Introduction to Cytoscape 3.1

Tutorial:Introduction to Cytoscape 3.1-part2

Slideshow Introduction to Cytoscape 3.1: Networks, Data, Styles, Layouts and App Manager [1]

Handout Introduction_to_Cytoscape_3.1:_Networks,_Data,_Styles,_Layouts_and_App_Manager.pdf [2]

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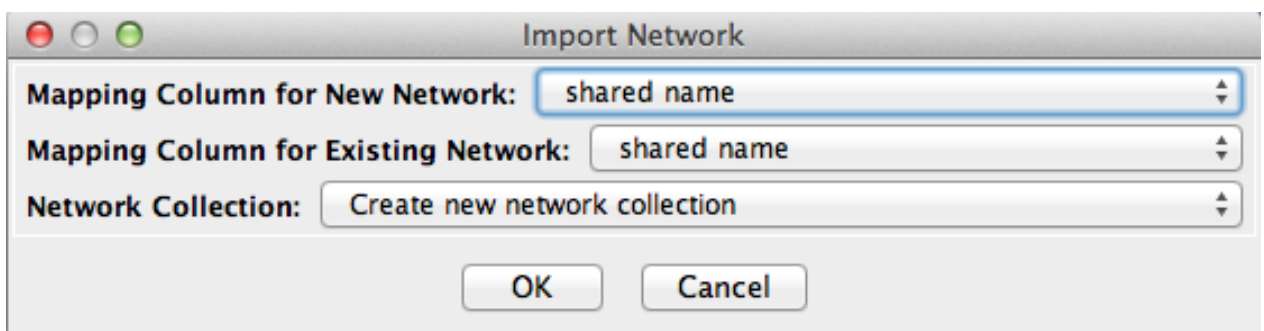
In the dialog, you can select to add the new network to an existing network collection or to create a new one. You can also select which column should be used for mapping between networks.

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 data value:

- 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 columns, but first, we need to import more data columns...

# Visualizing Data on Networks

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

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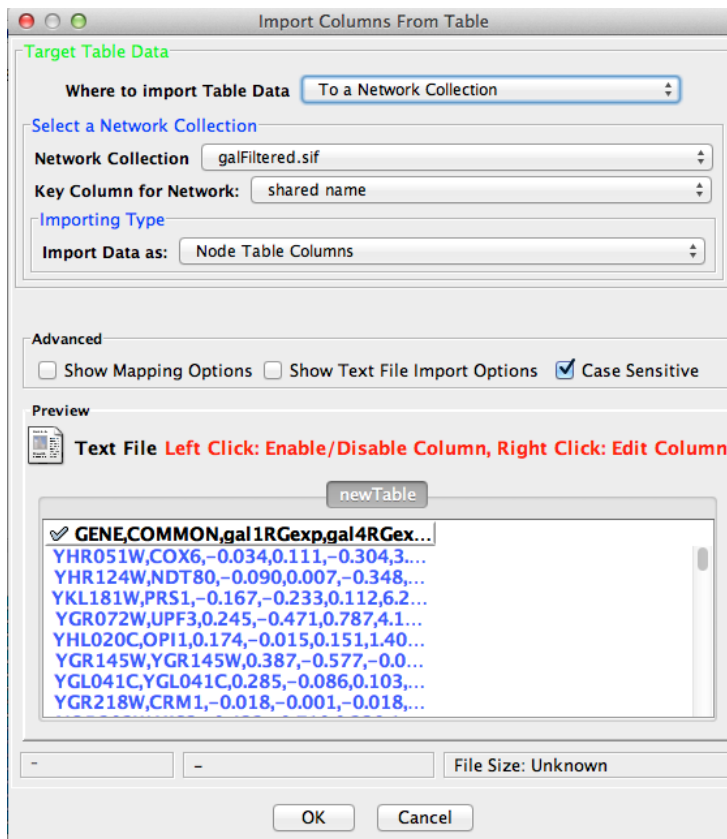
- In the **Select a Network Collection** section, choose the network to import the data columns to, and the column used as key to map to.
- Next, under **Import Data As**, select **Node Table Columns**.

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 **Column Names** section, select **Transfer first line as column names**

- Click **OK** to import.

You've successfully loaded data!

Viewing Data Columns

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 following data columns: gal1RGexp, gal4RGexp, and gal80Rexp.
- Return to the **Table Panel** by clicking away from the column 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 **Styles** tab in the **Control Panel** and select **Sample1** in the **Current Style** drop-down.

Styles lists a set of default styles. In the next section you will customize a style to highlight your data values. Details on editing and creating Styles here.

Editing Data Columns

So far, we have selected a couple of columns to display in the Table Panel. Next, we will explore columns and the Table Panel in more depth.

- Type *mcm1* in the **Search:** box. This will select the node:*YMR043W*, and display the columns for that node in the **Table Panel**.

- We're going add a new column for *MCM1*. Click on the **Create New Column** icon and select **New Single Column → String**.
- Type in **pdb** for the name of the column -- this will define a new string column type for nodes, and add it to the **Table Panel**.
- Now click into the empty cell for newly-created **pdb** column 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** column to be the second column position by dragging the column header to be behind the **name** column.
- Finally, select a number of nodes and note that the columns 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 Styles

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

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

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

Modifying the Style

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

The **Styles** interface is divided into 3 tabs, for **Node**, **Edge** and **Network** properties. For each property, there are 3 columns describing the current **Default** (meaning the default value for the current mapping), **Mapping** and any **Bypass**. A pre-defined set of properties is displayed by default. Additional properties for display can be selected by clicking the **Properties** drop-down at the top of the list of properties. The **Styles** interface also lists any pre-defined styles in the **Current Style** drop-down at the top of the interface. In the below figures, node fill color is mapped using a continuous mapping (**Cm**), with grey as the default color, and the currently selected node has a visual style bypass defined (yellow).
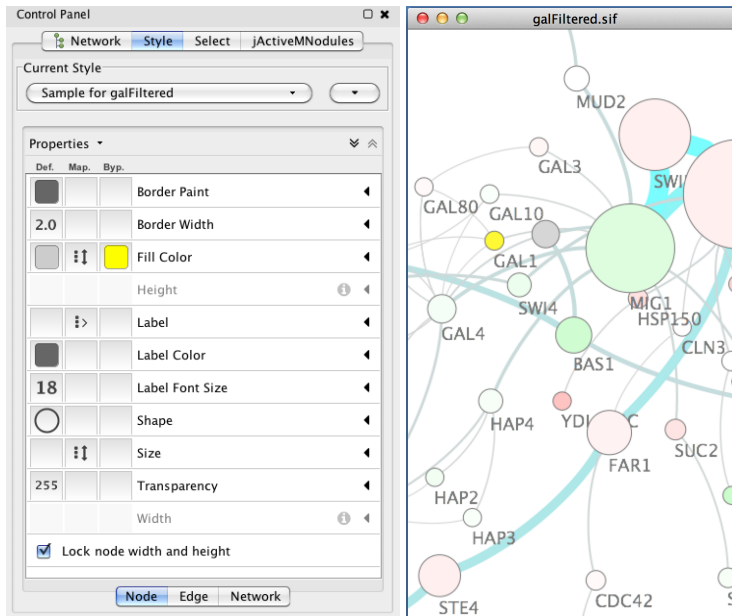

- To start, select the **Styles** tab on the Control Panel.
- Under the **Node** tab, find **Fill Color** and click on the arrow on the right side to expand.
- Click on the value 'gal1RGexp' to select an alternative data value to map to node color: select 'gal80Rexp'. Notice the changes in the network display.
- Click on the gradient color mapping to open the **Continous Mapping 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 its 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.

Creating a Style

- In the **Current Style** section, start a new style by clicking the **Options...** button [▾] and selecting **Create new Style**.
- Enter a name for your custom style and click **OK**.
- Find **Fill Color** under the **Node** tab and click the right-side arrow to expand.
- For **Column**, click on **-- select value --** and select the value 'gal1RGexp' to map expression fold values. For **Mapping Type** select 'Continuous Mapping'. Click on the gradient to open the gradient editor:
    - 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. Drag to center at 0.0. Leave as white color.
    - Close gradient dialog.
- Next, we want to edit the properties for Node Size.
- Under the **Node** tab, expand **Size** and select 'gal1RGsig' to map p-values. For **Mapping Type** select 'Continuous Mapping'. 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.
    - 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 data value = 1E-4 and Node Size = 40.0.
- Click 'OK' in the gradient dialog and explore the visualization you have created!

This creates a pseudo-exponential gradient mapping:
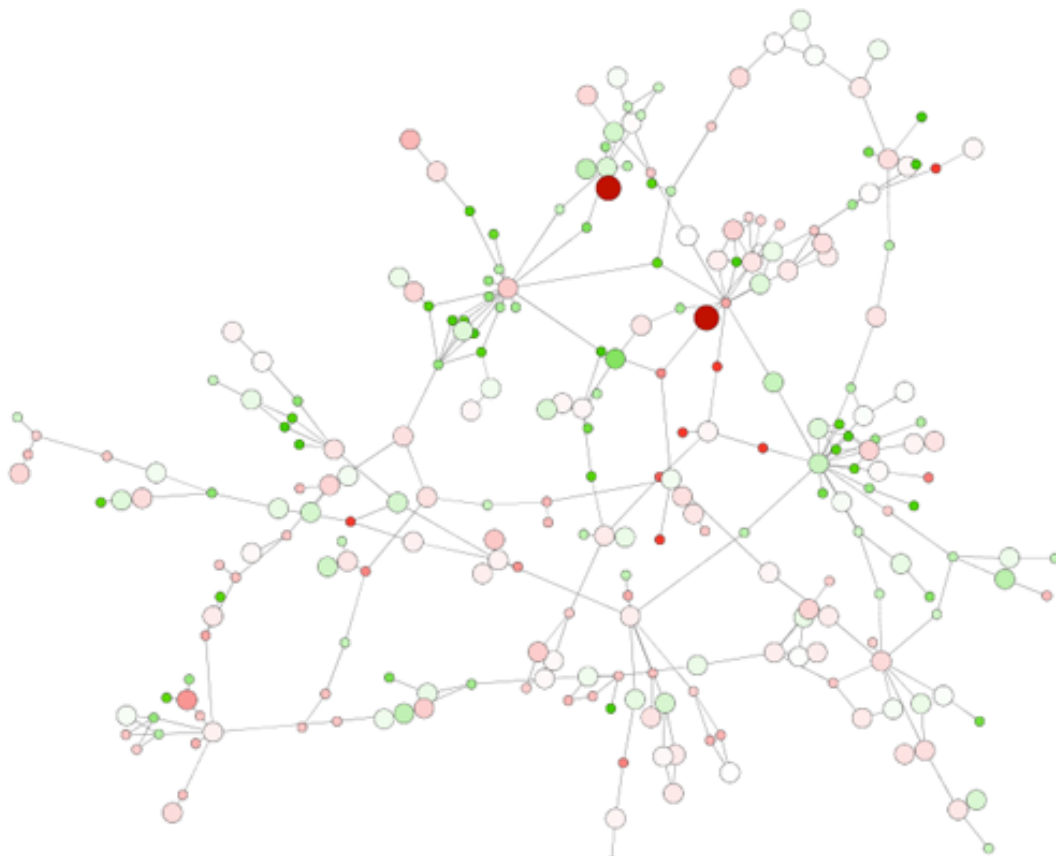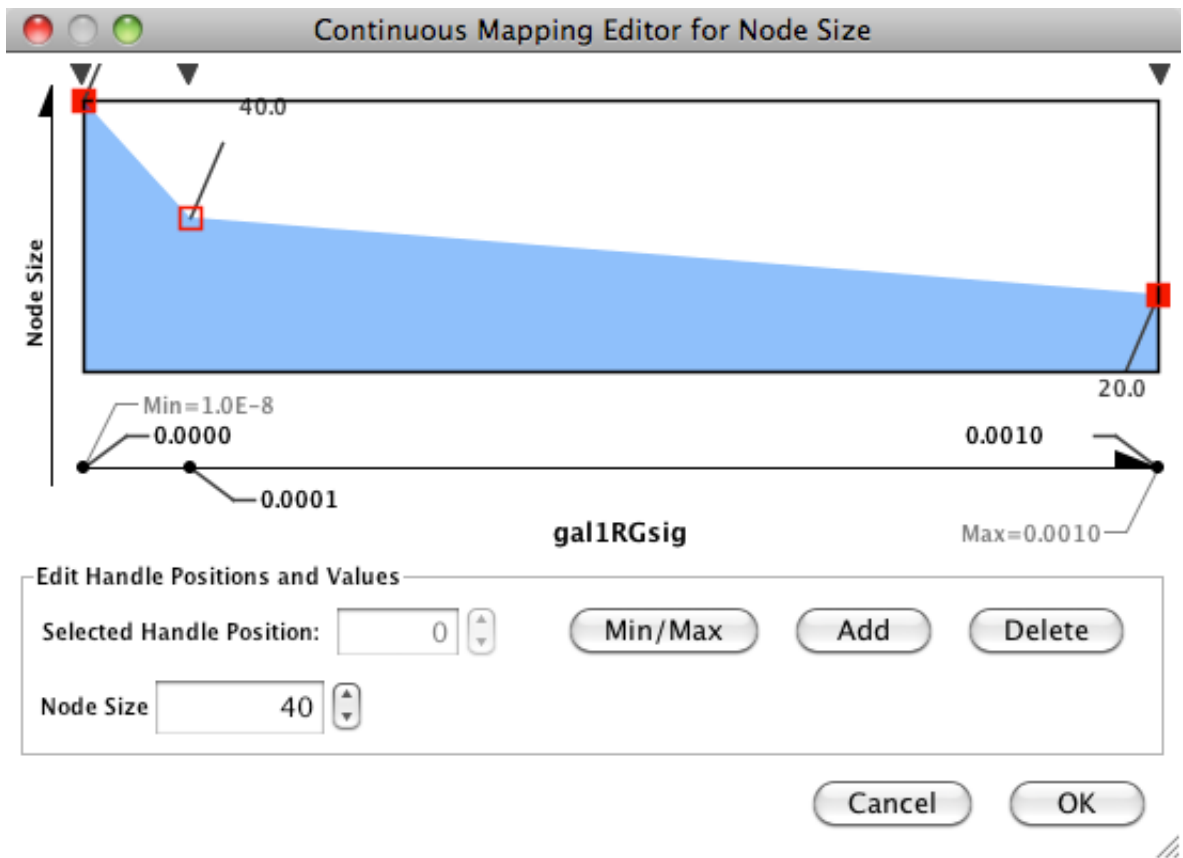
- Zoom by selecting an area and clicking
- Use the bird's-eye-view panel (bottom-left) to pan around network

- Try switching the Style by switching 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 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:
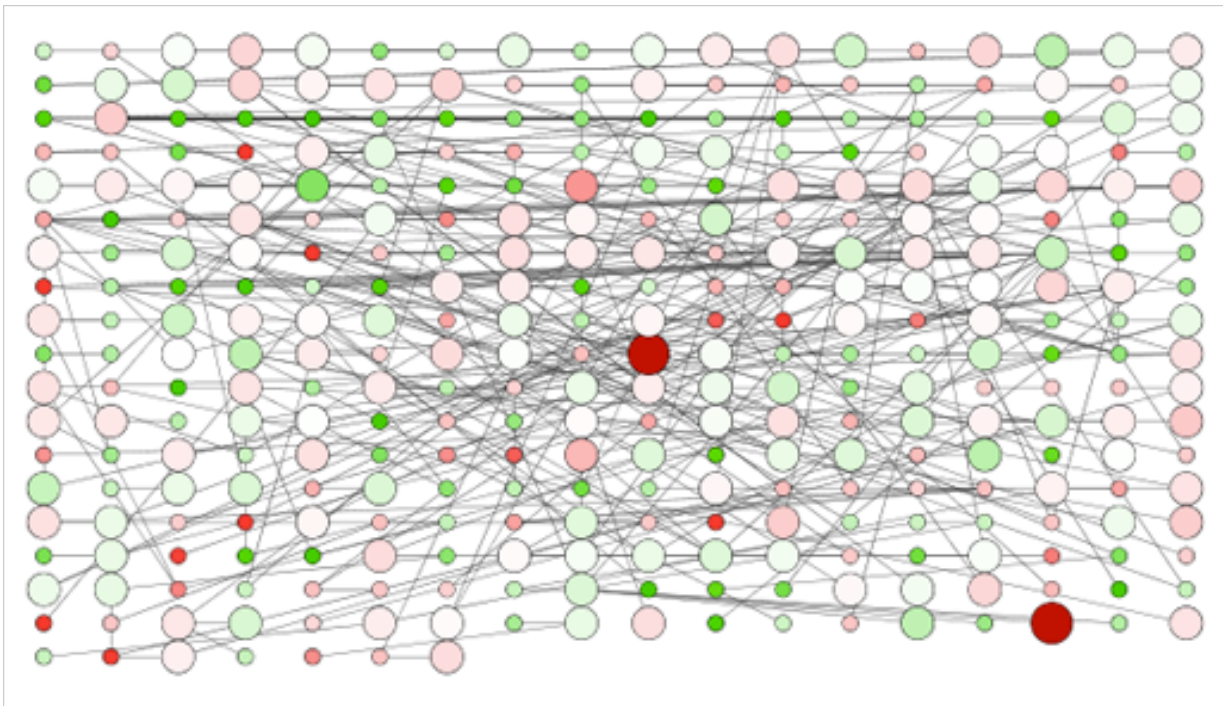
- Now, select **Edit → Undo: Grid Layout** and notice how your network reverts to the previous condition. Many (but not all) of Cytoscape's actions may be undone.
- Select a group of nodes in your network and again select **Layout → Grid Layout**. Notice that this now has a sub-menu with two options: **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
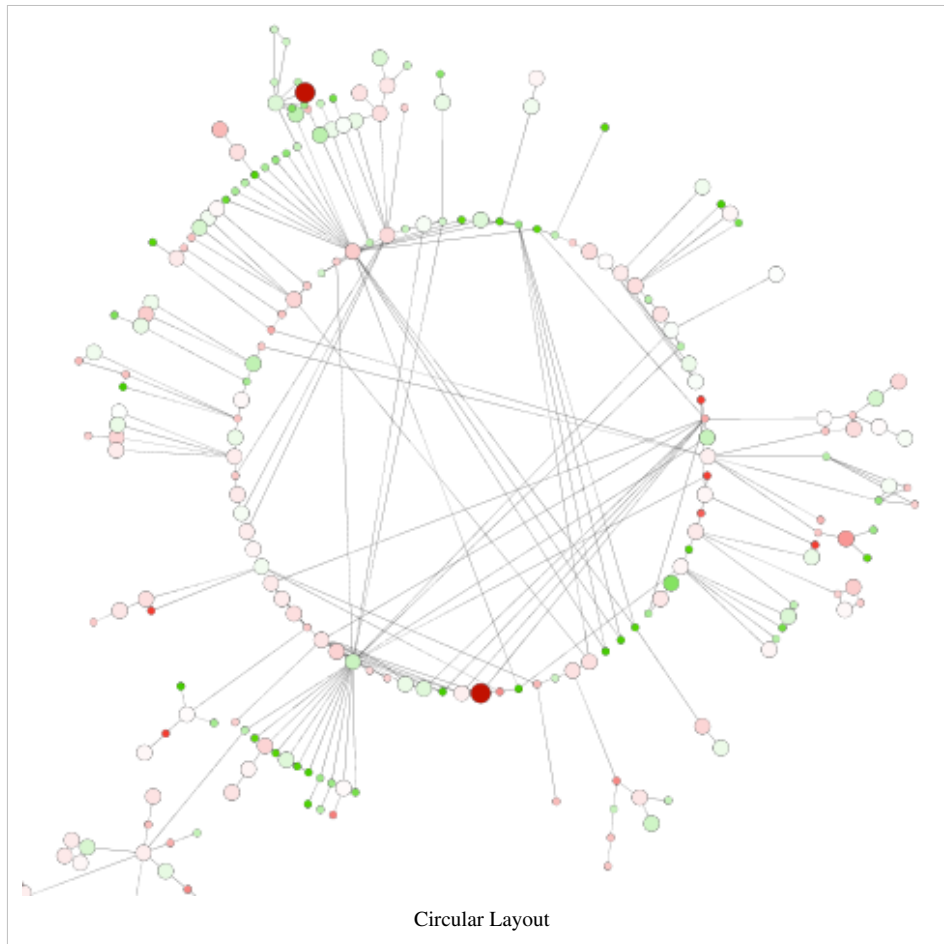
Hierarchical Layout

- **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
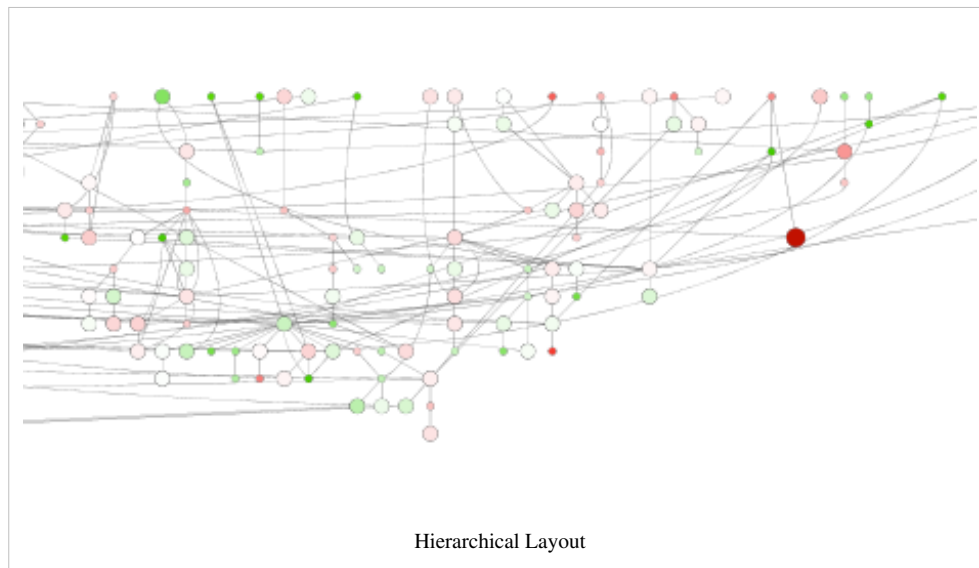
Data-Driven Simple Layouts

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 Circle Layout**: Orders the node around a circle based on the value of a selected column
- **Group Attributes Layout**: Groups the nodes based on the value of a selected column

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 column **degree** to every node, which is very useful for coloring nodes.

Degree Sorted Circle Layout
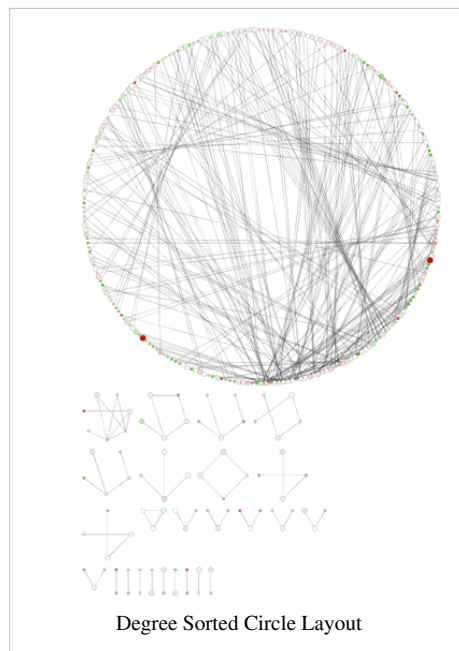
Attribute Circle Layout

- 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 columns to layout.

Attribute Circle Layout
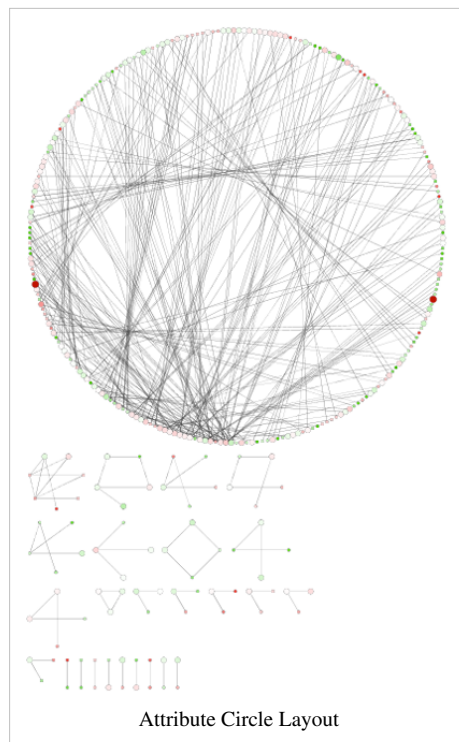
Group Attributes Layout

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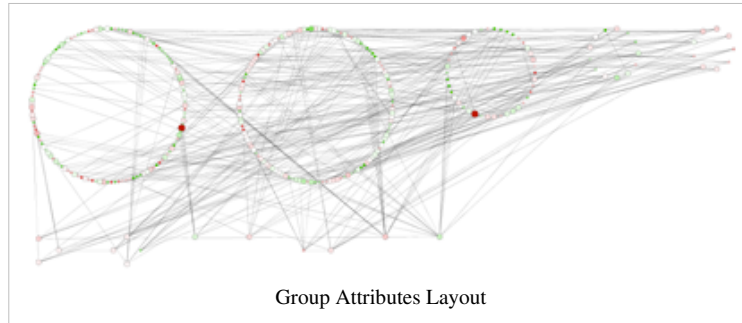
These layouts are useful to represent data columns associated with the nodes of a network, however, they don't provide much information about the network structure itself. For that, using more complicated layouts are required.

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 [3]).

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
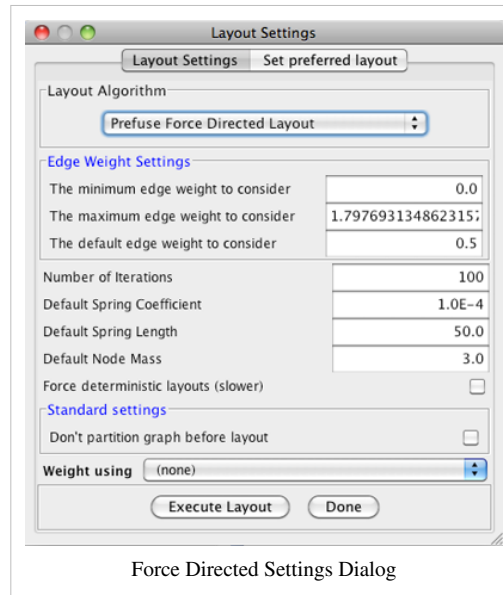
- Lets start by creating a layout using the default parameters.
    - Select **Execute Layout**.
    - Note how this exposes more of the structure of the network than any of the previous layouts.
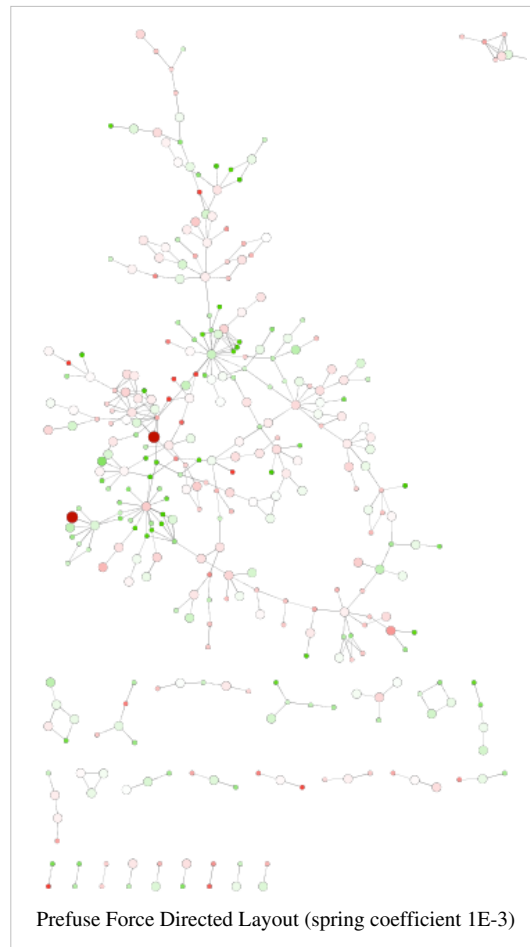
Prefuse Force Directed Layout
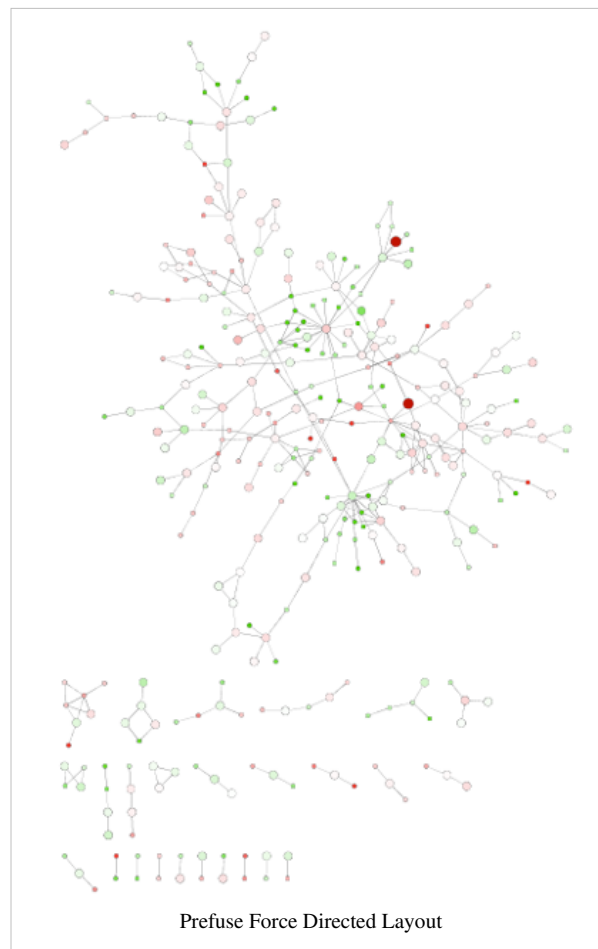
Now, let's see what the parameters do.

- 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)
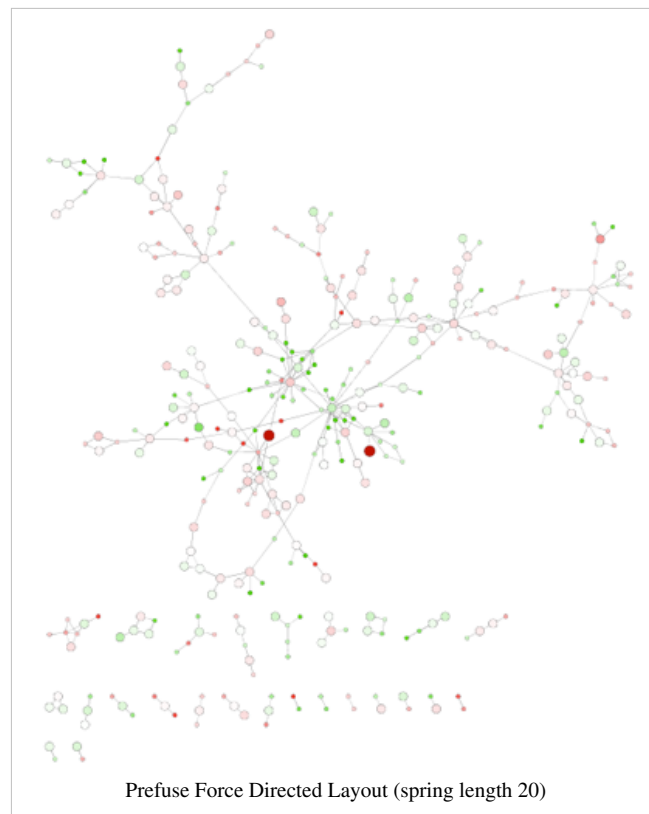
- Finally, lets change **Default Spring Length** back to **50** and the **Default Spring Coefficient** to **1E-3**. The spring coefficient is a measure of the strength of the spring.
- Now click **Execute Layout**. Note that the network remains pretty compact, even though we've reset the default spring 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 column 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**.
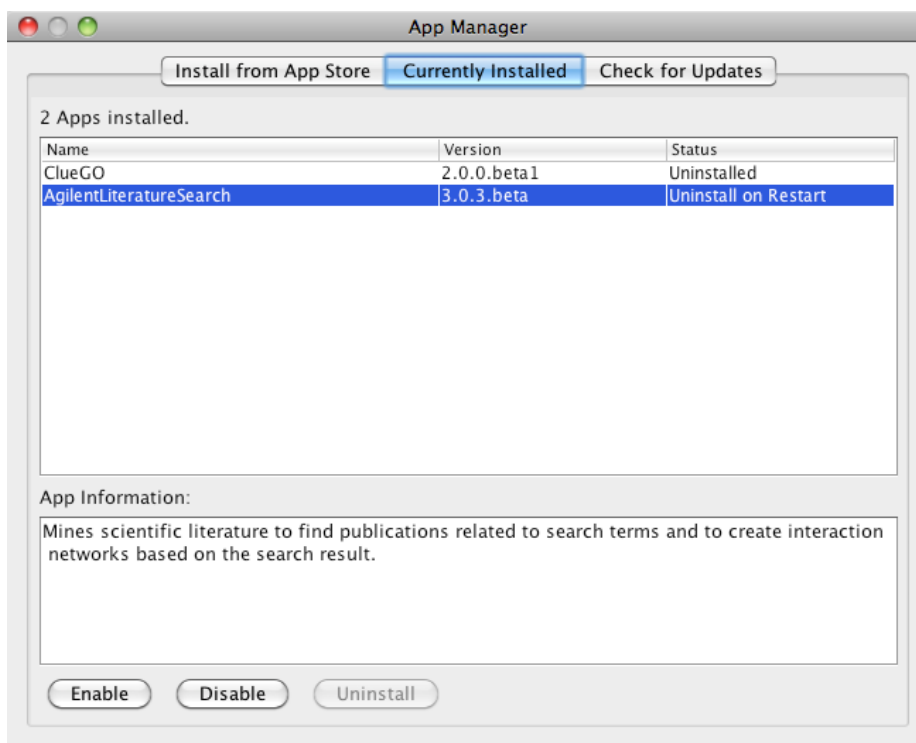
- **Currently Installed** folder lists any apps already installed. To find out more about a specific app, click on its name to display some basic information on the bottom of the window.
- **Install from App Store** tab displays an interface for interacting with the Cytoscape App Store.

  - 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.

References

[1] http://opentutorials.rbvi.ucsf.edu/index.php?title=Tutorial:Introduction_to_Cytoscape_3.1-part2&ce_slide=true&ce_style=cytoscape

[2] http://opentutorials.rbvi.ucsf.edu/index.php/File:Introduction_to_Cytoscape_3.1-part2.pdf

[3] http://prefuse.org

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