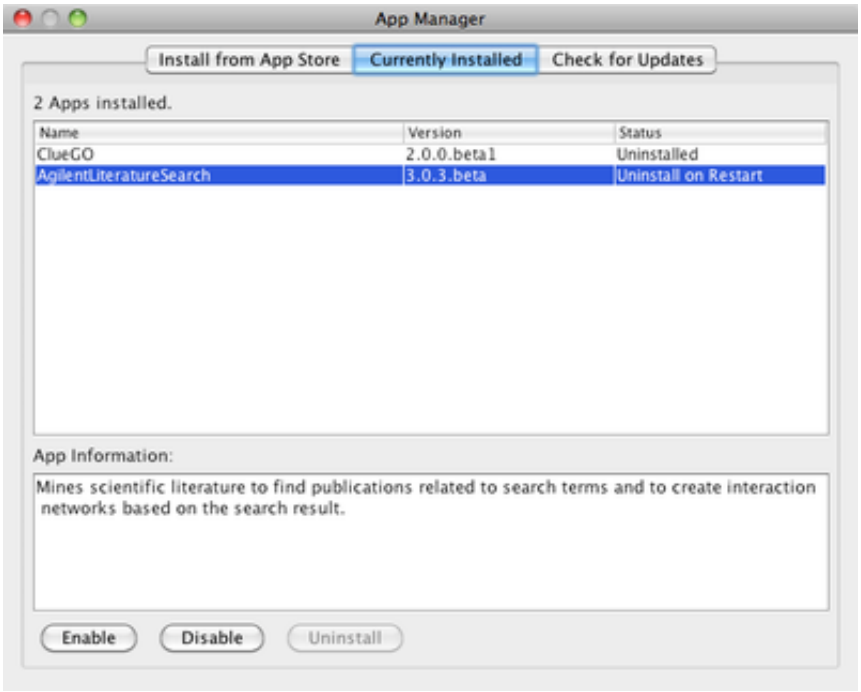
App Manager

The App Manager allows users to quickly and conveniently add extra features to Cytoscape directly from within Cytoscape, eliminating the need for manual searches through different websites to install and update

apps.

If you do not have Internet access enabled, you will not see the list of available apps or be able to automatically update existing ones; however, you will still be able to view and delete previously installed apps.

- Go to **Apps → App Manager**. The **App Manager** has three tabs: **Install from App Store**, **Currently Installed** and **Check for Updates**.



- **Currently Installed** folder lists any apps already installed. To find out more about a specific app, click on its name to display some basic information on the bottom of the window.
- **Install from App Store** tab displays an interface for interacting with the Cytoscape App Store.
  - To install **jActiveModules**: Search for "jactive". Select **jActiveModules** from the search results.
  - Click on the Install button at the bottom of the window
  - Click on close to exit the **App Manager**.
  - Go to the **Apps** menu and **jActiveModules** should appear in the list of apps.

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