
Cytoscape User Manual

Release 3.10.0

The Cytoscape Consortium

Aug 02, 2023

Contents

1	Introduction	3
2	Launching Cytoscape	5
2.1	System Requirements	5
2.2	Getting Started	5
3	Command Line Arguments	9
4	Quick Tour of Cytoscape	11
4.1	Starter Panel	11
4.2	Basic Features	12
4.3	The Menus	14
4.4	Network Management	19
4.5	Network View Tools	23
5	Creating Networks	25
5.1	Import Fixed-Format Network Files	25
5.2	Import Networks from Unformatted Table Files	27
5.3	Import Networks from Public Databases	32
5.4	Create a New Network or Edit One Manually	35
6	Nested Networks	39
6.1	Creating Nested Networks	39
6.2	Visualization of Nested Networks	39
7	Supported Network File Formats	41
7.1	SIF Format	41
7.2	NNF	43
7.3	GML Format	47
7.4	XGMML Format	47
7.5	SBML (Systems Biology Markup Language) Format	48
7.6	BioPAX (Biological PAthways eXchange) Format	48
7.7	GraphML	48
7.8	Delimited Text Table and Excel Workbook	48
7.9	Cytoscape.js JSON	48
7.10	Cytoscape CX	53

8	Node and Edge Column Data	55
8.1	Import Data Table Files	55
8.2	Legacy Cytoscape Attributes Format	57
8.3	Import Data Table from Public Databases	61
8.4	Mapping Identifiers	63
9	Column Data Functions and Equations	65
9.1	Column Formulas	65
9.2	The Formula Builder	70
9.3	A Note for App Writers	72
10	Finding and Filtering Nodes and Edges	73
10.1	Search Bar	73
10.2	The Select Menu	74
10.3	cyChart	75
10.4	Filters	80
10.5	Diffusion	89
11	Navigation and Layout	91
11.1	Basic Network Navigation	91
11.2	Other Mouse Behaviors	92
11.3	Manual Layout	94
11.4	Node Layout Tools	94
11.5	Edge Bend and Automatic Edge Bundling	96
11.6	Automatic Layout Algorithms	99
11.7	yFiles Layouts	109
11.8	Layout Parameters	111
12	Styles	113
12.1	What are Styles?	113
12.2	Introduction to the Style Interface	120
12.3	Introduction to Style	123
12.4	Images, Charts and Gradients	126
12.5	Styles Tutorials	133
12.6	Advanced Topics	160
12.7	Managing Styles	167
13	Network Annotations	169
13.1	Types of Annotations	170
13.2	The Annotation Panel	170
13.3	Creating Annotations	171
13.4	Selecting Annotations	172
13.5	Moving Annotations Backwards and Forwards	173
13.6	Renaming Annotations	173
13.7	Editing Annotations	174
13.8	Deleting Annotations	175
13.9	Grouping Annotations	175
14	Command Panel	177
15	Cytoscape Web Browser	179
15.1	Cytoscape Web Browser Window	180
15.2	Cytoscape Web Browser in Results Panel	181
15.3	Why Cytoscape Web Browser?	181

16 Merge	183
16.1 Merge Networks	183
16.2 Merge Tables	184
17 Analyzer	187
17.1 Network Analysis	187
17.2 NetworkAnalyzerDemo	188
18 Enrichment Table	191
18.1 Organism and Gene ID	191
18.2 Running Enrichment Analysis	192
18.3 Filter Results	192
18.4 Charts	193
18.5 Term Selection	193
18.6 Optional Settings	193
18.7 Enrichment Map Generation	194
18.8 Export results	194
18.9 Automation	194
19 Cytoscape Preferences	195
19.1 Managing Properties	195
19.2 Managing Bookmarks	197
19.3 Managing Proxy Servers	198
19.4 Managing Group Settings	199
19.5 Managing OpenCL Settings	201
20 Linkout	203
20.1 Adding and Removing Links	204
21 Panels	207
21.1 Managing Panels	208
21.2 Other Features	213
22 Rendering Engine	217
22.1 What is Level of Detail (LOD)?	217
23 Export Your Data	219
23.1 Raw Data Export	219
23.2 Exporting for Publication	226
24 Cytoscape and OpenCL (Computing on the GPU)	237
24.1 What it is for?	237
24.2 Setup & Configuration	237
24.3 OpenCL/GPU Troubleshooting	238
25 Cytoscape.js and Cytoscape	239
25.1 What is Cytoscape.js?	239
25.2 Data Exchange between Cytoscape and Cytoscape.js	242
25.3 Export Styles to Cytoscape.js	243
25.4 Build Your Own Web Application with Cytoscape.js	243
26 Cytoscape Automation	245
26.1 R and Python Packages	245
26.2 Commands	245
26.3 CyREST Interface Layer	246

27 Cytoscape Privacy Policy	251
28 Basic Expression Analysis Tutorial	253

The Cytoscape User Manual copyright is owned by The Cytoscape Consortium, and is made available under the same GPL license as Cytoscape itself: LGPL 2.1, the GNU Lesser General Public License, version 2.1, February 1999 available in text at <http://www.gnu.org/licenses/lgpl-2.1.html>.

Copyright (c) 2001-2023 The Cytoscape Consortium

Table of Contents

CHAPTER 1

Introduction

This version of Cytoscape builds upon the 3.x architecture, developer API and set of user controls established. If you're familiar with former versions of Cytoscape, this version will feel completely familiar and you'll be all set to go. In future releases, we will continue to tweak and improve both the software and the documentation. This manual will be updated to reflect all the latest changes.

If you would prefer to learn by doing, consider starting with the [Basic Expression Analysis Tutorial](#).

*This manual describes the installation and use of Cytoscape. For a more thorough understanding of Cytoscape and its ecosystem, we highly recommend reading the **Welcome Letter** accessible on the <http://cytoscape.org> website.*

Launching Cytoscape

Cytoscape is a Java application verified to run on the Linux, Windows, and Mac OS X platforms. Although not officially supported, other UNIX platforms such as Solaris or FreeBSD may run Cytoscape if Java version 8 is available for the platform.

2.1 System Requirements

The system requirements for Cytoscape depend on the size of the networks you want to load, view and manipulate.

Note that as of Cytoscape v3.2, networks are loaded faster and in less memory than with previous versions. While this is good news, networks created on v3.2 on a given memory configuration (e.g., 1GB) may not be loadable by prior Cytoscape versions on the same memory configuration.

*Specific system requirements, limitations, and configuration options apply to each platform, as described in the **Release Notes** available on the <http://cytoscape.org> website.*

2.2 Getting Started

2.2.1 Install Java

Cytoscape requires Java 17.

- We recommend a 64 bit Java Runtime Environment (JRE) such as OpenJDK 17.
- While Cytoscape versions prior to v3.2 run on Java 6, Oracle and other JVM suppliers have dropped Java 6 support. Consequently, Cytoscape v3.2 and later don't support Java 6. With v3.3, we also dropped support for Java 7, and with the release of Cytoscape v3.8 we dropped support for Java 8. With v3.10, we dropped support for Java 11, for the same reason.

For additional information, select the Release Notes button on the [Cytoscape website](http://cytoscape.org).

2.2.2 Install Cytoscape

Downloading and Installing

There are a number of options for downloading and installing Cytoscape. See the download page at the <http://cytoscape.org> website for all options.

- Automatic installation packages exist for Windows, Mac OS X, and Linux platforms – best for most users.
- You can install Cytoscape from a compressed archive distribution.
- You can build Cytoscape from the source code. You can check out the latest and greatest software from our [Git repository \(https://github.com/cytoscape/cytoscape\)](https://github.com/cytoscape/cytoscape).

Unattended Installation

The easiest and most common way to install Cytoscape is by executing an [automatic installation package](#) downloaded from the Cytoscape web site. This will bring up a wizard that will lead you through the process, presenting choices for the installation directory, license agreement, file associations and privacy settings.

The installation process can be automated and made silent by executing the installation package with the “-q” command parameter (e.g., “Cytoscape_3_10_0-RC1_windows_64bit.exe -q”) from a command line or script. For this to succeed, your execution environment must already have sufficient privileges to install software (e.g., for Windows: administrator privileges). With a “-q” parameter, the installation package will automatically choose all default settings.

More automation flexibility is available using other settings and pre-programmed response files, as described in Appendix A of the [Install4j manual \(http://resources.ej-technologies.com/install4j/help/doc/help.pdf\)](http://resources.ej-technologies.com/install4j/help/doc/help.pdf).

Cytoscape Directories

Cytoscape installations (regardless of platform) contain the following files and directories:

The *p/* directory signifies the program directory, which varies from platform to platform. For Cytoscape to work properly, all files should be left in the directory in which they were unpacked. The core Cytoscape application assumes this directory structure when looking for the various libraries needed to run the application.

The *u/* directory signifies the user’s home directory, which varies from user to user and from platform to platform. To change the user home directory from the default, one can set the Java environment variable `user.home` to the desired directory – this is useful when Cytoscape is installed on a workstation, but the home directory is stored on a central file server. `user.home` can be set by adding the following option to the Cytoscape.vmoptions file or the `_JAVA_OPTIONS` environment variable, substituting the desired path as appropriate:

-Duser.home=/path/to/desired/home

Your operating system may have other mechanisms for setting environment variables – see your operating system documentation for further details.

A quick note on upgrading your Cytoscape installation

If you have a previous Cytoscape installation you have two options:

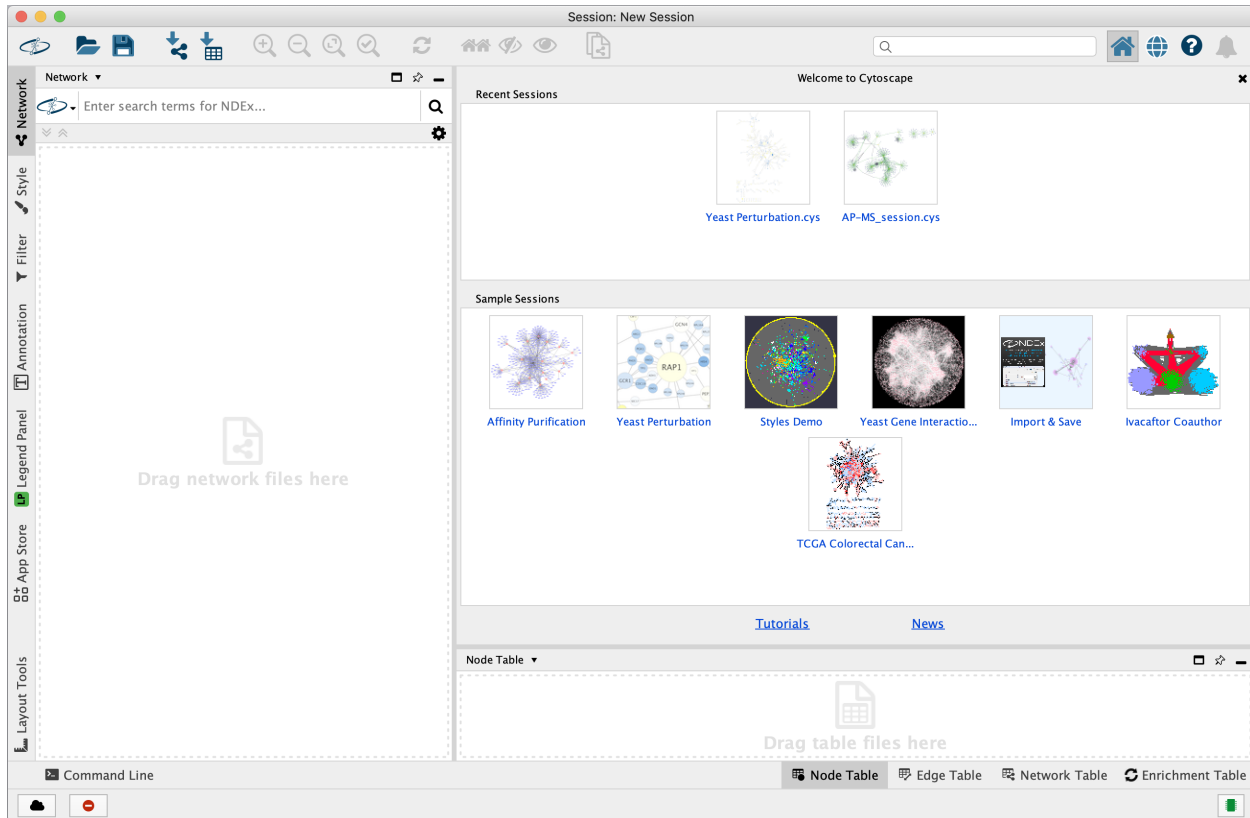
1. Starting with a clean slate. For this you should delete your previous installation directory and the `CytoscapeConfiguration` directory (see below for the location of this directory).
2. Just keep what you have and simply pick a distinct, new directory for installation. In the unlikely event that you should encounter any problem, delete the `.props` files in your `CytoscapeConfiguration` directory. If that doesn’t help try deleting the `CytoscapeConfiguration` directory. This latter step will cause you to

lose all of the apps that you have installed via the App Store, so only do that if you are having problems or if you don't mind reinstalling your apps. The core apps will not be affected by this step.

2.2.3 Launch the Application

As with any application, launch Cytoscape by double-clicking on the icon created by the installer, by running `cytoscape.sh` from the command line (Linux or Mac OS X) or by double-clicking `cytoscape.bat` or the Program Launch icon (Windows).

After launching Cytoscape a window will appear that looks like this:



If your Cytoscape window does not resemble this, further configuration may be required. Consult the **Release Notes** available on the <http://cytoscape.org> website.

2.2.4 Note on Memory Consumption

For most regular users, Cytoscape will estimate and reserve the proper amount of memory. An incorrect estimate may result in Cytoscape hanging at startup or Cytoscape unable to load your network. Unless Cytoscape fails to start or open your network, it has likely estimated the available memory correctly, and you can continue to the [Quick Tour](#). If Cytoscape misjudges the memory size or can't allocate enough memory, it could be that you're running with a **32 bit JRE** and could get better results by installing a **64 bit JRE** – see the Install Java section above.

When Cytoscape starts, it displays the current memory usage in the lower right corner of the main interface. You can click on the **Memory** button at any time to access an option to **Free Unused Memory**. While most users won't need to use this option, it can be useful for users who have multiple large networks loaded.

Overall Memory Size for Cytoscape

By default, Cytoscape uses an estimate for initial and maximum memory allocation based on your operating system, system architecture (32 or 64 bit), and installed memory. You can change Cytoscape's initial and/or maximum memory size by editing the *Cytoscape.vmoptions* file, which resides in the same directory as the Cytoscape executable. The file contains one option per line, with each line terminated by a linefeed, and an extra linefeed at the end of the file. Note that for the MacOS platform, the situation is slightly different – if you are launching Cytoscape by clicking on the Cytoscape icon, you must edit the *.../Cytoscape.app/Contents/vmoptions.txt* file instead. To access this in Finder, you will need to right-click the Cytoscape app icon and select **Show Package Contents**, which will display the Contents subdirectory that contains *vmoptions.txt*.

For example, if you want Cytoscape to initially allocate 2GB of memory and use up to a maximum of 4GB, edit the *Cytoscape.vmoptions* file to contain the following lines (... do not forget the linefeed at the end of each line, and an extra linefeed at the end of the file!):

-Xms2GB

-Xmx4GB

Stack Size

There is one more option related to memory allocation. Some of the functions in Cytoscape use larger stack space (a temporary memory for some operations, such as layout). Since this value is set independently from the values above, sometimes layout algorithms fail due to an *out of memory* error. To avoid this, you can set a larger heap size for Cytoscape tasks by using the **taskStackSize** option in the *cytoscape3.props* file (located in the *CytoscapeConfiguration* directory). This can be edited within Cytoscape using the Preferences Editor (**Edit** → **Preferences** → **Properties...**) - look for **taskStackSize**. The value should be specified in bytes.

Command Line Arguments

Cytoscape recognizes a number of optional command line arguments, including run-time specification of network files, node and edge data files, and session files. This is the output generated when Cytoscape is executed with the *-h* or *-help* flag:

```
usage: cytoscape.{sh|bat} [OPTIONS]
-h,--help                Print this message.
-v,--version              Print the version number.
-s,--session <file>      Load a cytoscape session (.cys) file.
-N,--network <file>      Load a network file (any format).
-P,--props <file>        Load cytoscape properties file (Java properties
                          format) or individual property: -P name=value.
-V,--vizmap <file>       Load vizmap properties file (Cytoscape VizMap
                          format).
-S,--script <file>       Execute commands from script file.
-R,--rest <port>         Start a rest service.
```

Any file specified for an option may be specified as either a path or as a URL. For example you can specify a network as a file (assuming that `myNet.sif` exists in the current working directory): `cytoscape.sh -N myNet.sif`.

Note: if there are spaces in the file path, be sure to put quotes around it: `cytoscape.bat -N "C:\Program Files\Cytoscape\sampleData\galFiltered.sif"`.

Or you can specify a network as a URL: `cytoscape.sh -N http://example.com/myNet.sif`.

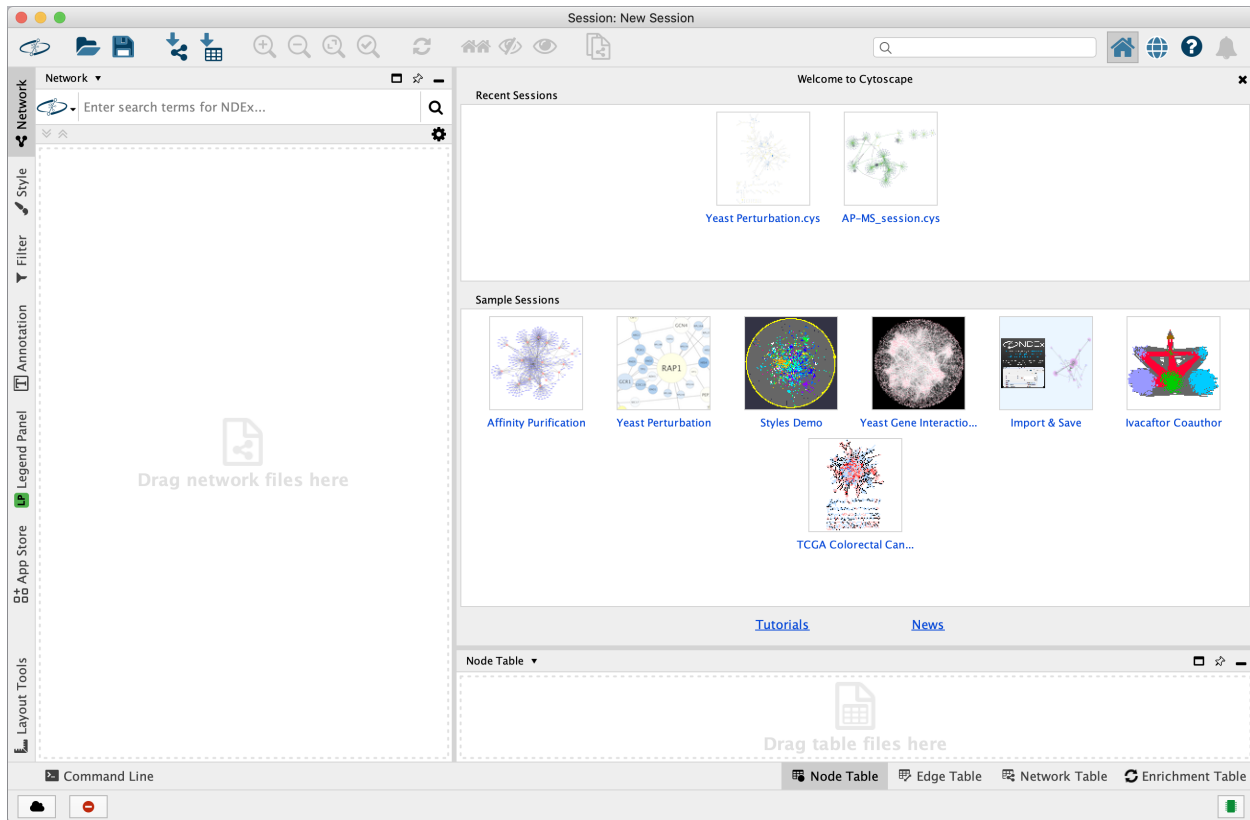
All options described above (except for starting a REST service) can be accessed from the menu once Cytoscape is running.

Quick Tour of Cytoscape

This chapter describes the basic layout and mechanics of using Cytoscape. If you would prefer to learn by doing, consider starting with the [Basic Expression Analysis Tutorial](#).

4.1 Starter Panel

When you start Cytoscape, you can access basic functions from the **Starter Panel**:



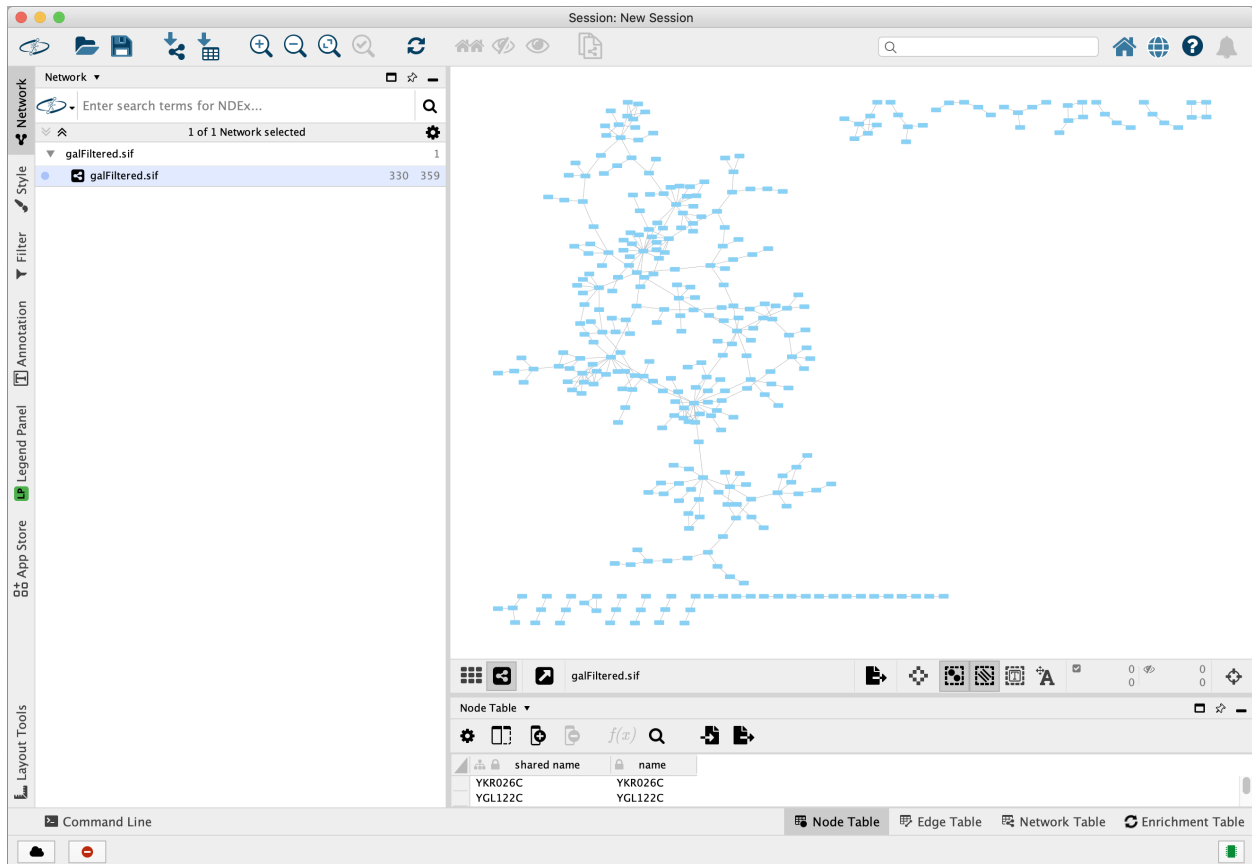
The **Starter Panel** is designed to give you quick access to a set of sample session files, as well as tutorials and Cytoscape news. The sample session files include a broad range of networks to give a sense of the diversity of interaction types, visualization styles and biological applications (see Network Table properties for more information about each sample session network). The **Starter Panel** will also present your own most recent sessions for quick access.

When you load a session file, the **Starter Panel** will disappear. You can display it at any time by choosing **View** → **Show Starter Panel**.

For information on user privacy, see the [Cytoscape Privacy Policy](#).


4.2 Basic Features

When a network is loaded, Cytoscape will look similar to the image below:




Most functionalities are self-explanatory, but we'll go through a concise explanation for clarity. The main window here has several components:

- The **Menu Bar** at the top (see below for more information about each menu).
- The **Tool Bar**, which contains icons for commonly used functions. These functions are also available via the menus. Hover the mouse pointer over an icon and wait momentarily for a description to appear as a tooltip. Right-clicking on the tool bar allows the contents to be customized.
- The **Network Panel** (**Network** panel of the **Control Panel**). At the top of the Network Panel is a Search bar, with direct access to multiple external resources.
- The main **Network View Window**, which displays the network. At the bottom of the network view are a set of network view tools.
- The **Table Panel** (bottom right panel), which displays columns of associated data for nodes, edges and network-wide, and enables you to modify the values of column data.

The **Network Panel** and **Table Panel** are dockable tabbed Panels. You can undock any of these panels by clicking on the **Float Window** control  in the upper-right corner of each panel. This is useful when you want assign the network panel as much screen space as possible. You will now have two Cytoscape windows, the main window, and a new window labeled Table Panel, similar to the one shown below. A popup will be displayed when you put the mouse pointer on a cell.

To dock the window again, click the **Dock Window** icon .

Clicking the **Minimize** icon  will minimize the panel; the panel can be shown again by choosing **View** → **Show**

and selecting the relevant panel, or by clicking on one of the tabs in the minimized panel, for example **Network** or **Node Table**, and then clicking the **Dock** icon.

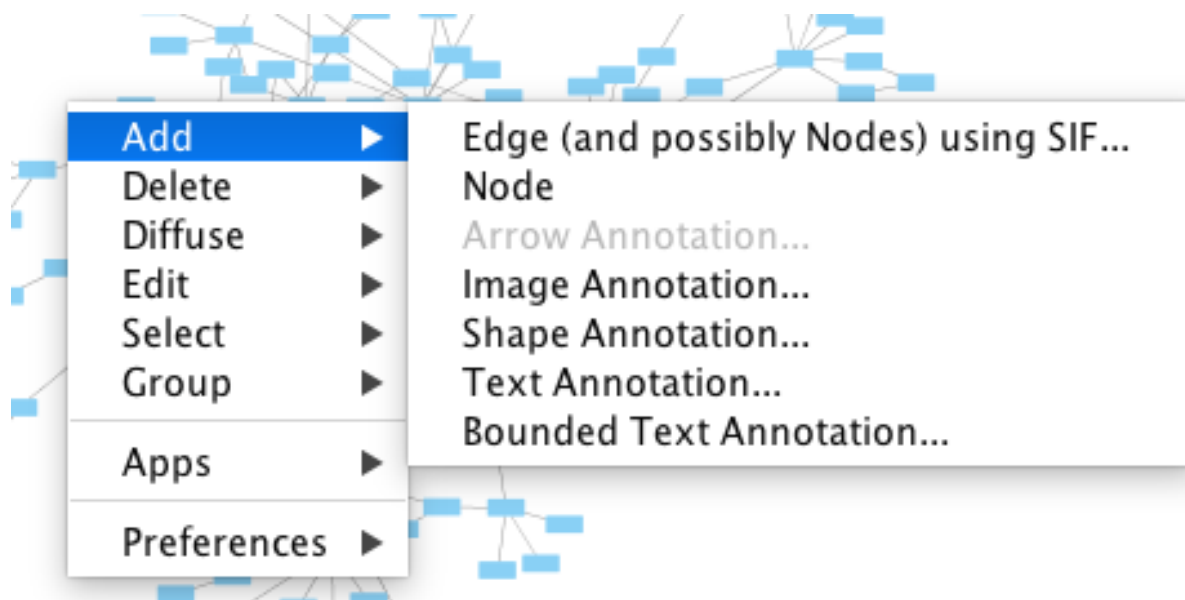


shared name	name
YKR026C	YKR026C
YGL122C	YGL122C
YGR218W	YGR218W
YGL097W	YGL097W
YOR204W	YOR204W
YLR249W	YLR249W
YPR080W	YPR080W
YBR118W	YBR118W

For more information on the panels in Cytoscape, see the [Panels](#) section.

4.2.1 Network Editing

Cytoscape also has an edit functionality that enables you to build and modify networks interactively within the network canvas. To edit a network, just right-click on the open space of network window, select the menu item **Add** → **Node**, a new node will be added to the canvas. To add an edge, right click on a node, choose the menu item **Edit** → **Add Edge**. Then select the target node, a new edge will be added between the two nodes. In a similar way annotation objects can be added; pictures, shapes or textboxes; much like in MS PowerPoint or similar software. Detailed information on network editing can be found in the [Editing Networks](#) section.



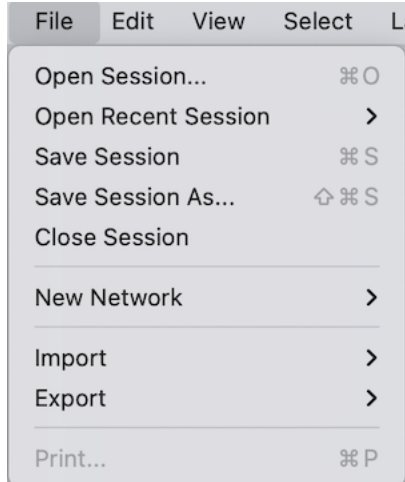
4.3 The Menus

4.3.1 File

The **File** menu contains most basic file functionality: **File** → **Open Session** for opening a Cytoscape session file; **File** → **New Network** for creating a new network, either blank for editing, or from an existing network; **File** → **Save** for

saving a session file; **File** → **Import** for importing data such as networks and tables; and **File** → **Export** for exporting data. **File** → **Export Network to Image** lets you export the network in either JPEG, PDF, PNG, PostScript or SVG format. **File** → **Export Network to Web Page** lets you export the entire session or a single network as a Web page using Cytoscape.js.

File → **Open Recent Session** will list recently opened session files for quick access. **File** → **Print...** allows printing.



4.3.2 Edit

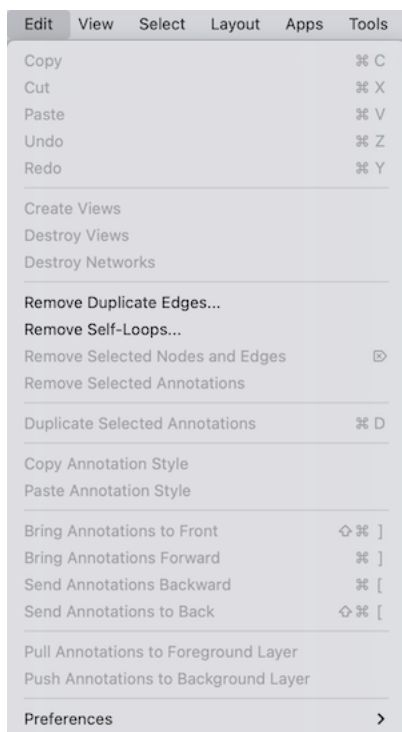
The **Edit** menu contains **Cut**, **Copy** and **Paste** functions, as well as **Undo** and **Redo** functions which undo and redo edits made in the **Table Panel**, edits to the network and to layout. The **Undo/Redo** functions work on the last 10 tasks performed.

There are also options for creating and destroying views (graphical representations of a network) and networks (the raw network data - not yet visualized), as well as an option for deleting selected nodes and edges from the current network. All deleted nodes and edges can be restored to the network via **Edit** → **Undo**.

Other editing options include; **Remove Duplicated Edges** will delete edges that are duplicates (having the same source and target nodes), keeping one edge, **Remove Self-Loops** removes edges that have the same source and target node, and **Delete Selected Nodes and Edges...** deletes a selected subset of the network. **Rename Network...** allows you to rename the currently selected network.

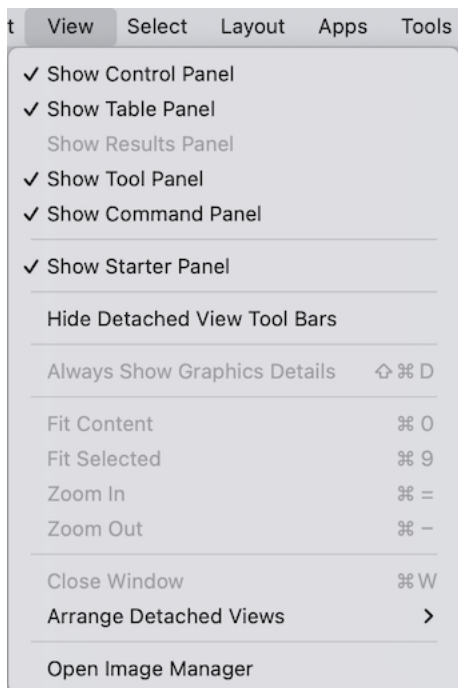
A set of functions for bringing annotations forward, backward etc, and pushing/pulling them to the foreground vs background layer are also available in the Edit menu.

Editing preferences for properties and apps are found under **Edit** → **Preferences** → **Properties...** More details on how to edit preferences can be found [here](#).



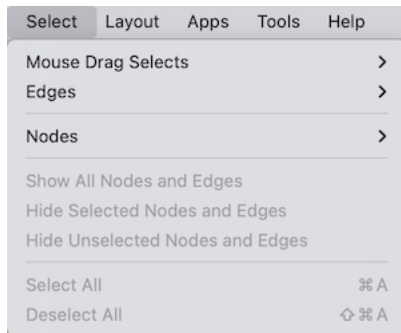
4.3.3 View

The **View** menu allows you to display or hide panels, including the **Control Panel**, **Table Panel**, **Result Panel**, **Tool Panel** and the **Command Panel**. In addition, it also provides a means for viewing the **Starter Panel**. It also provides the control of other view-related functionality.



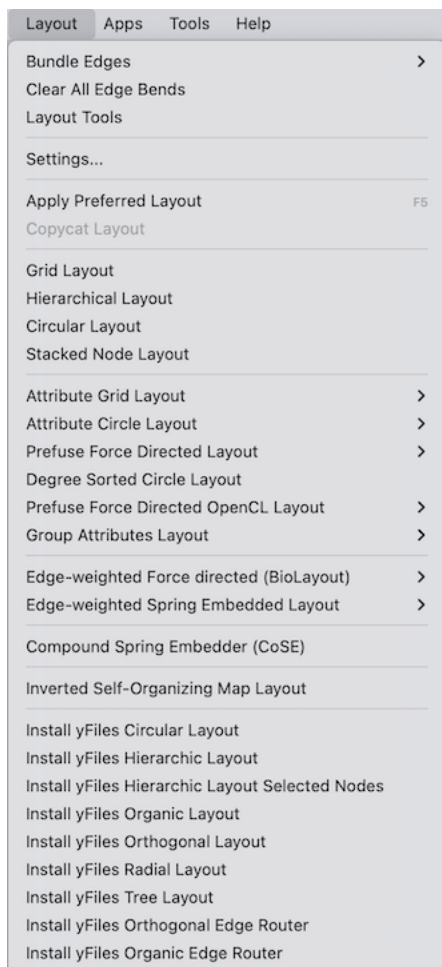
4.3.4 Select

The **Select** menu contains different options for selecting nodes and edges.



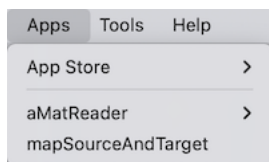
4.3.5 Layout

The **Layout** menu has an array of features for visually organizing the network. The features in the top portion of the network (**Bundle Edges**, **Clear All Edge Bends**, **Node Layout Tools**) are tools for manipulating the network visualization. The bottom section of the menu lists a variety of layout algorithms which automatically layout a network.



4.3.6 Apps

The **Apps** menu gives you access to the **App Store** (**Apps** → **App Store**) for managing (install/update/delete) your apps and may have options added by apps that have been installed. Depending on which apps are loaded, the apps that you see may be different than what appear here. The below picture shows a Cytoscape installation without installed apps.



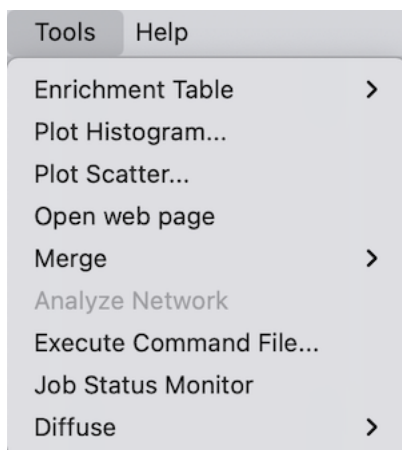
Note: A list of available Cytoscape apps with descriptions is available online at: <http://apps.cytoscape.org>.

In previous versions of Cytoscape, apps were called plugins and served a similar function.

4.3.7 Tools

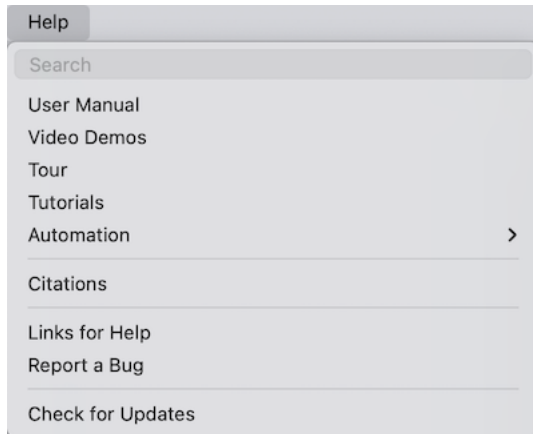
The **Tools** menu contains advanced features like **Enrichment Table**, **cyChart**, **Analyze Network**, **Open web page**, **Merge**, **Execute Command File...**, **Job Status Monitor** and **Diffuse**.

Cytoscape Web Browser allows for viewing any html page directly in Cytoscape. The web browser can be opened in a separate window or can be launched in the **Results Panel**.

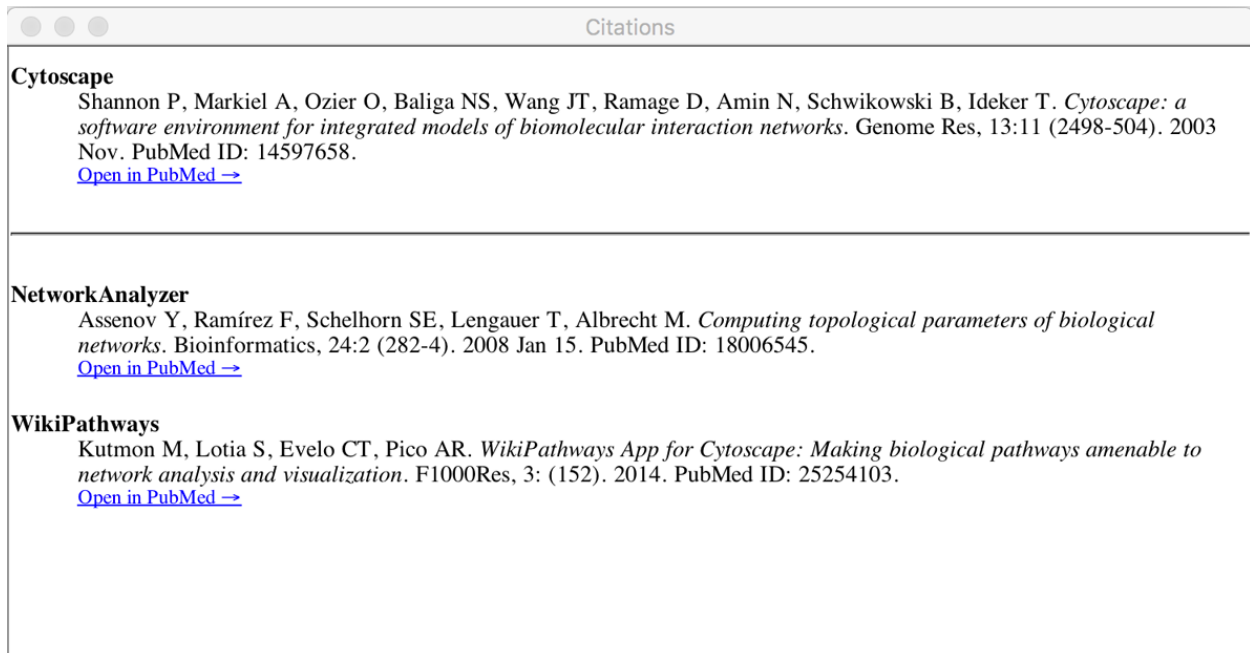


4.3.8 Help

The **Help** menu allows you to launch the online help viewer and browse and search this manual. It also provides direct access to a **Tour of Cytoscape**, as well as a full listing of Cytoscape tutorials. Tutorial content opens automatically in the **Cytoscape Web Browser**. Video demos are also linked to directly from the Help menu.



The **Citations** option displays the main literature citation for Cytoscape, as well as a list of literature citations for installed apps. The list will be different depending on the set of apps you have installed.

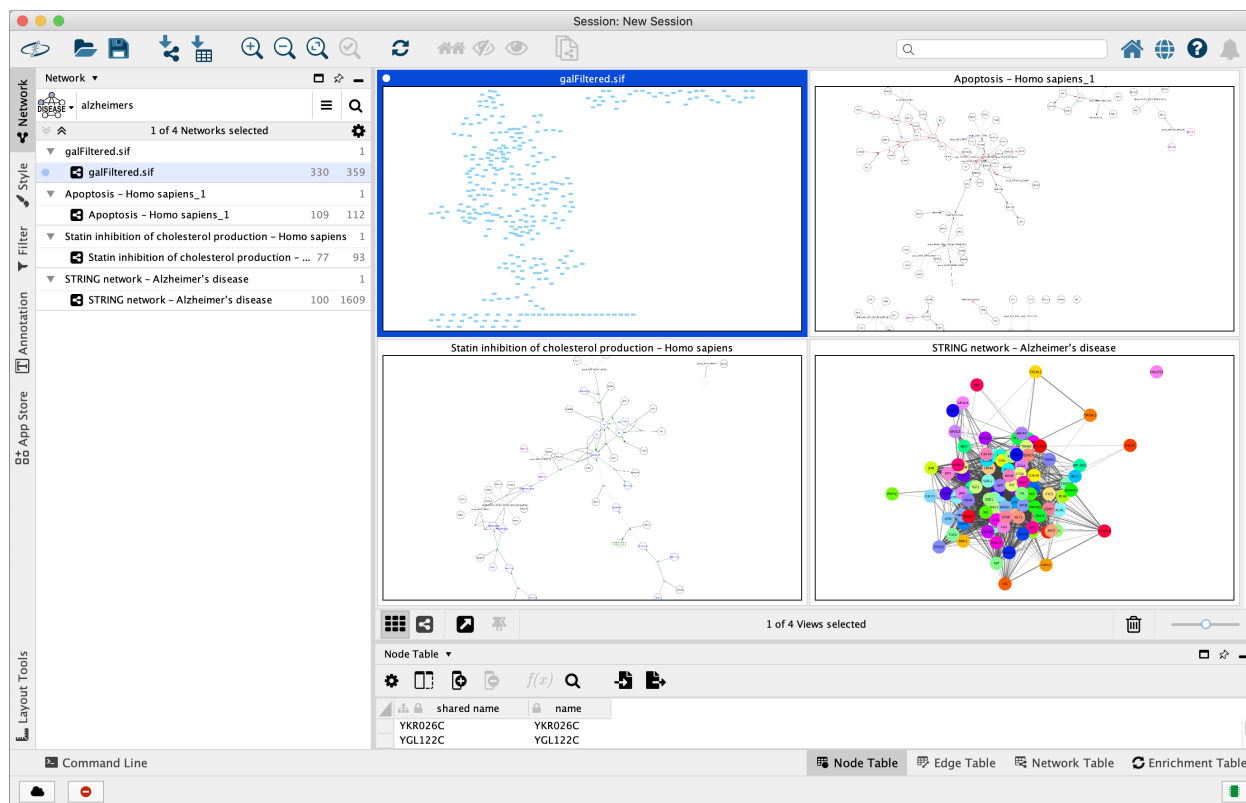


The **Help** menu also allows you to connect directly to **Cytoscape Help Desk** and the **Bug Report** interface.

4.4 Network Management

Cytoscape allows multiple networks to be loaded at a time, either with or without a view. A network stores all the nodes and edges that are loaded by the user and a view displays them.

An example where a number of networks have been loaded is shown below:



The network manager (in the **Control Panel**) shows the networks that are loaded. Clicking on a network here will make that view active in the main window, if the view exists.

- Each network has a name and size (number of nodes and edges), which are shown in the network manager. The number of nodes and edges is shown by default but this can be disabled under **Options** → **Show Number of Nodes and Edges**.
- If a network is loaded from a file, the network name is the name of the file. The list of networks can be sorted alphabetically by network name by clicking on the **Options** button at the top right and selecting **Sort Network by Name**.
- By default, the network provenance history is also shown in the **Network Panel**, for example showing if a network originated as a subnetwork from another network. This can be disabled under **Options** → **Show Network Provenance History**.

Some networks are very large (thousands of nodes and edges) and can take a long time to display. For this reason, a network in Cytoscape may not contain a view. Networks that have a view are in normal black font and networks that don't have a view are highlighted in red. You can create or destroy a view for a network by right-clicking the network name in the network manager or by choosing the appropriate option in the **Edit** menu. You can also destroy previously loaded networks this way.

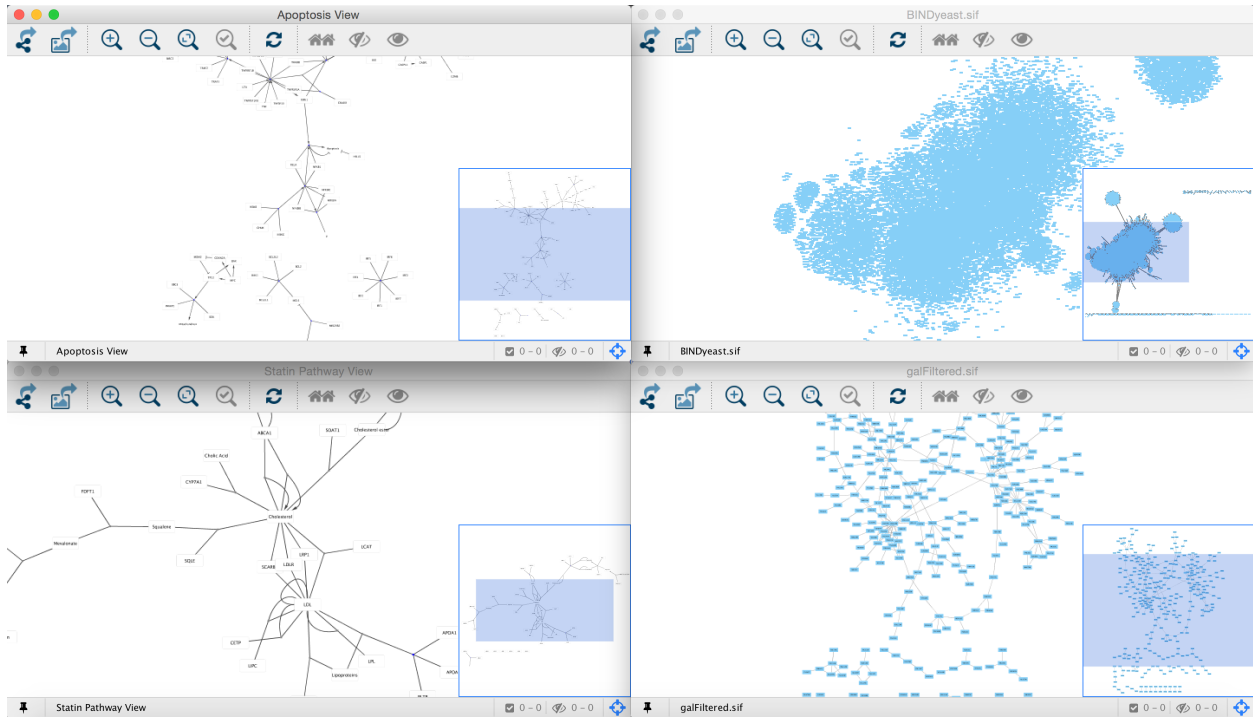
Certain operations in Cytoscape will create new networks. If a new network is created from an old network, for example by selecting a set of nodes in one network and copying these nodes to a new network (via the **File** → **New Network** option), it will be shown immediately follows the network that it was derived from.

Network views can also be detached (undocked) from the main Cytoscape window. When detached, a view window can be dragged to another monitor, resized, maximized and minimized by using the normal window controls for your operating system. Notice, however, that closing a view window does not destroy it, but simply reattaches it to the Cytoscape window.

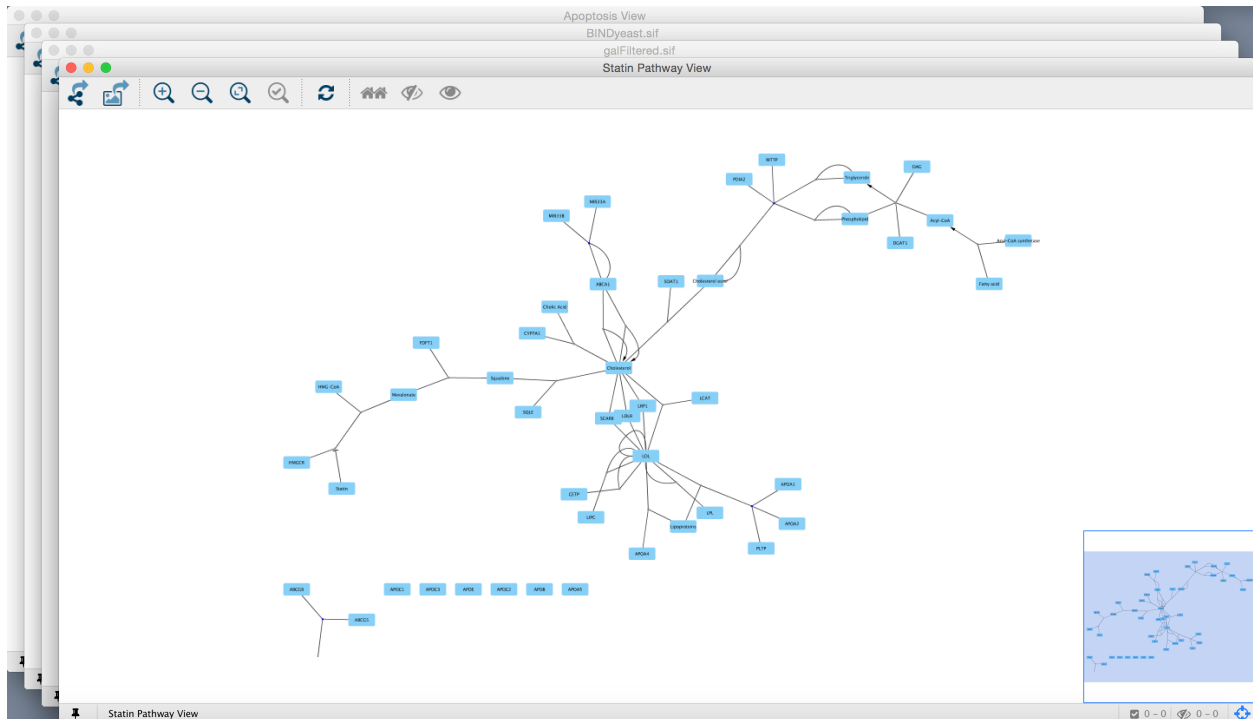
4.4.1 Arrange Network Windows

When you have detached network view windows, you can arrange them by selecting one of these options under **View** → **Arrange Detached Views**:

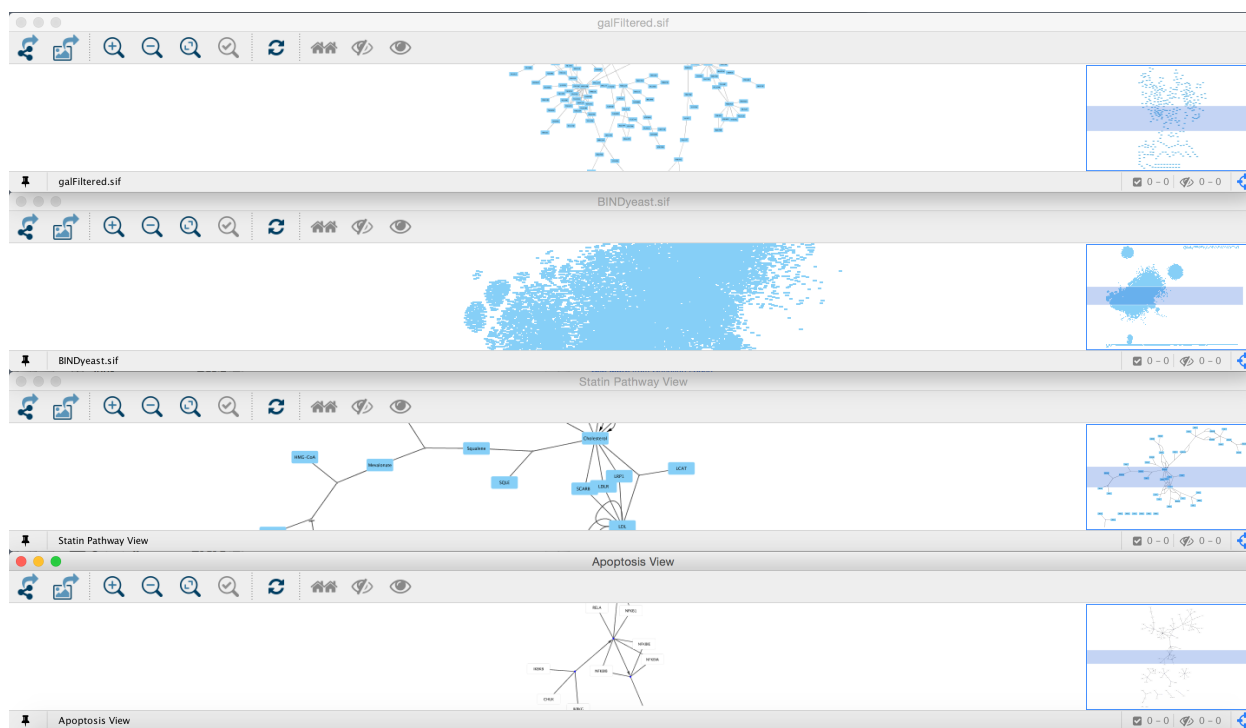
Grid



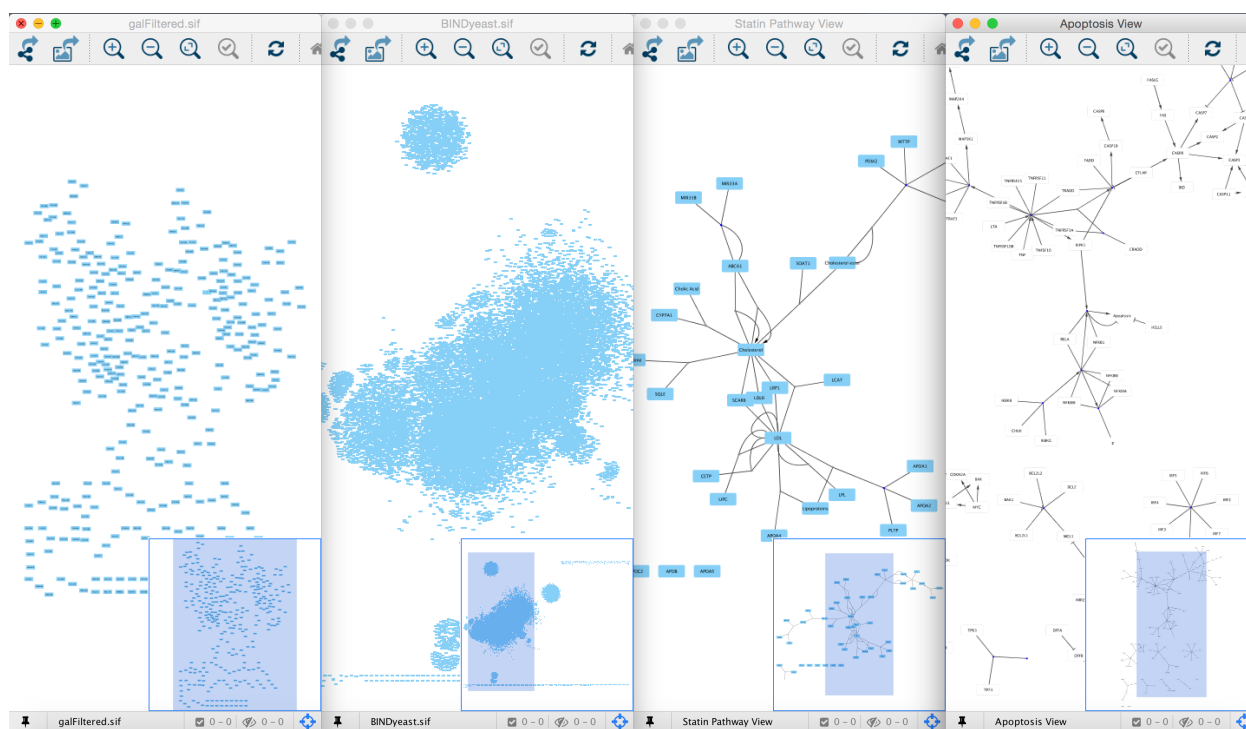
Cascade



Vertical Stack



Side by Side



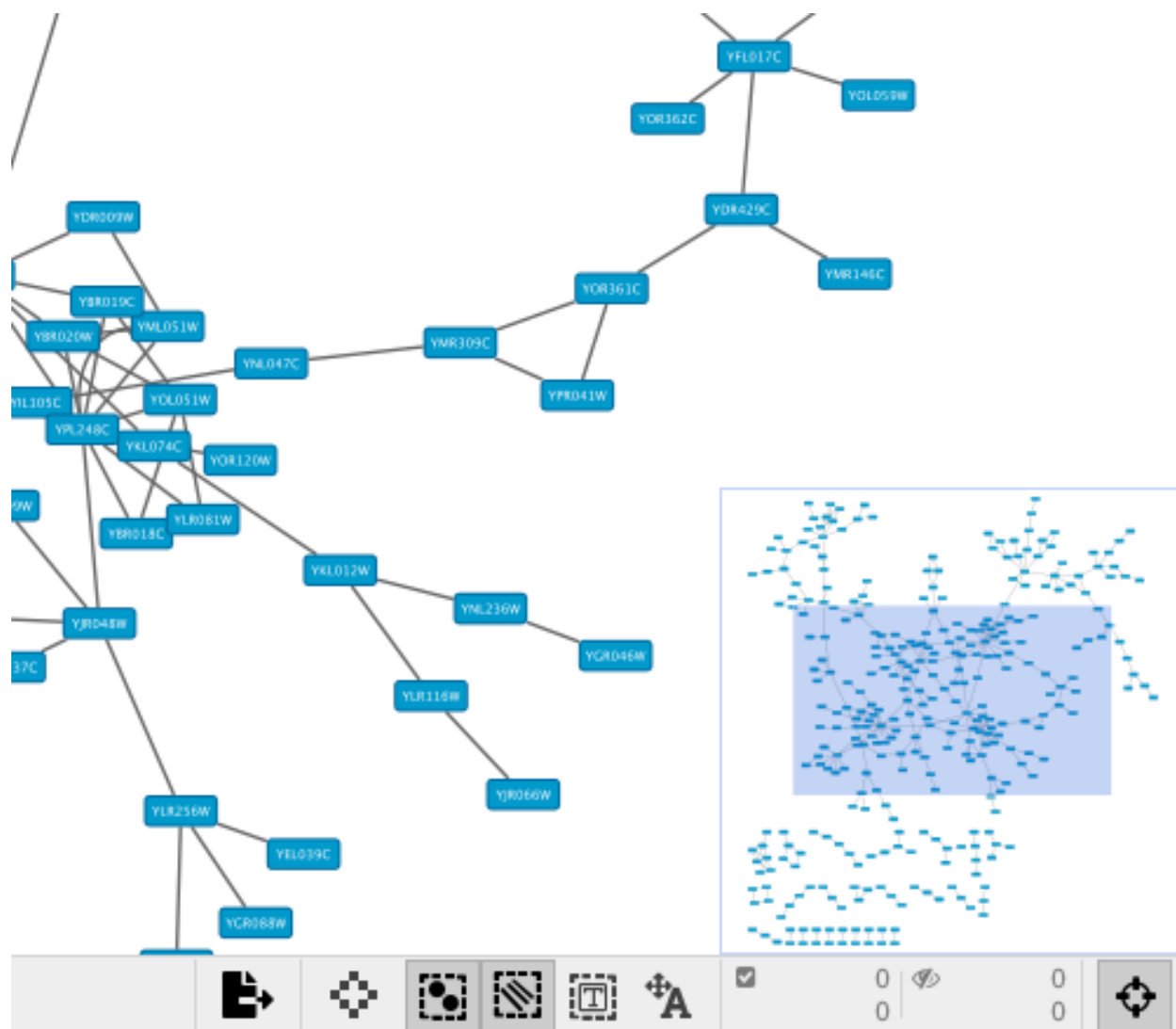
4.5 Network View Tools

At the bottom of the Network View Window is a set of network tools:



- **Show Grid** will arrange all loaded networks as a grid.
- **Show Network** will show the currently selected network.
- **Detach View** detaches the network view window from the main Cytoscape window.
- **Export to File...** gives you options to export the network or image.
- **Always Show Graphics Details** forces the rendering of graphics details. It is turned off by default.
- **Toggle Node Selection** allows you to turn off/on node selection. It is turned on by default.
- **Toggle Edge Selection** allows you to turn off/on edge selection. It is turned on by default.
- **Toggle Annotation Selection** allows you to turn off/on annotation selection. It is turned off by default.
- **Toggle Label Selection** allows you to turn off/on node/edge label selection. It is turned off by default.
- **Hide Navigator** lets you hide the Navigator ("bird's eye view").

The **Navigator** (or bird's eye view) shows an overview of the network. It can be used to navigate around a large network view. The blue rectangle indicates the portion of the network currently displayed in the network view window, and it can be dragged with the mouse to view other portions of the network. Zooming in will cause the rectangle to appear smaller and vice versa.



Creating Networks

There are 4 different ways of creating networks in Cytoscape:

1. Importing pre-existing, fixed-format network files.
2. Importing pre-existing, unformatted text or Excel files.
3. Importing data from from public databases.
4. Creating an empty network and manually adding nodes and edges.

5.1 Import Fixed-Format Network Files

Network files can be specified in any of the formats described in the [Supported Network Formats](#) section. Networks are imported into Cytoscape via **File** → **Import**. The network file can either be located directly on the local computer, or found on a remote computer (in which case it will be referenced with a URL).

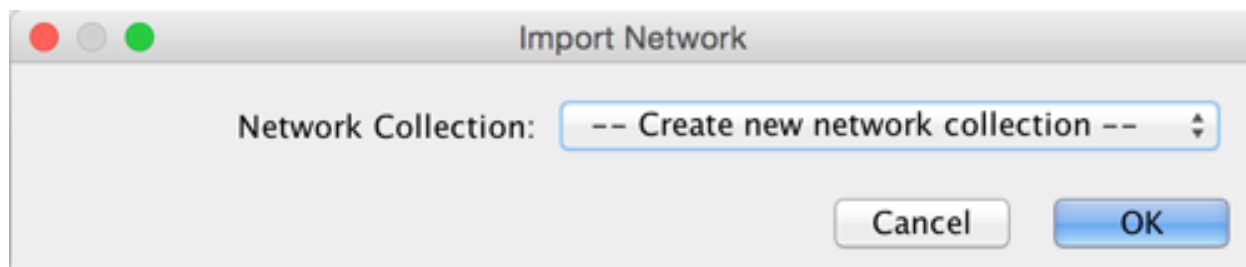
5.1.1 Load Networks from Local Computer

In order to load a network from a local file you can select **File** → **Import** → **Network from File...** or click on



on the tool bar. Choose the correct file in the file chooser dialog and press **Open**. Some sample network files of different types have been included in the sampleData folder in Cytoscape.

After you choose a network file, another dialog will pop up. Here, you can choose either to create a new network collection for the new network, or load the new network into an existing network collection. When you choose the latter, make sure to choose the right mapping column to map the new network to the existing network collection.



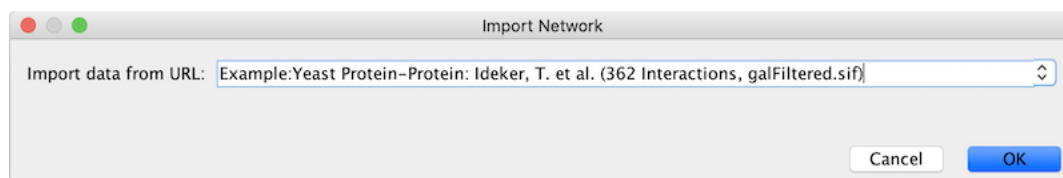
Network collections in Cytoscape are used to organize related networks, for example subnetworks. Networks in a collection are linked through the **shared name** node attribute; the **shared name** attribute will be added upon import. This attribute is useful when you want to change a node name across all networks in a collection.

Alternatively, you can simply drag and drop a network file from the desktop into the **Network** tab of the **Control Panel**, rather than selecting the file from the menu option.

Network files in SIF, GML, and XGMML formats may also be loaded directly from the command line using the `-N` option.

5.1.2 Load Networks from a Remote Computer (URL import)

To load a network from a remote file, select **File** → **Import** → **Network from URL...** In the import network dialog, insert the appropriate URL, either manually or using URL bookmarks. Bookmarked URLs can be accessed by clicking on the arrow to the right of the text field (see the Bookmark Manager in [Preferences](#) for more details on bookmarks). Also, you can drag and drop links from a web browser to the URL text box. Once a URL has been specified, click on the OK button to load the network.



For network files stored in cloud storage, the default URL does not always work in Cytoscape and requires transformation before it can be used. Here are examples of transformation of the default URL for some common cloud storage options:

Dropbox

- Default URL: <https://www.dropbox.com/s/077w3i4500dxrsm/galFiltered.sif?dl=0>
- Cytoscape URL: <https://dl.dropboxusercontent.com/s/077w3i4500dxrsm/galFiltered.sif>

Instructions: Replace `www.dropbox.com` with `dl.dropboxusercontent.com` AND remove `?dl=0`

Google Drive

For files smaller than 100K:

- Default: https://drive.google.com/file/d/1hHO4ErMx7HMo-_sRV_PfeoM3lnn6ZDLw/view?usp=sharing
- Cytoscape URL: https://drive.google.com/uc?export=download&id=1hHO4ErMx7HMo-_sRV_PfeoM3lnn6ZDLw

Instructions: Replace `file/d/` with `uc?export=download&id=` AND remove `/view?usp=sharing`

You may see an intermediate import window, described in the section below, where you may need to change the delimiter and define source, target and interaction. For this particular example, in **Advanced** change the **Delimiter** to **Space**, unselect **Use first line as column names** and set the first column as **Source**, the third column as **Target** and the second column as **Interaction Type**.

GitHub

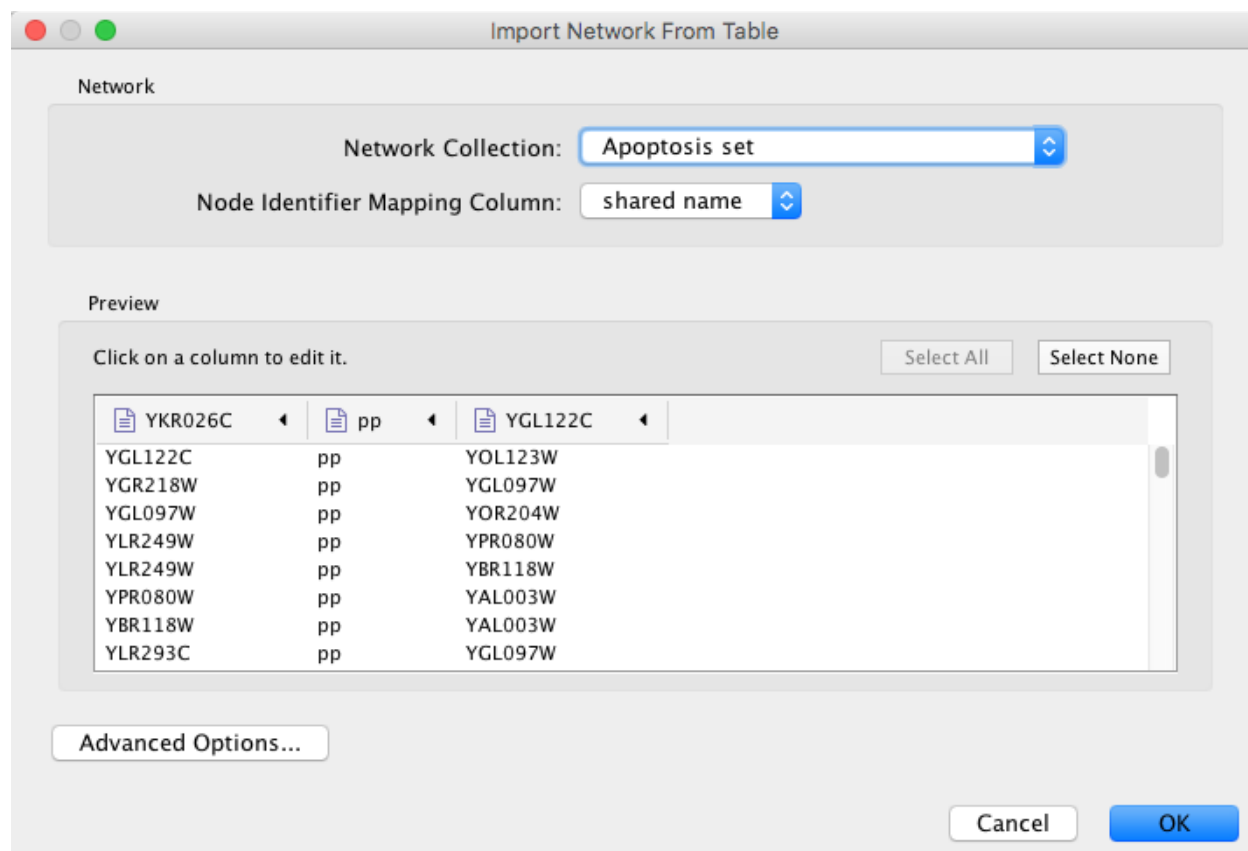
- Default URL: `https://github.com/bdemchak/cytoscape-jupyter/blob/main/sanity-test/data/galFiltered.sif`
- Cytoscape URL: `https://raw.githubusercontent.com/bdemchak/cytoscape-jupyter/main/sanity-test/data/galFiltered.sif`

Instructions: Replace `github.com` with `raw.githubusercontent.com` AND remove `/blob`

Another issue for network import is the presence of firewalls, which can affect which files are accessible to a computer. To work around this problem, Cytoscape supports the use of proxy servers. To configure a proxy server, go to **Edit** → **Preferences** → **Proxy Settings...** This is further described in the [Preferences](#) section.

5.2 Import Networks from Unformatted Table Files

Cytoscape supports the import of networks from delimited text files and Excel workbooks using **File** → **Import** → **Network from File...** An interactive GUI allows users to specify parsing options for specified files. The screen provides a preview that shows how the file will be parsed given the current configuration. As the configuration changes, the preview updates automatically. In addition to specifying how the file will be parsed, the user must also choose the columns that represent the source and target nodes as well as an optional edge interaction type. For detailed instructions, see Basic Operations below.



5.2.1 Supported File Types

The import function supports delimited text files and Microsoft Excel Workbooks. For Excel Workbooks with multiple sheets, one sheet can be selected for import at a time. The following is a sample table file:

The network table files should contain at least two columns for creating network with edges. If the file has only one column, the created network will not contain any edges. The interaction type is optional in this format. Therefore, a minimal network table looks like the following:

One row in a network table file represents an edge and its edge data columns. This means that a network file is considered a combination of network data and edge column data. A table may contain columns that aren't meant to be edge data. In this case, you can choose not to import those columns by clicking on the column header in the preview window. This function is useful when importing a data table like the following (1):

Unique ID A	Unique ID B	Alt ID A	Alt ID B	interaction detection methods	species A	species B	Interactor types	Source database	Interactoin ID
7025	5747	TRIP6	PTK2	w HPRD	Mammalia	Homo sapiens	protein protein	HPRD Marcotte	0
4174	7311	MCM5	UBA52	neighboring_reaction	Homo sapiens	Homo sapiens	protein protein	Reactome	1
7040	7040	TGFB1	TGFB1	nmr	Homo sapiens	Homo sapiens	protein protein	BIND	2

This data file is a tab-delimited text file and contains network data (interactions), edge data, and node data. To import network and edge data from this table, choose *Unique ID A* as source, *Unique ID B* as target, and *Interactor types* as interaction type. Next, turn off columns used for node data (*Alt ID A*, *species B*, etc.). Other columns can be imported as edge data.


The network import function cannot import node table columns - only edge table columns. To import node table columns from this table, please see the [Node and Edge Column Data](#) section of this manual.

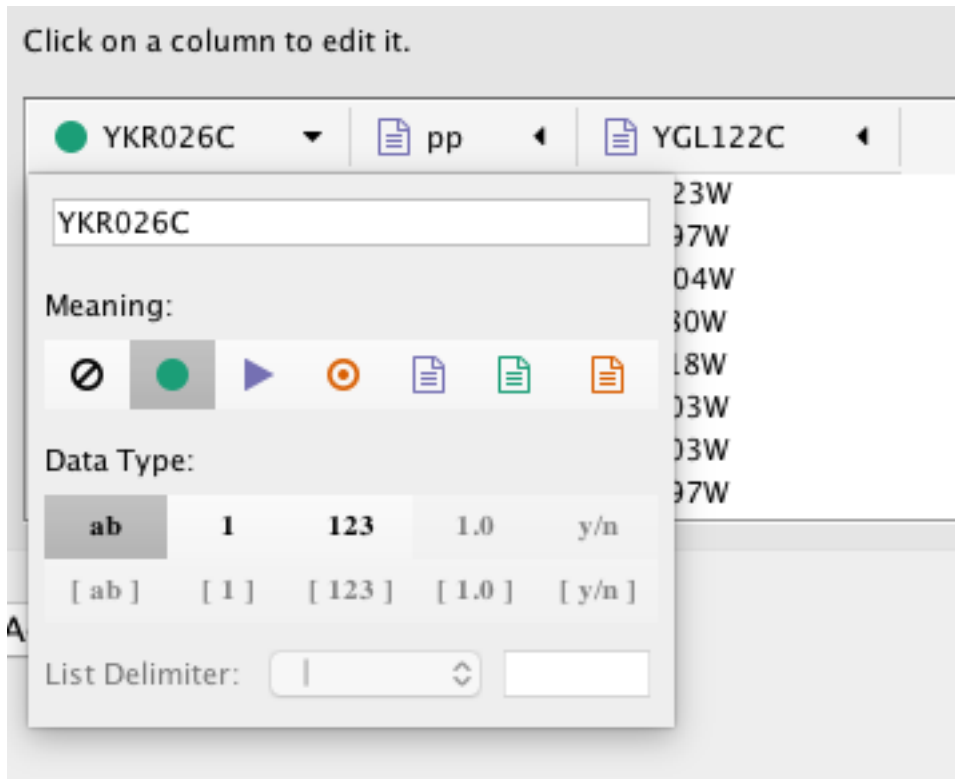
Note (1): This data was adapted from the *A merged human interactome* datasets by Andrew Garrow, Yeyejide Adeleye and Guy Warner (Unilever, Safety and Environmental Assurance Center, 12 October 2006).


5.2.2 Basic Operations

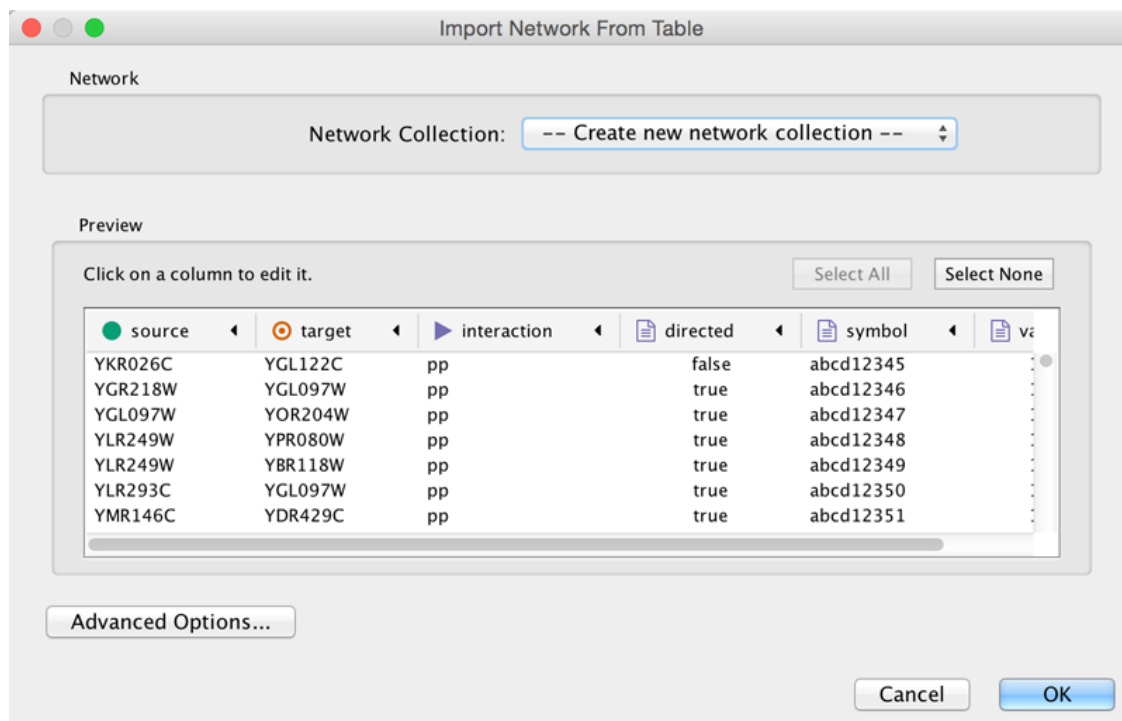
To import network from text/Excel tables, please follow these steps:



1. Select **File** → **Import** → **Network from File...** or click on  on the tool bar.
2. Select a table file in the file chooser dialog.
3. Define the interaction parameters by specifying which columns of data contain the **Source Interaction**, **Target Interaction**, and **Interaction Type**. Clicking on the arrow to the right of any column header will bring up the interface for selecting source, interaction and target:



4. (Optional) Define edge table columns, if applicable. Network table files can have edge table columns in addition to network data.
 - Enable/Disable Table Columns: You can enable/disable column data by selecting the  symbol in the column editor.



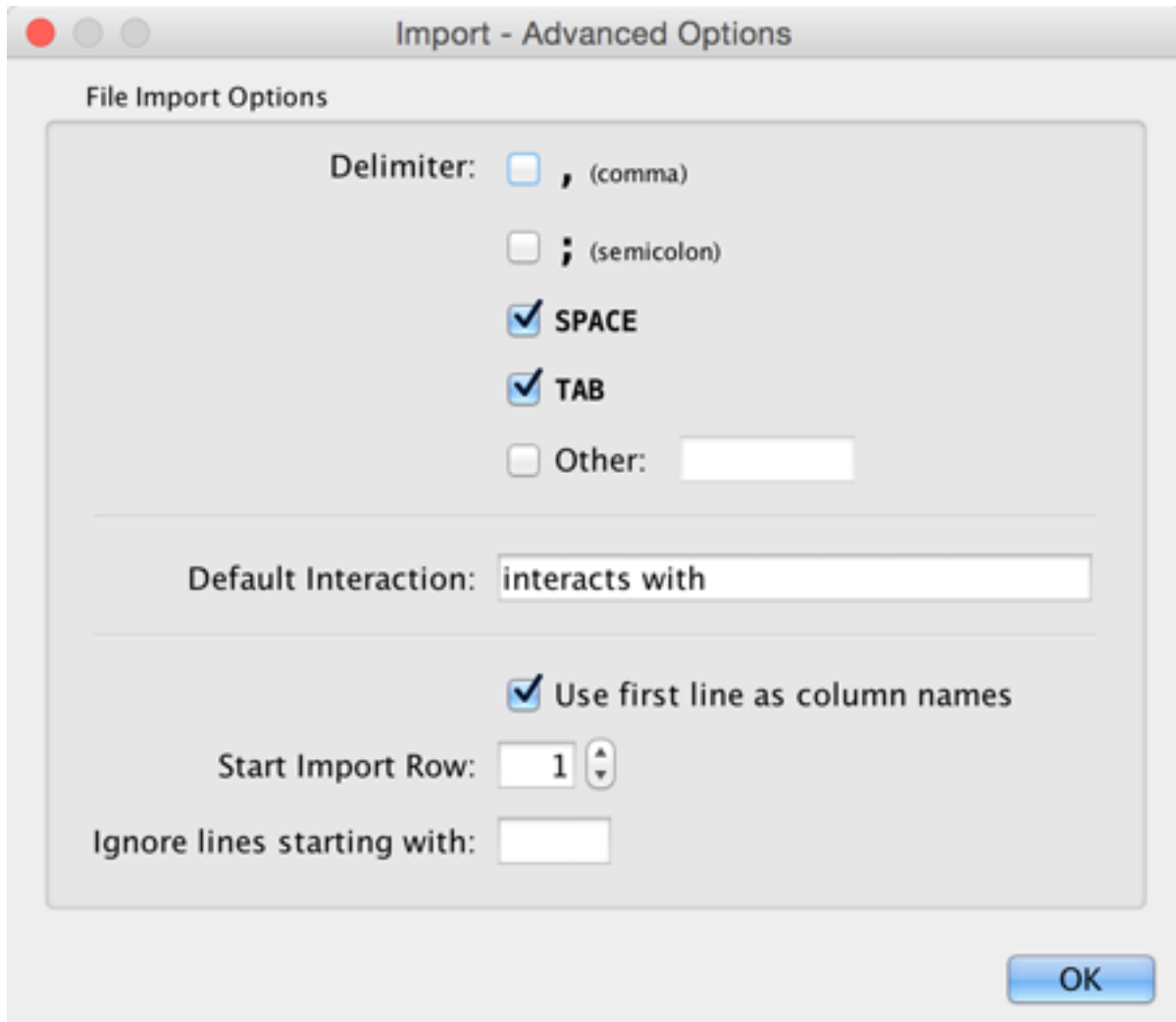
- **Change Column Name and Data Types:** You can also modify the column name and data type in the column editor. For more detail, see **Modify Column Name/Type** below.

5. Click the **OK** button.

Import List of Nodes Without Edges

The table import feature supports lists of nodes without edges. If you select only a source column, it creates a network without interactions. This feature is useful with the node expansion function available from some web service clients. Please read the section **Importing Networks from External Database** for more detail.

5.2.3 Advanced Options

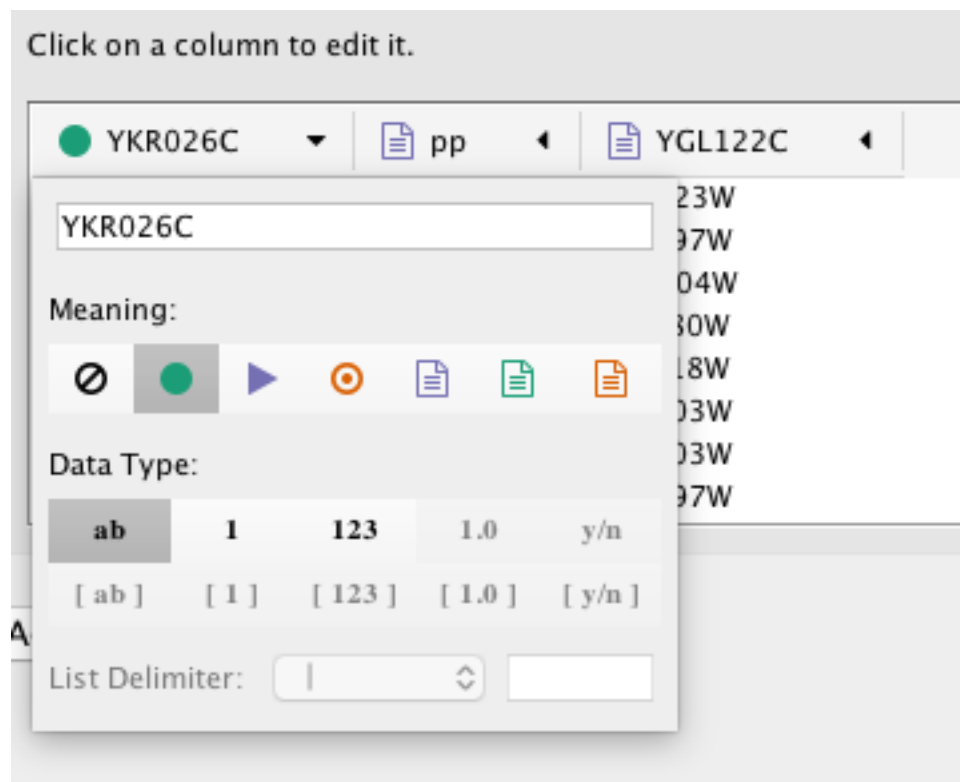


You can select several options by clicking the **Advanced Options** button in the main import interface.

- **Delimiter:** You can select multiple delimiters for text tables. By default, *Tab* and *Space* are selected as delimiters.
- **Default Interaction**
- **Transfer first line as column names:** Selecting this option will cause all edge columns to be named according to the first data entry in that column.
- **Start Import Row:** Set which row of the table to begin importing data from. For example, if you want to skip the first 3 rows in the file, set 4 for this option.
- **Ignore lines starting with:** Rows starting with this character will not be imported. This option can be used to skip comment lines in text files.

5.2.4 Modify Column Name/Type

In the **Import Network from Table** interface, you can change the name and data type of column by clicking on any column header:



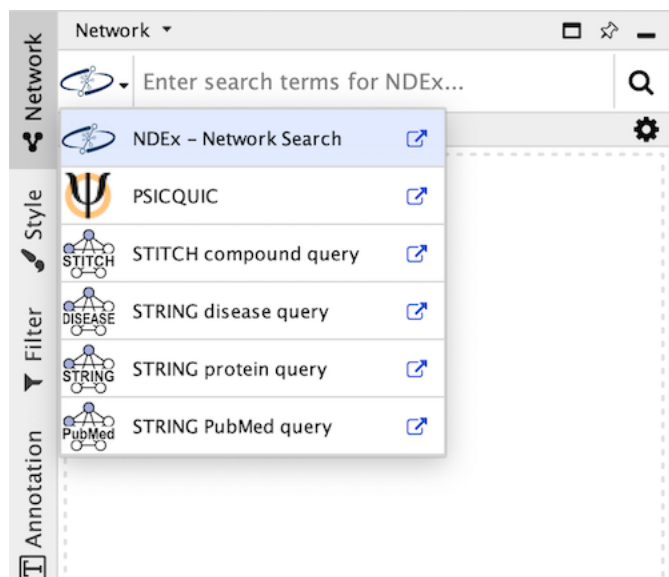
Column names and data types can be modified here.

- **Modify Column Name** - type in a new column name.
- **Modify Column Data Type** - The following column data types are supported:
 - String
 - Boolean (True/False)
 - Integer
 - Floating Point
 - List of (one of) String/Boolean/Integer/Floating Point

Cytoscape has a basic data type detection function that automatically suggests the column data type according to its entries. This can be overridden by selecting the appropriate data type from the radio buttons provided. For lists, a global delimiter must be specified (i.e., all cells in the table must use the same delimiter).

5.3 Import Networks from Public Databases

Cytoscape allows you to import networks from public databases. Users can access various kinds of databases through this function, under **File** → **Import** → **Network from Public Databases...** A **Search bar** is also available at the top of the **Network** panel in the **Control Panel**. From the search bar, you can directly access several public databases.



5.3.1 What is a Web Service?

A web service is a standardized, platform-independent mechanism for computers to interact over the internet. These days, many major biological databases publish their data with a web service API:

- List of Biological Web Services: <https://incubator.apache.org/projects/taverna.html>
- Web Services at the EBI: <https://www.ebi.ac.uk/Tools/common/tools/help/>

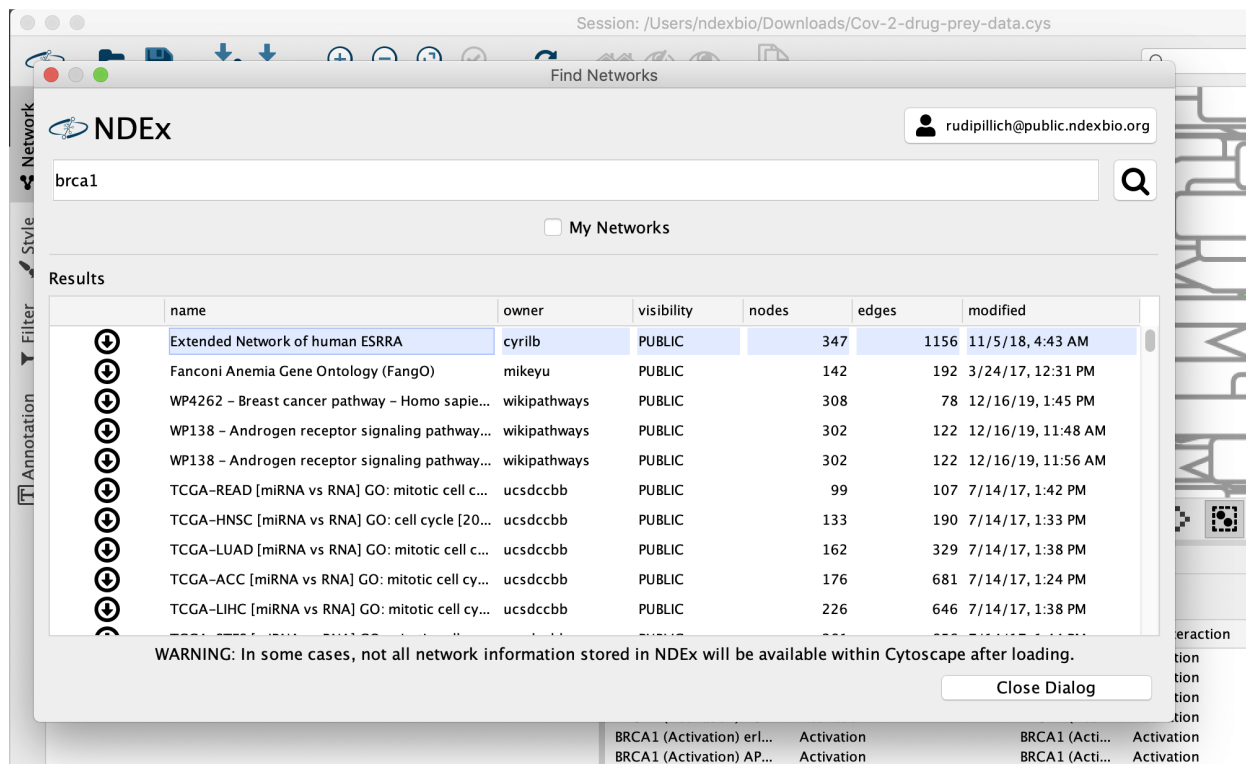
Cytoscape core developer team have developed several web service clients using this framework. Cytoscape supports many web services including:

- **PSICQUIC**: Standard web service for biological interaction data sets. The full list of PSICQUIC-compatible databases is available [here](#). PSICQUIC is available from the **Search bar**.
- **Pathway Commons**: Integrated data from pathway and network resources. The full list of supported resources is available [here](#). Pathway Commons is available from **File** → **Import** → **Network** → **Public Databases...**
- **STITCH** and **STRING**: STITCH is a database of known and predicted interactions between chemicals and proteins. STRING is a database of known and predicted protein-protein interactions. STITCH and STRING are available from the **Search bar** and from **File** → **Import** → **Network** → **Public Databases...**
- **NDEx**: The Network Data Exchange (NDEx) Project provides an open-source framework where scientists and organizations can share, store, manipulate, and publish biological network knowledge. NDEx is available from the **Search bar**, from **File** → **Import** → **Network from NDEx...** and in the **Toolbar** via the **NDEx Button**.

5.3.2 Example: Retrieving Networks from NDEx

- In the **Search bar**, select NDEx from the drop-down menu and type in one or more search terms, such as BRCA1.
- Click **Enter** to start the search.
- The CyNDEx-2 **Find Networks** dialog window will open and show the search results
- By default, results are returned in order of relevance based on the search terms you provided; you can change the sorting criteria by clicking on the column headers.

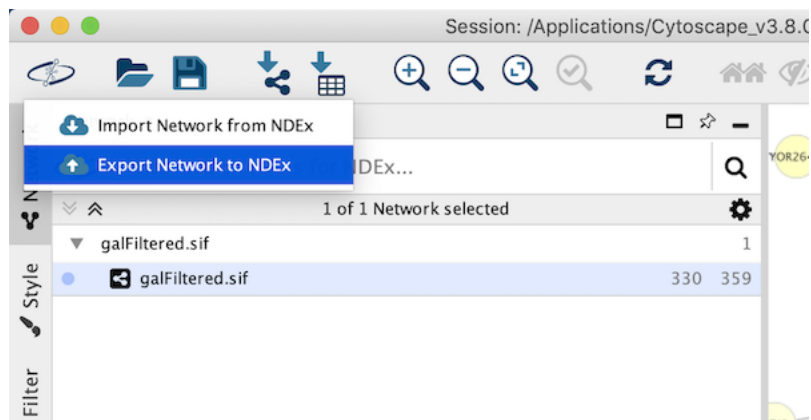
- Mark the **My Networks** checkbox at the top of the results table to only display the results that you own (you must have an NDEx account and a profile associated to the CyNDEx Browser. . . see the section [Export options](#) for more details).
- Click the **Black Arrow Icon** on the left hand side of a network to import it into Cytoscape and visualize it. When you have finished loading networks, dismiss the dialog window by clicking the **Close Dialog** button.



You can also find a network via its UUID by using the `uuid:` selector in your search (e.g., `uuid:50e3dff7-133e-11e6-a039-06603eb7f303`)

CyNDEx-2, like NDEx, uses standard [Lucene Syntax](#) as its network search language. For additional information, see [Searching Networks in NDEx](#). More information about CyNDEx-2, see the [CyNDEx-2 App Store](#) page.

Finally, It is also possible to access the NDEx Import and Export dialogs via the NDEx button in the main **Cytoscape Toolbar**, which will display the two options on click.

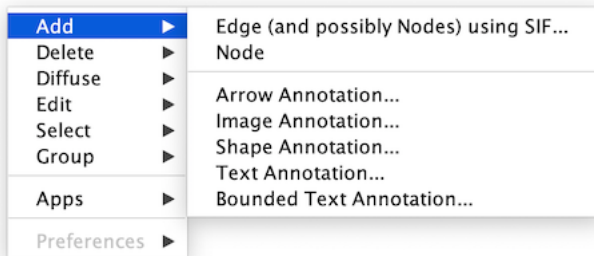


5.4 Create a New Network or Edit One Manually

A new, empty network can also be created and nodes and edges manually added. To create an empty network, go to **File** → **New Network** → **Empty**, and then manually add network components by right clicking on the network canvas or on a node. You can edit an existing network using the same process.

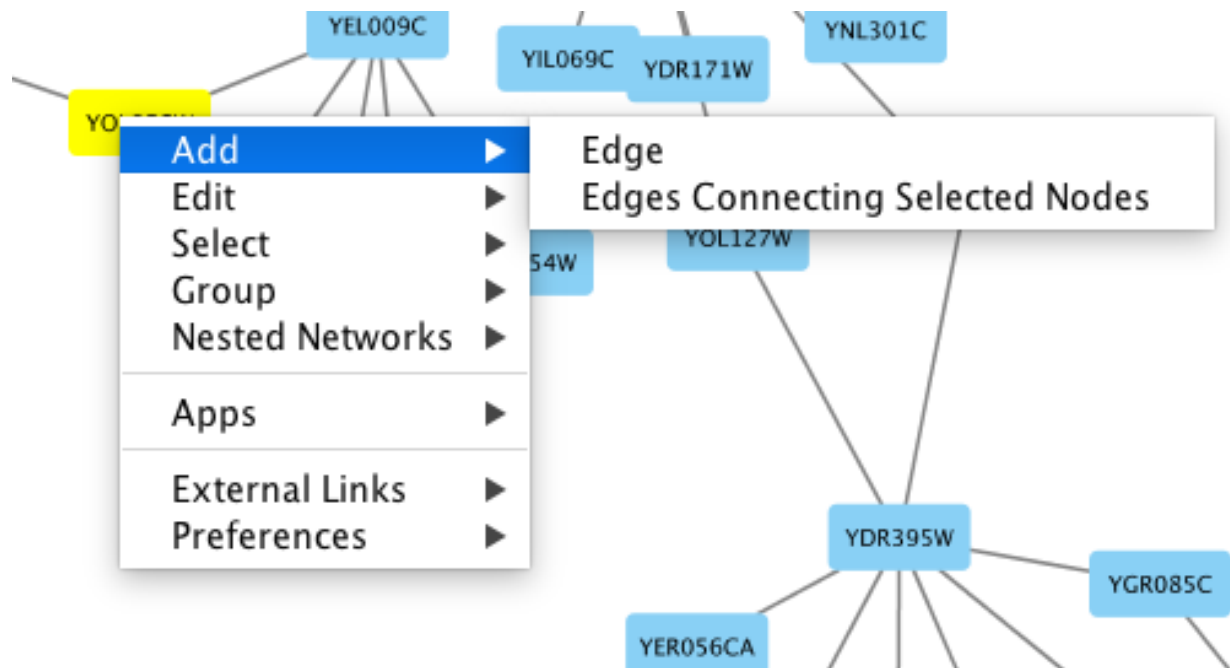
5.4.1 Adding a Node

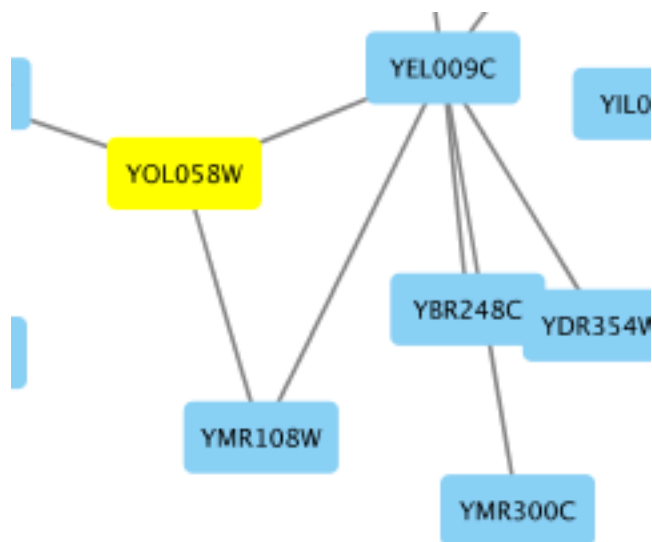
To add a new node, right-click on an empty space of the network view panel. Select **Add** → **Node** item from the pop-up menu.



5.4.2 Adding an Edge

To add an edge to connect nodes, right-click on the source node. Select **Edit** → **Add Edge** from the pop-up menu. Next, click on the target node. The Images below show the two steps for drawing an edge between two nodes. You can abort the drawing of the edge by pressing Esc key. You can also select two or more nodes to connect and in the right-click menu select **Add** → **Edges Connecting Selected Nodes** to create edges connecting all selected nodes.



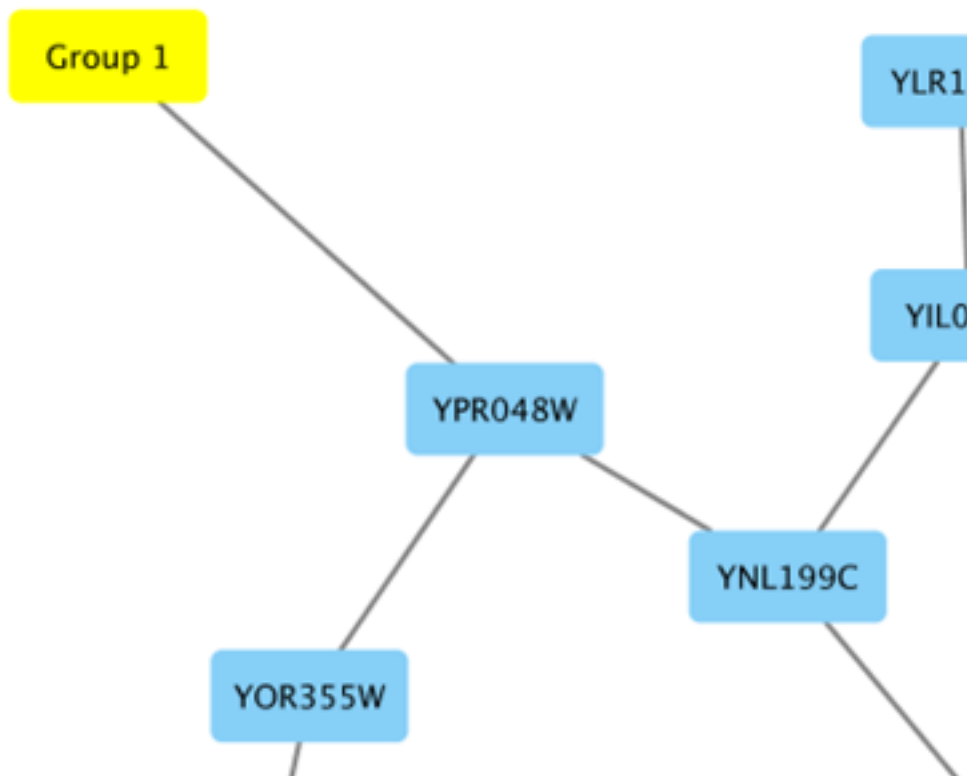


You can delete nodes and edges by selecting a number of nodes and edges, then selecting **Edit** → **Cut**. You can also delete selected nodes and edges from the **Edit** menu, under **Edit** → **Delete Selected Nodes and Edges...** You can recover any nodes and edges deleted from a network by going to **Edit** → **Undo**.

5.4.3 Grouping Nodes

Any number of nodes can be grouped together and displayed as either one group node or as the individual nodes. To create a group, select two or more nodes and right-click to select **Group** → **Group Selected Nodes**. You will be prompted to select a name for the group node. Once a group is created, you can use the right-click menu to collapse or expand the group. You can also quickly collapse/expand a group by double-clicking on the group node or any of its children to toggle back and forth.

Collapsed group



Expanded group

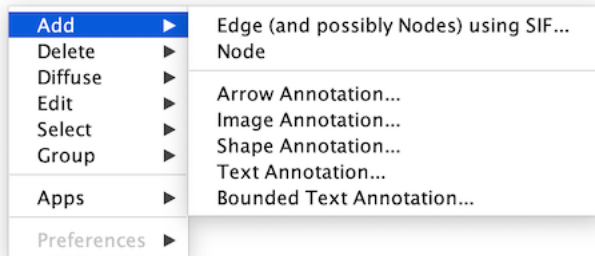


The appearance and behavior of grouped nodes depends on the [group settings](#) in effect when the group is created.

Settings can be managed for the entire Cytoscape session (via **Edit** → **Preferences** → **Group Preferences...**) or for a specific group (right-click **Preferences** → **Group Preferences...**).

5.4.4 Adding Network Annotations

Annotations in the form of text, images or shapes can be added to the network canvas by right-clicking anywhere on the canvas and selecting one of the **Annotation** choices in the **Add** menu. You can add an image of your own, choose from a shapes library or add either plain or bounded text. Shapes and text are customizable and any added annotations can be edited from the right-click context menu.



Nested Networks

Cytoscape has the ability to associate a **Nested Network** with any node. A nested network is any other network currently defined in Cytoscape. This capability allows for creation of network hierarchies as well as circular relationships. For example, various module-finding plugins make use of nested networks in the overview network that they generate. There each node representing a module contains a nested network.

Note that **Nested Networks** are similar in concept to **Groups**, but with very different consequences. A Nested Network incorporates an independent network that does not share nodes or attributes with the current network – it can be edited only as a separate network collection or in a separate Cytoscape session. Its nodes cannot be connected to nodes in the current network and cannot be found or filtered using Cytoscape functions or apps. Conversely, nodes in a Group are part of the current network, can have edges to nodes outside of the group, and can be found or filtered using Cytoscape functions or apps.

Most often, **Groups** are more functional and easier to use.

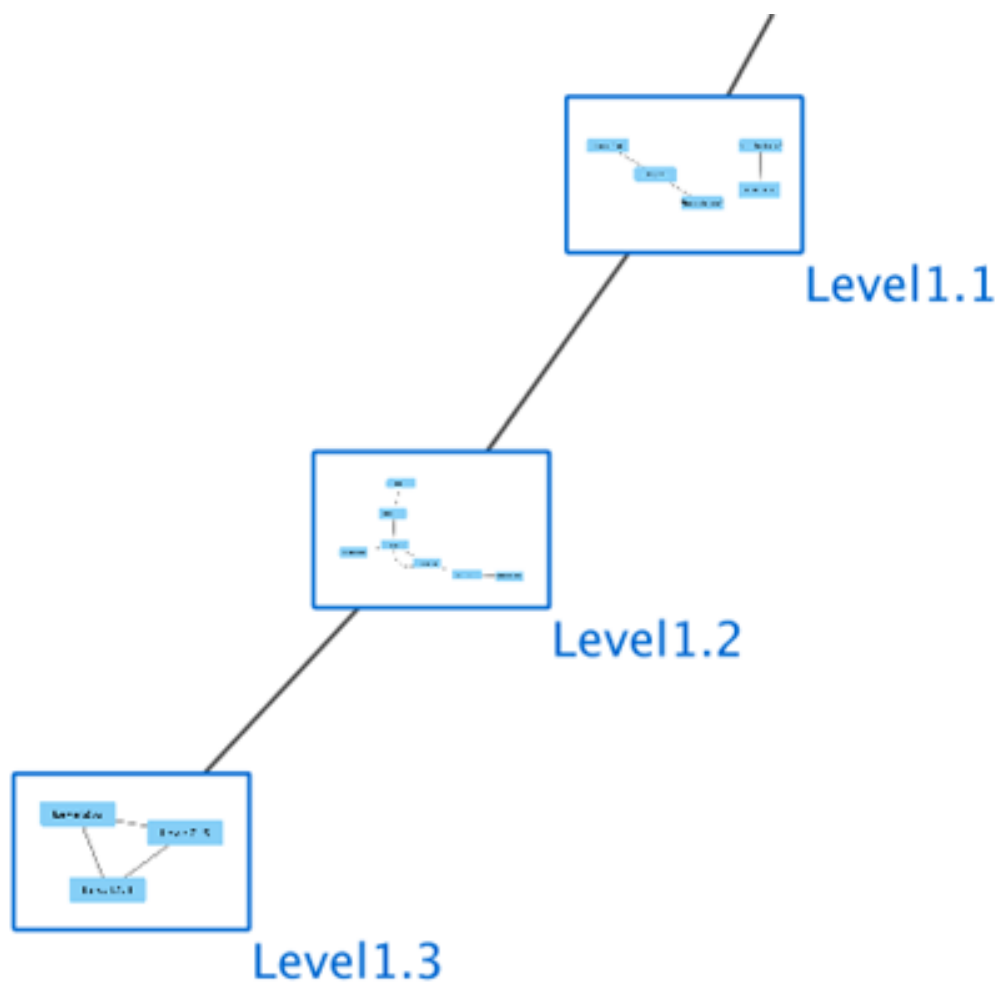
6.1 Creating Nested Networks

There are currently two ways in which a user can create nested networks.

- By importing a Nested Network Format (NNF) file. (See: **NNF Network Format**).
- By manually constructing networks and assigning nested networks to individual nodes through the right-click node context menu. (See **Nested Network Node Context Menu**).

6.2 Visualization of Nested Networks

Nodes containing nested networks that are zoomed in sufficiently display an image for the nested network. If no current network view exists for the nested network the image will be a default icon, otherwise it will be a low-resolution rendering of the nested network's current layout.



Supported Network File Formats

Cytoscape can read network/pathway files written in the following formats:

- Simple interaction file (SIF or .sif format)
- Nested network format (NNF or .nnf format)
- Graph Markup Language (GML or .gml format)
- XGMML (extensible graph markup and modelling language).
- SBML
- BioPAX
- GraphML
- Delimited text
- Excel Workbook (.xls, .xlsx)
- [Cytoscape.js JSON](#)
- [Cytoscape CX](#)

The SIF format specifies nodes and interactions only, while other formats store additional information about network layout and allow network data exchange with a variety of other network programs and data sources. Typically, SIF files are used to import interactions when building a network for the first time, since they are easy to create in a text editor or spreadsheet. Once the interactions have been loaded and network layout has been performed, the network may be saved to GML or XGMML format for interaction with other systems. All file types listed (except Excel) are text files and you can edit and view them in a regular text editor.

7.1 SIF Format

The simple interaction format is convenient for building a graph from a list of interactions. It also makes it easy to combine different interaction sets into a larger network, or add new interactions to an existing data set. The main

disadvantage is that this format does not include any layout information, forcing Cytoscape to re-compute a new layout of the network each time it is loaded.

Lines in the SIF file specify a source node, a relationship type (or edge type), and one or more target nodes:

```
nodeA <relationship type> nodeB
nodeC <relationship type> nodeA
nodeD <relationship type> nodeE nodeF nodeB
nodeG
...
nodeY <relationship type> nodeZ
```

A more specific example is:

```
node1 typeA node2
node2 typeB node3 node4 node5
node0
```

The first line identifies two nodes, called node1 and node2, and a single relationship between node1 and node2 of type typeA. The second line specifies three new nodes, node3, node4, and node5; here “node2” refers to the same node as in the first line. The second line also specifies three relationships, all of type typeB and with node2 as the source, with node3, node4, and node5 as the targets. This second form is simply shorthand for specifying multiple relationships of the same type with the same source node. The third line indicates how to specify a node that has no relationships with other nodes. This form is not needed for nodes that do have relationships, since the specification of the relationship implicitly identifies the nodes as well.

Duplicate entries are ignored. Multiple edges between the same nodes must have different edge types. For example, the following specifies two edges between the same pair of nodes, one of type xx and one of type yy:

```
node1 xx node2
node1 xx node2
node1 yy node2
```

Edges connecting a node to itself (self-edges) are also allowed:

```
node1 xx node1
```

Every node and edge in Cytoscape has a name column. For a network defined in SIF format, node names should be unique, as identically named nodes will be treated as identical nodes. The name of each node will be the name in this file by default (unless another string is mapped to display on the node using styles). This is discussed in the section on [Styles](#). The name of each edge will be formed from the name of the source and target nodes plus the interaction type: for example, sourceName (edgeType) targetName.

The tag “edgeType” can be any string. Whole words or concatenated words may be used to define types of relationships, e.g. geneFusion, cogInference, pullsDown, activates, degrades, inactivates, inhibits, phosphorylates, upRegulates, etc.

Some common interaction types used in the Systems Biology community are as follows:

```
pp ..... protein - protein interaction
pd ..... protein -> DNA
(e.g. transcription factor binding upstream of a regulating gene.)
```

Some less common interaction types used are:

```
pr ..... protein -> reaction
rc ..... reaction -> compound
cr ..... compound -> reaction
```

(continues on next page)

(continued from previous page)

```
gl ..... genetic lethal relationship
pm ..... protein-metabolite interaction
mp ..... metabolite-protein interaction
```

7.1.1 Delimiters

Whitespace (space or tab) is used to delimit the names in the simple interaction file format. However, in some cases spaces are desired in a node name or edge type. The standard is that, if the file contains any tab characters, then tabs are used to delimit the fields and spaces are considered part of the name. If the file contains no tabs, then any spaces are delimiters that separate names (and names cannot contain spaces).

If your network unexpectedly contains no edges and node names that look like edge names, it probably means your file contains a stray tab that's fooling the parser. On the other hand, if your network has nodes whose names are half of a full name, then you probably meant to use tabs to separate node names with spaces.

Networks in simple interactions format are often stored in files with a `.sif` extension, and Cytoscape recognizes this extension when browsing a directory for files of this type.

7.2 NNF

The NNF format is a very simple format that unlike SIF allows the optional assignment of single nested network per node. No other node columns can be specified. There are only 2 possible line formats:

- A node *node* contained in a *network*:

```
network node
```

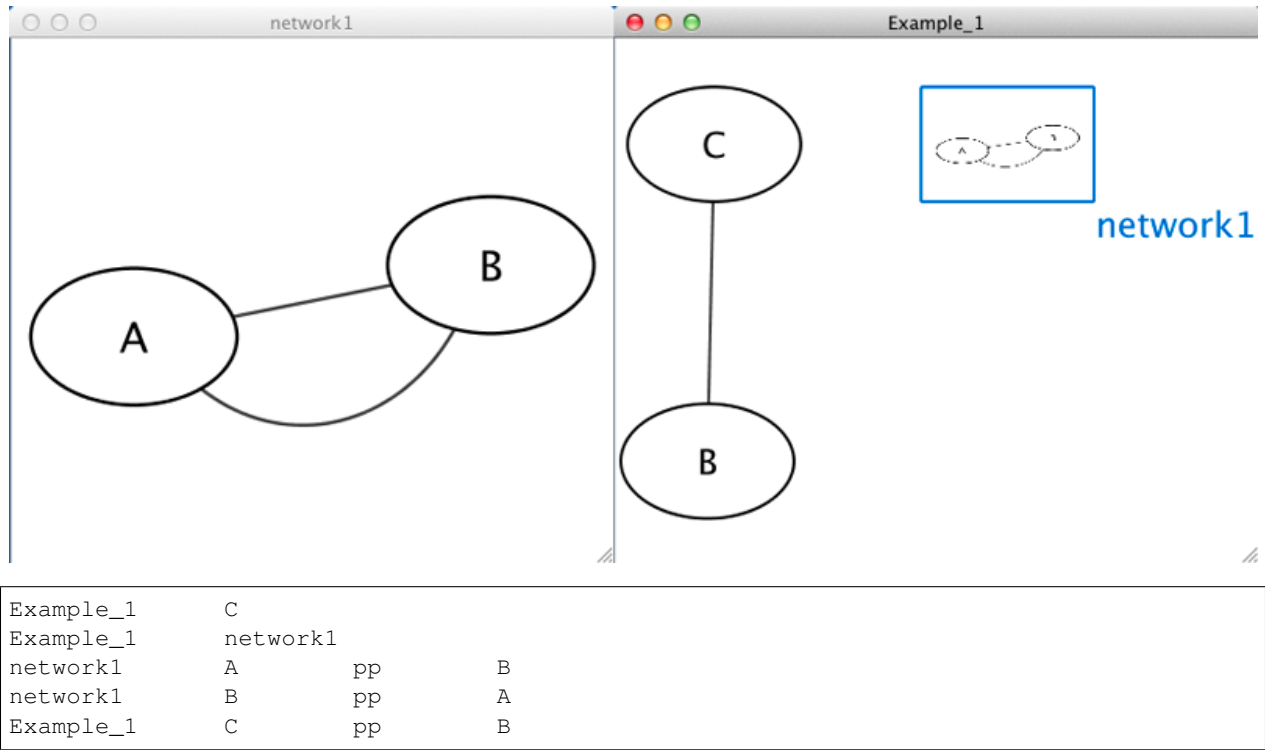
- 2 nodes linked together contained in a network:

```
network node1 interaction node2
```

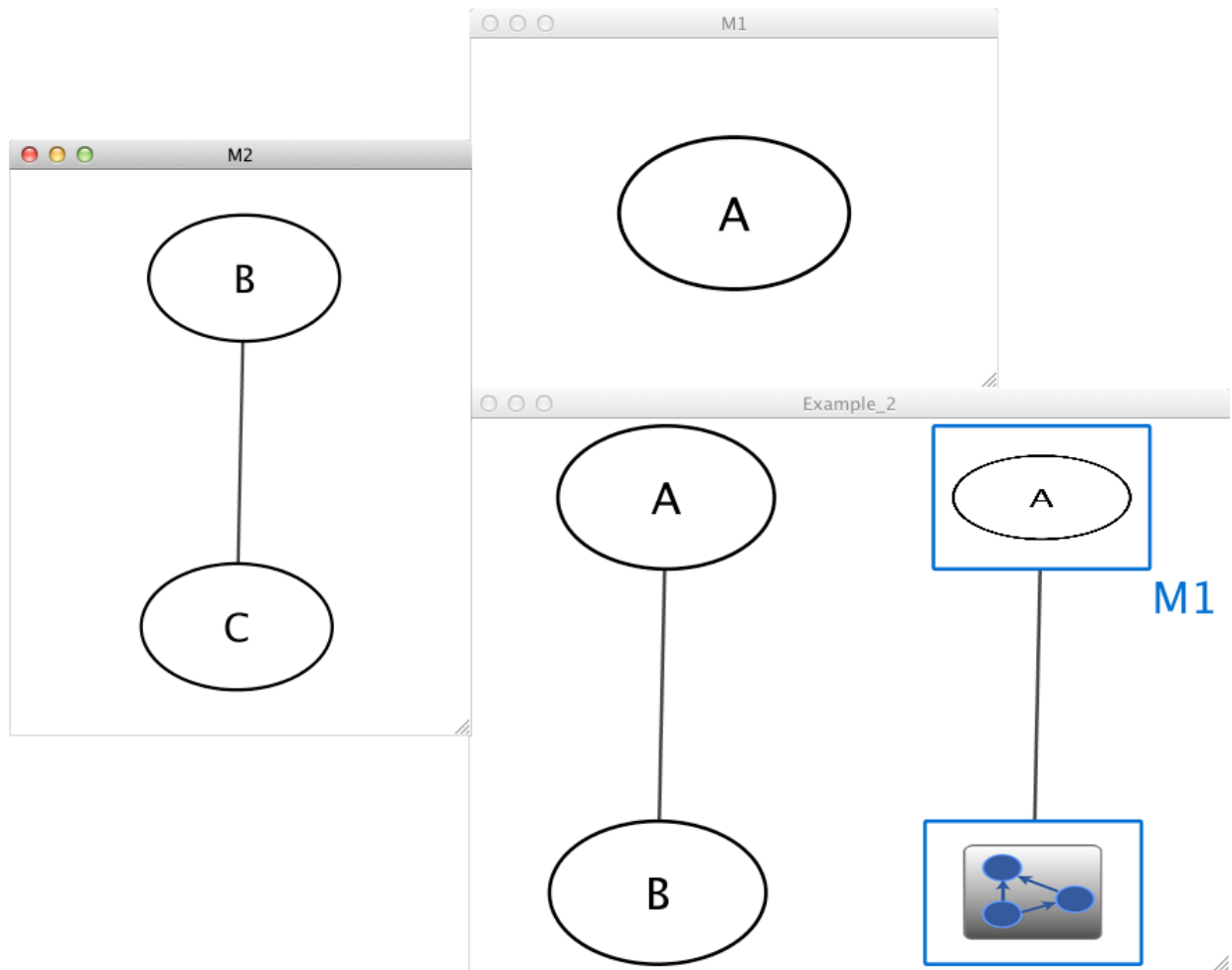
If a network name (first entry on a line) appeared previously as a node name (in columns 2 or 4), the network will be nested in the node with the same name. Also, if a name that has been previously defined as a network (by being listed in the first column), later appears as a node name (in columns 2 or 4), the previously defined network will be nested in the node with the same name. In summary: any time a name is used as both, a network name, and a node name, this implies that the network will be nested in the node of the same name. Additionally comments may be included on all lines. Comments start with a hash mark '#' and continue to the end of a line. Trailing comments (after data lines) and entirely blank lines anywhere are also permissible. Please **note** that if you load multiple NNF files in Cytoscape they will be treated like a single, long concatenated NNF file! If you need to embed spaces, tabs or backslashes in a name, you must escape it by preceding it with a backslash, so that, e.g. an embedded backslash becomes two backslashes, an embedded space a backslash followed by a space etc.

7.2.1 Examples

Example 1

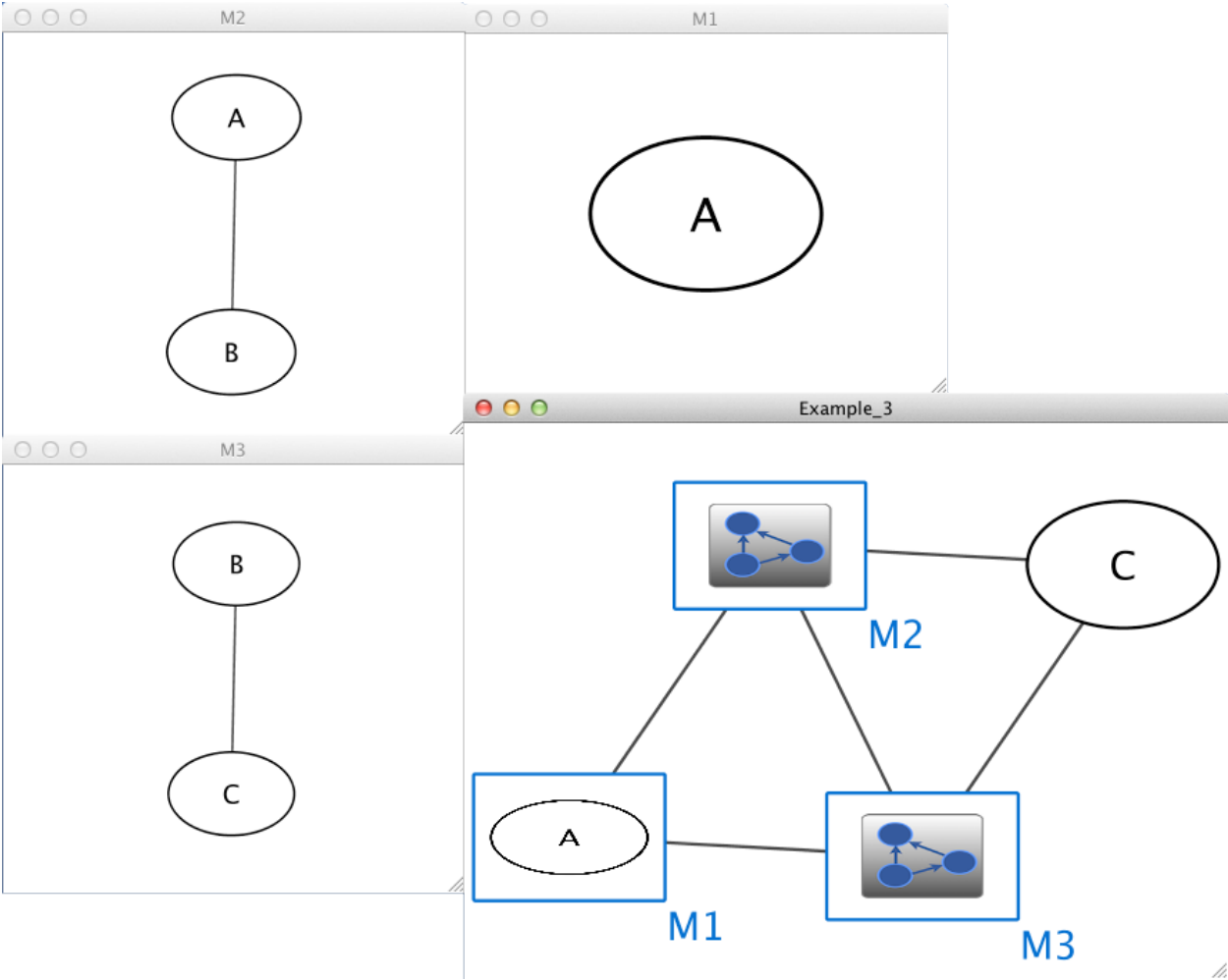


Example 2

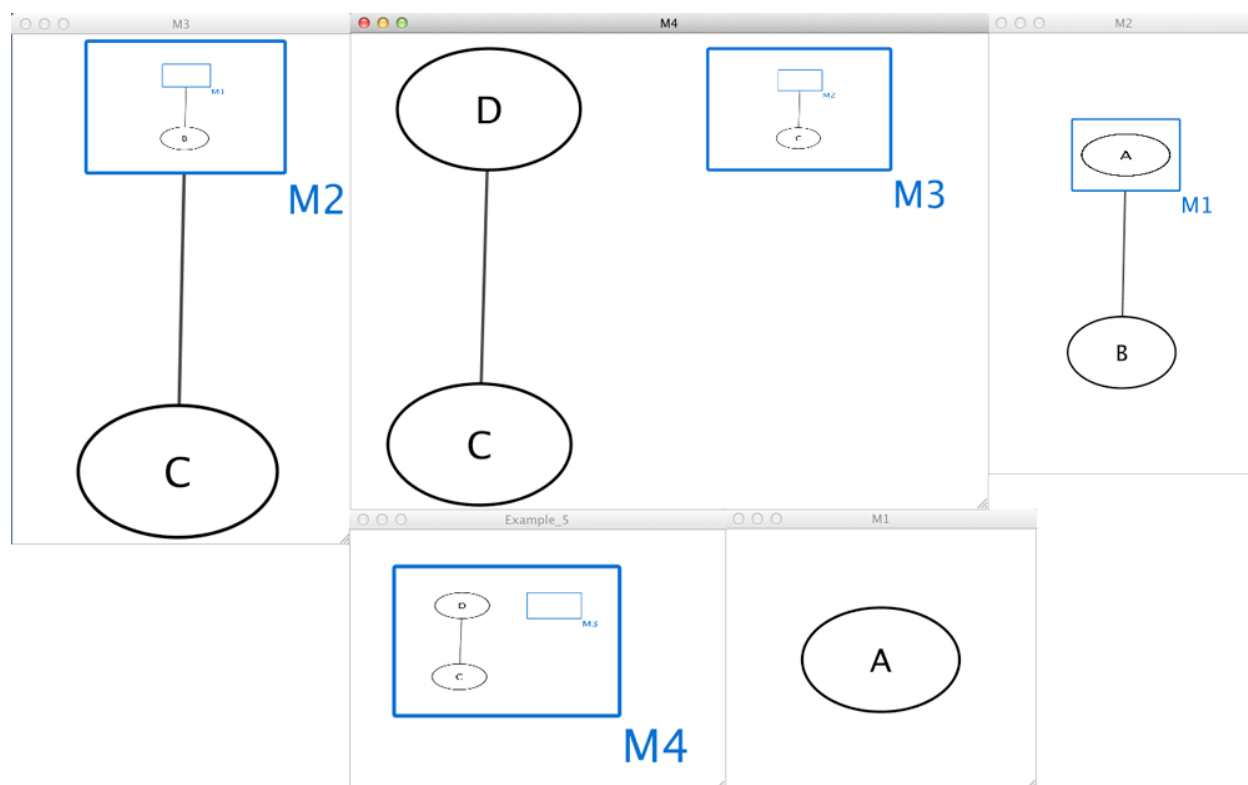


Example_2	M1		
Example_2	M2		
M1	A		
M2	B	pp	C
Example_2	A	pp	B
Example_2	M1	im	M2

Example 3



Example_3	M1	im	M2
Example_3	M3	im	M1
Example_3	M2	im	M3
Example_3	C	pp	M3
Example_3	M2	pp	C
M1	A		
M2	A	pp	B
M3	B	pp	C

Example 4

Example_4	M4		
M4	D		
M4	M3		
M3	M2	pp	C
M2	M1	pp	B
M1	A		
M4	C	pp	D

7.3 GML Format

In contrast to SIF, GML is a rich graph format language supported by many other network visualization packages. The GML file format specification is available at:

<http://graphviewer.nl/misc/gmlanguage/gml-technical-report.pdf>

It is generally not necessary to modify the content of a GML file directly. Once a network is built in SIF format and then laid out, the layout is preserved by saving to and loading from GML. Properties specified in a GML file will result in a new style named `Filename.style` when that GML file is loaded.

7.4 XGMML Format

XGMML is the XML evolution of GML and is based on the GML definition. In addition to network data, XGMML contains node/edge/network column data. More information on Wikipedia:

<https://en.wikipedia.org/wiki/XGMML>

XGMML is now preferred to GML because it offers the flexibility associated with all XML document types. If you're unsure about which to use, choose XGMML.

There is a java system property "cytoscape.xgmml.repair.bare.ampersands" that can be set to "true" if you have experience trouble reading older files.

This should only be used when an XGMML file or session cannot be read due improperly encoded ampersands, as it slows down the reading process, but this is still preferable to attempting to fix such files using manual editing.

7.5 SBML (Systems Biology Markup Language) Format

The Systems Biology Markup Language (SBML) is an XML format to describe biochemical networks. SBML file format specification is available at:

<http://sbml.org/documents/>

7.6 BioPAX (Biological Pathways eXchange) Format

BioPAX is an OWL (Web Ontology Language) document designed to exchange biological pathways data. The complete set of documents for this format is available at:

<http://www.biopax.org/>

7.7 GraphML

GraphML is a comprehensive and easy-to-use file format for graphs. It is based on XML. The complete set of documents for this format is available at:

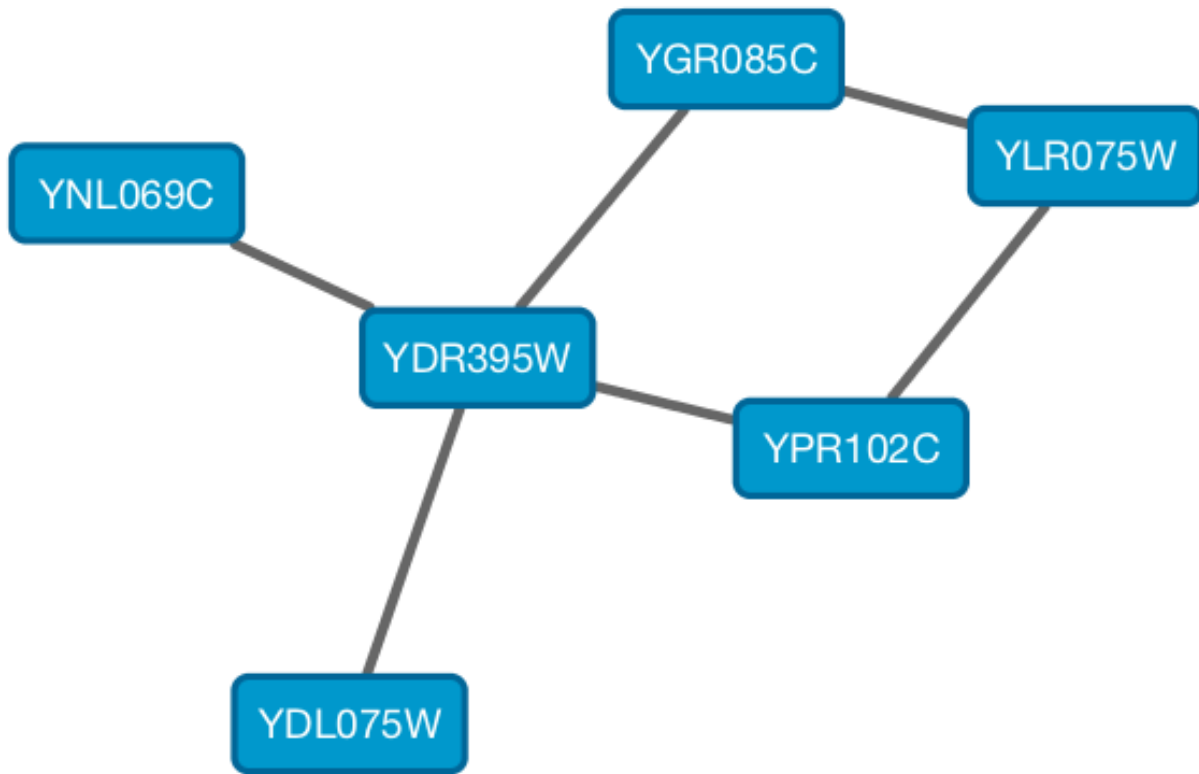
<http://graphml.graphdrawing.org/>

7.8 Delimited Text Table and Excel Workbook

Cytoscape has native support for Microsoft Excel files (.xls, .xlsx) and delimited text files. The tables in these files can have network data and edge columns. Users can specify columns containing source nodes, target nodes, interaction types, and edge columns during file import. Some of the other network analysis tools, such as igraph (<https://igraph.org/>), has feature to export graph as simple text files. Cytoscape can read these text files and build networks from them. For more detail, please read the Import Free-Format Tables section of the **Creating Networks** section.

7.9 Cytoscape.js JSON

From Cytoscape 3.1.0 on, Cytoscape supports **Cytoscape.js** JSON files. You can use this feature to export your network visualizations to web browsers. Cytoscape.js has two ways to represent network data, and currently both reader and writer support only the array style graph notation. For example, this network in Cytoscape:



will be exported to this JSON:

```

{
  "elements" : {
    "nodes" : [ {
      "data" : {
        "id" : "723",
        "selected" : false,
        "annotation_Taxon" : "Saccharomyces cerevisiae",
        "alias" : [ "RPL31A", "RPL34", "S000002233", "ribosomal protein L31A (L34A)" ],
        "shared_name" : "YDL075W",
        "SUID" : 723,
        "degree_layout" : 1,
        "name" : "YDL075W"
      },
      "position" : {
        "x" : 693.0518315633137,
        "y" : -49.47506554921466
      },
      "selected" : false
    }, {
      "data" : {
        "id" : "726",
        "selected" : false,
        "annotation_Taxon" : "Saccharomyces cerevisiae",
        "alias" : [ "RP23", "RPL16B", "S000005013", "ribosomal protein L16B (L21B)" ],
        "shared_name" : "YNL069C",

```

(continues on next page)

(continued from previous page)

```

    "SUID" : 726,
    "degree_layout" : 1,
    "name" : "YNL069C"
  },
  "position" : {
    "x" : 627.3147710164387,
    "y" : -205.99251969655353
  },
  "selected" : false
}, {
  "data" : {
    "id" : "658",
    "selected" : false,
    "annotation_Taxon" : "Saccharomyces cerevisiae",
    "alias" : [ "RPL11B", "S000003317", "ribosomal protein L11B (L16B) (rp39B) ↵
↵(YL22) " ],
    "shared_name" : "YGR085C",
    "SUID" : 658,
    "degree_layout" : 2,
    "name" : "YGR085C"
  },
  "position" : {
    "x" : 804.3092778523762,
    "y" : -245.6235926946004
  },
  "selected" : false
}, {
  "data" : {
    "id" : "660",
    "selected" : false,
    "annotation_Taxon" : "Saccharomyces cerevisiae",
    "alias" : [ "KAP108", "S000002803", "SXM1" ],
    "shared_name" : "YDR395W",
    "SUID" : 660,
    "degree_layout" : 8,
    "name" : "YDR395W"
  },
  "position" : {
    "x" : 730.8733342488606,
    "y" : -157.50702317555744
  },
  "selected" : false
}, {
  "data" : {
    "id" : "579",
    "selected" : false,
    "annotation_Taxon" : "Saccharomyces cerevisiae",
    "alias" : [ "RPL11A", "S000006306", "ribosomal protein L11A (L16A) (rp39A) ↵
↵(YL22) " ],
    "shared_name" : "YPR102C",
    "SUID" : 579,
    "degree_layout" : 2,
    "name" : "YPR102C"
  },
  "position" : {
    "x" : 841.1395696004231,
    "y" : -130.77909119923908

```

(continues on next page)

(continued from previous page)

```

    },
    "selected" : false
  }, {
    "data" : {
      "id" : "578",
      "selected" : false,
      "annotation_Taxon" : "Saccharomyces cerevisiae",
      "alias" : [ "GRC5", "QSR1", "RPL10", "S000004065", "ribosomal protein L10" ],
      "shared_name" : "YLR075W",
      "SUID" : 578,
      "degree_layout" : 2,
      "name" : "YLR075W"
    },
    "position" : {
      "x" : 910.3755162556965,
      "y" : -217.0562556584676
    },
    "selected" : false
  } ],
  "edges" : [ {
    "data" : {
      "id" : "659",
      "source" : "658",
      "target" : "578",
      "selected" : false,
      "interaction" : "pp",
      "shared_interaction" : "pp",
      "shared_name" : "YGR085C (pp) YLR075W",
      "SUID" : 659,
      "name" : "YGR085C (pp) YLR075W"
    },
    "selected" : false
  }, {
    "data" : {
      "id" : "661",
      "source" : "658",
      "target" : "660",
      "selected" : false,
      "interaction" : "pp",
      "shared_interaction" : "pp",
      "shared_name" : "YGR085C (pp) YDR395W",
      "SUID" : 661,
      "name" : "YGR085C (pp) YDR395W"
    },
    "selected" : false
  }, {
    "data" : {
      "id" : "724",
      "source" : "660",
      "target" : "723",
      "selected" : false,
      "interaction" : "pp",
      "shared_interaction" : "pp",
      "shared_name" : "YDR395W (pp) YDL075W",
      "SUID" : 724,
      "name" : "YDR395W (pp) YDL075W"
    }
  },

```

(continues on next page)

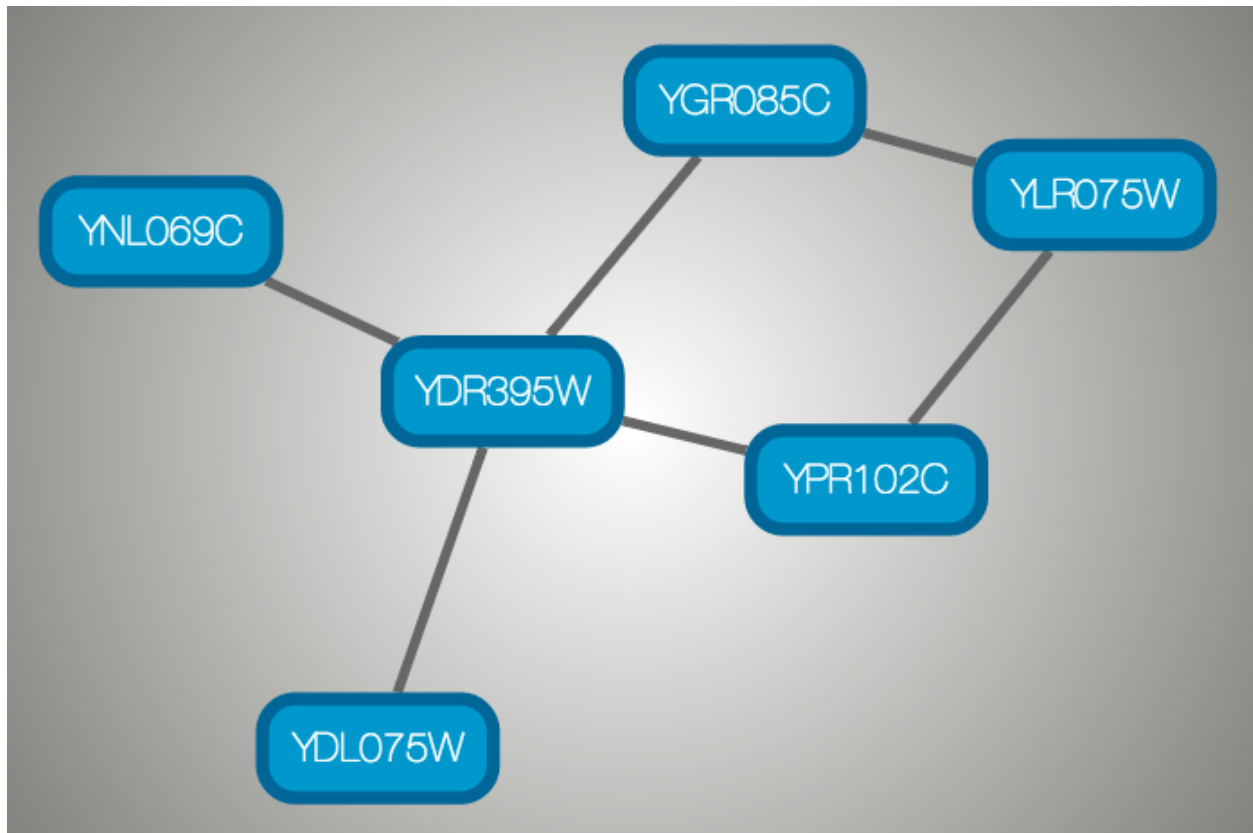
(continued from previous page)

```

    "selected" : false
  }, {
    "data" : {
      "id" : "733",
      "source" : "660",
      "target" : "579",
      "selected" : false,
      "interaction" : "pp",
      "shared_interaction" : "pp",
      "shared_name" : "YDR395W (pp) YPR102C",
      "SUID" : 733,
      "name" : "YDR395W (pp) YPR102C"
    },
    "selected" : false
  }, {
    "data" : {
      "id" : "727",
      "source" : "660",
      "target" : "726",
      "selected" : false,
      "interaction" : "pp",
      "shared_interaction" : "pp",
      "shared_name" : "YDR395W (pp) YNL069C",
      "SUID" : 727,
      "name" : "YDR395W (pp) YNL069C"
    },
    "selected" : false
  }, {
    "data" : {
      "id" : "580",
      "source" : "578",
      "target" : "579",
      "selected" : false,
      "interaction" : "pp",
      "shared_interaction" : "pp",
      "shared_name" : "YLR075W (pp) YPR102C",
      "SUID" : 580,
      "name" : "YLR075W (pp) YPR102C"
    },
    "selected" : false
  } ]
}

```

And this is a sample visualization in Cytoscape.js:



7.9.1 Important Note

Export network and table to Cytoscape.js feature in Cytoscape creates a JSON file **WITHOUT** style. This means that you need to export the style in a separate JSON file if you apply style to your network. Please read the [Style](#) section for more details.

7.10 Cytoscape CX

CX is a JSON-based transfer format that enables diverse Cytoscape Cyberinfrastructure (CI) services to exchange networks while preserving all network-related information. It is designed for flexibility, modularity, and extensibility, and as a message payload in common CI REST protocols. It enables applications to standardize on core aspects of networks, coordinate on more specific or unique standards, and to ignore or omit irrelevant aspects. It is not intended as an optimized format for storage or for specific functionality in applications.

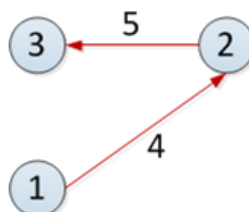
CX is an Aspect-Oriented Network Interchange Format, where the base information is a list of nodes. Independent data structures (called aspects) organize and elaborate on nodes and each other. The core of CX defines five aspects, though a more comprehensive [CX document](#) describes many more aspects.

The **nodes** aspect contains only the identifiers of the network's nodes, The **edges** aspect contains identifiers for each edge along with the identifiers of the nodes the edge connects. The **networkAttributes** aspect contains name-value pairs describing the network. The **nodeAttributes** and "edgeAttributes" aspects contain name-value pairs attached to specifically identified nodes and edges.

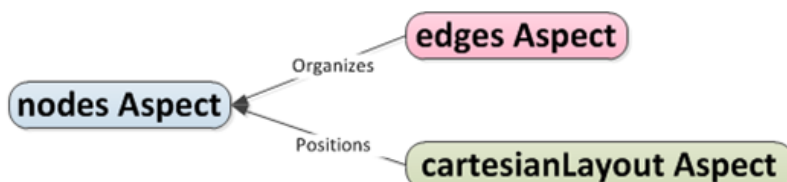
Critically, applications are free to add and maintain their own aspects without coordinating or negotiating with disinterested applications.

As an illustration using the picture below, a three node network can be described as a list of nodes (**nodes** aspect) and edges that link them (**edges** aspect). If the network has been laid out, a separate aspect (**cartesianLayout** aspect) can describe the position of each node. More concretely, a CX encoding would have three nodes in the **nodes** aspect, each with unique IDs. The **edges** aspect references each node by ID, with each edge having its own ID. Finally, the **cartesianLayout** aspect ties coordinates to nodes by ID. In fact, a network may have many aspects, describing node and edge attributes, subnetworks, visual properties, groups and so on.

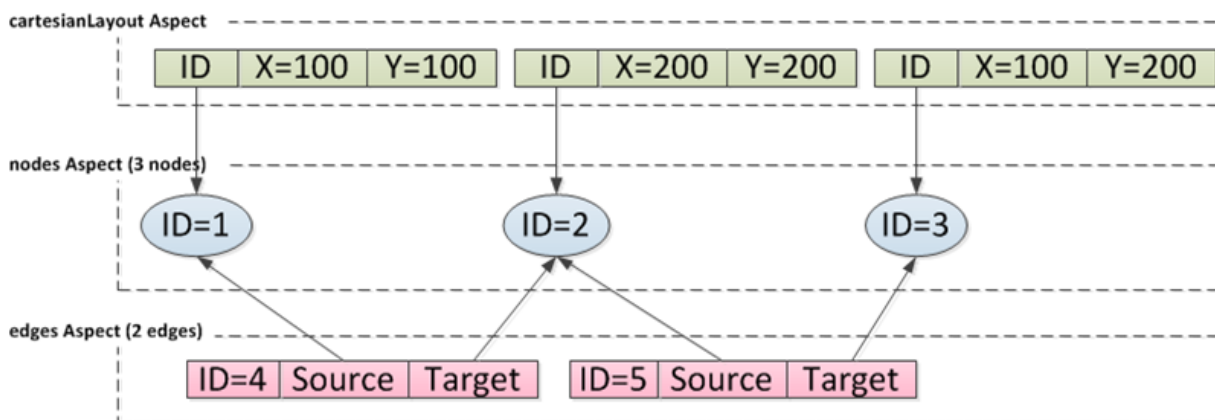
Example Graph



Aspect Relationships



CX Encoding



The actual JSON encoding for a CX stream is described in the [CX document](#). It would appear something like this:

```

{
  "nodes": [{"@id": 1}, {"@id": 2}, {"@id": 3}],
  "edges": [{"s": 1, "@id": 4, "t": 2},
            {"s": 2, "@id": 5, "t": 3}],
  "cartesianLayout": [{"x": 100, "node": 1, "y": 100},
                     {"x": 200, "node": 2, "y": 200},
                     {"x": 100, "node": 3, "y": 200}]
}
  
```

Node and Edge Column Data

Interaction networks are useful as stand-alone models. However, they are most powerful for answering scientific questions when integrated with additional information. Cytoscape allows the user to add arbitrary node, edge and network information to Cytoscape as node/edge/network data columns. This could include, for example, annotation data on a gene or confidence values in a protein-protein interaction. These column data can then be visualized in a user-defined way by setting up a mapping from columns to network properties (colors, shapes, and so on). The section on [Styles](#) discusses this in greater detail.

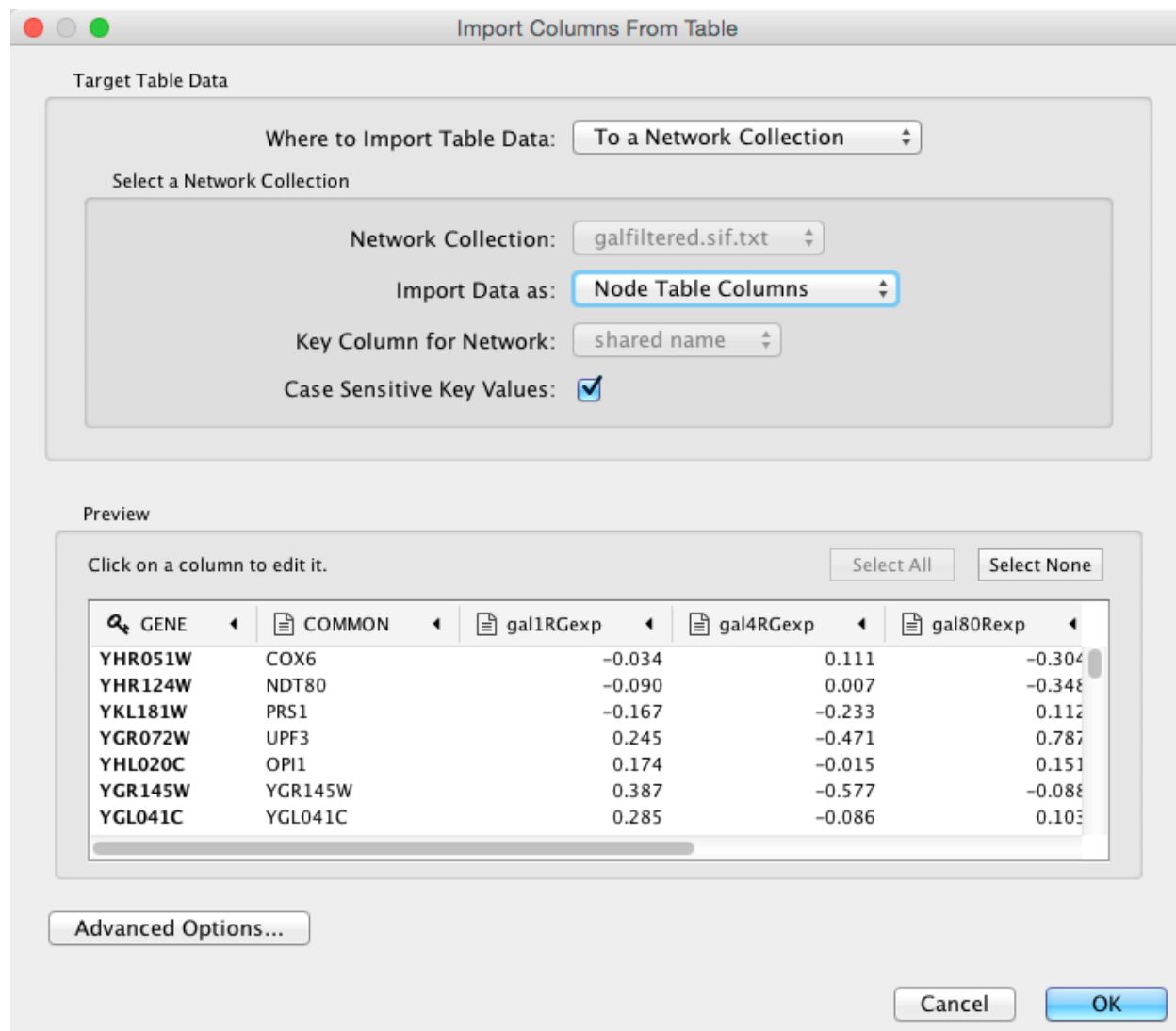
8.1 Import Data Table Files



Cytoscape offers support for importing data from delimited text and MS Excel data tables.

Sample Data Table 1

The data table file should contain a primary key column and at least one data column. The maximum number of data columns is unlimited. The **Alias** column is an optional feature, as is using the first row of data as column names. Alternatively, you can specify each column name from the **File** → **Import** → **Table from File...** user interface.

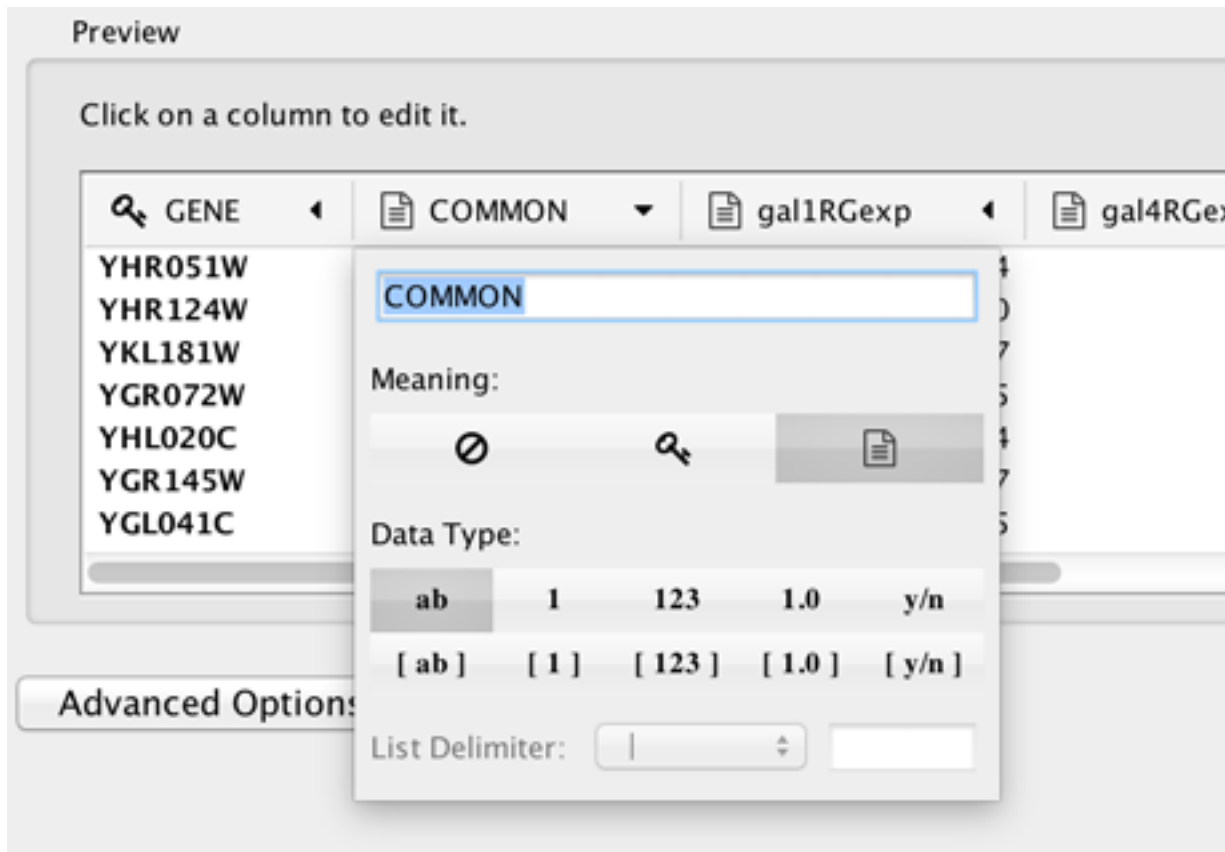
8.1.1 Basic Operation



1. Select **File** → **Import** → **Table from File...**. Alternatively, you can simply drag and drop the file from the desktop into the **Table Panel**, or click the **Import Table from File...**  in the **Table Panel** interface.
2. Select a data file. The file can be either a text or Excel (.xls/.xlsx) file.
3. In the **Target Table Data** section, choose where to import the data to. You can choose an existing network collection, a specific network only, or you can choose to import the data to an **Unassigned Table** (described below).
4. Depending on what you choose in the **Where to import Table Data** drop-down, you will need to select a network collection or specific network. You will also need to select **Import Data as**, that is whether the data is node, edge or network table columns.
5. If the table is not properly delimited in the preview panel, change the delimiter in the **Advanced Options** panel. The default delimiter is tab. This step is not necessary for Excel Workbooks.
6. By default, the first column is designated as the primary key, as designated by the key  icon. Make sure the column designated as key matches what's selected under **Key Column for Network** (i.e. the key in the

network. To set another column as the key instead, click the arrow at next to the column title and select the key symbol.

7. Similarly, to change the data type of a column, for example from integer to string, click the arrow next to the column title, and select the correct data type.



1. Click **OK** to import.

Unassigned Table

As of Cytoscape 3.1, it is possible to import data tables without assigning them to existing networks, meaning the data doesn't have to correspond to any nodes/edges currently loaded. If a data table is imported as unassigned and a network is later imported that maps to the data in terms of nodes or edges, the data will link automatically. This is useful when loading a large dataset (for example expression data), defining a **Style** for visualizing the data on networks and later loading individual networks to view the data, for example from an online database. This feature allows the data to be automatically linked to any network that is applicable, without having to load the data for each network.

8.2 Legacy Cytoscape Attributes Format

In addition to tabular data, the simple attribute file format used in previous versions of Cytoscape is still supported. Node and edge data files are simply formatted: a node data file begins with the name of the column on the first line (note that it cannot contain spaces). Each following line contains the name of the node, followed by an equals sign and the data value. Numbers and text strings are the most common data types. All values for a given column must have the same type. For example:

```
FunctionalCategory
YAL001C = metabolism
YAR002W = apoptosis
YBL007C = ribosome
```

An edge data file has much the same structure, except that the name of the edge is the source node name, followed by the interaction type in parentheses, followed by the target node name. Directionality counts, so switching the source and target will refer to a different (or perhaps non-existent) edge. The following is an example edge data file:

```
InteractionStrength
YAL001C (pp) YBR043W = 0.82
YMR022W (pd) YDL112C = 0.441
YDL112C (pd) YMR022W = 0.9013
```

Since Cytoscape treats edge data as directional, the second and third edge data values refer to two different edges (source and target are reversed, though the nodes involved are the same).

Each data column is stored in a separate file. Node and edge data files use the same format, and have the suffix *.attrs*.

Node and edge data may be loaded via the **File** → **Import** → **Table** menu options, just as data table files are.

When expression data is loaded using an expression matrix, it is automatically loaded as node data unless explicitly specified otherwise.

Node and edge data columns are attached to nodes and edges, and so are independent of networks. Data values for a given node or edge will be applied to all copies of that node or edge in all loaded network files, regardless of whether the data file or network file is imported first.

8.2.1 Detailed file format (Advanced users)

Every data file has one header line that gives the name of the data column, and optionally some additional meta-information about that data column. The format is as follows:

```
columnName (class=JavaClassName)
```

The first field is always the column name: it cannot contain spaces. If present, the class field defines the name of the class of the data values. For example, **java.lang.String** or **String** for strings, **java.lang.Double** or **Double** for floating point values, **java.lang.Integer** or **Integer** for integer values, etc. If the value is actually a list of values, the class should be the type of the objects in the list. If no class is specified in the header line, Cytoscape will attempt to guess the type from the first value. If the first value contains numbers in a floating point format, Cytoscape will assume **java.lang.Double**; if the first value contains only numbers with no decimal point, Cytoscape will assume **java.lang.Integer**; otherwise Cytoscape will assume **java.lang.String**. Note that the first value can lead Cytoscape astray: for example,

```
floatingPointDataColumn
firstName = 1
secondName = 2.5
```

In this case, the first value will make Cytoscape think the values should be integers, when in fact they should be floating point numbers. It's safest to explicitly specify the value type to prevent confusion. A better format would be:

```
floatingPointDataColumn (class=Double)
firstName = 1
secondName = 2.5
```

or

```
floatingPointDataColumn
firstName = 1.0
secondName = 2.5
```

Every line past the first line identifies the name of an object (a node in a node data file or an edge in a edge data file) along with the String representation of the data value. The delimiter is always an equals sign; whitespace (spaces and/or tabs) before and after the equals sign is ignored. This means that your names and values can contain whitespace, but object names cannot contain an equals sign and no guarantees are made concerning leading or trailing whitespace. Object names must be the node ID or edge ID as seen in the left-most column of the **Table Panel** if the data column is to map to anything. These names must be reproduced exactly, including case, or they will not match.

Edge names are all of the form:

```
sourceName (edgeType) targetName
```

Specifically, that is

```
sourceName space openParen edgeType closeParen space targetName
```

Note that tabs are not allowed in edge names. Tabs can be used to separate the edge name from the = delimiter, but not within the edge name itself. Also note that this format is different from the specification of interactions in the SIF file format. To be explicit: a SIF entry for the previous interaction would look like

```
sourceName edgeType targetName
```

or

```
sourceName whiteSpace edgeType whiteSpace targetName
```

To specify lists of values, use the following syntax:

```
listDataColumnName (class=java.lang.String)
firstObjectName = (firstValue::secondValue::thirdValue)
secondObjectName = (onlyOneValue)
```

This example shows a data column whose value is defined as a list of text strings. The first object has three strings, and thus three elements in its list, while the second object has a list with only one element. In the case of a list every data value uses list syntax (i.e. parentheses), and each element is of the same class. Again, the class will be inferred if it is not specified in the header line. Lists are not supported by **Styles** and so can't be mapped to network properties.

8.2.2 Newline Feature

Sometimes it is desirable to for data values to include linebreaks, such as node labels that extend over two lines. You can accomplish by inserting into the data value. For example:

```
newlineDataColumn
YJL157C = This is a long\nline for a label.
```



8.2.3 Table Panel

shared name	shared interaction	name	interaction	stringdb score	stringdb interspecies	stringdb textmining	stringdb database
RANBP9 (pp) KRAS	pp	RANBP9 (pp...	pp	0.903		0.057	
RANBP9 (pp) ATM	pp	RANBP9 (pp...	pp	0.633		0.433	
RANBP9 (pp) SRC	pp	RANBP9 (pp...	pp	0.484		0.169	
RANBP9 (pp) STXBP4	pp	RANBP9 (pp...	pp	0.438		0.438	
RANBP9 (pp) HRAS	pp	RANBP9 (pp...	pp	0.905		0.073	
ARHGEF5 (oo) SRC	oo	ARHGEF5 (o...	oo	0.714		0.54	

Node Table | **Edge Table** | Network Table

When Cytoscape is started, the **Table Panel** appears in the bottom right of the main Cytoscape window. This browser can be hidden and restored using the F5 key or by unchecking the **View** → **Show Table Panel** menu option. Like other panels, the browser can be undocked by pressing the little icon in the top right corner.




To swap between displaying node, edge, and network data tables use the tabs on the bottom of the **Table Panel**. By default, the **Table Panel** displays columns for all nodes and edges in the selected network. To display columns for

only selected nodes/edges, click the **Change Table Mode** button  at the top left. To change the columns that are displayed, click the **Show Column**  button and choose the columns that are to be displayed (select various columns by clicking on them, and then click elsewhere on the screen to close the column list).

Editing the Table Panel and Values

Most column values can be edited by double-clicking the cell (only the ID cannot be edited). Newline characters can be inserted into String columns either by pressing **Enter** or by typing `\n`. Once finished editing, click outside of the editing cell in the Table Panel or press **Shift-Enter** to save your edits. Pressing **Esc** while editing will undo any changes.

Rows in the panel can be sorted alphabetically by specific column by clicking on a column heading. A new column

can be created using the **Create New column**  button, and must be one of four types - integer, string, real number (floating point), or boolean. Columns can be deleted using the **Delete Columns...**  button. **NOTE: Deleting columns removes them from Cytoscape, not just the Table Panel!** To remove columns from the panel without deleting them, simply unselect the column using the **Select Columns**  button.

Columns in the **Table Panel** can be renamed by right-clicking on the column header and selecting **Rename Column...** The **Table Panel** supports name spaces, so if you have several columns with related information, you can create a namespace. Namespace and column name are separated by a double colon (::). For example, if the data includes multiple columns with cellular compartment information, you can edit the column titles in the format **compartment::cytosol**, **compartment::endosome** etc, which will create a namespace **compartment** with several associated columns. It is then possible to perform operations such as **Show/Hide** on all columns in a namespace.

1. Load a network, for example *galFiltered.sif*.
2. Select **File** → **Import** → **Table from Public Databases...**
3. You will first be asked to select from a set of web services. For this example, we will choose **ENSEMBL GENES 104**.

1. In the **Import Data Table from Public Databases** dialog, select a **Service**. Since the galFiltered network is from yeast, select **ENSEMBL GENES - SACCHAROMYCES CEREVISIAE**.
2. For **Key Column in Cytoscape**, select *COMMON* for **Column** and *Gene Name(s)* for **Data Type**.

Import Table from Public Databases

Data Source: **BioMart Client**

About

bio::mart

Service

Ensembl Genes 103 - Saccharomyces cerevisiae genes (R64-1-1) ...

Key Column in Cytoscape

Column: **COMMON**

Data Type: **Gene Name(s) [e.g. SCO2]**

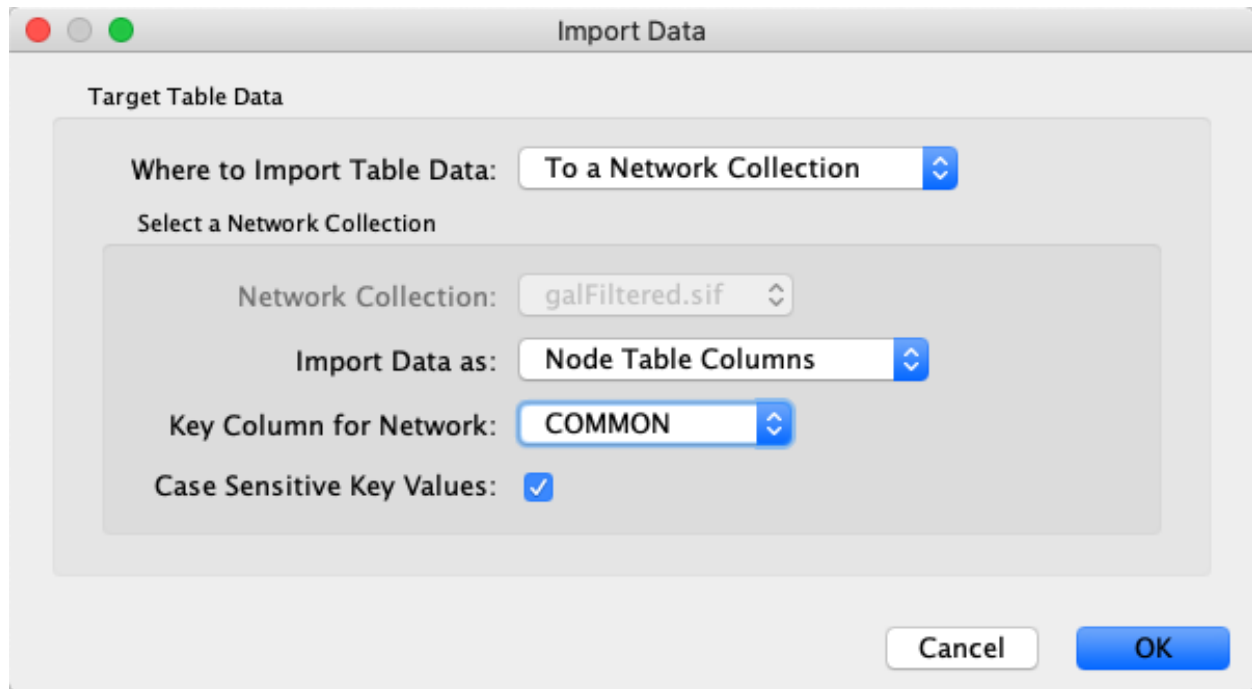
Import Settings

- ☐ PANTHER end (hmmpantther_end)
- ☐ PANTHER start (hmmpantther_start)
- ☒ **PDB ID (pdb)**
- ☐ PHI-base accession ID (phi)
- ☐ PIRSF ID (pirsf)
- ☐ PIRSF end (pirsf_end)
- ☐ PIRSF start (pirsf_start)
- ☐ PROSITE patterns ID (scanprosite)
- ☐ PROSITE patterns end (scanprosite_end)
- ☐ PROSITE patterns start (scanprosite_start)
- ☐ PROSITE profiles ID (pfscan)
- ☐ PROSITE profiles end (pfscan_end)

Select All Select None

Cancel **Import**

1. Select the data columns you want to import.
2. Select **Import**.
3. In the **Import Data** interface, select *COMMON* for **Key Column for Network**.



When import is complete, you can see the newly imported data columns in the Table Panel.

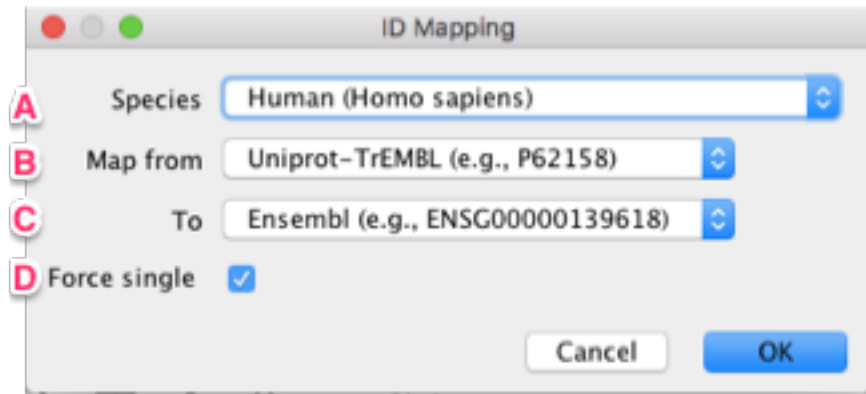
Node Table					
shared name	name	Degree	COMMON	PDB ID	Pfam ID
YDL194W	YDL194W	1	SNF3		PF00083
YDR277C	YDR277C	2	MTH1		PF17235
YBR043C	YBR043C	1	YBR043C		
YPR145W	YPR145W	1	ASN1		PF13537
YER054C	YER054C	2	GIP2		PF03370
YBR045C	YBR045C	3	GIP1		
YBL079W	YBL079W	1	NUP170	3IS5	PF08801
YIR345W	YIR345W	1	YIR345W		

8.4 Mapping Identifiers

A common problem in integrating multiple data sources is differences in terminology. Standardized identifiers have many dialects. Some databases are specific to a particular organism or genome. Others span those boundaries. [BridgeDB](#) is a web service devoted to solving the id mapping problem. Cytoscape contains simple access to BridgeDB. If you need more esoteric species or data sources, there is an [installable BridgeDB app](#) to access a fuller feature set.

[Ensembl](#) is used as the canonical taxonomy. A translation between two arbitrary data sources is generally achieved by mapping each through Ensembl.

To map an identifier from one source to another, right click on the column header of your identifier. Select the option to **Map Column...**



A. The mapping is always constrained by species to prevent senseless matches across species. You must choose a species (once) for this feature to function properly. The choices for the Data Source and Target are determined by the species.

B. Based on the items in the column you chose we can make a reasonable assumption as to the database as to use as the source for your mapping. If this is not the source, you can override it in the Map from field.

C. The target database of the identifier mapping. This list is filtered by species and curated down to the most common options. A full list of supported targets is [here](#).

D. In some cases where there are multiple answers, the **Force Single** option limits the result to the first answer returned by the service. If the option is off, a list of results will appear in the column.

Column Data Functions and Equations

9.1 Column Formulas

9.1.1 Introduction

Columns may contain formulas that are evaluated on-demand and result in a value.

9.1.2 Syntax

Basic Syntax

A formula always starts with an equals sign '='. This signifies that the value in the table cell is a formula.

Example: `=ABS($otherColumn + LOG(10.2))`

The type of the value returned by a formula must match the column type, or be easily converted to the column type. For example, if a formula returns a numeric value in a string column, the numeric value will be converted to a string. However if a formula returns a string value in a numeric column, the string cannot be automatically converted to a number, so it will result in an error being shown.

All numeric values will be accepted for a boolean (or logical) column data where non-zero will be interpreted as **true** and zero as **false**. Floating point values will be converted using the rules of the Excel(tm) **INT** function. Parentheses can be used for grouping and to change evaluation order.

Functions

Cytoscape provides a set of functions that perform specific tasks and calculations. A function is written as the name of the function, then an opening bracket '(', then an optional comma-separated list of arguments, then a closing bracket ')'. Example: `=MAX(10, 20)` Example: `=IF($otherColumn, "UP", "DOWN")` Example: `=NOW()`

Attributes

Attributes are named references to other columns in the same table as the formula, and result in the value of the column cell for the same node, edge or network.

An attribute reference is written by placing the column name after a dollarsign (\$).

Example: **\$columnName**

If the column name contains spaces, special characters or a namespace identifier then the name must be placed between curly braces.

Example: **\${column name with spaces}** Example: **\${namespace::columnName}**

Special characters such as commas must be escaped with a leading backslash.

Example: **\${name with \, comma}**

You may provide a default value that will be used if the column value is blank. Place a colon (:) and the value after the column name.

Example: **\${columnName:0.0}**

Finally, column names are case sensitive.

Operators

An operator is written between two operands.

Example: **=\$x + 1**

Numeric operators: + addition, - subtraction, * multiplication, / division, ^ exponentiation

Text operators: & string concatenation

Logical operators (operate on boolean values true/false): < less than, > greater than, >= greater than or equal, <= less than or equal, = equal, <> not equal

The operator precedence rules follow those of standard arithmetic.

Literal Values

String (text) literals are between double quotes, example: **"abc"**

Numeric literals, example: **123**

Floating point literals, example: **123.45**

Boolean (logical) literals: **true, false**

In order to embed a double-quote or a backslash in a string they have to be escaped with a leading backslash, therefore the string **"\"** must be written as **"\"**.

Conditional IF

A conditional is written as a function named 'IF' with three arguments: **IF(condition, a, b)**. If the condition evaluates to true then the value of the **a** argument is returned, otherwise the **b** argument is returned.

Example: **IF(\$x = \$y, "equal", "different")**

9.1.3 Supported Functions

Currently we support the following functions:

Cytoscape-specific network functions

- Degree – the degree of a node, meaning how many edges connect to it.
- InDegree – the indegree of a node.
- IsDirected – Returns true if this edge is directed, false otherwise.
- OutDegree – the outdegree of a node.
- SourceID – the ID of the source node of an edge.
- TargetID – the ID of the target of an edge.

Numeric Functions

- Abs – Returns the absolute value of a number.
- ACos – Returns the arccosine of a number.
- ASin – Returns the arcsine of a number.
- ATan2 – Returns the arctangent of two numbers x and y.
- Average – Returns the average of a group of numbers.
- Combin – Returns number of combinations of n objects, with k chosen at any one time.
- Cos – Returns the cosine of an angle given in radians.
- Cosh – Returns the hyperbolic sine of its argument.
- Degrees – Returns its argument converted from radians to degrees.
- Exp – Returns e raised to a specified number.
- GeoMean – the geometric mean of a set of numbers.
- HarMean – the harmonic mean of a set of numbers.
- Ln – Returns the natural logarithm of a number.
- Log – Returns the logarithm of a number to a specified base.
- Max – Returns the maximum of a group of numbers.
- Median – Returns the median of a list of numbers.
- Min – Returns the minimum of a group of numbers.
- Mod – Calculates the modulus of a number.
- Mode – the mode of a set of numbers.
- NormDist – Returns the pdf or CDF of the normal distribution.
- Permut – Returns the number of permutations for a given number of objects.
- Pi – Returns an approximation of the value of p.
- Product – Returns the product the given numbers.

- Radians – Returns its argument converted from degrees to radians.
- Round – Rounds a number to a specified number of decimal places.
- Sign – Implements the signum function. Returns -1,0,+1 based on the number being negative, zero, or positive.
- Sin – Returns the sine of an angle given in radians.
- Sinh – Returns the hyperbolic sine of its argument.
- Sqrt – Calculates the square root of a number.
- StDev – Returns the sample standard deviation of a list of numbers.
- Sum – Returns the sum of all of its arguments.
- Tan – returns the tangent of its argument in radians.
- Tanh – returns the hyperbolic tangent of its argument in radians.
- Trunc – Truncates a number.
- Var – sample variance.

Text Functions

- Concatenate – Concatenates two or more pieces of text.
- Left – Returns a prefix of s string.
- Len – Returns the length of a string.
- Listtostring – Converts a list to a string, given a separator.
- Lower – Converts a string to lowercase.
- Mid – Selects a substring of some text.
- Right – Returns a suffix of a string.
- Split – Splits a text string into substrings around matches of a delimiter. Returns a list of strings.
- Substitute – Replaces some text with other text.
- Text – Format a number using the Java *DecimalFormat* class' conventions.
- Upper – Converts a string to uppercase.
- Value – Converts a string to a number.

List Functions

- Blist – Returns a list of boolean values.
- Count – Returns the number of numeric values in a list.
- First – Returns the first entry in a list.
- Flist – Returns a list of floating point numbers.
- Ilist – Returns a list of integer numbers.
- Largest – Returns the kth largest element of a list of numbers.
- Last – Returns the last entry in a list.
- Len – Returns the length of a string (ie number of characters in the string), or the length of a list.

- Nth – Returns the n-th entry in a list.
- Slist – Returns a list of strings.

Logical/Boolean Functions

- And – Returns the logical conjunction of any number of boolean values.
- If – Returns one of two alternatives based on a boolean value.
- Not – Returns the logical negation of a boolean value.
- Or – Returns the logical disjunction of any number of boolean values.

Date/Time Functions

- Now – Returns a string representation of the current date and time.
- Today – returns a string representation of the current date.

Other Functions

- Booleantablecell – Returns the value in the column for the specified SUID
- Doubletablecell – Returns the value in the column for the specified SUID
- Error – Throws an exception at runtime.
- Integertablecell – Returns the value in the column for the specified SUID
- Longtablecell – Returns the value in the column for the specified SUID
- Stringtablecell – Returns the value in the column for the specified SUID

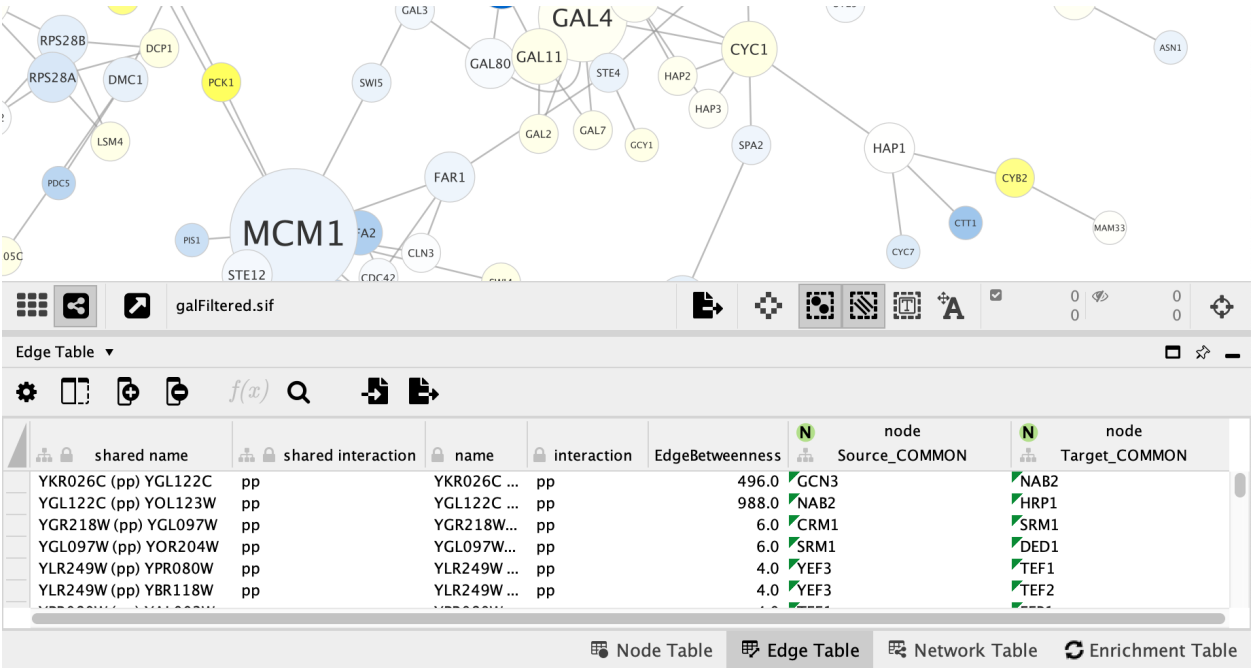
9.1.4 Map Source and Target Nodes

By default, Cytoscape adds columns for source and target node to the **Edge Table**, using equations. This mapping happens automatically when a network is opened, and the **shared name** column is used for the mapping. However, the selection of which **Node Table** column to use is customizable.

To update the mapping, go to **Apps** → **mapSourceAndTarget**. It is possible to select more than one **Node Table** column for the mapping, resulting in multiple sets of source and target node columns in the **Edge Table**.

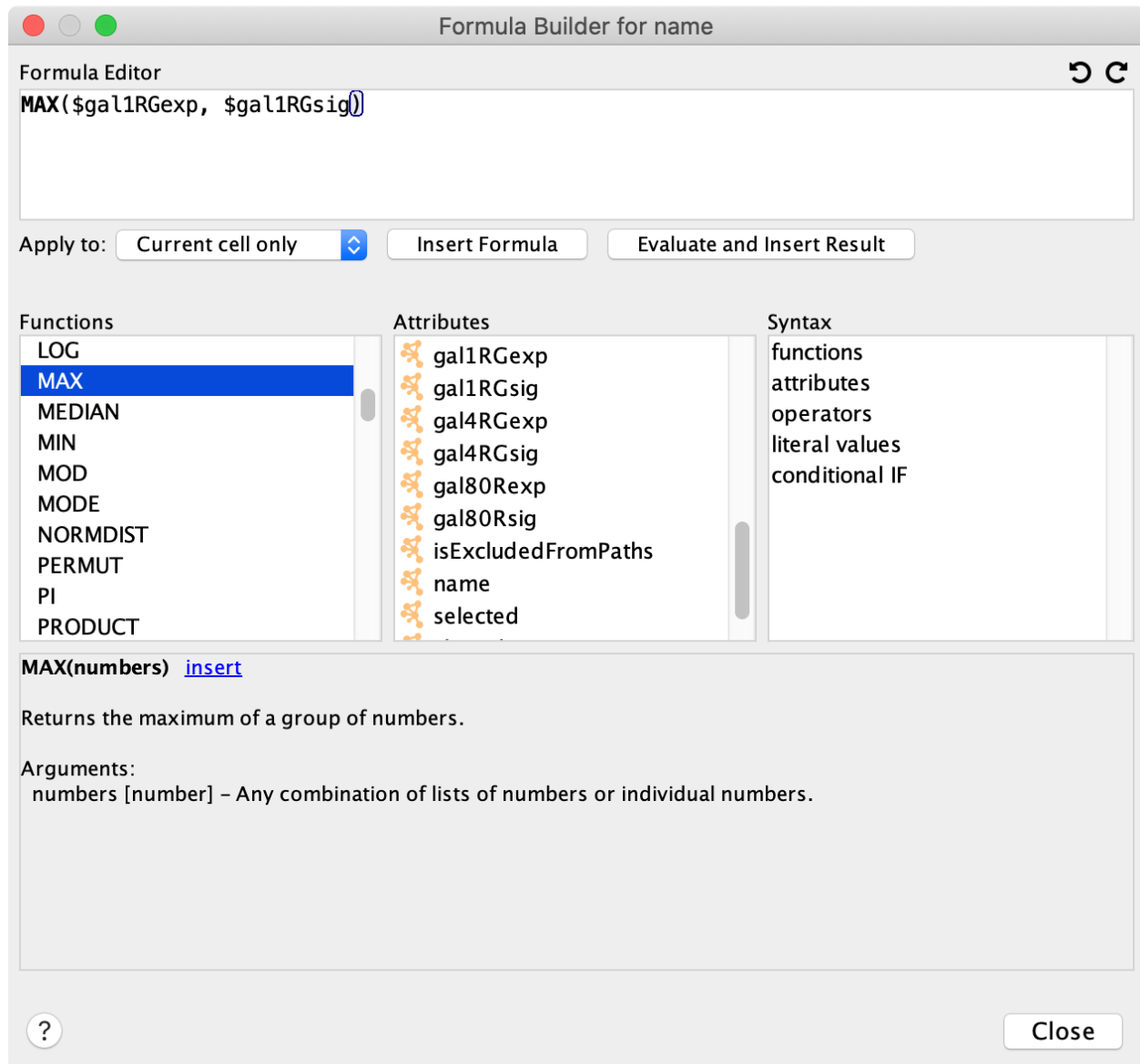
To turn off automatic mapping, go to **Edit** → **Properties** → **Cytoscape Preferences** and then select **mapSourceAndTarget** from the drop-down. Change the value of the **autoMap** property to **FALSE**.

The screenshot below shows the source and target node column mappings, using the node column **COMMON**.



9.2 The Formula Builder

In order to ease the creation of formulas as well as to facilitate discovery of built-in functions we provide a **Formula Builder** in the **Table Panel**. The Formula Builder is opened by clicking the $f(x)$ button. This should bring up the **Formula Builder** which looks like this:



At the top is a text area called the **Formula Editor**. The text for a formula may be typed directly into this area. At the top-right of the text area are buttons for **Undo** and **Redo**.

When the formula is ready click the **Insert Formula** button to insert the formula into the table. Depending on what is selected in the combo box, the formula can be inserted into the selected cell only, the entire column, or just the cells for nodes/edges that are currently selected. If there is a syntax error in the formula it will be reported immediately when the **Insert Formula** button is clicked.

Normally formulas are re-evaluated on demand as needed. For example if a formula contains an attribute reference to another column, and the value in that column changes, then the formula is re-evaluated. This re-evaluation sometimes has disadvantages, for example re-evaluation can sometimes be slow for very large networks. Instead of inserting the formula itself you may click the **Evaluate and Insert Result** button. This will evaluate the formula immediately and just insert the result into the selected cells.

Below the **Formula Editor** is an area used for documentation.

- The **Functions** area lists all functions that are available. Click on a function name to view documentation on what the function does and how it can be used. Click the **insert** link in the documentation area to insert the function into the **Formula Editor** at the location of the cursor.

- The **Attributes** area lists all available columns in the current table that can be referenced from the formula. Click the **insert** link in the documentation area to insert an attribute reference into the Formula Editor at the location of the cursor.
- The **Syntax** area provides documentation on formula syntax.

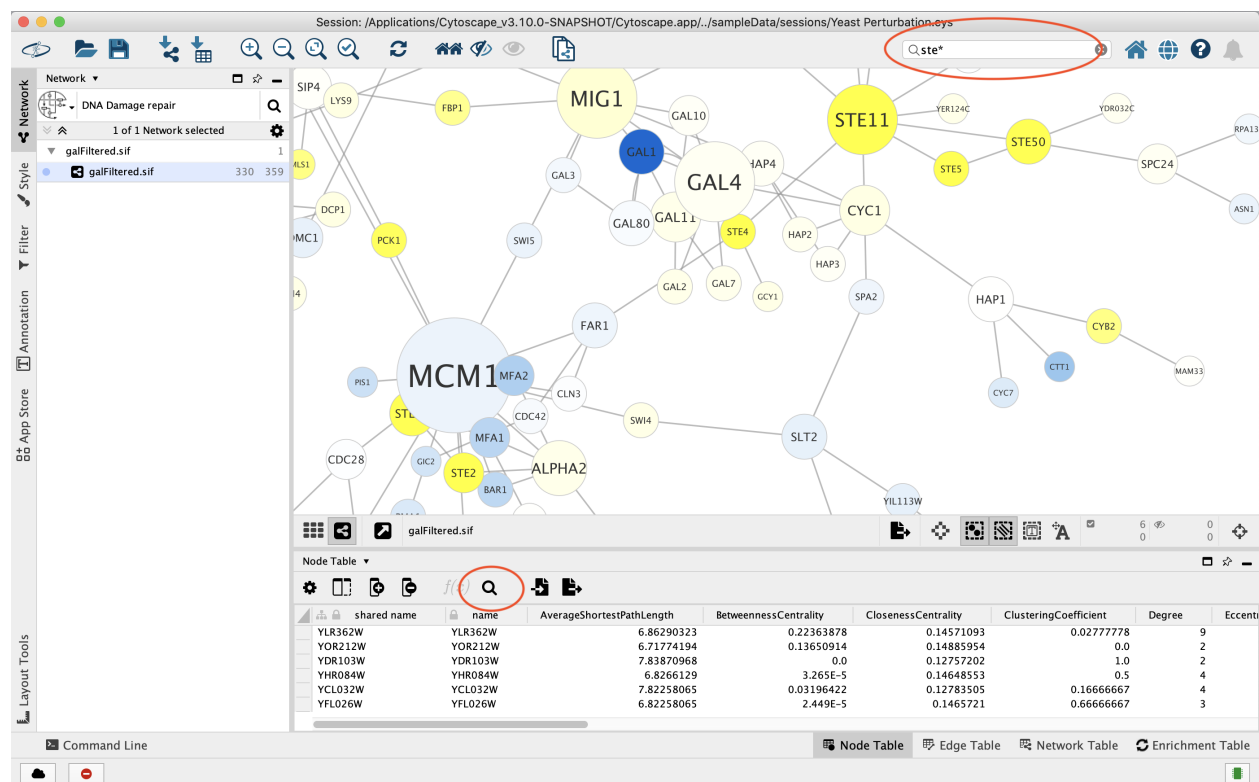
9.3 A Note for App Writers

It is relatively easy to add your own built-in formula functions. A simple function can probably be implemented in 15 to 20 minutes. It can then be registered via the parser and becomes immediately available to the user. It will be available in the in the **Formula Builder**.

Finding and Filtering Nodes and Edges

10.1 Search Bar

You can search for nodes and edges by column value directly through the search field in the **Tool Bar**, and by clicking the **Search Table** button in the **Table Panel** for **Node** and **Edge** tables. For example, to select nodes or edges with a column value that starts with *STE*, type `ste*` in the search bar. The search is case-insensitive. The `*` is a wildcard character that matches zero or more characters, while `?` matches exactly one character. So `ste?` would match *STE2* but would not match *STE12*. Searching for `ste*` would match both.



To search a specific column, you can prefix your search term with the column name followed by a `:`. For example, to select nodes and edges that have a **COMMON** column value that starts with *STE*, use `common:ste*`. If you don't specify a particular column, all columns will be searched.

10.1.1 Query Syntax

The query syntax uses the standard Lucene QueryParser with a few modifications.

To search for column values that contain special characters you need to escape those characters using a `\`. For example, to search for *GO:1232*, use the query `GO\ : 1232`. The complete list of special characters is:

```
+ - & | ! ( ) { } [ ] ^ " ~ * ? : \ space
```

10.2 The Select Menu

The **Select** → **Nodes** and **Select** → **Edges** menus provide several mechanisms for selecting nodes and edges. Most options are fairly straightforward and self-explanatory.

A set of keyboard shortcuts for selecting nodes, edges and annotations are also available. Note that these keyboard shortcuts work regardless of which **Selection Mode** for mouse click or drag-selection.

Select → **Mouse Drag Selects** includes the same options for **Selection Mode** for mouse click- or drag-selection as the current **Selection Mode** in the **Network View Tools**.

Select → **Nodes** → **Largest subnetwork** selects the largest connected component in the current network. This operation is useful when working with a partitioned network consisting of two or more distinctly connected graphs. After selecting the largest subnetwork, a new network can easily be created from the selection.

Select → **Nodes** → **From ID List File...** selects nodes based on node identifiers found in a specified file. The file format is simply one node id per line:

```
Node1
Node2
Node3
...
```

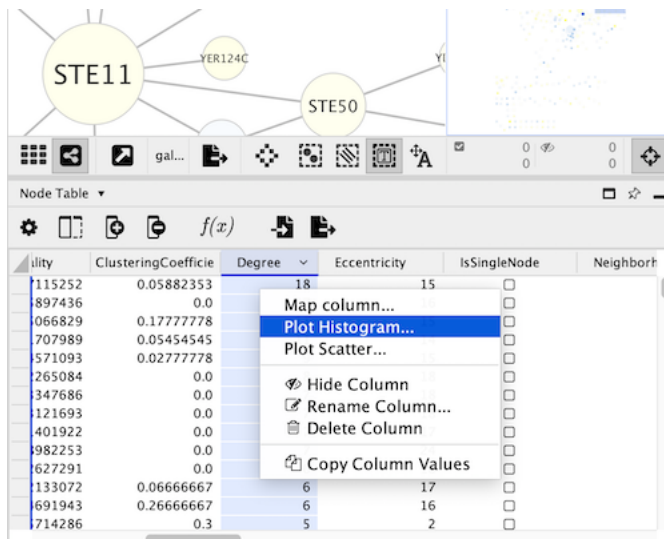
10.3 cyChart

CyChart is a charting package available as a core app in Cytoscape. **CyChart** provides simple 1D and 2D plots of numerical values from node or edge tables. Selection in the chart will reciprocally select nodes or edges in the network. This provides another way to visualize and interact with your data in Cytoscape.

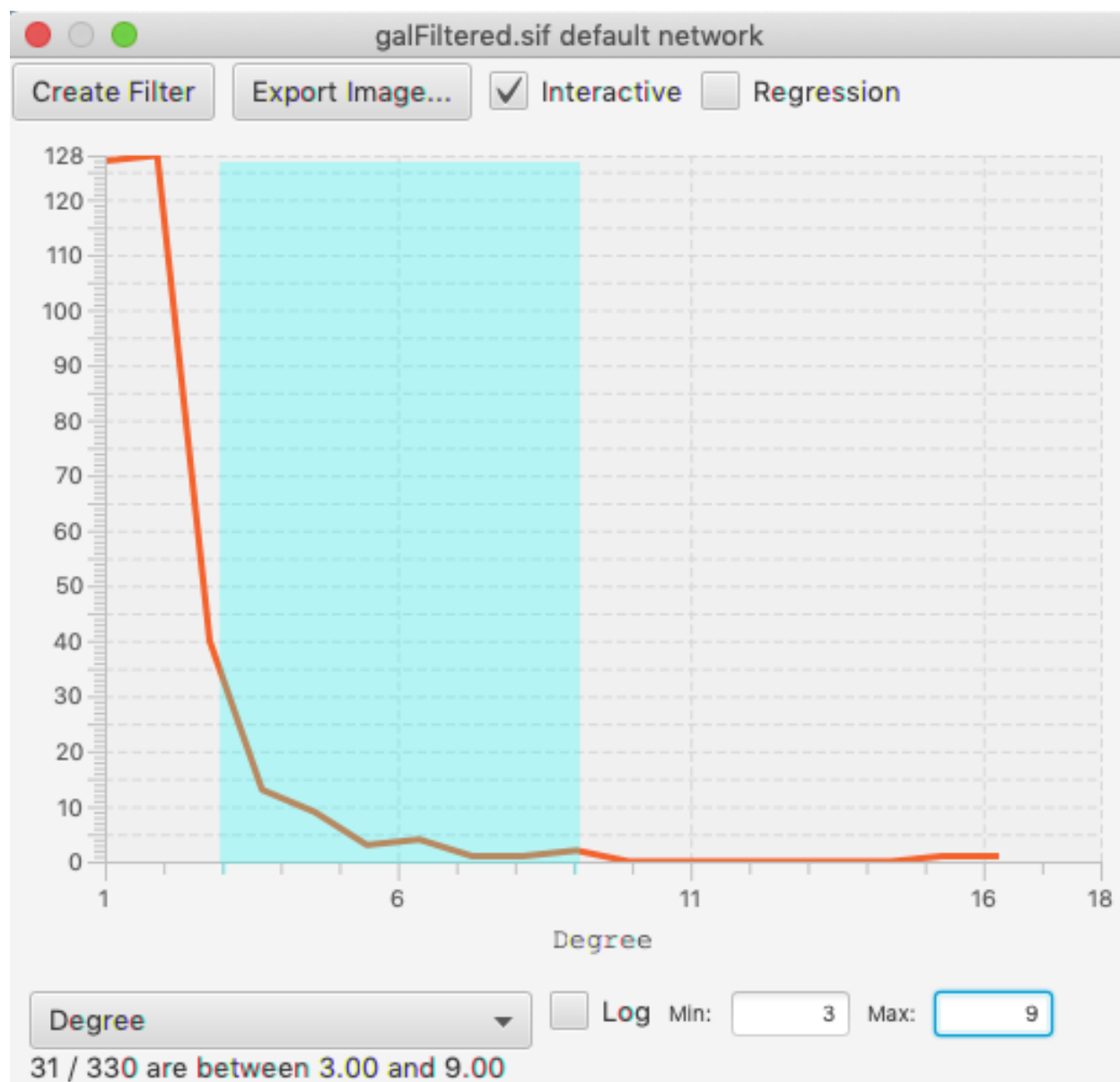
10.3.1 Histograms

A histogram shows the distribution of a variable in bins over a range. It shows the user where the most common values are and whether the values are distributed uniformly (flat line), normally (the bell curve) or have strong modes (hills and valleys). This can be particularly useful for finding pockets of the data that express similar ranges, such as positively and negatively expressed genes.

To create a histogram using **cyChart**, open the right-click on the header of a numeric column in the **Node** or **Edge Table**, and select the command **Plot Histogram...** CyChart options are also available in the **Tools** menu.



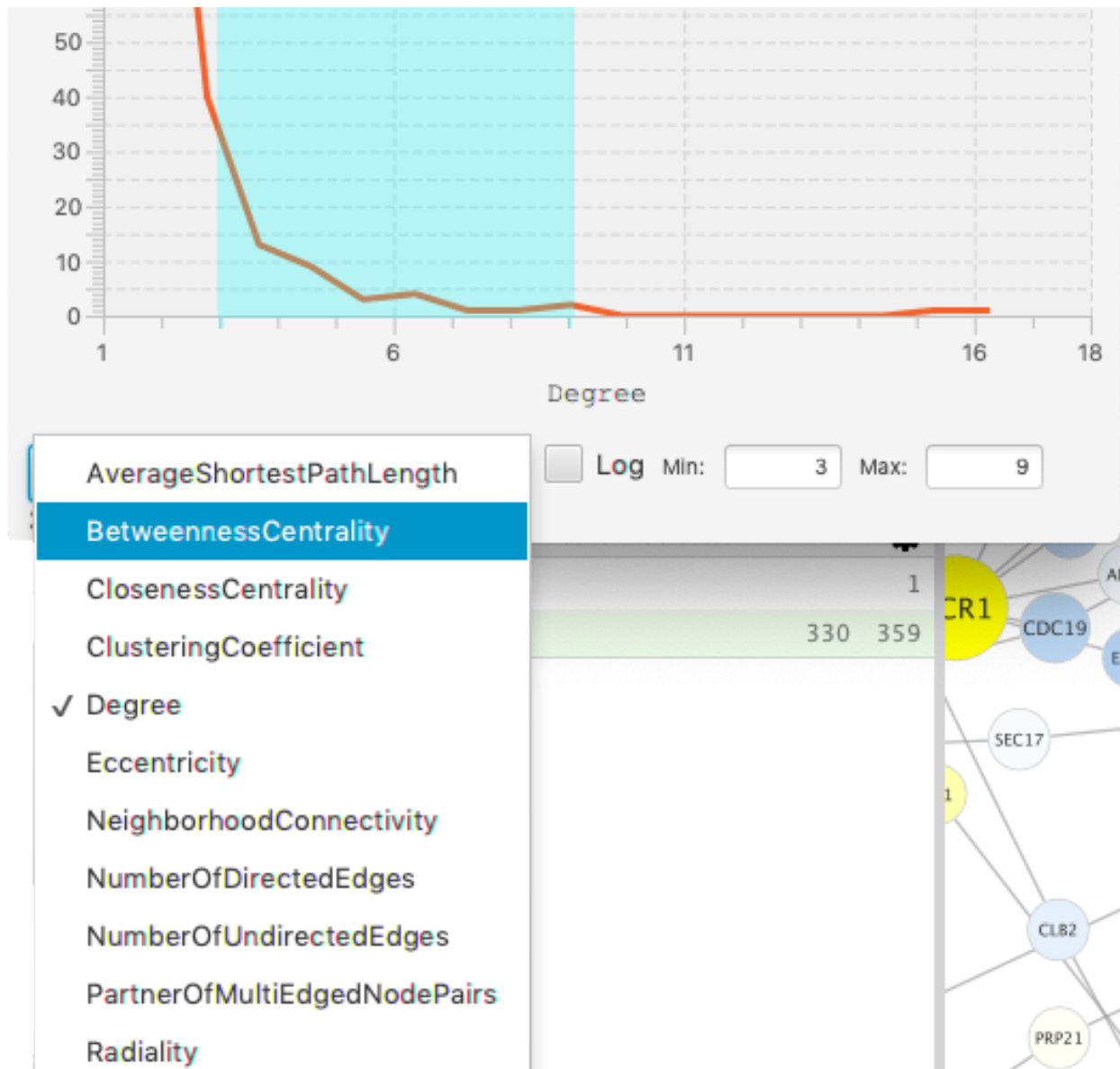
The structure of the **cyChart** window has a header with common functions and settings, the content of the chart, and a footer with the selections status and the controls to set the axes.



To select a range within a histogram, click and drag left or right. You should see a color change in the background of the data. To edit an existing selection, drag in the middle of the selection to move the entire selection, or on either edge of the selection to edit just the start or end of the range. To clear the selection, click outside of the range.

If the chart is in its interactive mode, you can see the main graph view changing its selection as the chart changes. However, in large networks this will over-stress the computer and become sluggish in the interface. Therefore, there is a check box in the header of **cyChart** to control whether selection is recomputed whenever the mouse moves, or occurs only at the end of your drag.

The footer is used to set the axes of the chart, and to show the status of the selection. Click on the popup choice box to see the list of available dimensions. The chart will be regenerated whenever you change either dimension. The current selection is lost when either axis changes.



[Note: the first invocation of the axis popups may take several seconds to respond. Subsequent clicks will be more responsive.]

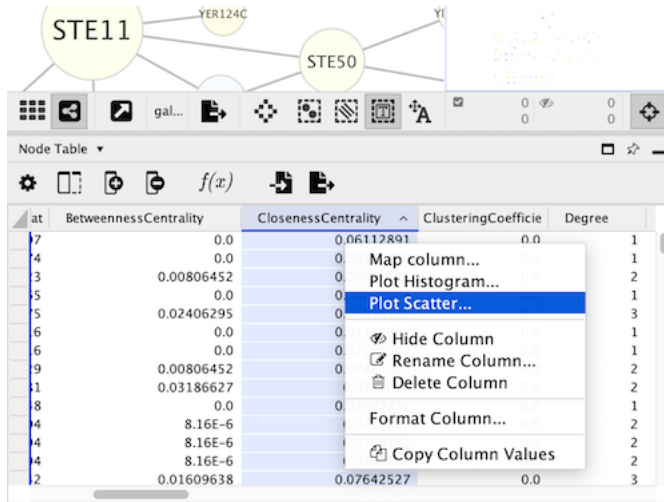
[Note: Logarithmic axes will be enabled in a future release.]

Regardless of the experiment size, the histogram is divided into 100 bins, smoothed, and plotted such that the Y value on the line is the number of nodes (edges) within that range. The bins have equal width (as opposed to equal area). This is a simplification of statistical rules to determine the number of bins in the sampling of the data, but is not unreasonable in the context where you are setting the ranges manually.

10.3.2 Scatter Charts

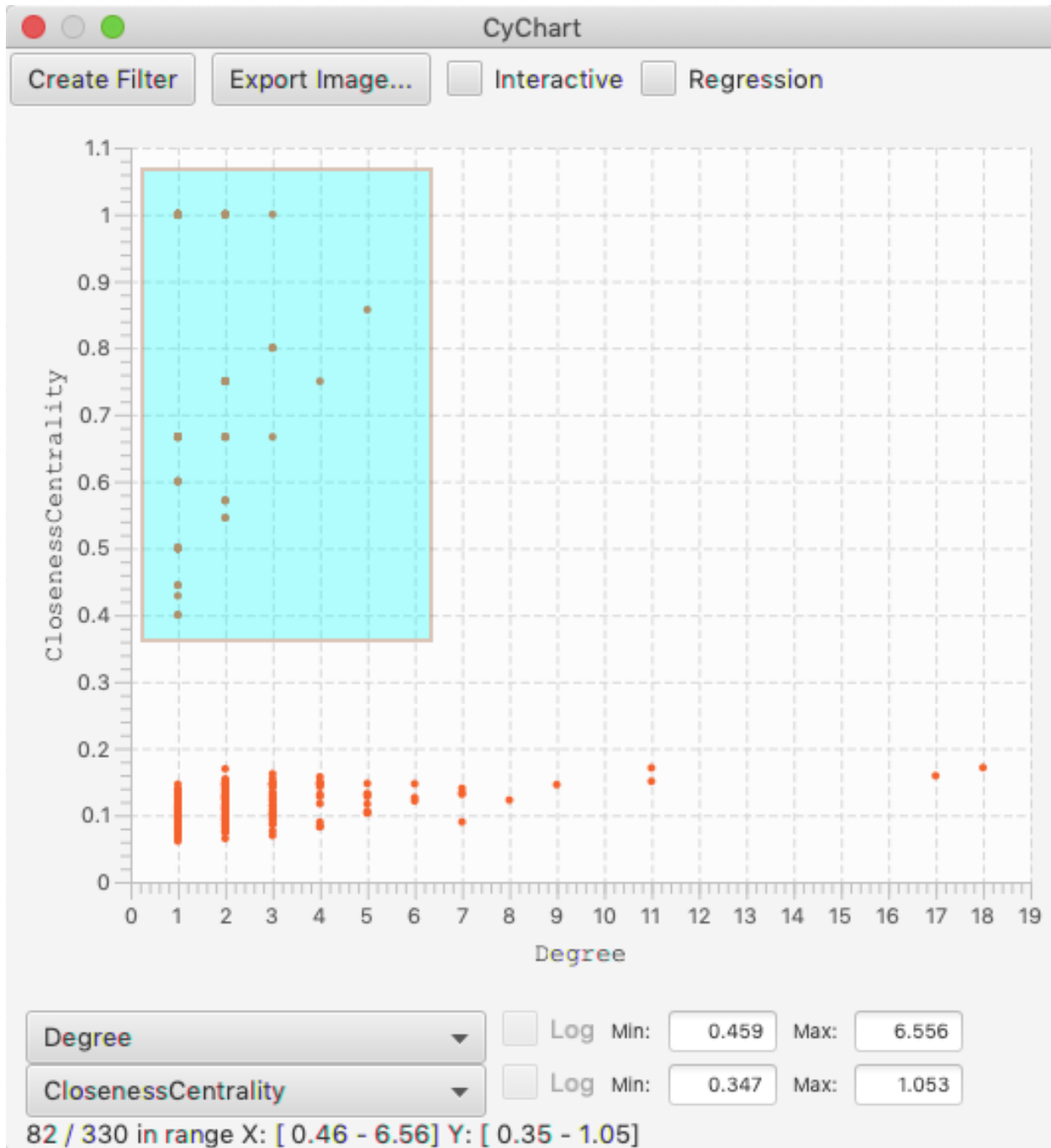
A scatter chart is a two dimensional plot with a dot drawn for each row in the table. Per standard, the domain is the horizontal (X) axis and the range is the vertical (Y) axis. Similar to the histograms, clicking and dragging within the chart will select a rectangle of dots, and change the current selection in your graph. You can edit the size of the selection by dragging any of the corners, or edit the position by clicking inside the rectangle.

Create the scatter chart by right-clicking on the header of the column you want as your X axis and select the command **Plot Scatter...**



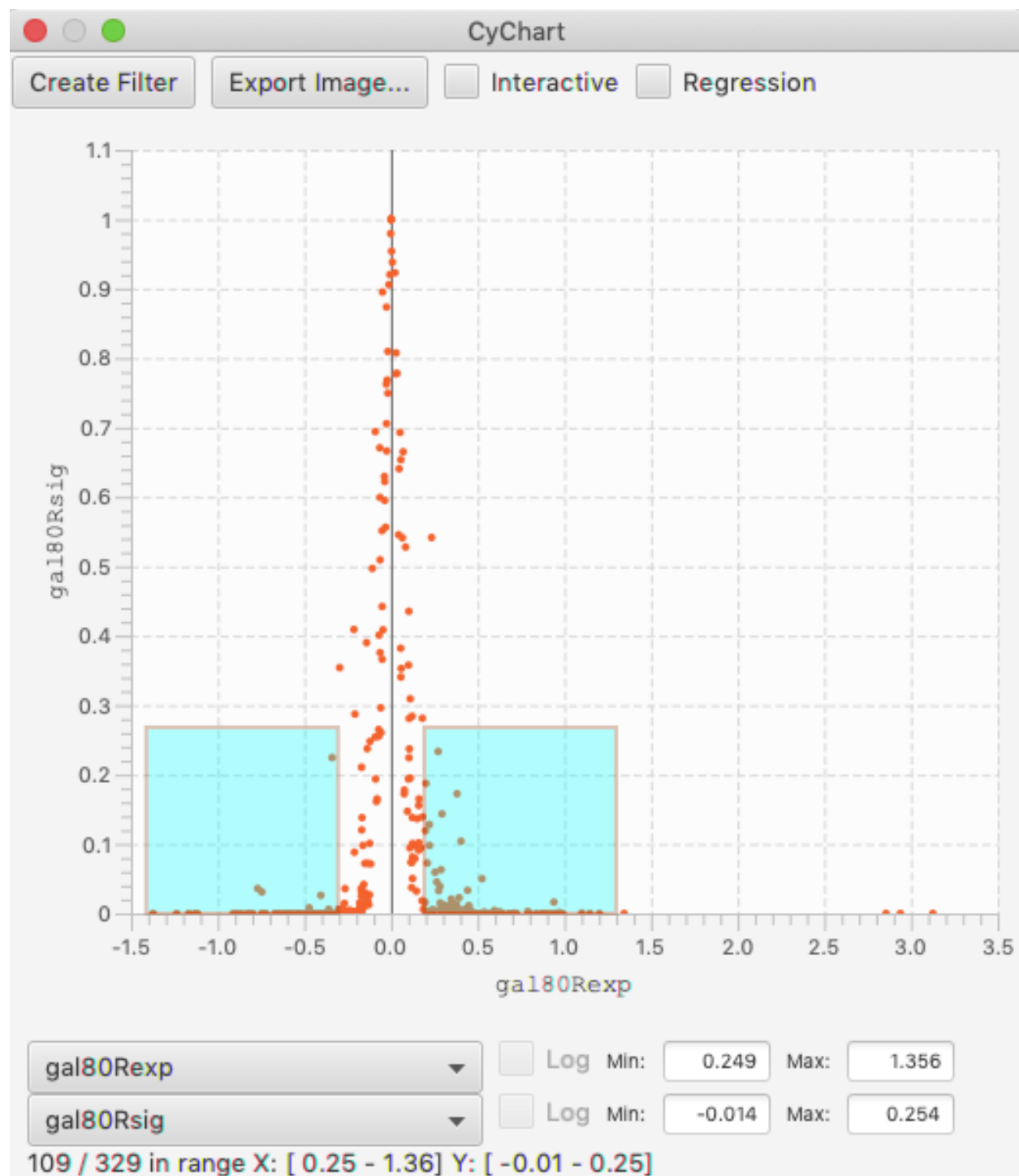
There is a **Regression** check box, which will add a regression line through the data. The regression is calculated with the linear least squares method. The slope, intercept and measure of the fit are shown with the line.

As with Histograms, the **Scatter Chart** has a check box to set whether the selection of nodes in your graph will update whenever the mouse moves, or only upon release. If there is annoying flicker when dragging your selection, you should turn off the Interactive mode.



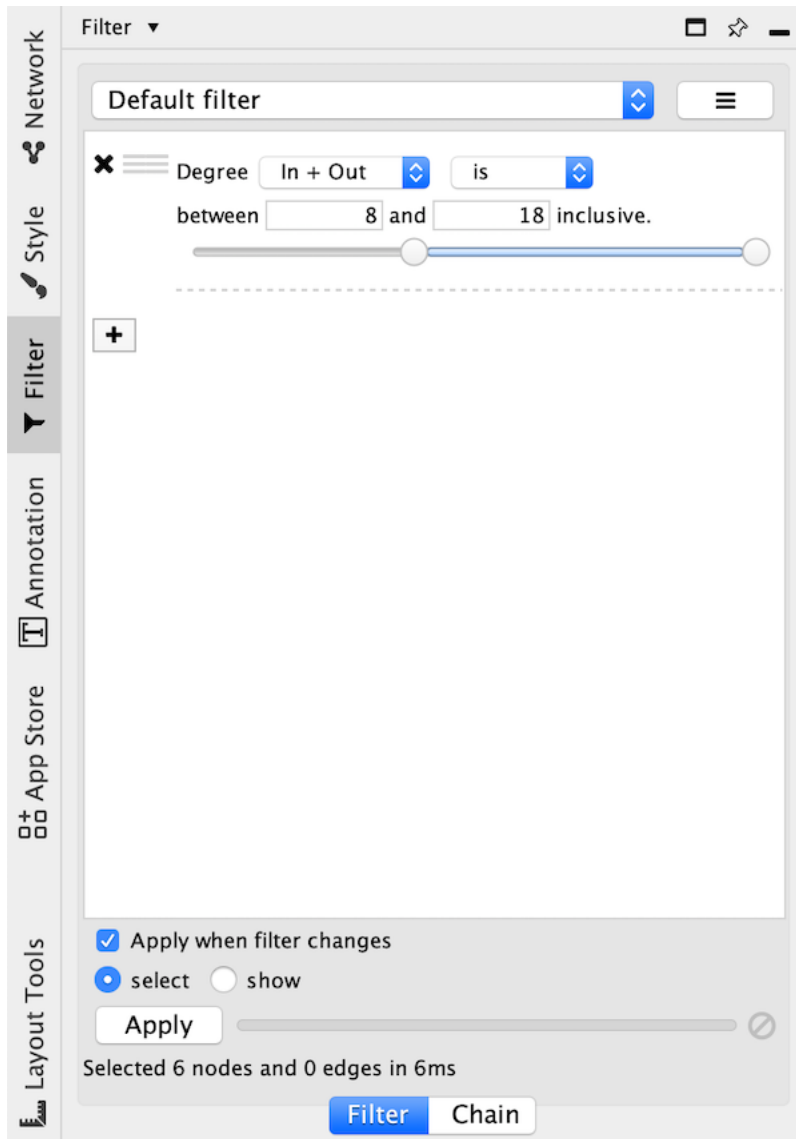
10.3.3 Volcano Plots

Volcano plots are a domain-specific type of scatter chart, where the X axis is an expression level, and the range is the significance of the measurement. These plots have the interesting characteristic that you are often interested in both positive and negative values, with a high value for the significance. In this case, it is useful to be able to select areas of a scatter chart symmetrically around the axis. This is done by holding the option key, as you drag. (This feature is only enabled when the X axis spans across 0, so if you don't see it appear, confirm that your table column has negative and positive values.)



10.4 Filters

The **Filter** tab in the **Control Panel** can be used to create selection expressions for selecting nodes and edges.




There are two tabs:

1. On the **Filter** tab are *narrowing* filters, which can be combined into a tree.
2. On the **Chain** tab are *chainable* transformers, which can be combined in a linear chain.

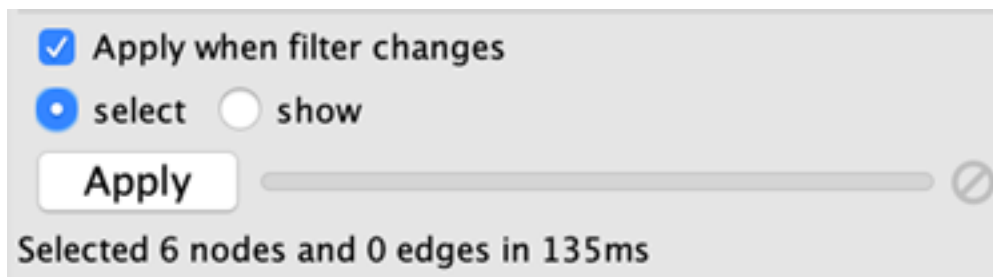
10.4.1 Narrowing Filters

Narrowing filters are applied to all the nodes and edges in the network, and are used to select a subset of the nodes and edges based on user-specified constraints. For example, you can find edges with a weight between 0 and 5.5, or nodes with degree less than 3 (connecting to 3 or less edges). A filter can contain an arbitrary number of sub-filters.

To add a filter click on the + button. To delete a filter (and all its sub-filters) click the x button. To move a filter grab the handle  with the mouse and drag and drop the filter on its intended destination. Dropping a filter on top of another filter will group the filters into a composite filter.

Interactive Filter Application Mode

Due to the nature of narrowing filters, Cytoscape can apply them to a network efficiently and interactively. Some filters even provide slider controls to quickly explore different thresholds. This is the default behavior on smaller networks. For larger networks, Cytoscape automatically disables this interactivity. You can override this by manually checking the **Apply when filter changes** box above the **Apply** button:



The **Apply** button will re-apply the active filter. On the opposite side of the progress bar is the cancel button, which will let you interrupt a long-running filter.

You also have the option to use the filter to show only the selected nodes by checking the **show** button. The **select** button is checked by default and simply selects nodes that pass the filter.

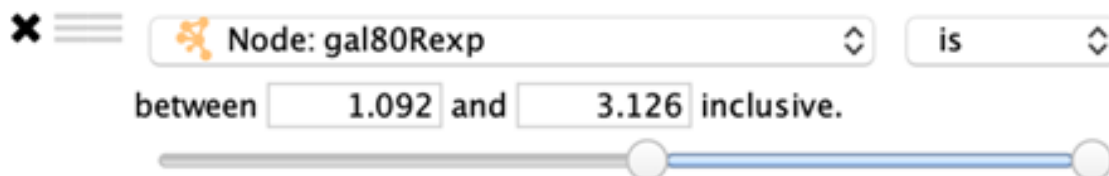
Cytoscape comes packaged with the following narrowing filters:

Column Filter

Column filters will match nodes or edges that have particular column values. Depending on the column data type a variety of matching options are provided:

- **Numeric Columns**

- A slider is shown that represents the minimum and maximum values in the column. Drag the two handles to select a range of values.
- The range values may also be entered manually.
- Options:
 - * **is**: Selects values that are inside the range.
 - * **is not**: Selects values that are outside the range.



- **String Columns**

- The text entered in the text box will be matched against the column values depending on the following options.
- Options:
 - * **contains**: Selects values that contain the text.
 - * **doesn't contain**: Selects values that do not contain the text.

- * **is**: Selects values that match the text exactly (case-insensitive).
- * **is not**: Selects values that do not match the text exactly (case-insensitive).
- * **regex**: Selects values that match a regular expression using [Java regular expression syntax](#). This allows for much more sophisticated matching than is provided by the above options.
- By default string matching is case insensitive. Case sensitive matching requires the use of a regular expression that starts with **(?-i)**. For example to match the text *ABC* in a case sensitive way use the following regular expression: **(?-i)ABC**.

A screenshot of a Cytoscape filter interface. On the left, there is a close button (X) and a menu icon (three horizontal lines). The main part of the interface is a filter rule: 'Node: name' followed by a dropdown arrow, then the operator 'contains' followed by another dropdown arrow. Below this, there is a text input field containing the value 'YDL19'.

• Boolean Columns

- Boolean columns can only contain three values: true, false or blank.
- Options:
 - * **true**: Selects values that are true.
 - * **false**: Selects values that are false.

A screenshot of a Cytoscape filter interface. On the left, there is a close button (X) and a menu icon (three horizontal lines). The main part of the interface is a filter rule: 'Node: isExcludedFromPaths' followed by a dropdown arrow. Below this, there is a text input field containing the value 'true'.

• List Columns

- Column filters for list columns are similar to their non-list counterparts, however there is one additional option...
- * **any element**: Matches if any value in the list matches the filter.
- * **each element**: Matches only if all of the values in the list match the filter.

A screenshot of a Cytoscape filter interface. On the left, there is a close button (X) and a menu icon (three horizontal lines). The main part of the interface is a filter rule: 'Node: attributes' followed by a dropdown arrow. Below this, there are two more dropdown arrows, the first containing 'any element' and the second containing 'contains'.

Degree Filter

The degree filter matches nodes with a degree that falls within the given minimum and maximum values, inclusive. You can choose whether the filter operates on the in-degree, out-degree or overall (in + out) degree.

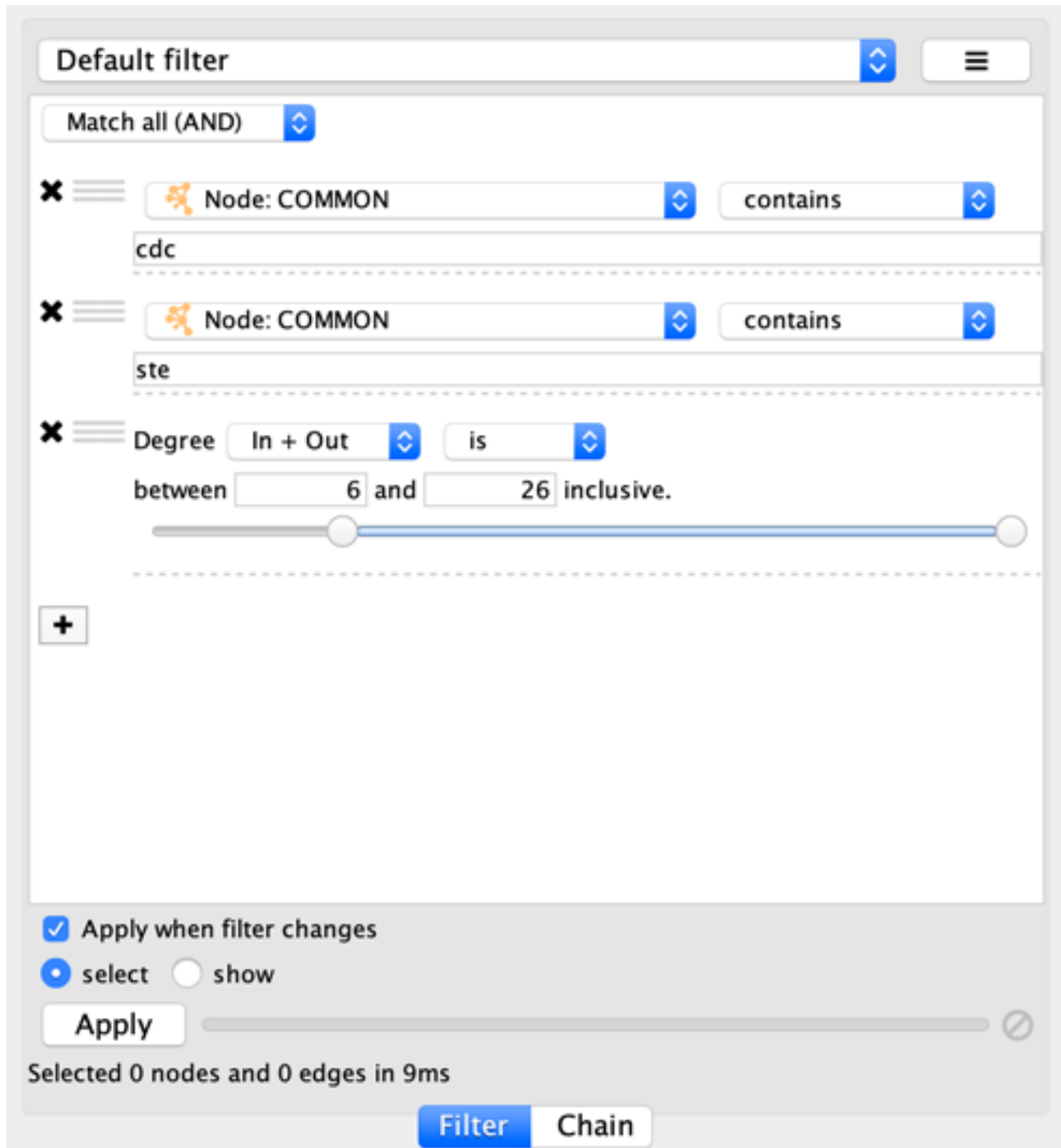
Topology Filter


The topology filter matches nodes having a certain number of neighbors which are within a fixed distance away, and which match a sub-filter. The thresholds for the neighborhood size and distance can be set independently, and the sub-filter is applied to each such neighbor node.

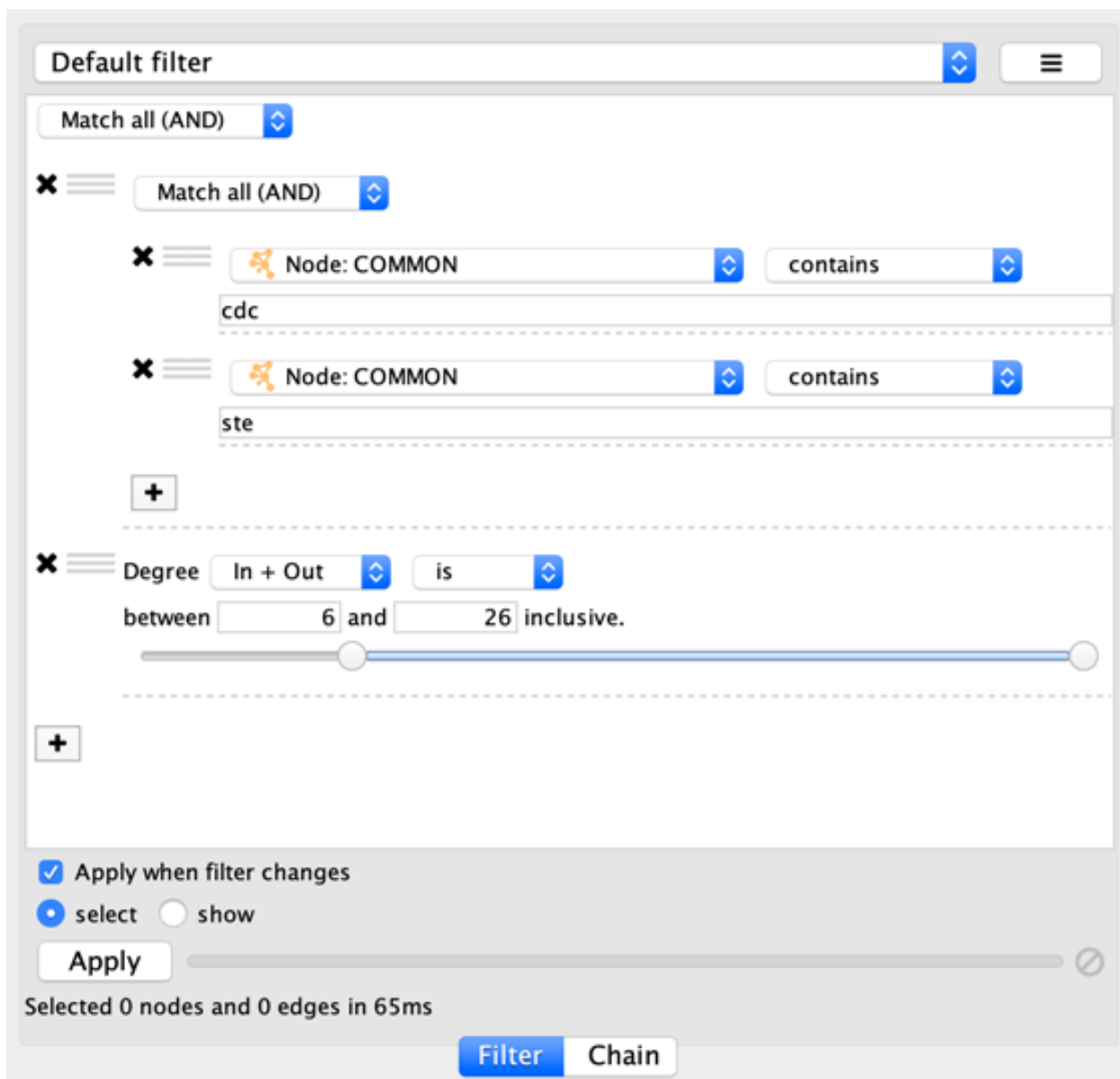
The topology filter will successfully match a node if the sub-filter matches against the required number of neighbor nodes.

Grouping and Organizing Filters

By default, nodes and edges need to satisfy the constraints of all your filters. You can change this so that instead, only the constraints of at least one filter needs to be met in order to match a node or edge. This behavior is controlled by the **Match all/any** drop-down box. This appears once your filter has more than one sub-filter. For example, suppose you wanted to match nodes with column **COMMON** containing `ste` or `cdc`, but you only want nodes with degree 5 or more, you'd first construct a filter that looks like this:



This filter will match nodes where **COMMON** contains **ste** **and** **cdc**. To change this to a logical **or** operation, drag either of the column filters by its handle  onto the other column filter to create a new group. Now change the group's matching behavior to **Match any**:



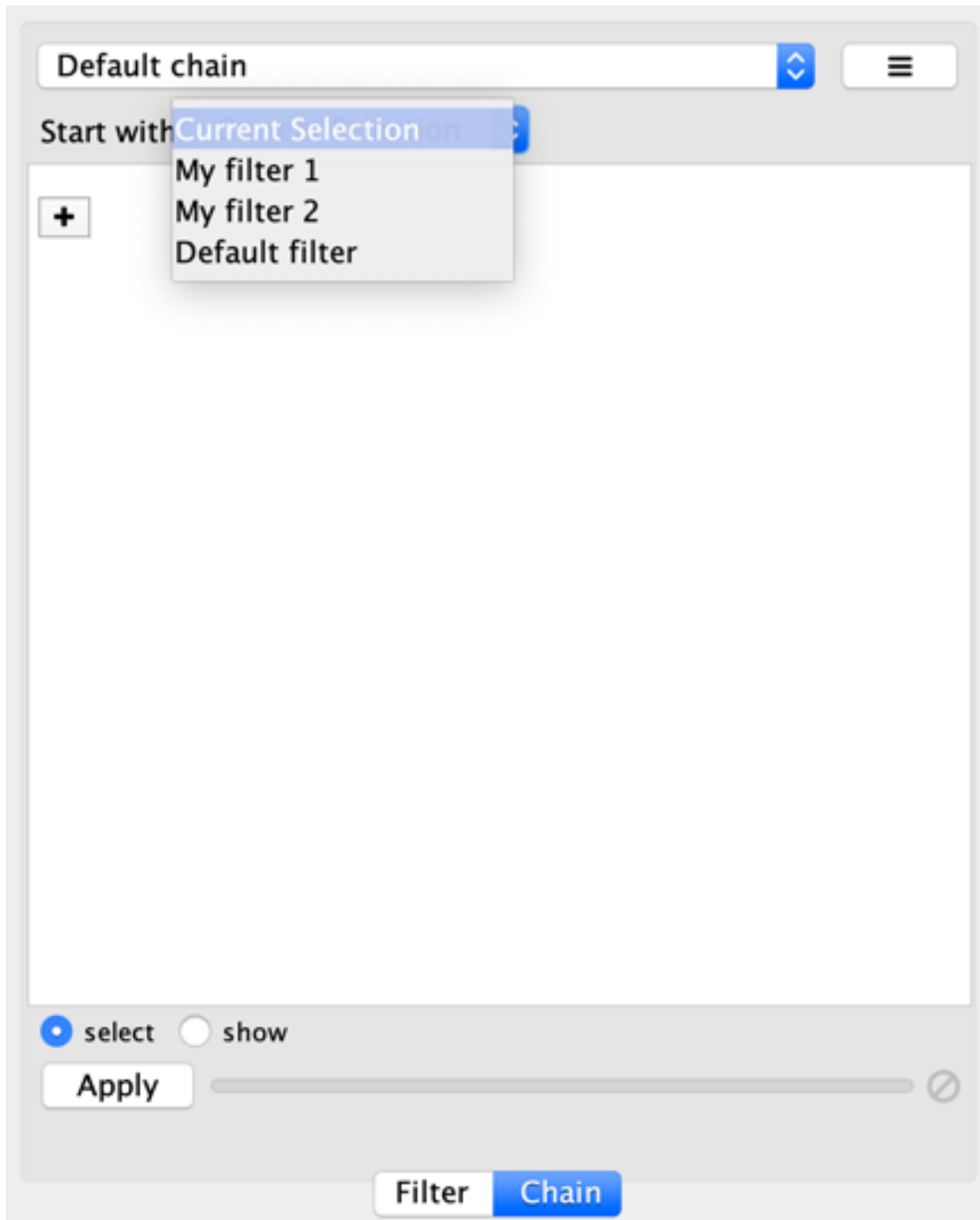
You can also reorder filters by dropping them in-between existing filters.

10.4.2 Chainable Transformers

The input to a chainable transformer is a set of nodes and edges, either the nodes and edges that are currently selected in the network, or the output of a narrowing filter. Chainable transformers can filter out nodes/edges, or include more nodes/edges. For example a chainable transformer can add nodes that are neighbours of the nodes in the input.

Chainable filters are combined in an ordered list. The nodes and edges in the output of a transformer become the input of the next transformer in the chain. The first transformer in the chain gets its input from the current selection or from a filter on the **Filter** tab. The output of the last transformer becomes the new selection.

You can specify the input to the first transformer in the chain by selecting a **Start with**, where **Current selection** refers to the nodes and edges currently selected. You can also choose a narrowing filter, which produces a different set of selected nodes and edges.



Chainable transformer can be reordered by dragging one by the handle and dropping it between existing transformer. Cytoscape currently bundles the following chainable transformers:

Edge Interaction Transformer

This transformer will go through all the input edges and selectively add their source nodes, target nodes, or both, to the output. This is useful for adding nodes that are connected to edges that match a particular filter.

Output options:

- **Add** (default): Automatically includes all input nodes and edges in the output, and adds source or target nodes from input edges to the output.
- **Replace with**: Does not automatically include input nodes and edges in the output. Only outputs nodes that match the filter.

Select options:

- **Source and target nodes** (default): Output both target and source nodes of selected edges.
- **Source nodes**: Output only source nodes of selected edges.
- **Target nodes**: Output only target nodes of selected edges.

A sub-filter may be added as well. When a sub-filter is present the source/target nodes must match the filter to be included in the output.

Node Adjacency Transformer

This transformer is used to add nodes and edges that are adjacent to the input nodes. A sub-filter may be specified as well.

Note that pressing the **Apply** button repeatedly may cause the selection to continuously expand. This allows adjacent nodes that are at greater distances to be added.

Output options:

- **Add** (default): Automatically includes all input nodes and edges in the output, and adds selected adjacent nodes and edges.
- **Replace with**: Only outputs the adjacent nodes/edges.

Select options:

- **Adjacent nodes**: Output nodes that are adjacent to the input nodes.
- **Adjacent edges**: Output edges that are adjacent (incident) to the input nodes.
- **Adjacent nodes and edges** (default): Output both nodes and edges that are adjacent to the input nodes.

Edge direction options. (Hidden by default, click the small arrow icon to reveal.):

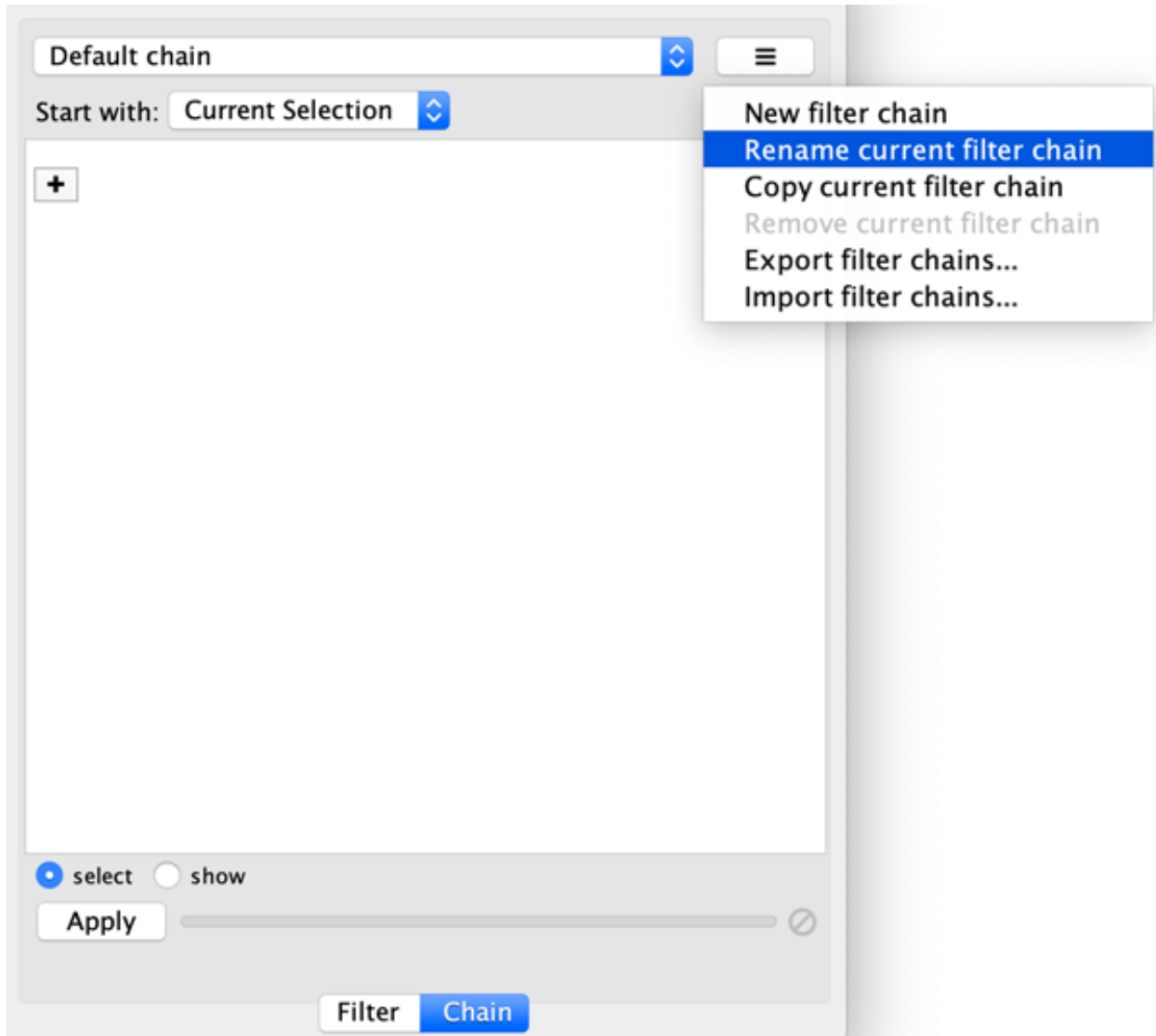
- **Incoming**: Only include adjacent nodes/edges when the adjacent edge is incoming.
- **Outgoing**: Only include adjacent nodes/edges when the adjacent edge is outgoing.
- **Incoming and Outgoing** (default): Ignore the directionality of adjacent edges.

Sub-filter options. (Available when a sub-filter has been added.):

- **Adjacent nodes** (default): The sub-filter is only applied to adjacent nodes. (Edges to the adjacent nodes are still included in the output.)
- **Adjacent edges**: The sub-filter is only applied to adjacent edges. (Nodes connected to the adjacent edges are still included in the output.)
- **Adjacent nodes and edges**: Both the adjacent edge and its connected node must match the filter. Note that for a filter to match an edge and a node at the same time it should be a compound filter that is set to **Match any (OR)**.

10.4.3 Working with Narrowing and Chainable Filters

The name of active filter appears in the drop-down box at the top of **Select** panel. Beside this is the options button which will allow you to rename, remove or export the active filter. It also lets you create a new filter, or import filters.



10.5 Diffusion

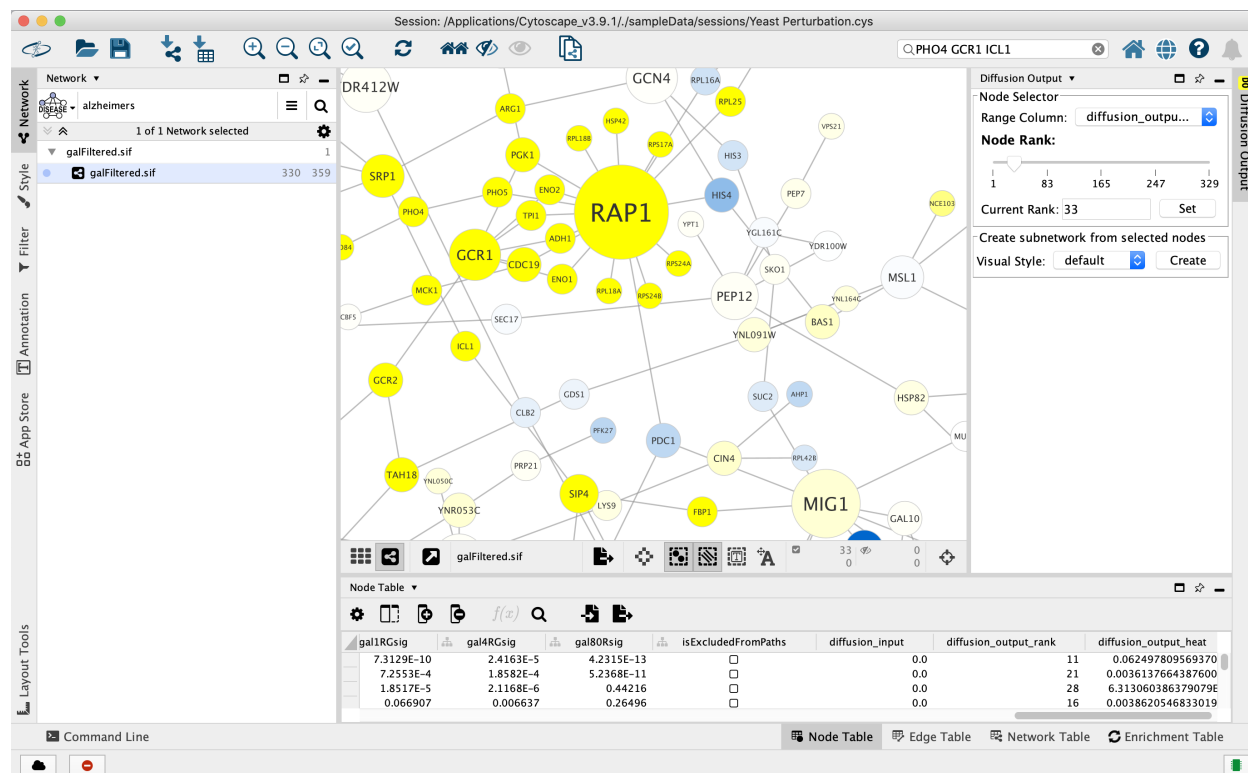
Cytoscape's Diffusion algorithm attempts to use a set of nodes and an entire interaction network to find the nodes most relevant to the original set. Conceptually, Diffusion applies heat to each node in the set, and lets the heat flow through connecting edges to adjacent nodes. It then produces a list of nodes ranked by the heat they accumulated. A node with many connections will tend to have a higher ranking, and an isolated node will tend to have low rank (and thus be excluded from the resulting node set).

By default, Diffusion uses the set of selected nodes as the heat sources, with each node having the same initial heat. At the end of a Diffusion, Cytoscape leaves the top 90th percentile of hot nodes selected. It allows you to use the Results panel to select a higher or lower percentile dynamically. It also stores the node's initial heat as a node

attribute in the *diffusion_input* column, and returns the heat and ranking values in the *diffusion_output_heat* and *diffusion_output_rank* columns.

An advanced Diffusion option allows you to specify initial heat values for each node via its *diffusion_input* attribute.

This figure shows the result of selecting the PHO4, GCR1 and ICL1 genes (via the [search bar](#)) and performing a Diffusion by either selecting **Tools** → **Diffuse** → **Selected Nodes** or right-clicking to **Diffuse** → **Selected Nodes**. Diffusion calculated the heat ranking of all 331 nodes in the network, and then selected the top 33.



To select more than 33 nodes, move the **Node Rank** slider in the Diffusion Output Results Panel to the right or enter a number greater than 33 in the **Current Rank** field. You can also select nodes using a heat value cutoff by using the **Range Column** to select a column containing heat values. Finally, you can use the **Visual Style** chooser and **Create** button to extract the selected nodes into a new network.

You can execute Diffusion multiple times on a network, thereby creating multiple *heat*, *output_heat* and *output_rank* columns.

11.1 Basic Network Navigation

Cytoscape uses a [Zoomable User Interface](#) for navigating and viewing networks. ZUIs use two mechanisms for navigation: zooming and panning. Zooming increases or decreases the magnification of a view based on how much or how little a user wants to see. Panning allows users to move the focus of a screen to different parts of a view.

11.1.1 Zoom

Cytoscape provides four mechanisms for zooming: toolbar buttons, menu options, keyboard shortcuts and the scroll wheel.

Use the zooming buttons located on the toolbar to zoom in and out of the interaction network shown in the current network display. Zoom icons are detailed below:



From Left to Right:

Zoom In

- Menu option: **View** → **Zoom In**
- Keyboard shortcut: **Ctrl-Plus** (**Command-Plus** on Mac OS X)

Zoom Out

- Menu option: **View** → **Zoom Out**
- Keyboard shortcut: **Ctrl-Minus** (**Command-Minus** on Mac OS X)

Fit Content: Zoom level is adjusted to fit the network to the window

- Menu option: **View** → **Fit Content**
- Keyboard shortcut: **Ctrl-0** (**Command-0** on Mac OS X)

Fit Selected: Zoom level is adjusted to zoom on any selected nodes

- Menu option: **View** → **Fit Selected**
- Keyboard shortcut: **Ctrl-9** (Command-9 on Mac OS X)

Using the scroll wheel, you can zoom in by scrolling up and zoom out by scrolling downwards. These directions are reversed on Macs with natural scrolling enabled (the default for Mac OS X Lion and newer versions).

11.1.2 Pan

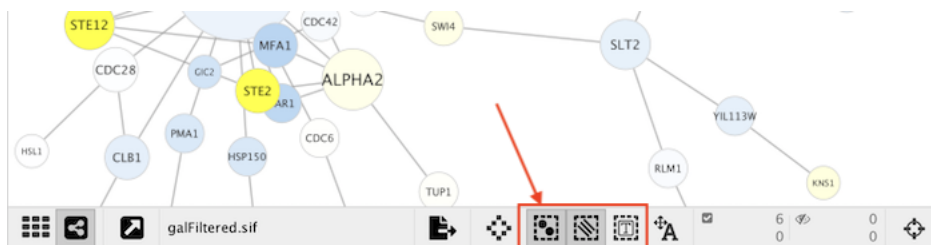
There are two ways to pan the network:




- Left-Click and Drag - You can pan the network view by holding down the left mouse button and moving the mouse.
- Dragging Box on **Network Overview** - You can also pan the view by left-clicking and dragging the blue box in the overview panel in the lower part of the view.

11.2 Other Mouse Behaviors

11.2.1 Select

- Click the left mouse button on a node, edge or annotation to select that element.
- Hold down the **Shift** or **Ctrl** key (Command on Mac) and left-click a node, edge or annotation to add it to the selection. Doing the same on a selected element unselects it.
- Hold down the left mouse button on the canvas background and drag the mouse while holding down the **Shift** or **Ctrl** key (Command on Mac) to select groups of nodes/edges/annotations using a classic rectangular selection area.
- Hold down the left mouse button on the canvas background and drag the mouse while holding down **Option + Shift** (Command + Shift on Mac) to select groups of nodes/edges/annotations using a lasso selection tool.
- Remember that the selection action (mouse click or drag-selection) only works if the **Selection Mode** for that element type (i.e. nodes, edges, annotations) is enabled. In order to enable or disable the selection of an element type, just toggle its corresponding button at the bottom of the network view (see image below) or use the options under the menu **Select** → **Mouse Drag Selects**.



- So if you don't want any **nodes** to be selected, toggle the button  off.
- And if you don't want any **edges** to be selected, toggle the button  off.
- Likewise, if you don't want any **annotations** to be selected, toggle the button  off.

11.2.2 Context

Click the right mouse button (or Ctrl+left mouse button on Macs) on a node/edge to launch a context-sensitive menu with additional information about the node/edge.

11.2.3 Node Context Menu

This menu can change based on the current context. For nodes, it typically shows:

- Add
- Diffuse
- Edit
- Select
- Group
- Nested Networks
- Apps
- External Links
- Preferences

Edges usually have the following menu:

- Diffuse
- Edit
- Select
- Apps
- External Links
- Preferences

Apps can contribute their own items into node and edge context menus. These additions usually appear in the **Apps** section of the context menu.

Nested Network Node Context Menu

- **Add Nested Network:** Lets the user select any network in Cytoscape as the current node's nested network. If the current node already has a nested network it will be replaced.
- **Remove Nested Network:** Removes the currently associated nested network from a node. The associated network is not deleted. Only the association between the node and the network is removed.
- **Go to Nested Network:** The current node's nested network will be the current network view and have the focus. Should a network view for the nested network not exist, it will be created.

More information about nested networks can be found in the [Nested Networks](#) section.

11.3 Manual Layout

The simplest method to manually organize a network is to click on a node and drag it. All of the selected nodes are moved together.

In addition to the ability to click on a node and drag it to a new position, Cytoscape now has the ability to move nodes using the arrow keys on the keyboard. By selecting one or more nodes using the mouse and clicking one of the arrow keys (\leftarrow , \uparrow , \rightarrow , \downarrow) the selected nodes will move one pixel in the chosen direction. If an arrow key is pressed while holding the Shift key down, the selected nodes will move 15 pixels in the chosen direction.

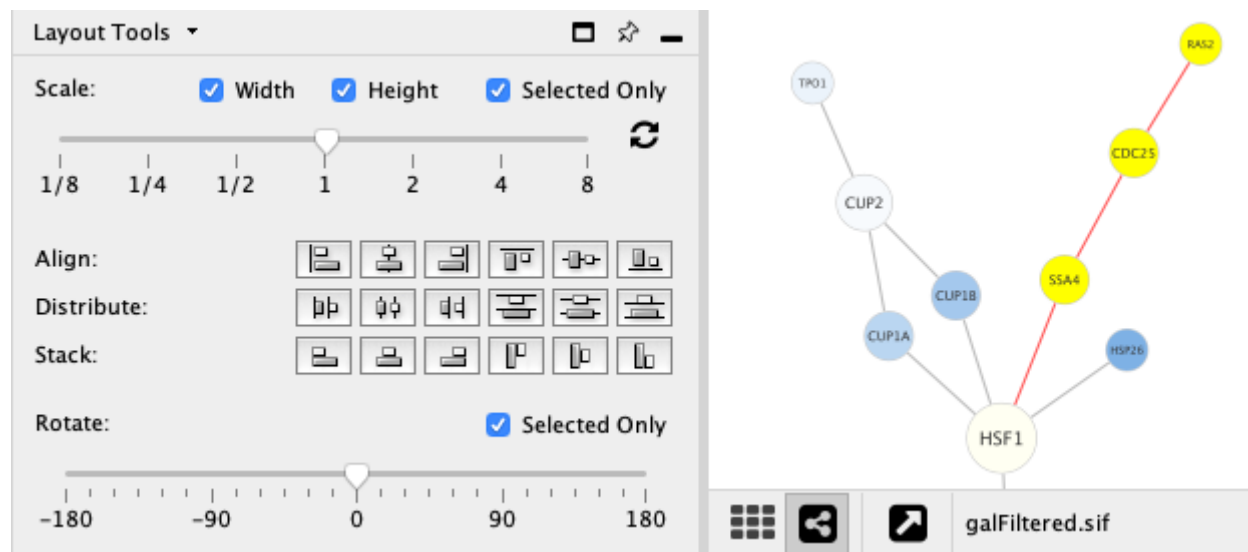
11.4 Node Layout Tools

The Tool Panel is available via the menu command **View** → **Show Tool Panel**, or via **Layout** → **Node Layout Tools**. It contains several **Node Layout Tools** that can help to automate or fine tune a layout.

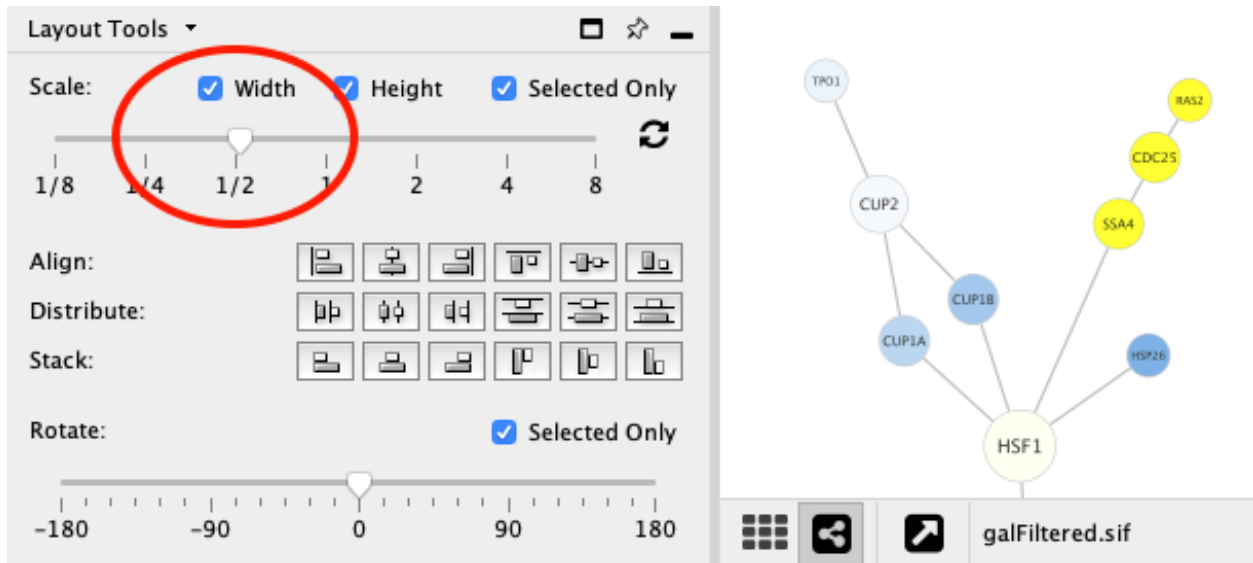
11.4.1 Scale

Adjust the Scale slider to change the length of edges. The position of the nodes will be scaled, not the node sizes. Node size can be adjusted using [Styles](#). The images below show selected (yellow) nodes scaled to 50% of the default value.

Before



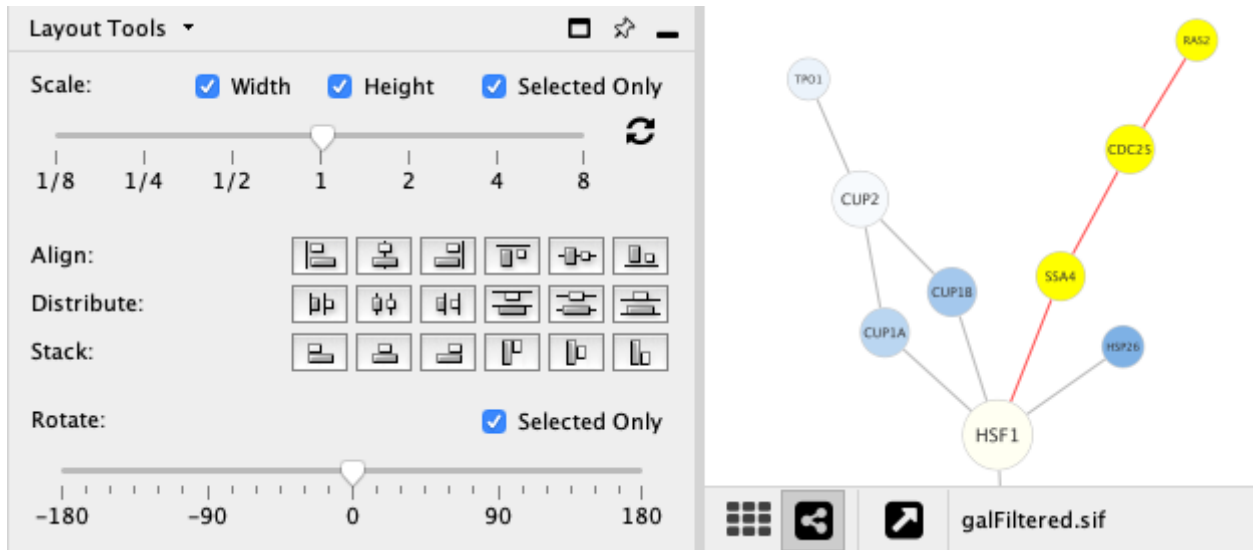
After



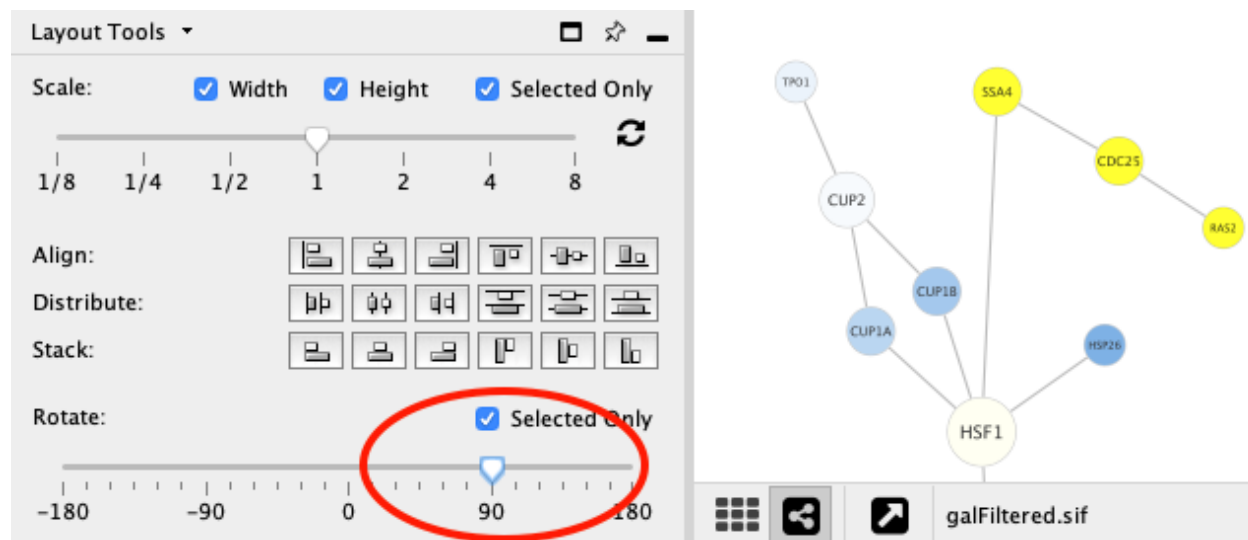
11.4.2 Rotate

The Rotate function will change the orientation of the entire network or a selected portion of the network. The images below show a network with selected nodes rotated 90 degrees.

Before



After



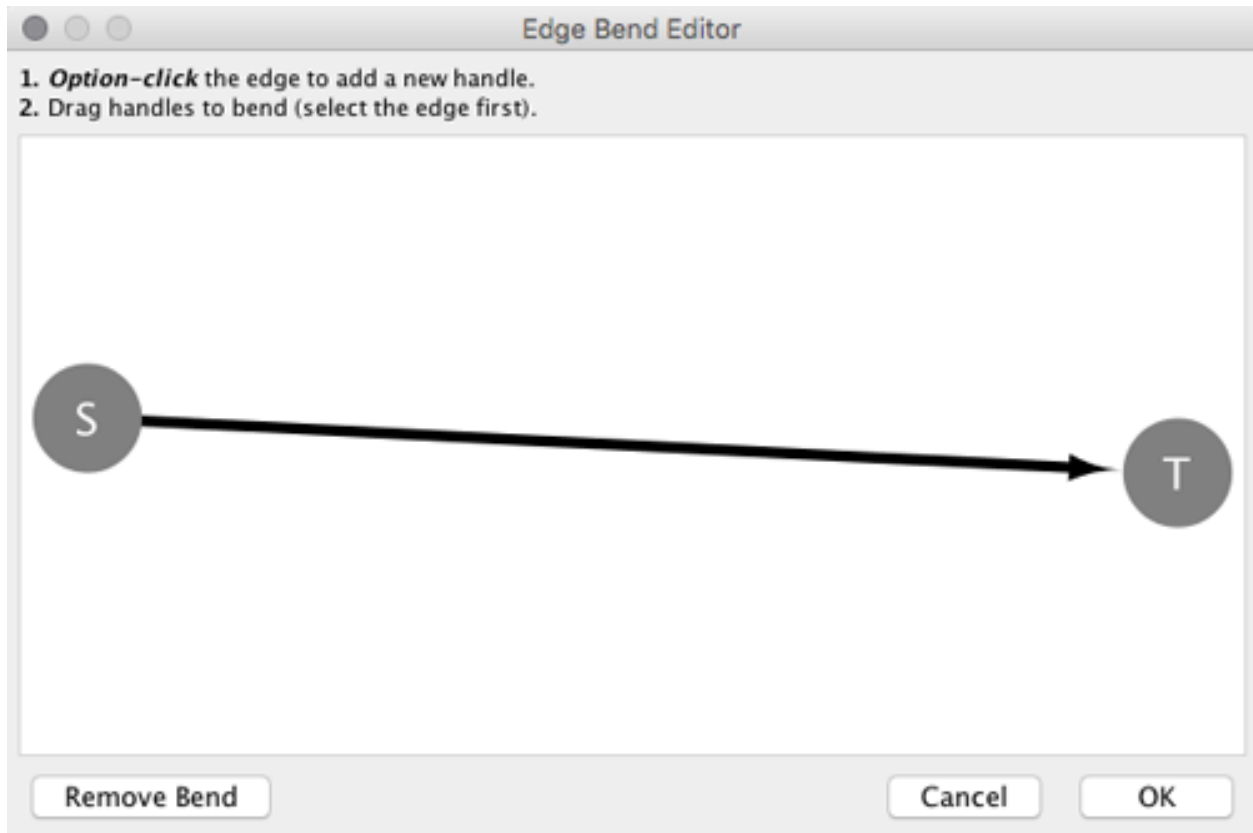
11.4.3 Align, Distribute and Stack

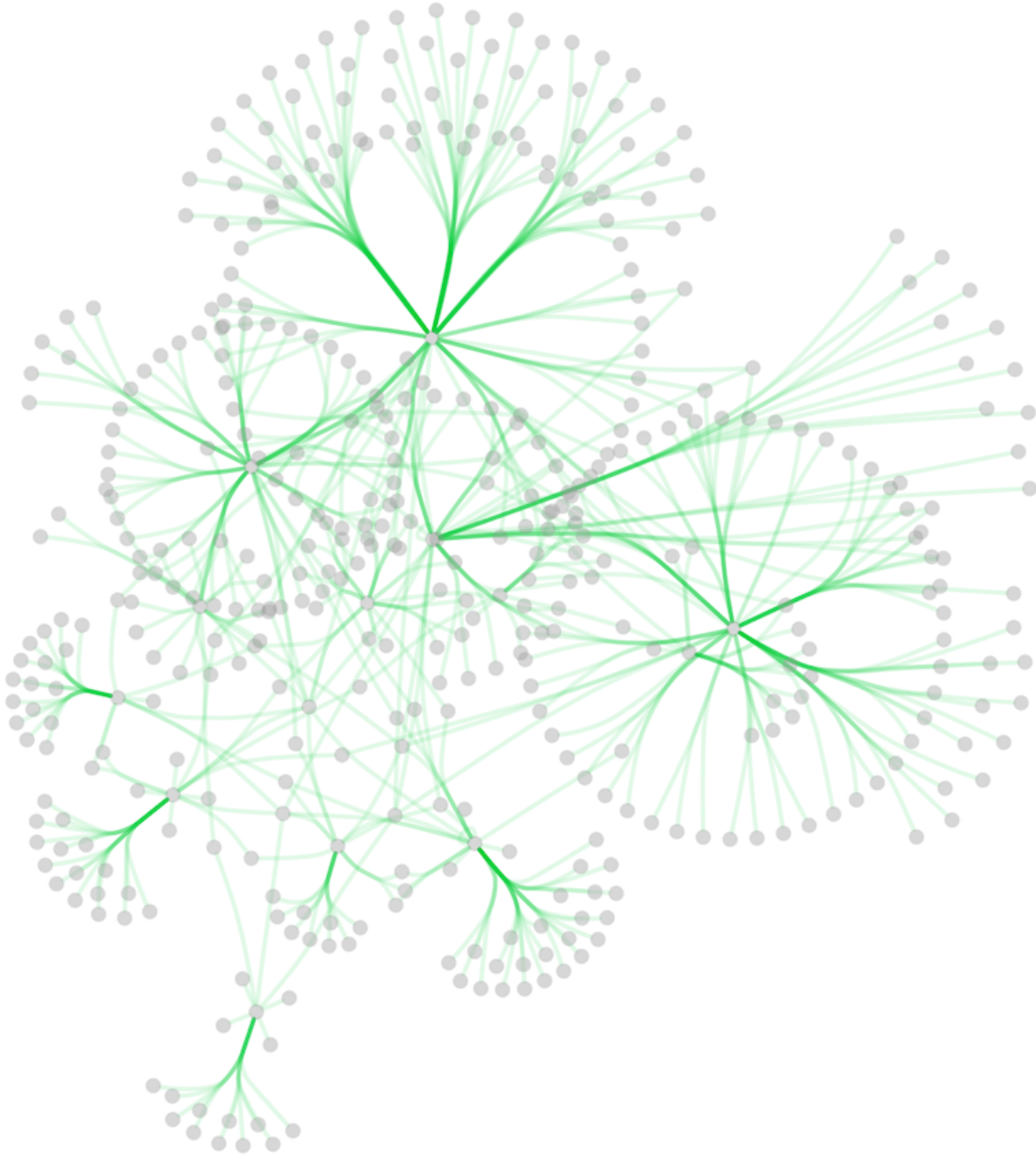
The **Tool Panel** contains buttons to set relative positions of nodes.

Align provides different options for either vertically or horizontally aligning selected nodes against a line. The differences are in what part of the node gets aligned, e.g. the center of the node, the top of the node, the left side of the node. **Distribute** evenly distributes selected nodes between the two most distant nodes along either the vertical or horizontal axis. The differences are again a function what part of the node is used as a reference point for the distribution. **Stack** vertically or horizontally stacks selected nodes with the full complement of alignment options. The table below provides a description of what each button does.

11.5 Edge Bend and Automatic Edge Bundling

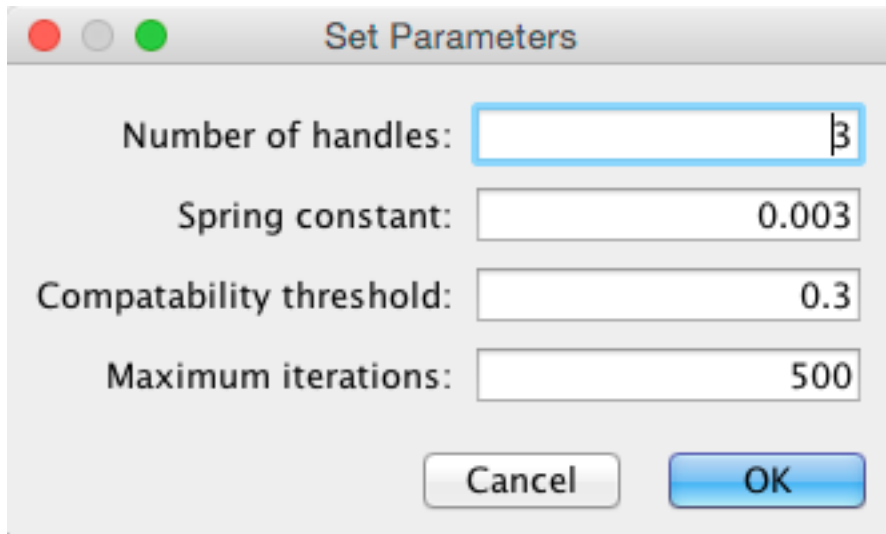
From Cytoscape 3.0, **Edge Bend** is a regular edge property and can be used as a part of a **Style**. Just like any other edge property, you can select a Default Value, a Mapping and use Bypass for select nodes. In the Style tab, select the **Bend** property from the **Properties** drop-down and click on either the Default Value, Mapping or Bypass cell to bring up the **Edge Bend Editor**. In the editor, you can add as many handles as you want to the edge using **Alt-Click** on Windows, **Option-Click** on Mac, or **Ctrl-Alt-Click** on Linux.





To clear all edge bends, select **Layout** → **Clear All Edge Bends**.

In addition to adding handles manually, you can use the **Bundle Edges** function to bundle all or selected edges automatically.



1. Select **Layout** → **Bundle Edges** → **All Nodes and Edges**.
2. Set parameters.
 - Details of the algorithm is described in [this paper](#).
3. Press **OK** to run. Edge bundling may take a long time if the number of edges is large.
 - If it takes too long, try decreasing **Maximum Iterations**.
 - For large, dense networks, try setting **Maximum iterations** in the range of 500 - 1000.

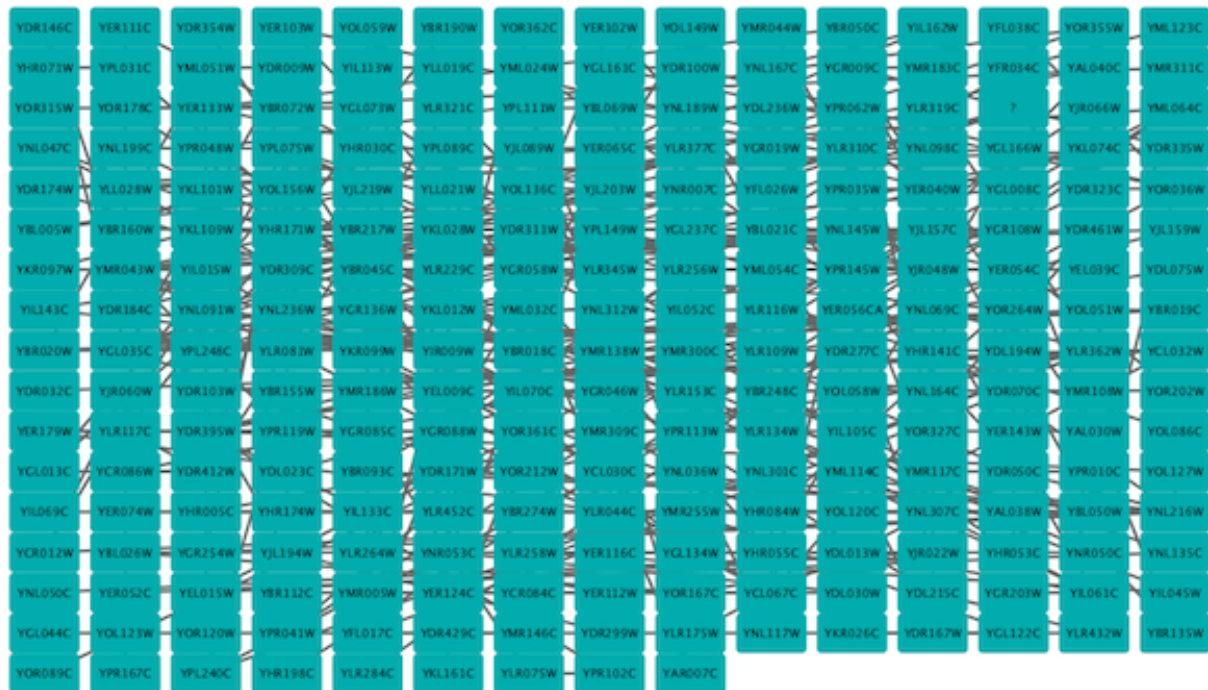
Note: The handle locations will be optimized for current location of nodes. If you move node positions, you need to run the function again to get proper result.

11.6 Automatic Layout Algorithms

The **Layout** menu has an array of features for organizing the network visually according to one of several algorithms, aligning and rotating groups of nodes, and adjusting the size of the network. Cytoscape layouts have three different sources, which are reflected in the **Layout** menu.

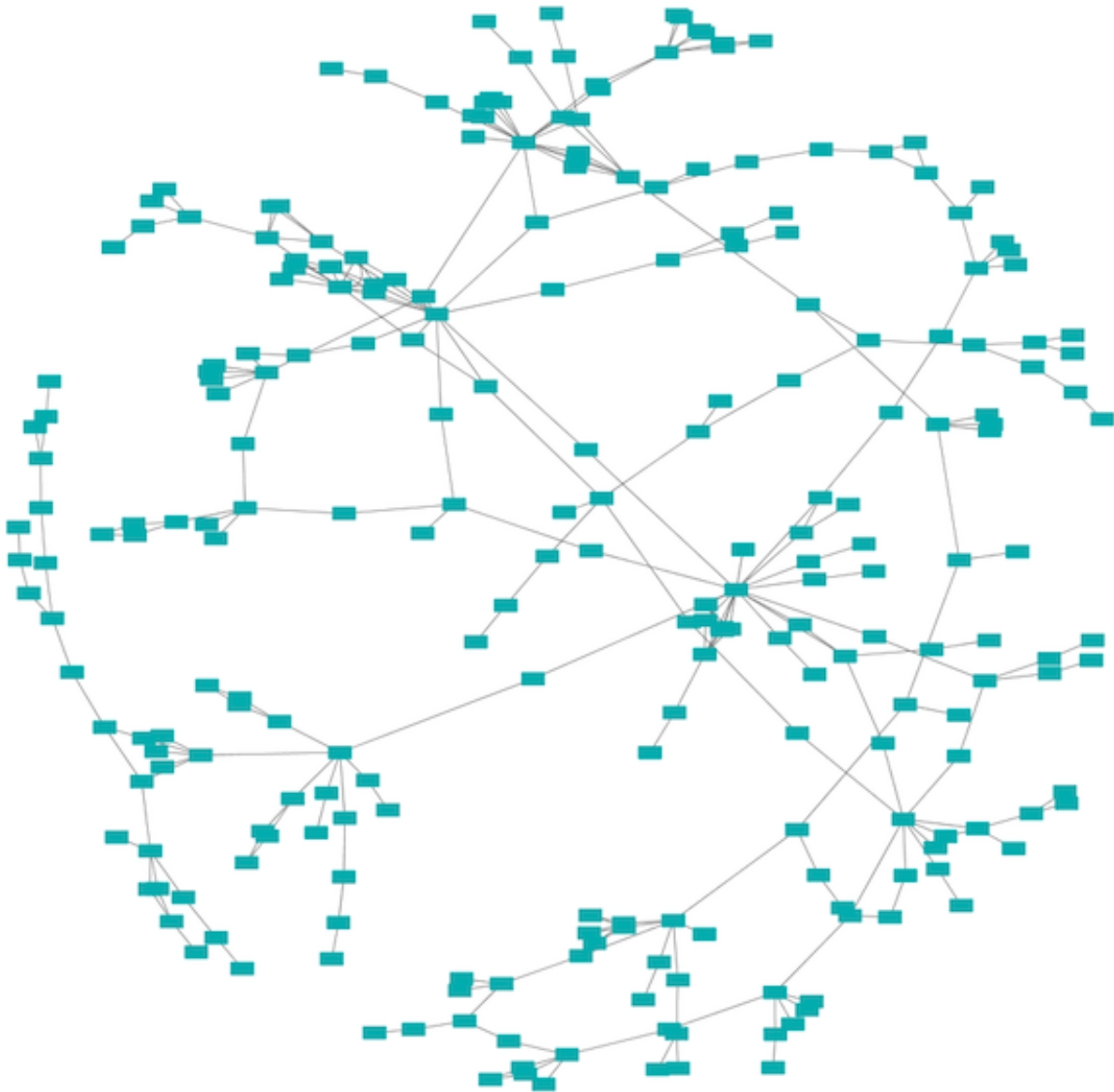
Cytoscape layouts have the option to operate on only the selected nodes, and all provide a **Settings...** panel to change the parameters of the algorithm. Most of the Cytoscape layouts also partition the graph before performing the layout. In addition, many of these layouts include the option to take either node or edge columns into account. A few of the layout algorithms are:

11.6.1 Grid Layout



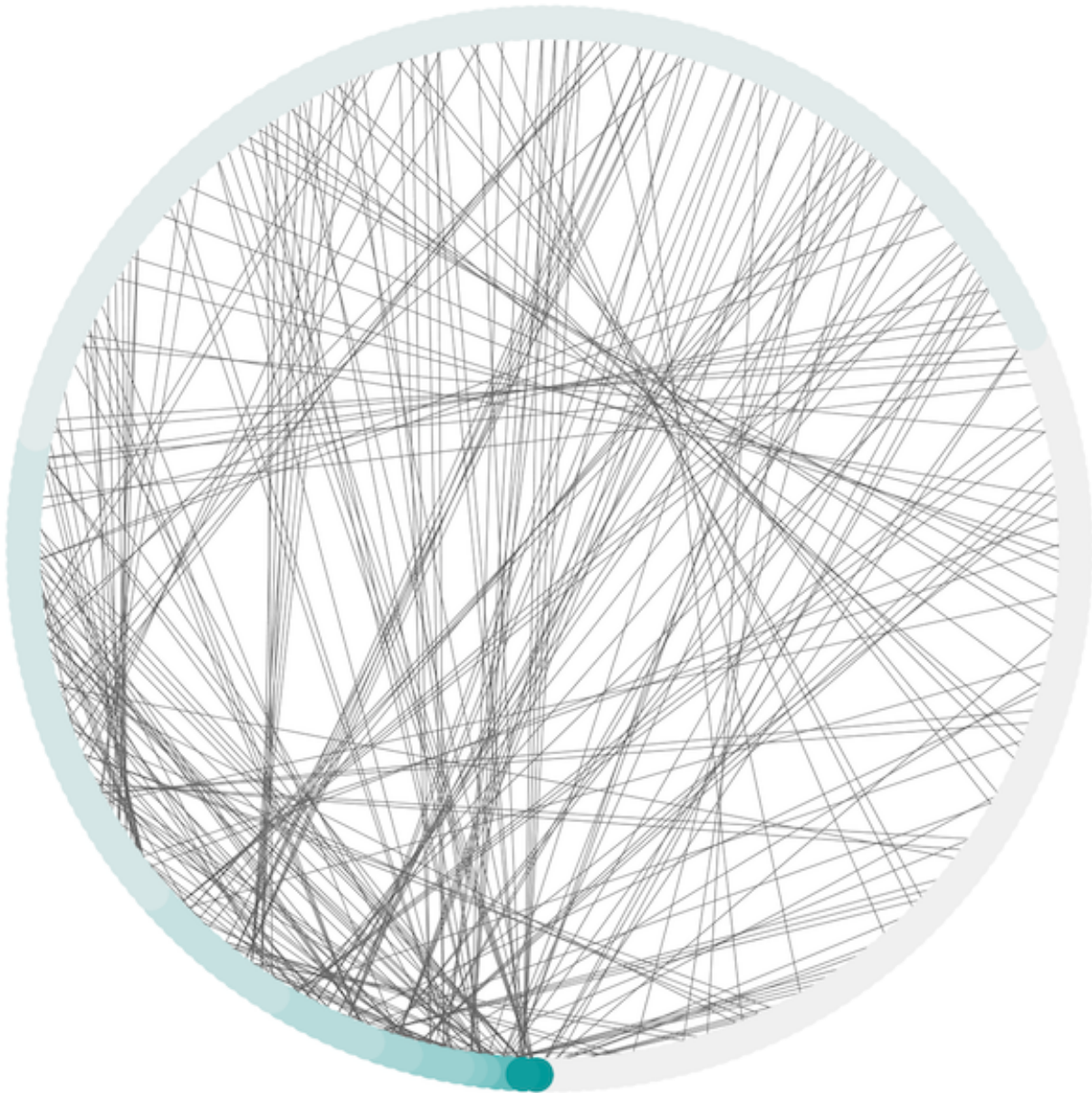
The grid layout is a simple layout that arranges all of the nodes in a square grid. This is the default layout and is always available as part of the Cytoscape core. It is available by selecting **Layout** → **Grid Layout**. A sample screen shot is shown above.

11.6.2 Edge-weighted Spring-Embedded Layout



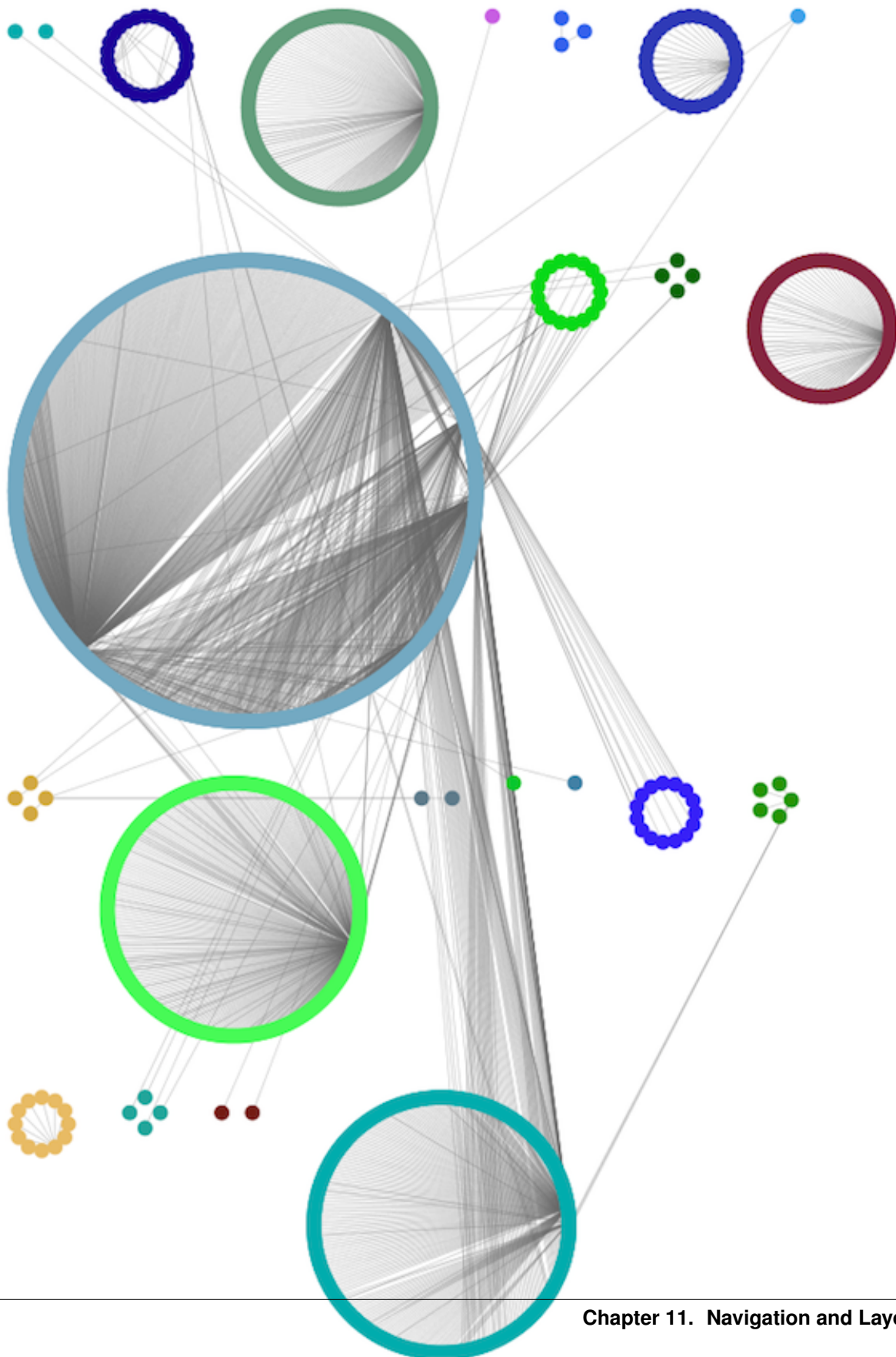
The spring-embedded layout is based on a force-directed paradigm as implemented by Kamada and Kawai (1988). Network nodes are treated like physical objects that repel each other, such as electrons. The connections between nodes are treated like metal springs attached to the pair of nodes. These springs repel or attract their end points according to a force function. The layout algorithm sets the positions of the nodes in a way that minimizes the sum of forces in the network. This algorithm can be applied to the entire network or a portion of it by selecting the appropriate options from **Layout** → **Edge-weighted Spring Embedded**.

11.6.3 Attribute Circle Layout



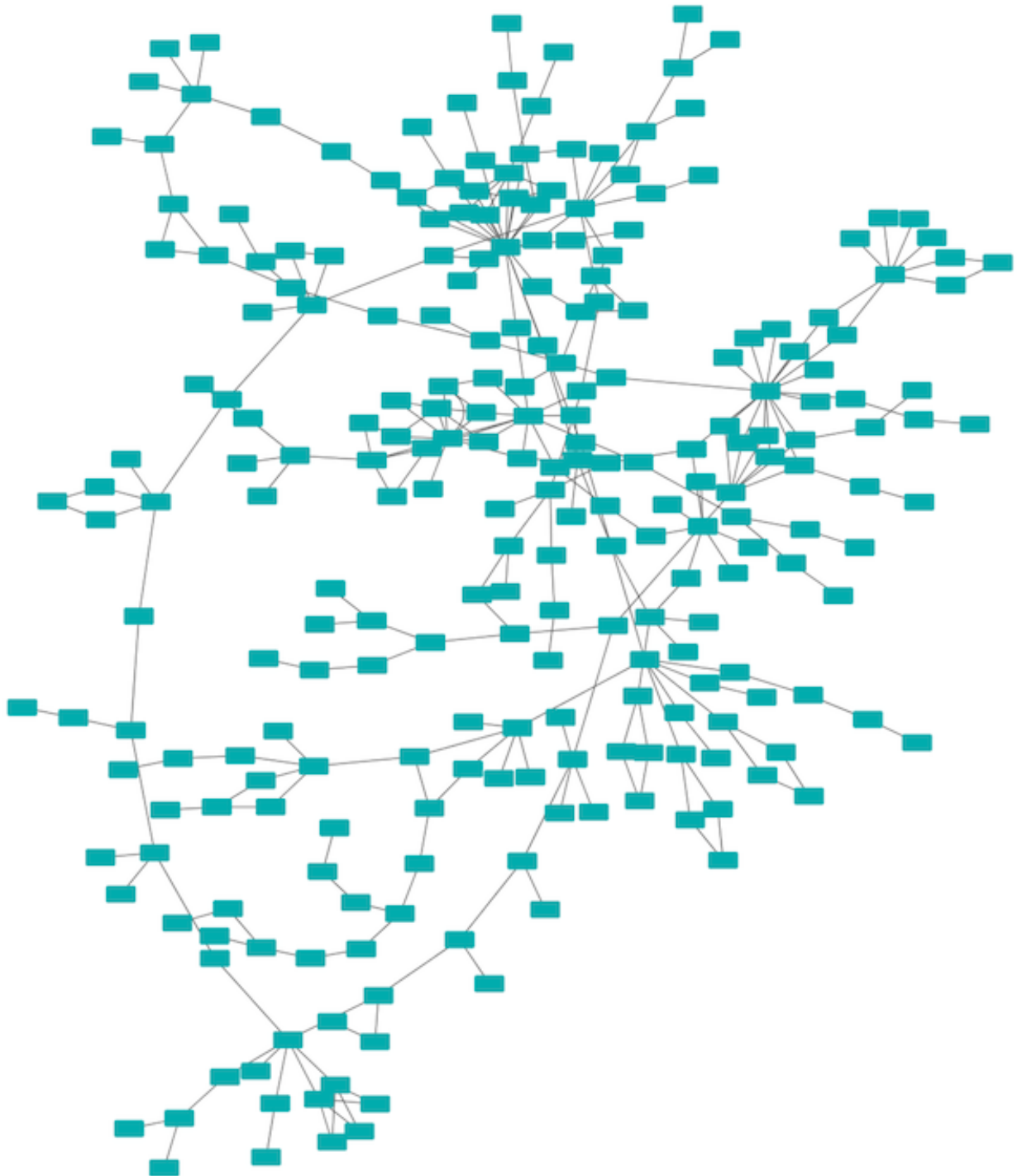
The **Attribute Circle** layout is a quick, useful layout, particularly for small networks, that will locate all of the nodes in the network around a circle. The node order is determined by a user-selected node column. The result is that all nodes with the same value for that column are located together around the circle. Using **Layout** → **Attribute Circle Layout** → *column* to put all nodes around a circle using *column* to position them. The sample screen shot above shows the a subset of the galFiltered network organized by node degree.

11.6.4 Group Attributes Layout



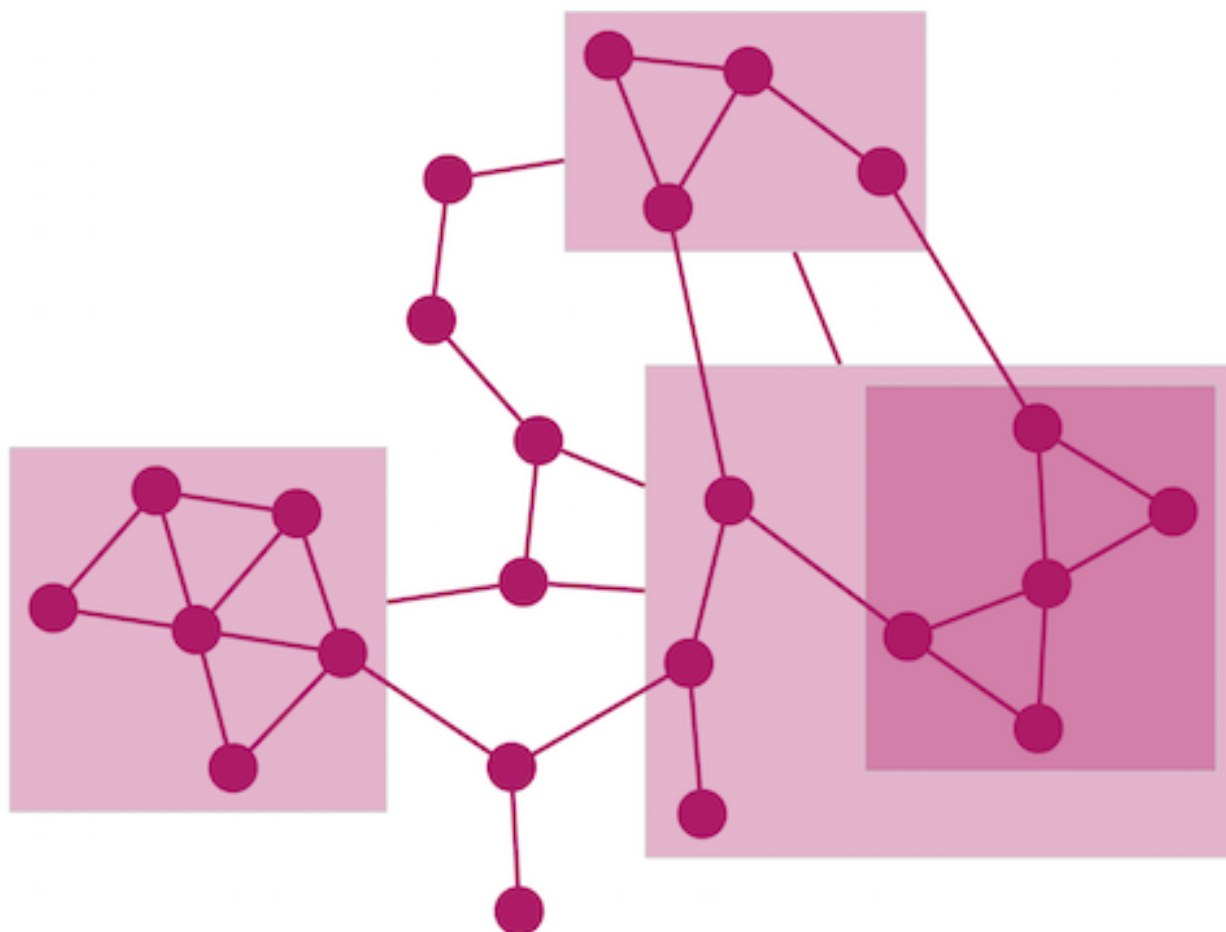
The **Group Attributes** layout is similar to the **Attribute Circle** layout described above except that instead of a single circle with all of the nodes, each set of nodes that share the same value for the column are laid out in a separate circle. The same network shown above (network generated by PSICQUIC Client) is shown above, using **Layout** → **Group Attributes Layout** → **taxonomy**.

11.6.5 Prefuse Force Directed Layout



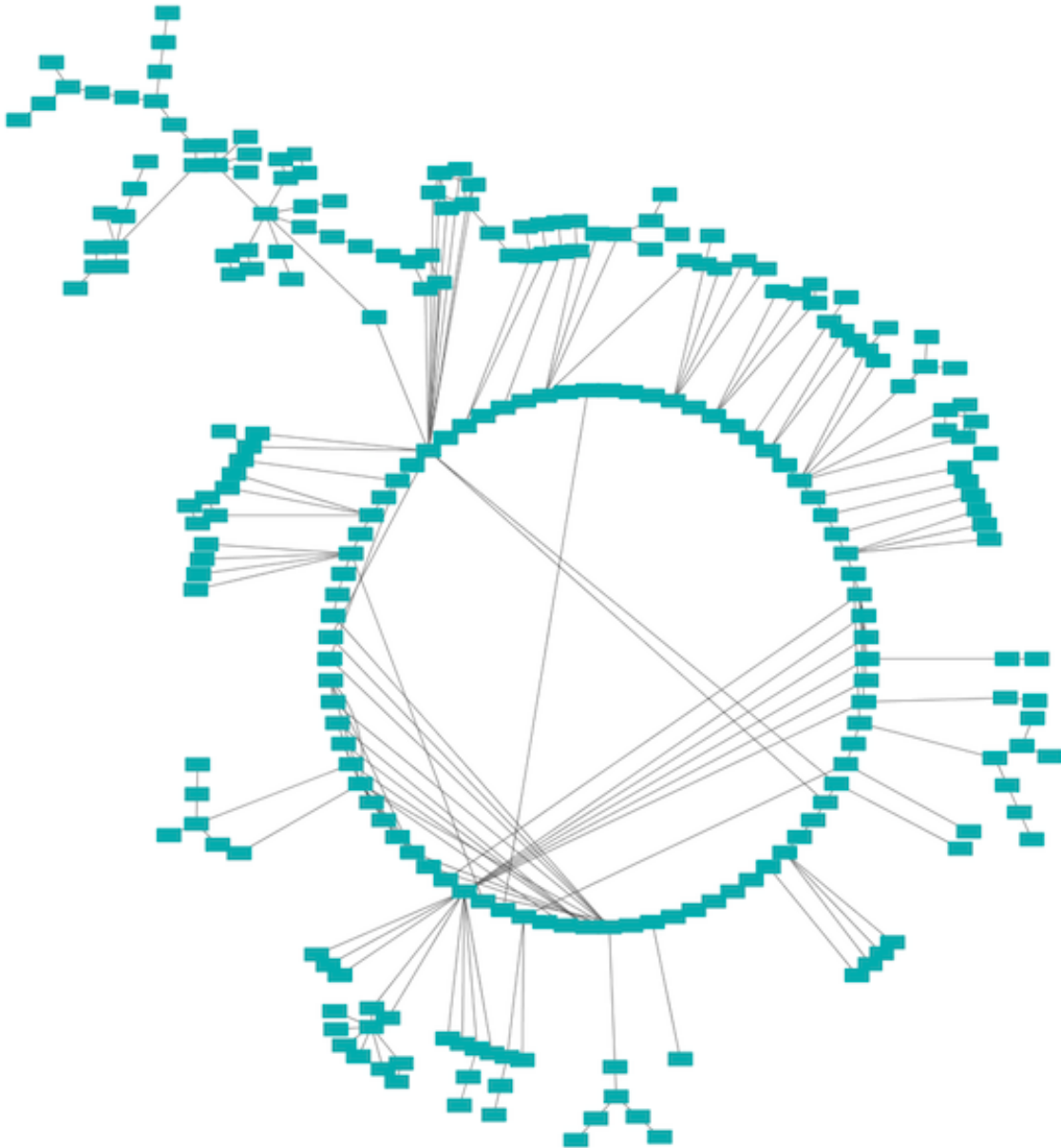
The force-directed layout is a layout based on the force-directed paradigm. This layout is based on the algorithm implemented as part of the prefuse toolkit provided by Jeff Heer. The algorithm is very fast and with the right parameters can provide a very visually pleasing layout. The **Force Directed Layout** will also accept a numeric edge column to use as a weight for the length of the spring, although this will often require more use of the **Settings...** dialog to achieve the best layout. This algorithm is available by selecting **Layout** → **Prefuse Force-Directed Layout** → **(unweighted)** or the edge column you want to use as a weight. A sample screen shot showing a portion of the galFiltered network provided in sample data is provided above.

11.6.6 Compound Spring Embedder Layout



The **Compound Spring Embedder (CoSE)** layout is based on the traditional force-directed layout algorithm with extensions to handle multi-level nesting (compound nodes), edges between nodes of arbitrary nesting levels and varying node sizes. It is the suggested Cytoscape layout for compound graphs, although it also works very well with noncompound graphs. It is available by selecting **Layout** → **Compound Spring Embedder (CoSE)**.

11.6.7 Circular Layout



This algorithm produces layouts that emphasize group and tree structures within a network. It partitions the network by analyzing its connectivity structure, and arranges the partitions as separate circles. The circles themselves are arranged in a radial tree layout fashion. This algorithm is available by selecting **Layout** → **Circular Layout**.

11.6.8 Hierarchical Layout



The hierarchical layout algorithm is good for representing main direction or flow within a network. Nodes are placed in hierarchically arranged layers and the ordering of the nodes within each layer is chosen in such a way that minimizes the number of edge crossings. This algorithm is available by selecting **Layout** → **Hierarchical Layout**.

11.6.9 Copycat Layout

The Copycat layout uses node positions in one network to lay out nodes in another network. Selecting **Layout** → **Copycat Layout** displays a dialog box that allows you to select the source network (which is already laid out) and the target network (which needs layout). By default, Copycat matches nodes in the source and target networks by node name, but you can choose any node attribute for this match.

As options, you can use **Select unmapped nodes** to cause Copycat to select target nodes that were not matched by nodes in the source network. This allows you to move them and possibly lay them out using other layout algorithms. You can use the **Layout unmapped nodes in a grid** option to preemptively move the unmatched target nodes away from the laid out target network.

11.7 yFiles Layouts

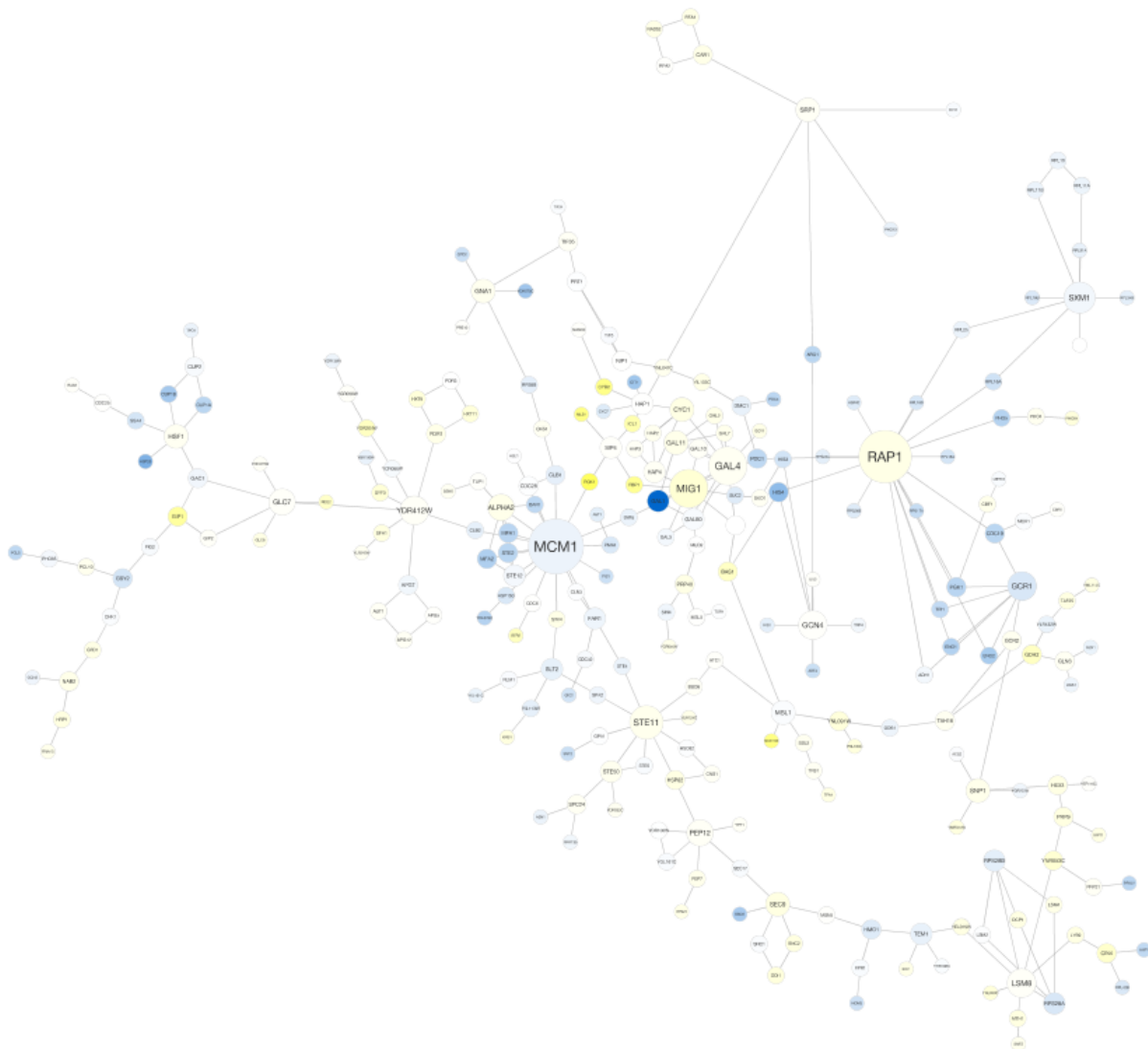
Cytoscape offers a set of layout algorithms based on the [yFiles library](#). As of Cytoscape 3.6, the yFiles algorithms are available directly through the [Cytoscape App Store](#). To install them, go to **Layout** → **Install yFiles**, which will direct you to the App Store. Click the **Install** button to proceed. You will be directed to a license agreement, and once yFiles is installed, the yFiles layouts will be available in the **Layout** menu.

The layout algorithms included in yFiles are:

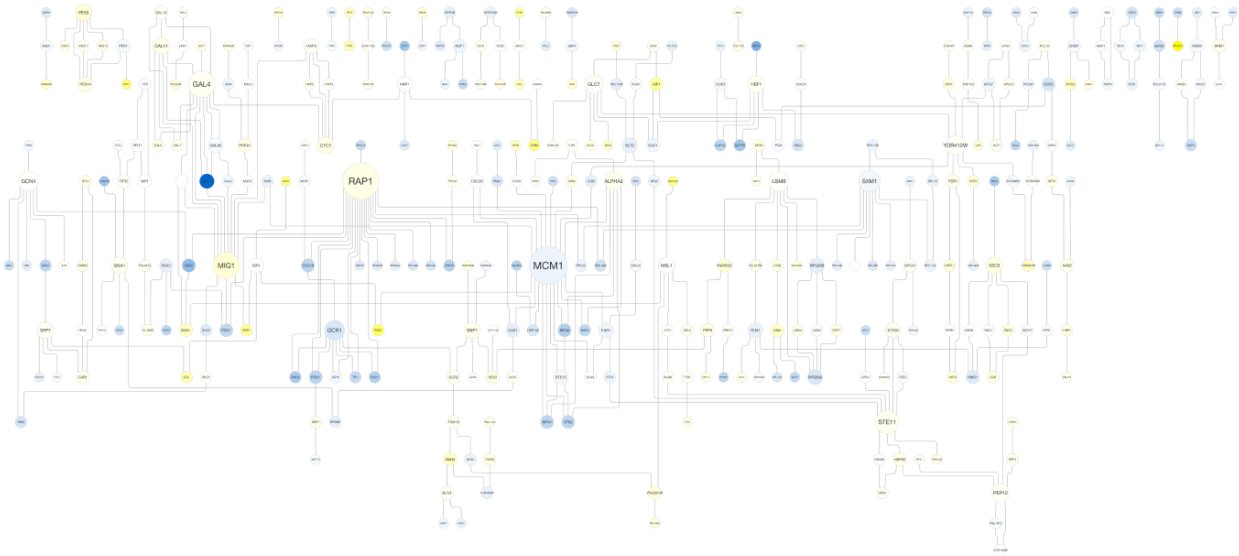
- Circular Layout
- Hierarchic Layout
- Hierarchic Layout Selected Nodes
- Organic Layout
- Orthogonal Layout
- Radial Layout
- Tree Layout
- Orthogonal Edge Router
- Organic Edge Router

Below are a few examples of yFiles layouts in Cytoscape, with more available from [yFiles](#).

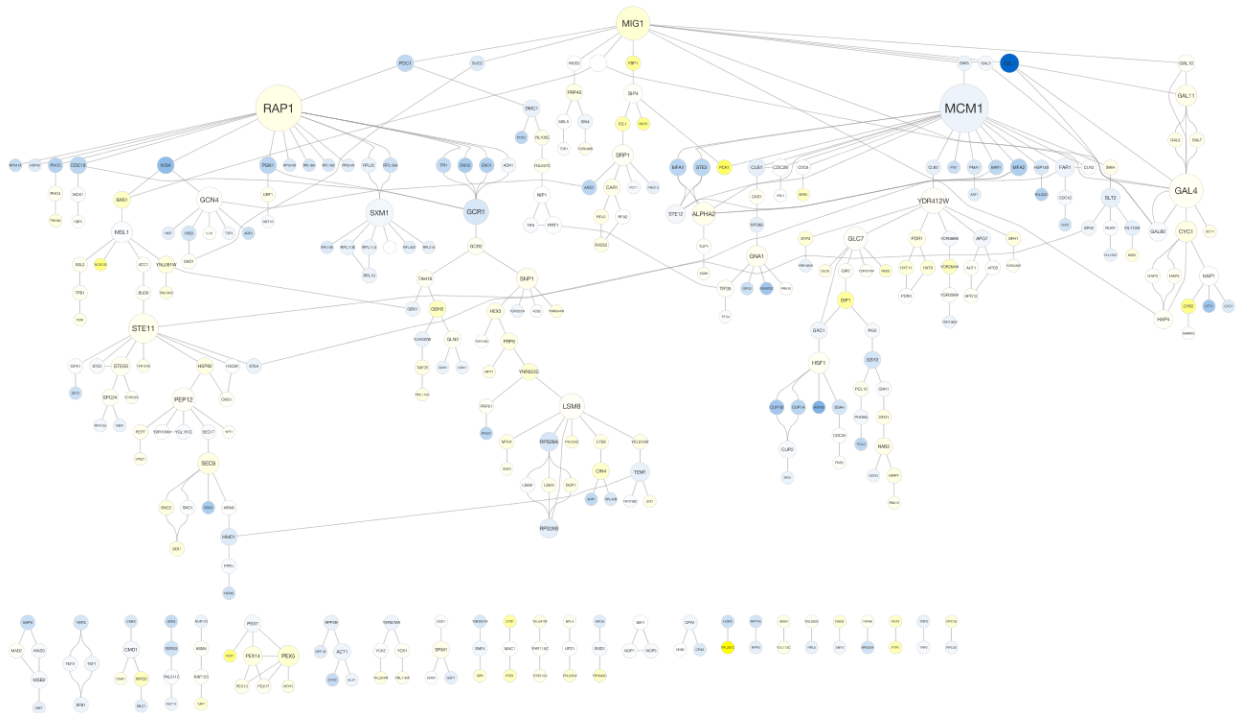
11.7.1 yFiles Organic Layout



11.7.2 yFiles Hierarchic Layout



11.7.3 yFiles Tree Layout



11.8 Layout Parameters

Many layouts have adjustable parameters that are exposed through the **Layouts** → **Settings...** menu option. The **Layout Settings** dialog, which allows you to choose which layout algorithm settings to adjust, is shown below. The

settings presented vary by algorithm and only those algorithms that allow access to their parameters will appear in the drop-down menu at the top of the dialog. Once you've modified a parameter, clicking the **Execute Layout** button will apply the layout.

The screenshot shows the 'Layout Settings' dialog box in Cytoscape. At the top, the 'Layout Algorithm' is set to 'Prefuse Force Directed Layout (default)'. Below this, there is a 'Make Default' button. The 'Edge column that contains the weights' is set to '(none)'. The 'Edge Weight Settings' section includes 'How to interpret weight values' set to 'Heuristic', and three input fields for 'The minimum edge weight to consider' (0E0), 'The maximum edge weight to consider' (1.79769E308), and 'The default edge weight to consider' (0.5). The 'Number of Iterations' is 100, 'Default Spring Coefficient' is 1E-4, 'Default Spring Length' is 50, and 'Default Node Mass' is 3. The 'Force deterministic layouts (slower)' checkbox is unchecked. The 'Standard Settings' section has a 'Don't partition graph before layout' checkbox, which is also unchecked. At the bottom, the 'Layout only selected nodes' checkbox is checked, and there are buttons for 'Reset Defaults', 'Apply Layout', and 'Done'.

Layout Settings

Layout Algorithm:

Prefuse Force Directed Layout (default) Make Default

Edge column that contains the weights: (none)

Edge Weight Settings

How to interpret weight values: Heuristic

The minimum edge weight to consider: 0E0

The maximum edge weight to consider: 1.79769E308

The default edge weight to consider: 0.5

Number of Iterations: 100

Default Spring Coefficient: 1E-4

Default Spring Length: 50

Default Node Mass: 3

Force deterministic layouts (slower): ☐

Standard Settings

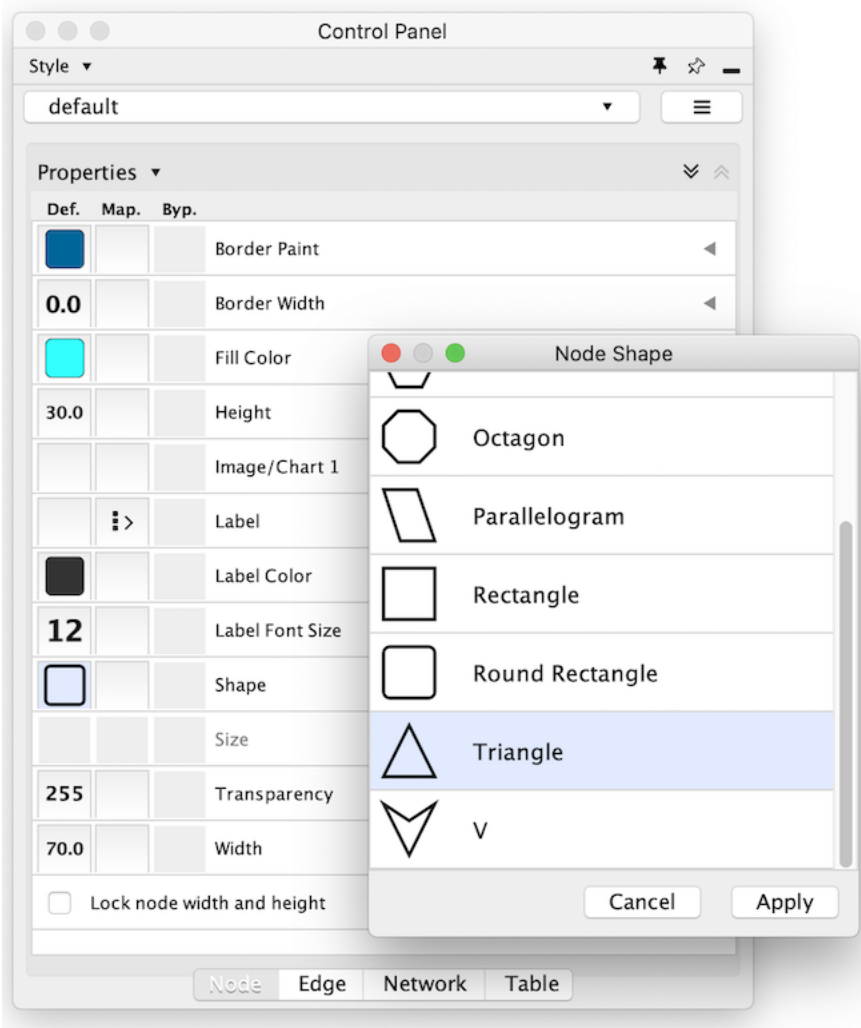
Don't partition graph before layout: ☐

☒ Layout only selected nodes Reset Defaults Apply Layout Done

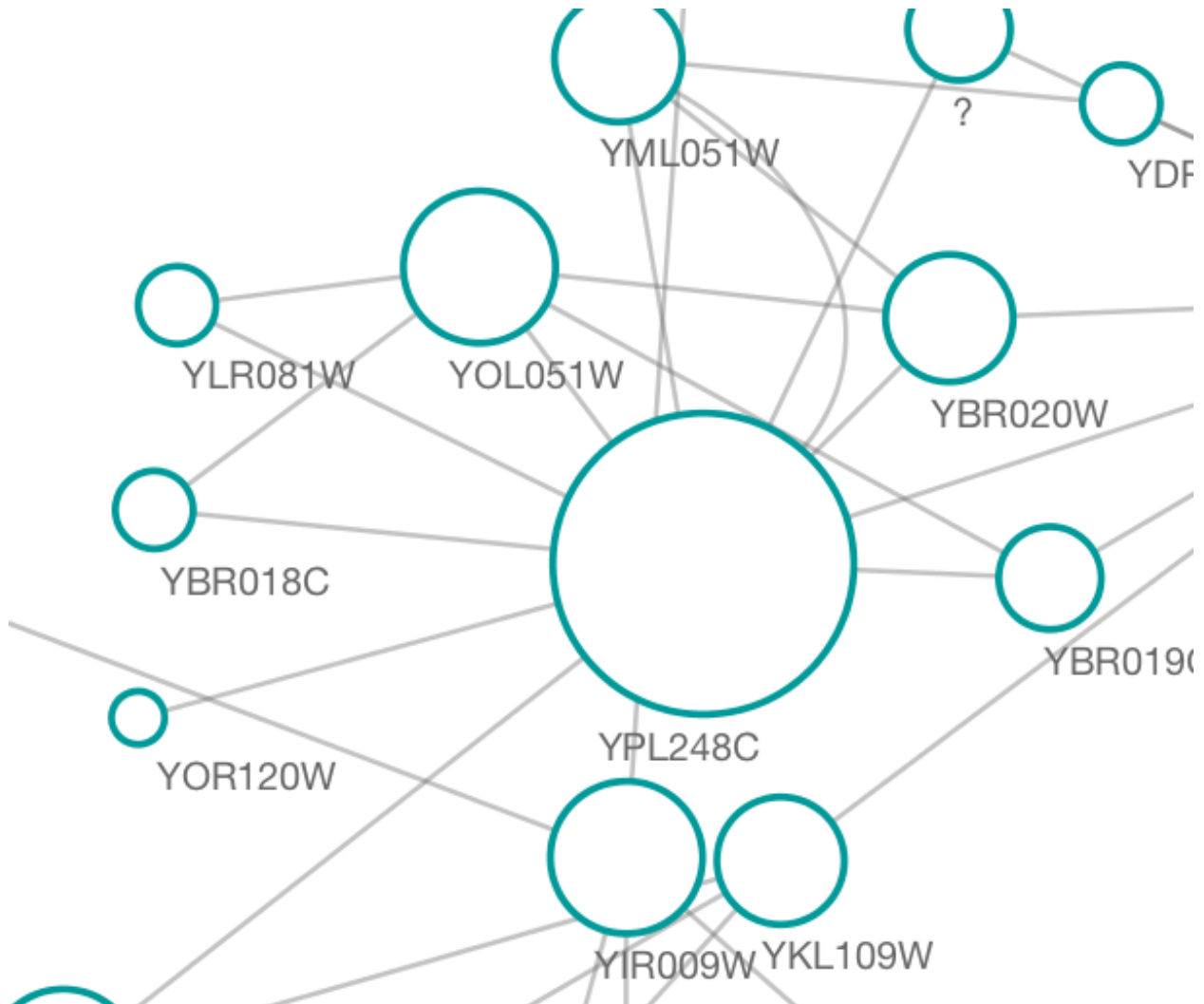
12.1 What are Styles?

One of Cytoscape's strengths in network visualization is the ability to allow users to encode any table data (name, type, degree, weight, expression data, etc.) as a property (such as color, size of node, transparency, or font type) of the network. A set of these encoded or mapped table data sets is called a **Style** and can be created or edited in the **Style** panel of the **Control Panel**. In this interface, the appearance of your network is easily customized. For example, you can:

Specify a default color and shape for all nodes.



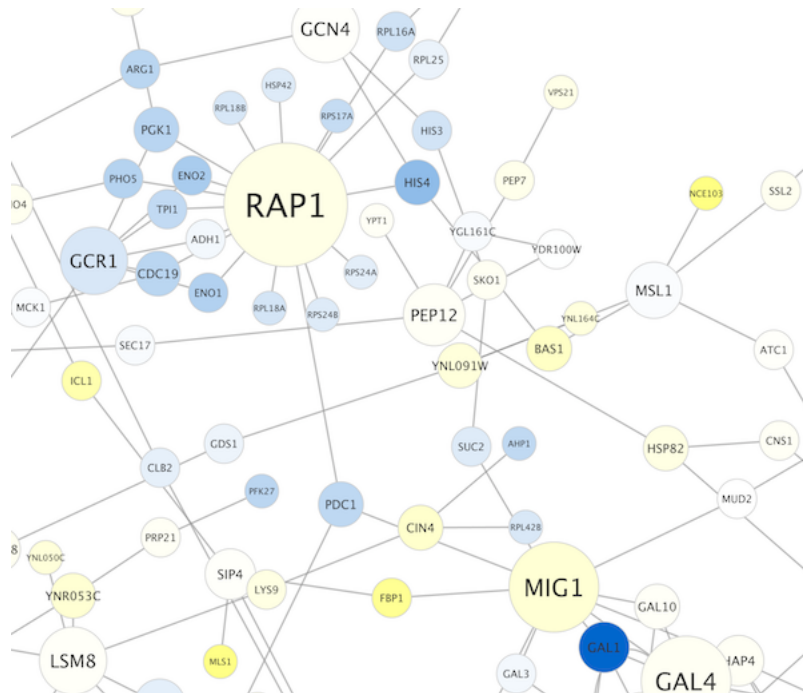
Set node sizes based on the degree of connectivity of the nodes. You can visually see the hub of a network...



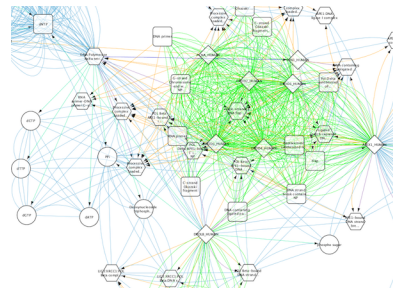
... or, set the font size of the node labels instead.



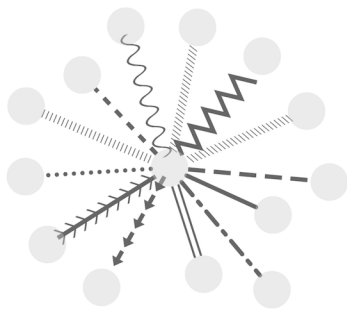
Visualize gene expression data along a color gradient.



Encode specific physical entities as different node shapes.



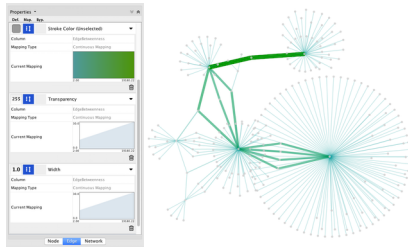
Use specific line types to indicate different types of interactions.



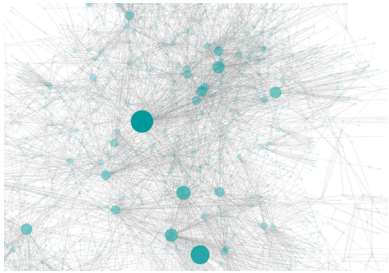
Control edge transparency (opacity) using edge weights.



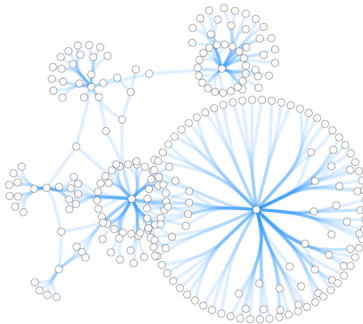
Control multiple edge properties using edge score.



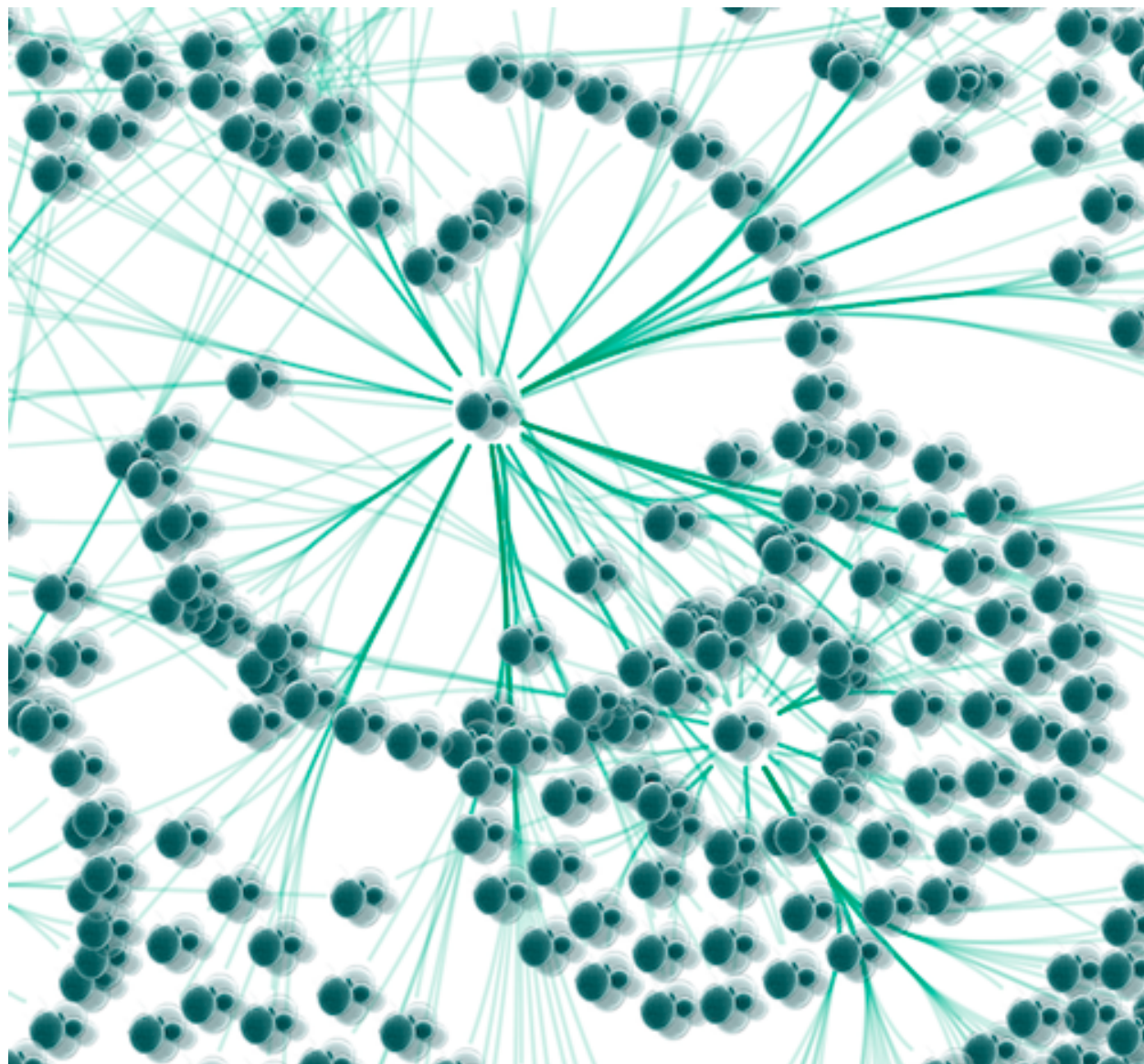
Browse extremely-dense networks by controlling the opacity of nodes.

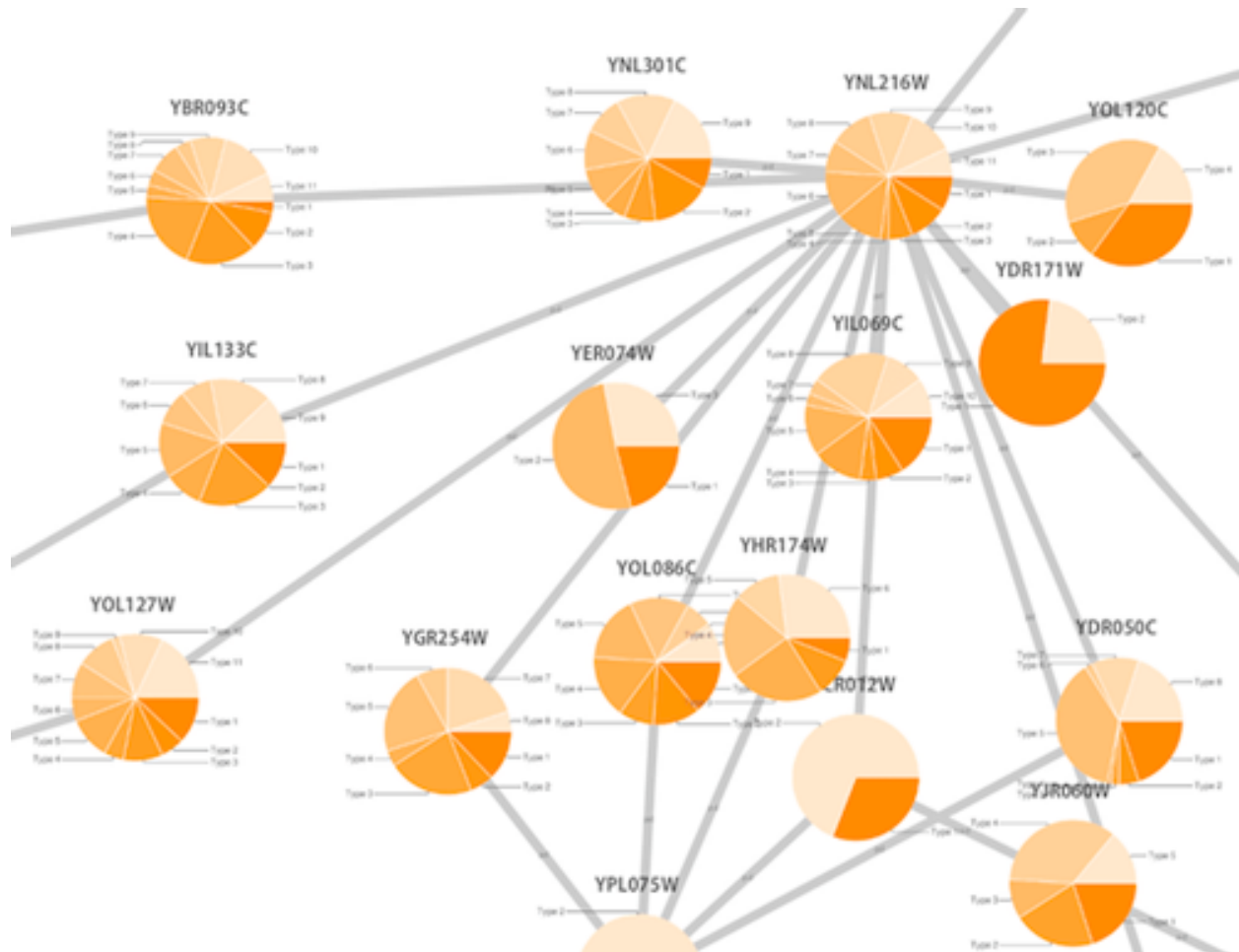


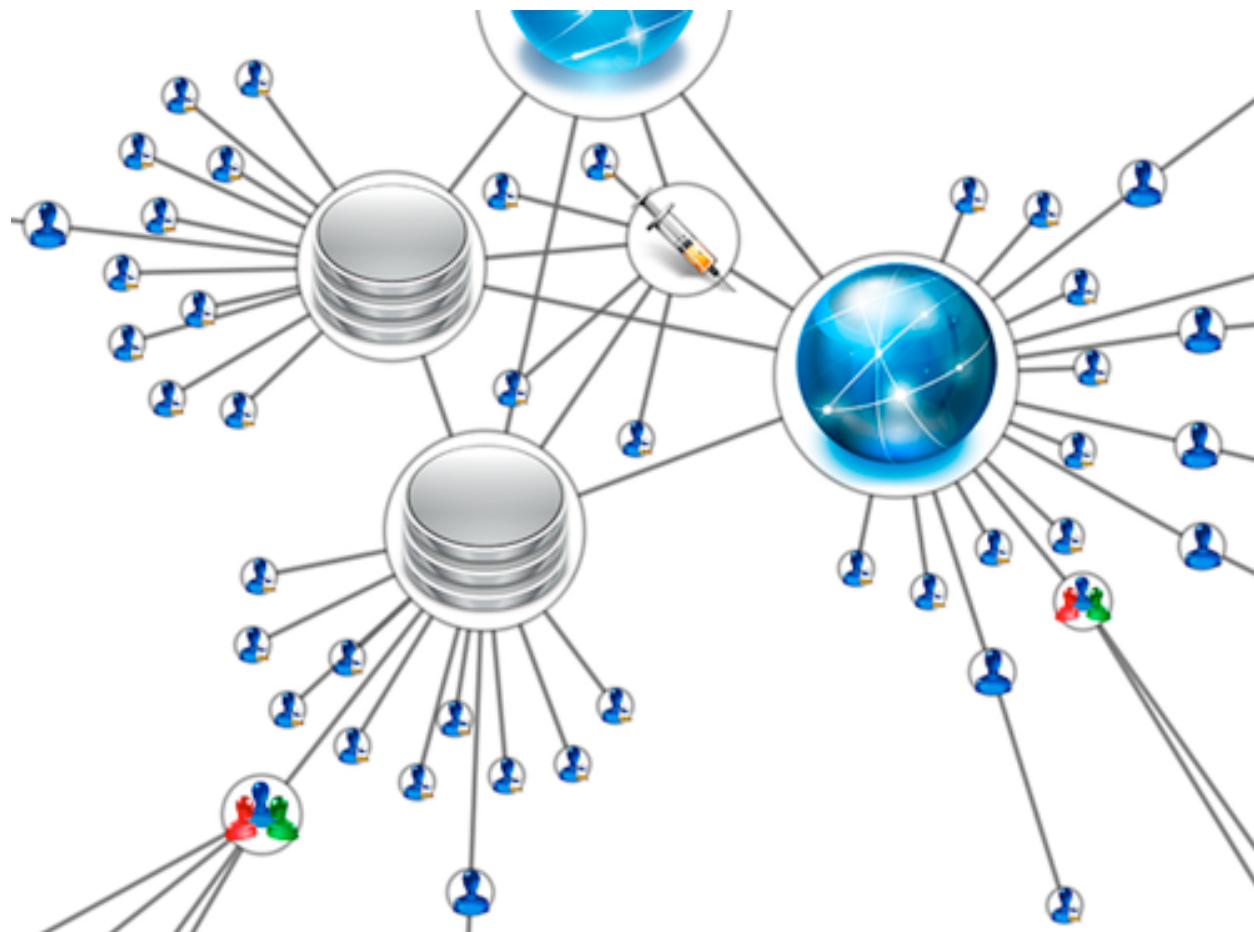
Show highly-connected region by edge bundling and opacity.



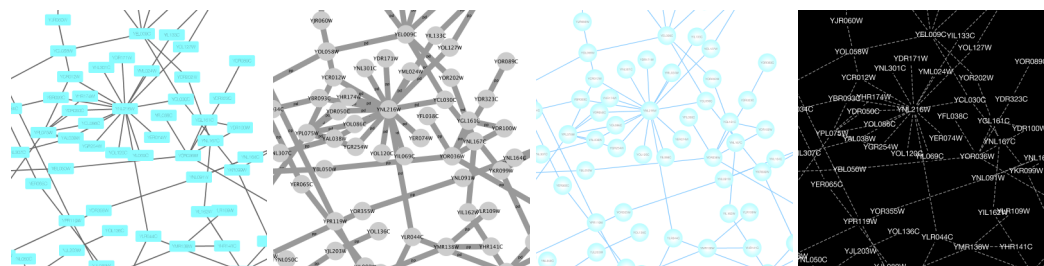
Add photo/image/graphics on top of nodes.





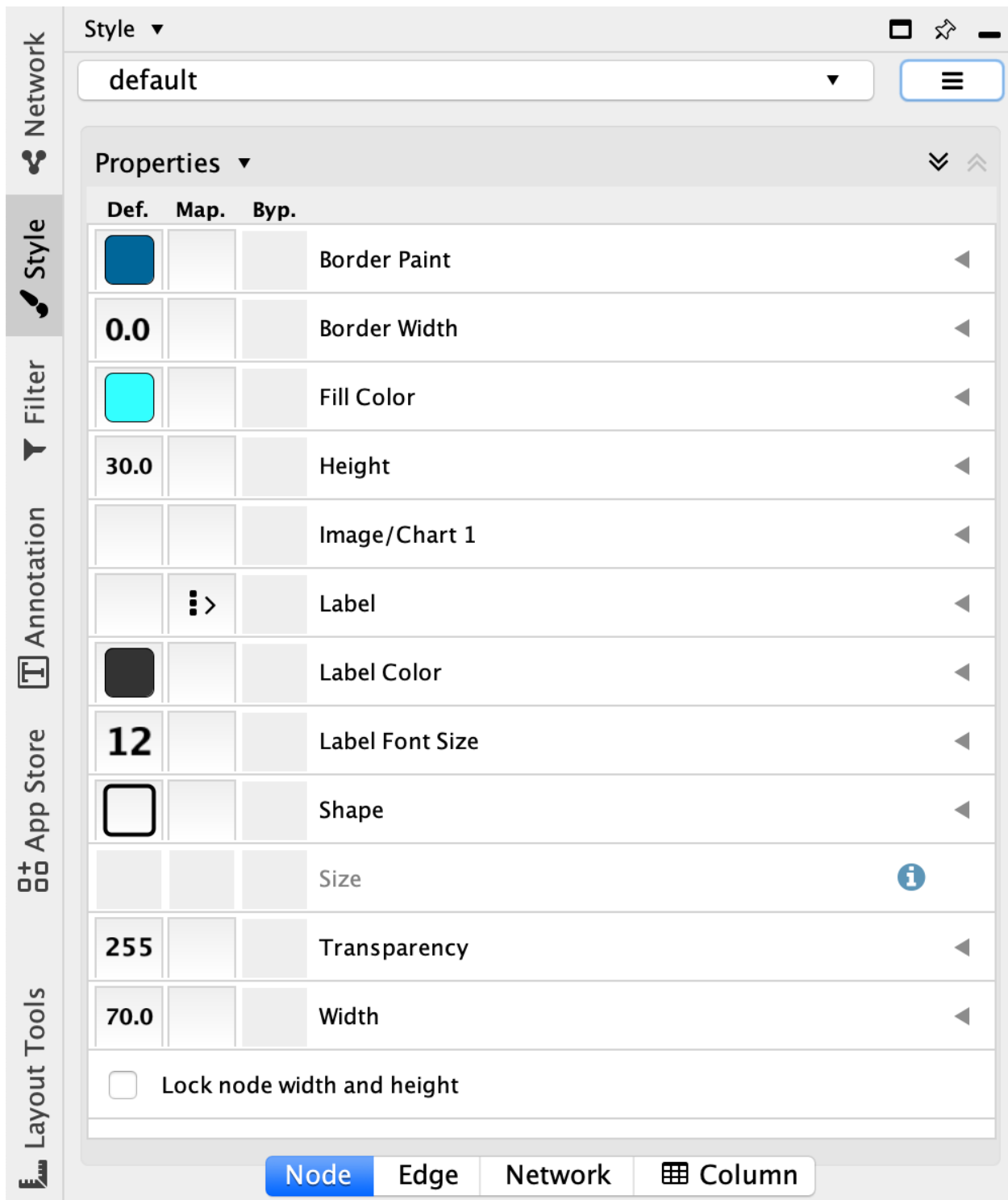


Cytoscape 3 has several sample styles. Below are a few examples of these applied to the *galFiltered.sif* network:

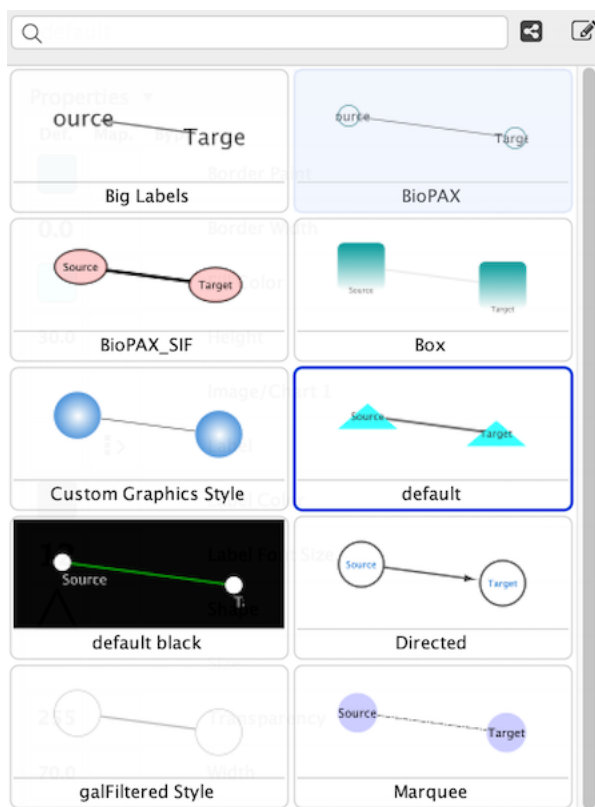





12.2 Introduction to the Style Interface

The **Style** interface is located under the **Style** panel of the **Control Panel**.



This interface allows you to create/delete/view and switch between different styles using the drop-down and the **Options** menu. With a specific style selected, the **Style** panel displays the details for a given style and is used to edit these details as well.



- At the top of the interface, there is a drop-down for selecting an pre-defined style.
- The list of available styles is searchable using the search field.
- The **Show only Applied Styles** button  will filter the list to display only the applied style.
- The list of available styles can be edited by clicking the **Edit..** . This will reveal a set of buttons for selecting and deleting styles.
- There is also an **Options** button  with options to rename, remove, create and copy a Style, and an option to create a legend for the selected style.
- The main area of the interface is composed of four tabs, for **Node**, **Edge** and **Network** properties, as well as a **Column** tab for setting mappings on individual columns in the **Node** and **Edge** tables of the “Table Panel”. Note that as of Cytoscape 3.10, **Column** styles are saved as part of the current style.
- Each tab contains a list of properties relevant to the current style, with a subset of properties shown by default. At the top of the list a **Properties** drop-down allows you to add additional properties to the list, show all properties, or save those currently shown as the new default.
- Each property entry in the list has 3 columns:
 - The **Default Value** shows just that, the default value for the property. Clicking on the **Default Value** column for any property allows you to change the default value.
 - **Mapping** displays the type of mapping currently in use for the property. Clicking on the **Mapping** column for any property expands the property entry to show the interface for editing the mapping. Details on the mapping types provided [here](#).
 - **Bypass** displays any style bypass for a selected node or edge. Note that a node/edge or subset of nodes/edges must be selected to activate the **Bypass** column. Clicking on the **Bypass** column for se-

lected node(s)/edge(s) allows you to enter a bypass for that property for selected node(s)/edge(s). There is no **Bypass** option for **Column** styles.

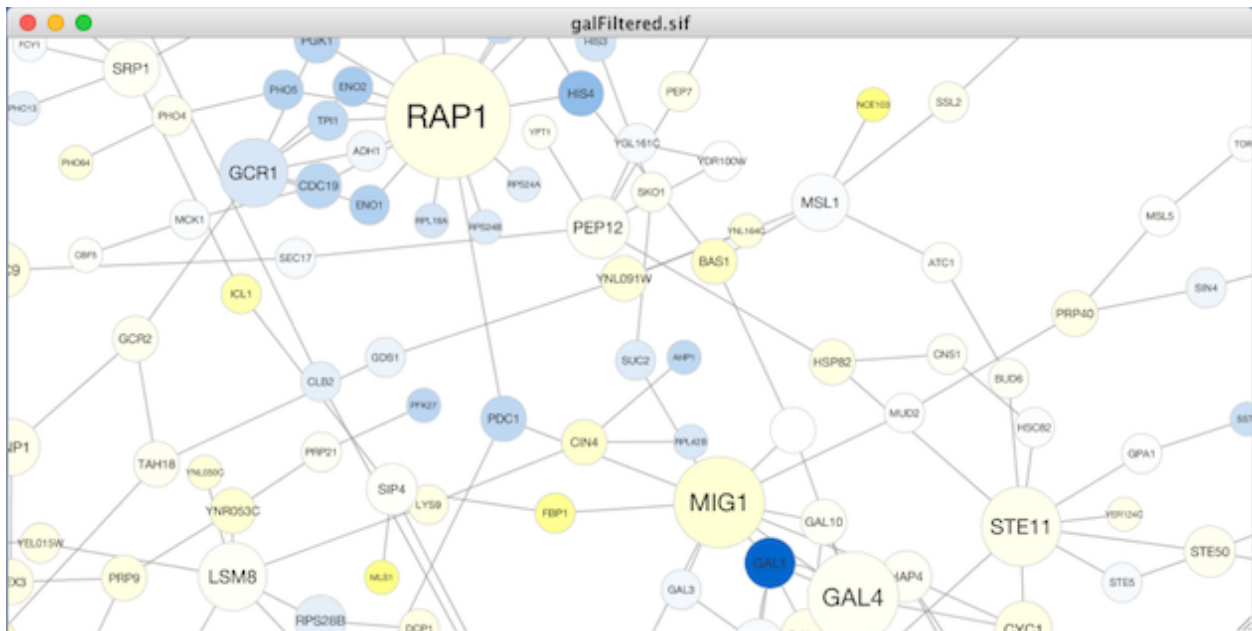
The **Default Value** is used when no mapping is defined for a property, or for nodes/edges not covered by a mapping for a particular property. If a **Mapping** is defined for a property, this defines the style for all or a subset of nodes/edges, depending on how the mapping is defined. A **Bypass** on a specific set of nodes/edges will bypass and override both the default value and defined mapping.

12.3 Introduction to Style

The Cytoscape distribution includes several predefined styles to get you started. To examine a few styles, try out the following example:

Step 1. Load some sample data

- Load a sample session file: From the main menu, select **File** → **Open...**, and select the file *sampleData/galFiltered.cys*.
- The session file includes a network, some annotations, and sample styles. By default, the style **galFiltered Style** is selected. Gene expression values for each node are colored along a color gradient between blue and yellow (where blue represents a low expression ratio and yellow represents a high expression ratio, using thresholds set for the **gal1RGexp** experiment bundled with Cytoscape in the *sampleData/galExpData.csv* file). Also, node size is mapped to the degree of the node (number of edges connected to the node) and you can see the hubs of the network as larger nodes. See the sample screenshot below:



Step 2. Switch between different styles

You can change the style by making a selection from the **Current Style** drop-down list, found at the top of the **Style** panel.

For example, if you select **Sample1**, a new style will be applied to your network, and you will see a white background and round blue nodes. If you zoom in closer, you can see that protein-DNA interactions (specified with the label **pd**) are drawn with dashed edges, whereas protein-protein interactions (specified with the label **pp**) are drawn with solid edges (see sample screenshot below).

12.3.2 Available Shapes and Line Styles

12.3.3 Edge Stacking

The **Edge Stacking** property determines how edges are visualized when there are multiple edges between a pair of nodes.

12.3.4 How Mappings Work

For each property, you can specify a default value or define a dynamic mapping. Cytoscape currently supports three different types of mappings:

1. Passthrough Mapping

- The values of network column data are passed directly through to properties. A passthrough mapping is typically used to specify node/edge labels. For example, a passthrough mapping can label all nodes with their common gene names.

2. Discrete Mapping

- Discrete column data are mapped to discrete properties. For example, a discrete mapping can map different types of molecules to different node shapes, such as rectangles for gene products and ellipses for metabolites.

3. Continuous Mapping

- Continuous data are mapped to properties. Depending on the property, there are three kinds of continuous mapping:
 - i. **Continuous-to-Continuous Mapping:** for example, you can map a continuous numerical value to node size.
 - ii. **Color Gradient Mapping:** This is a special case of continuous-to-continuous mapping. Continuous numerical values are mapped to a color gradient.
 - iii. **Continuous-to-Discrete Mapping:** for example, all values below 0 are mapped to square nodes, and all values above 0 are mapped to circular nodes.
- However, note that there is no way to smoothly morph between circular nodes and square nodes.

The table below shows mapping support for each property.

Legend

Node Mappings

Edge Mappings

Text Passthrough Mapping

In Cytoscape 2.8.0 and later versions, the **Passthrough Mapping** can recognize some text representations of values. This means, if you have a string column named **Node Size Values**, you can directly map those values as the node size by setting **Node Size Values** as controlling column for the **Node Size** property, with a **Passthrough Mapping**. The following value types are supported:

- **Colors:** [Standard color names supported by all browsers](#) or RGB representation in hex
- **Numerical Values:** Automatically mapped to the specified property.
- **Images:** URL String. If the URL is valid and an actual image data exists there, Cytoscape automatically downloads the image and maps it to the node.

Examples

Color Passthrough Mapping

Node Size Passthrough Mapping

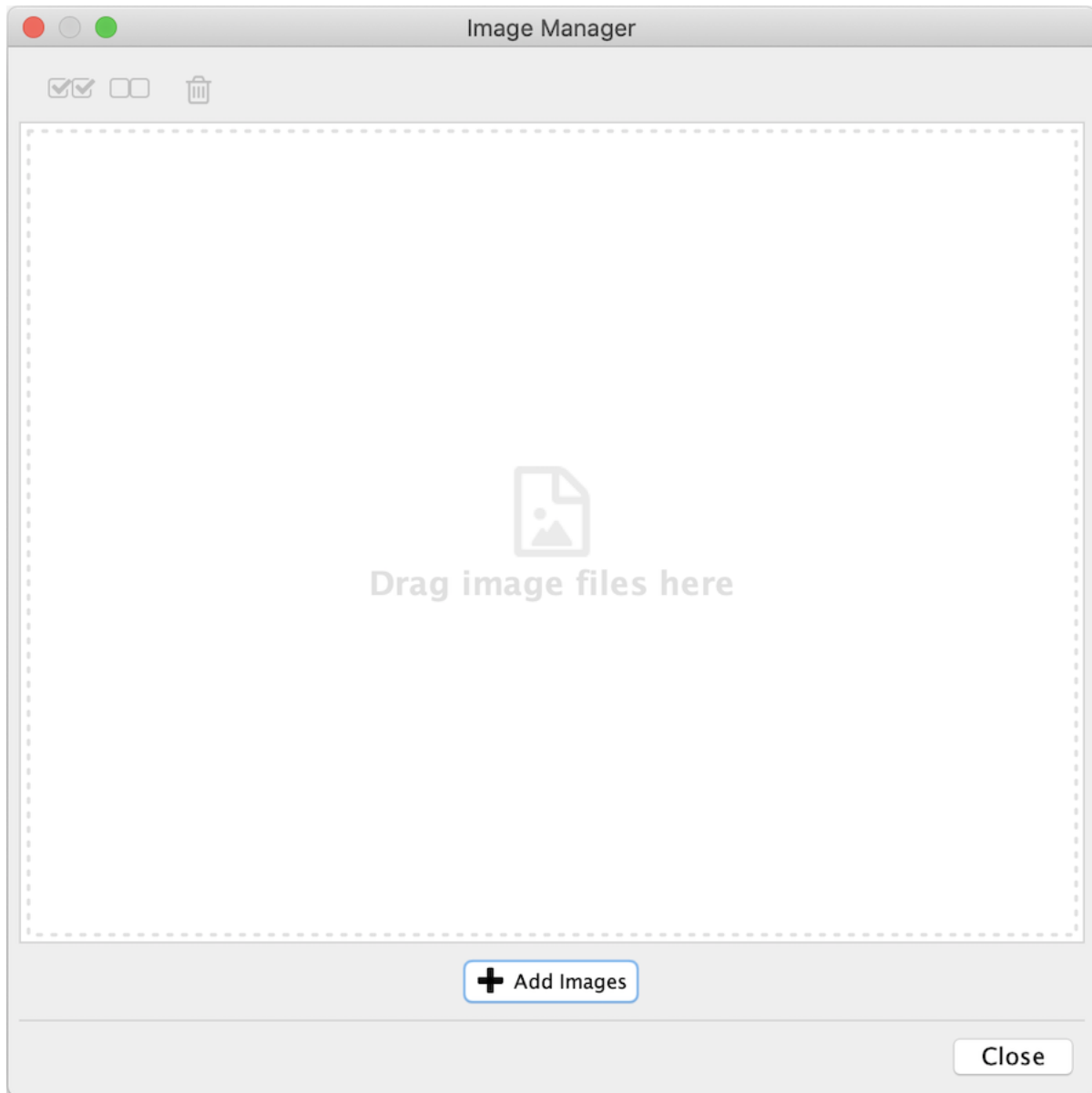
Image Passthrough Mapping

12.4 Images, Charts and Gradients

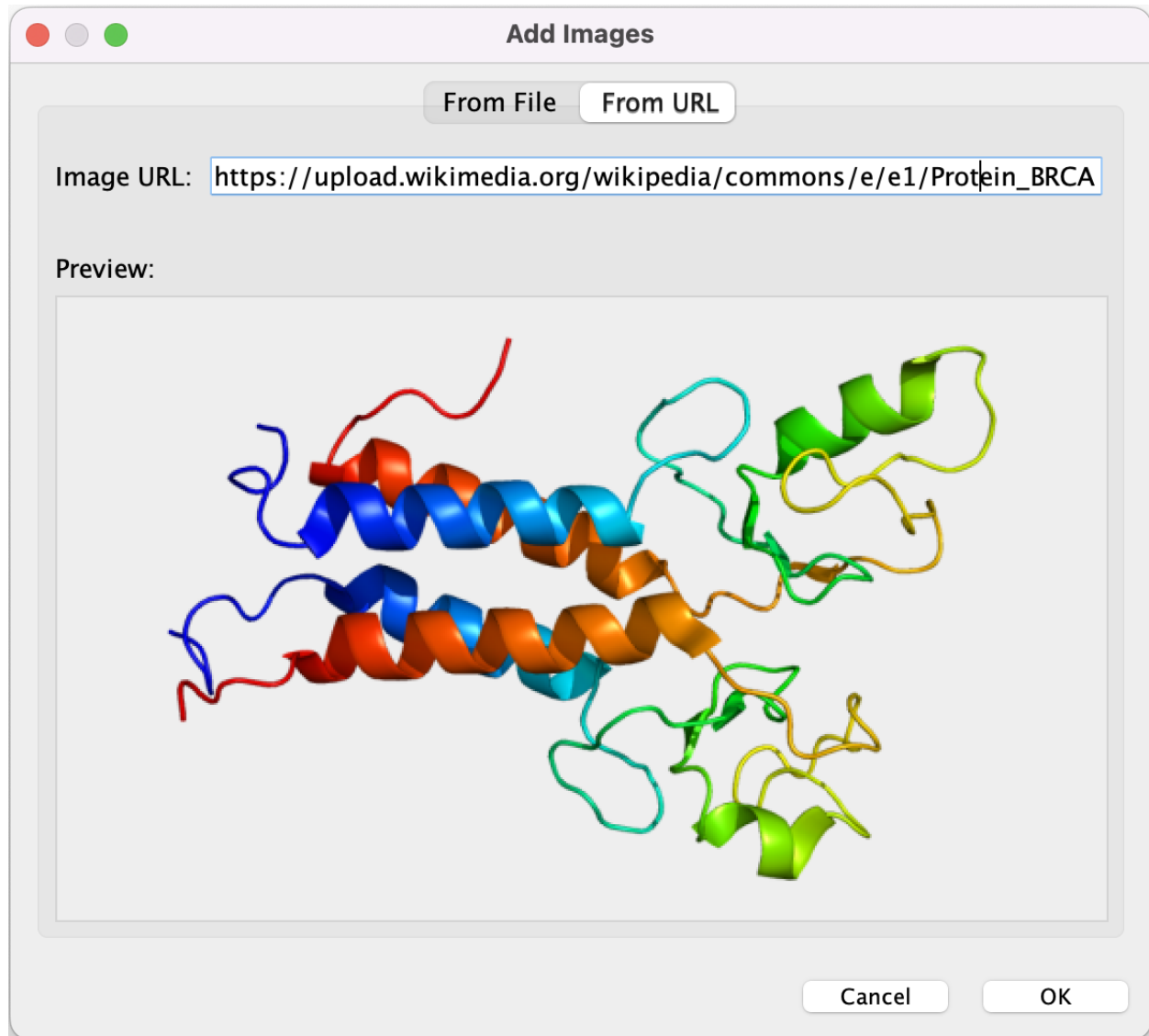
Cytoscape allows you to set custom graphics to nodes. Using the **Style** interface, you can map **Image/Chart** properties to nodes like any other property. Cytoscape provides a set of images and you can also add your own images in the **Image Manager**, as well as remove or modify existing ones.

12.4.1 Managing Images

The **Image Manager** is available under the menu option **View** → **Open Image Manager...**:

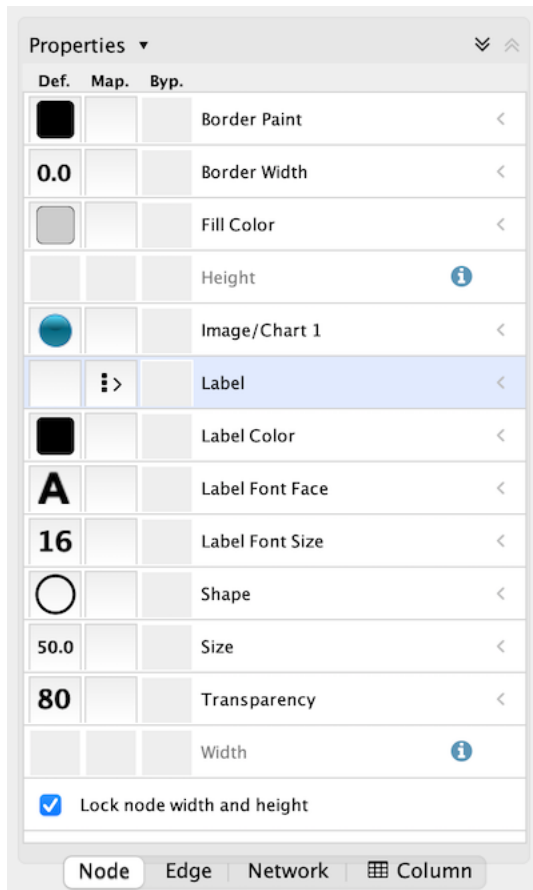


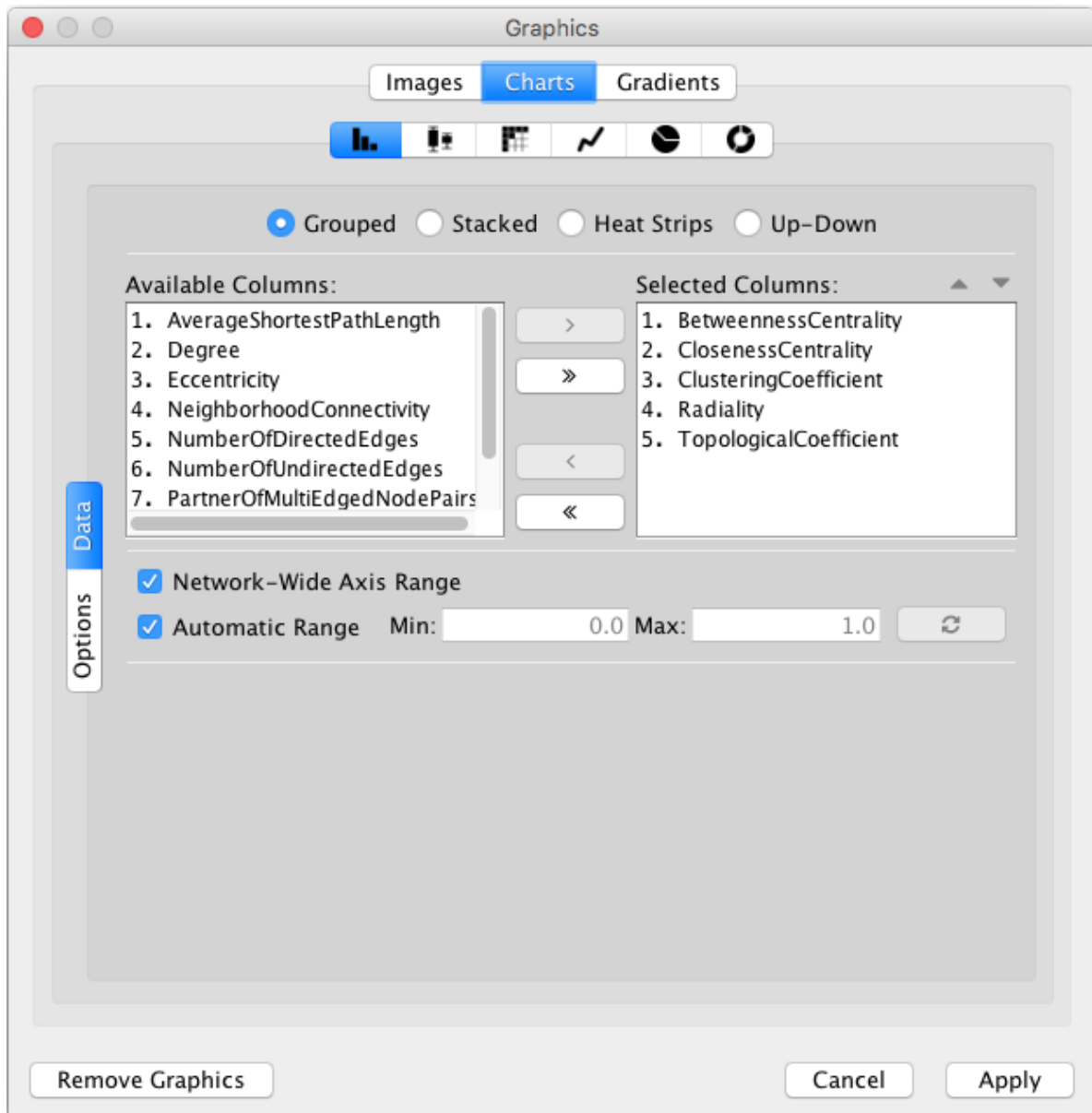
- You can add images by drag-and-drop of image files.
- To add images from a web browser or local file system, click the **Add Images** button and add your images under **From File** or **From URL**.

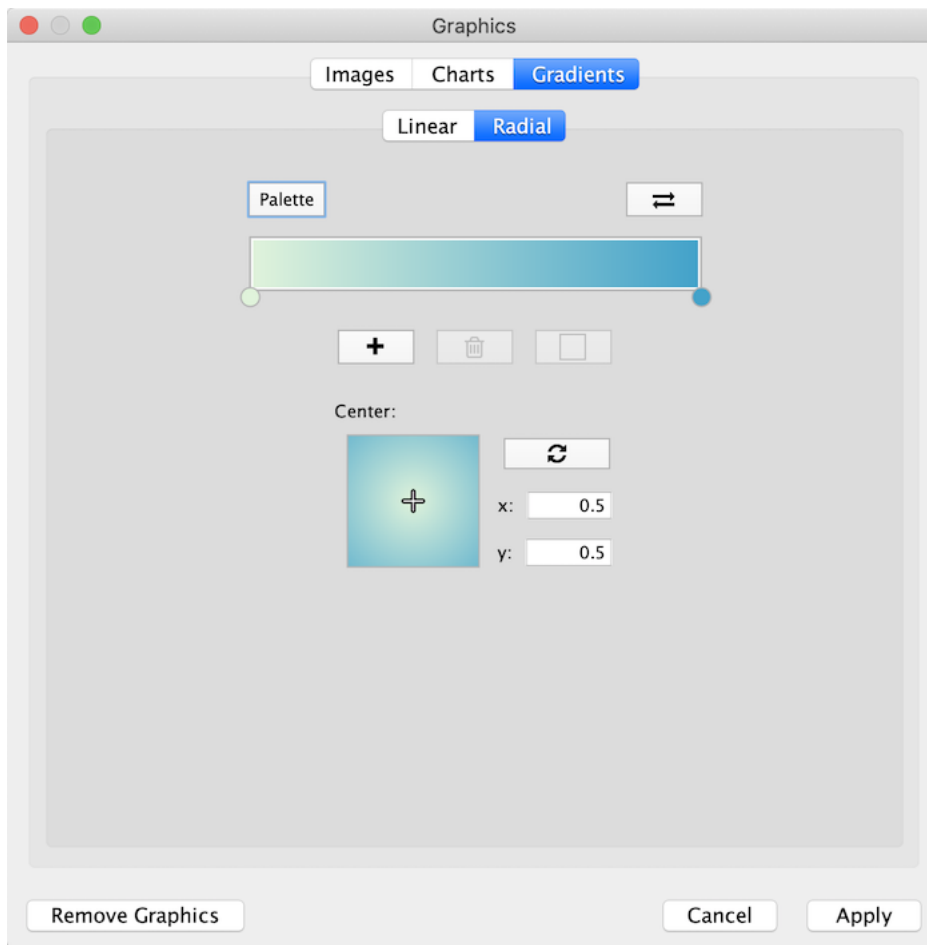


- If you want to add one or more images from a folder, select all the images you want to add under **From File**.
- To remove images from the current session's image library, simply select one or more images and press the **Remove Selected Images** button (trash icon).

12.4.2 Using Graphics in Styles







- To add a graphic, first add one **Image/Chart** property to the properties list in the **Style** interface (on the **Node** tab, select **Properties** → **Paint** → **Custom Paint *n*** → **Image/Chart *n***). Next, click the **Default Value** column of the **Image/Chart** property to bring up the **Graphics** dialog. Select an image, a chart or a gradient and then click **Apply**. By default, graphics are automatically resized to be consistent with the **Node Size** property.
- To remove an image, chart or gradient, click the **Remove Graphics** button on the **Graphics** dialog.

Graphics Positions

Each **Image/Chart** property is associated with a position. You can edit its position by using the UI available in the **Default Value** column for the **Image/Chart Position** property that has the same number. For instance, the **Image/Chart Position 2** value modifies the position of **Image/Chart 2**.

- **Note:** Setting graphics positions for *Linear* or *Radial* gradients has no effect, as they are always centered on the node.

Z-Ordering

The number that appears with the **Image/Chart** property represents an ordering of layers. Basic node color and shape are always rendered first, then node **Image/Chart 1**, **2**, ..., through **9**.

12.4.3 Saving and Loading Images

In general, saving and loading images is automatic. When you quit Cytoscape, all of the images in the **Image Manager** will be saved automatically. There are two types of saving:

1. To a session file
 - When you save the current session to a file, the images used in the current styles will be saved to that file. For example, if you have a style with a discrete mapping for **Image/Chart 1**, all images used in the style will be saved to the session file. Other images will **not** be saved in your session file. This is because your image library can be huge when you add thousands of images to the Image Manager and it takes a very long time to save and load the session file.
2. Automatic saving to CytoscapeConfiguration/images3 directory
 - When you select **File** → **Quit** (Windows and Linux) or **Cytoscape** → **Quit Cytoscape** (Mac OS X), all of the images in the Image Manager will be saved automatically to your Cytoscape settings directory. Usually, they are saved in YOUR_HOME_DIRECTORY/CytoscapeConfiguration/images3.

In any case, images will be saved automatically to your system or session and will be restored when you restart Cytoscape or load a session.

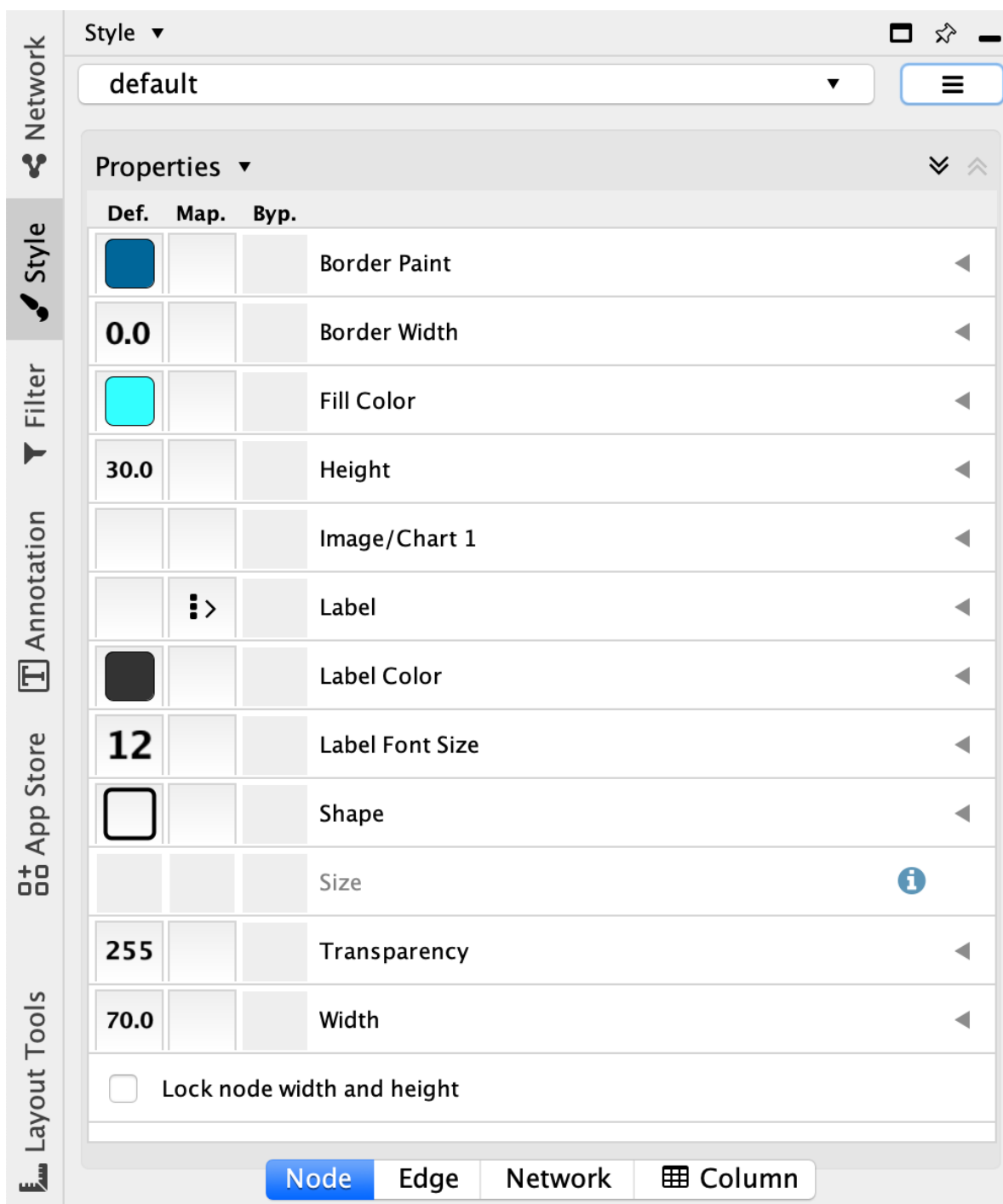
12.5 Styles Tutorials


The following tutorials demonstrate some of the basic **Style** features. Each tutorial is independent of the others.

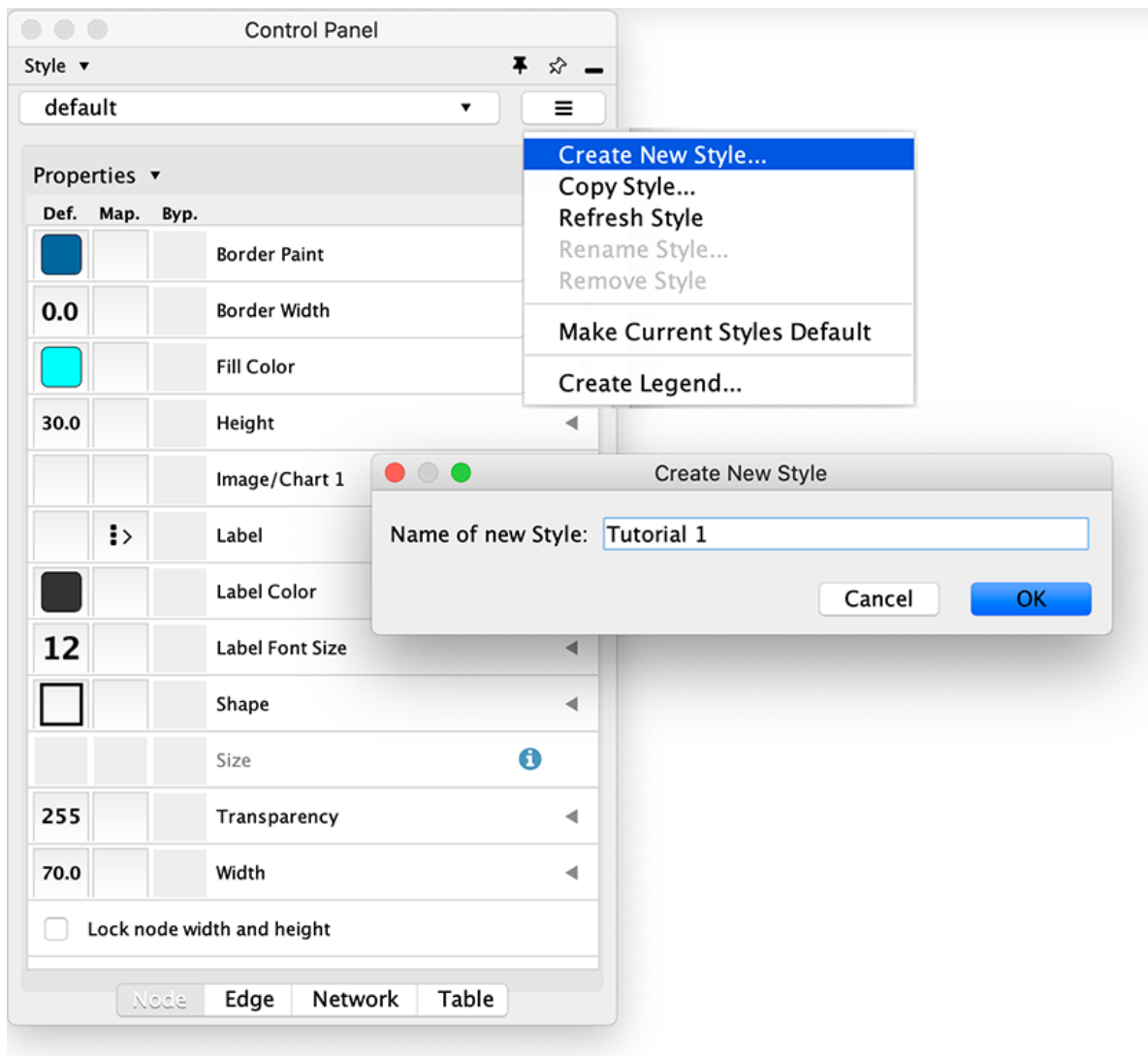
12.5.1 Tutorial 1: Creating a Basic Style and Setting Default Values

The goal of this tutorial is to learn how to create a new style and set some default values.

1. **Load a sample network:** From the main menu, select **File** → **Import** → **Network from File...**, and select `sampleData/galFiltered.sif`.
2. **Create some node/edge statistics:** The **Network Analyzer** calculates some basic statistics for nodes and edges. From the main menu, select **Tools** → **Analyze Network**, and click **OK**. All statistics are stored as regular table data.
3. Select the **Style** panel in the **Control Panel**.

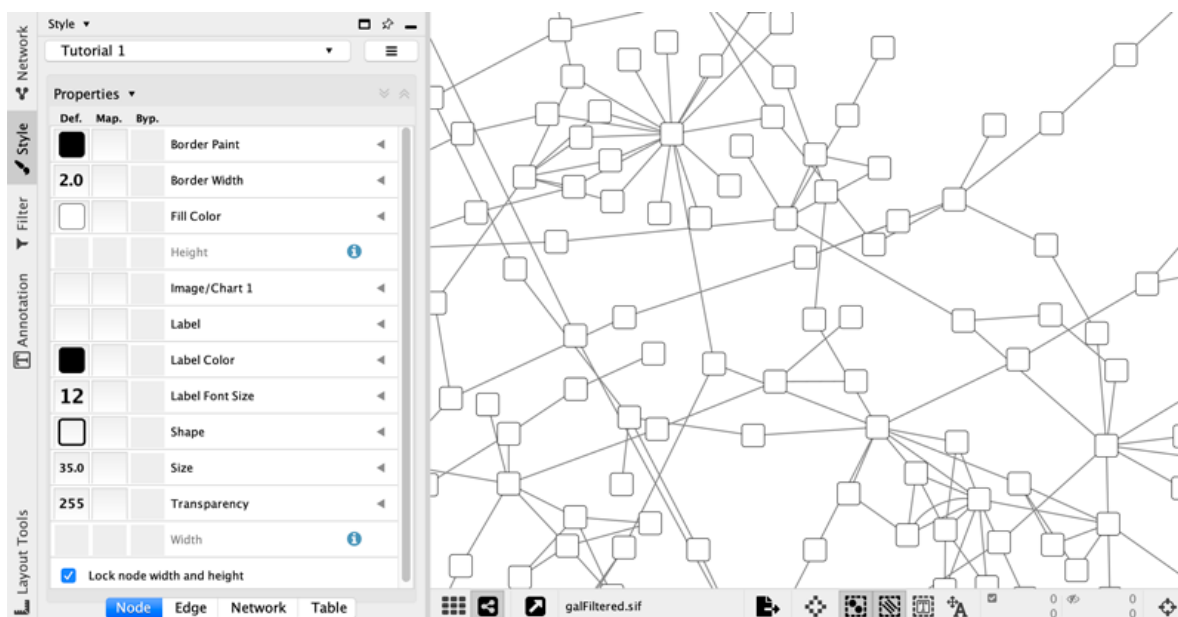


4. **Create a new style:** Click the **Options**  drop-down, and select **Create New Style**. Enter a name for your new style when prompted.



Since no mappings are set up yet, only default values are defined for some of the properties. From this panel, you can create node/edge mappings for all properties.

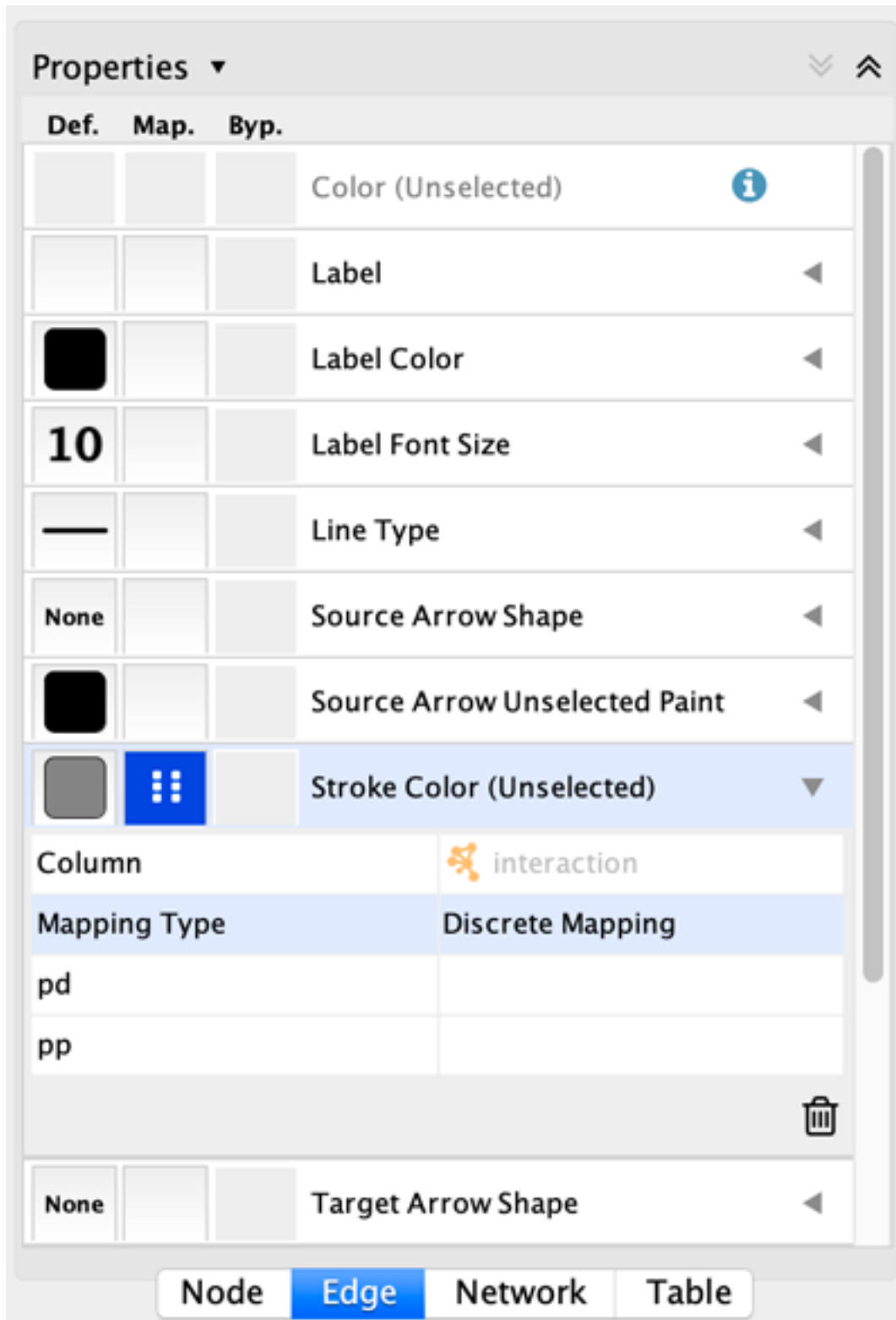
1. **Change the default node color and shape:** To set the default node shape to triangles, click the **Default Value** column for the **Shape** property. A list of available node shapes will be shown. Select the **Triangle** item and click the **Apply** button. You can edit other default values in the same way. In the example shown below, the node shape is set to **Round Rectangle**, while **Fill Color** is set to white. The new style is automatically applied to the current network, as shown below.






12.5.2 Tutorial 2: Creating a New Style with a Discrete Mapping

Now you have a network with a new style. The following section demonstrates how to create a new style that has a discrete mapping. The goal is to draw protein-DNA interactions as dashed lines, and protein-protein interactions as solid lines.

1. **Find the property:** In the **Edge** tab of the **Style** panel, find the **Stroke Color (Unselected)** property. If it is not already visible in the properties sheet, add it by selecting the drop-down item **Properties** → **Paint** → **Color (Unselected)** → **Stroke Color (Unselected)**.
2. **Choose a data column to map to:** Expand the entry for **Stroke Color (Unselected)** by clicking the arrow icon on the right. Click the **Column** entry and select *interaction* from the drop-down list that appears.
3. **Set the mapping type:** Under **Mapping Type**, select **Discrete Mapping**. All available column values for *interaction* will be displayed, as shown below.

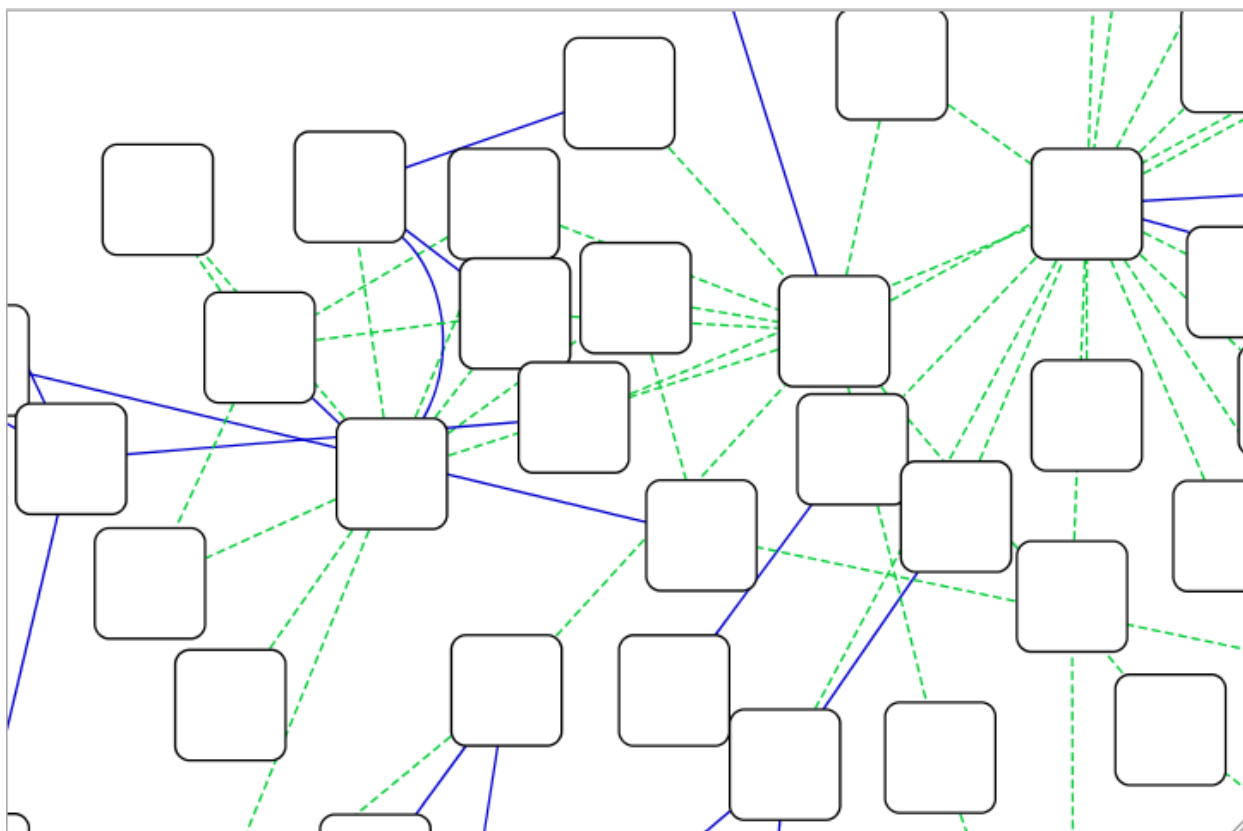


4. **Set the mapped values:** Click the empty cell next to *pd* (protein-DNA interactions). On the right side of the cell, click on the ... button that appears. A popup window will appear with all available palettes and color collections, you can select an individual color from any color palette. Select green or similar, and the change will immediately appear on the network window.

Stroke Color (Unselected) ▼	
Column	interaction
Mapping Type	Discrete Mapping
pd	 R:0 G:204 B:51 - #00CC33
pp	 R:0 G:0 B:204 - #0000CC
	

Repeat step 4 for *pp* (protein-protein interactions), but select a darker color. Then repeat steps 3 through 4 for the **Line Type** property, by selecting the correct line style (**Dash** or **Solid**) from the list.

Now your network should show *pd* interactions as dashed green lines and *pp* interactions as solid lines. A sample screenshot is provided below.



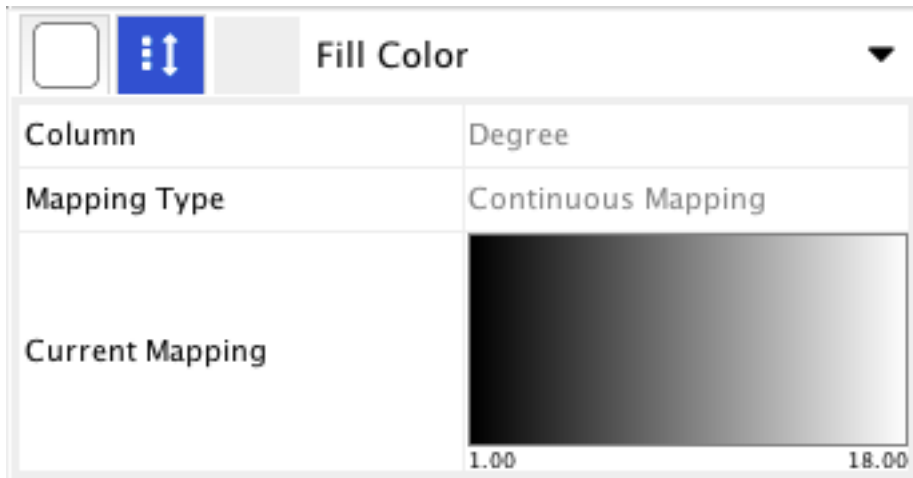
12.5.3 Tutorial 3: Creating a New Style with a Continuous Mapping

At this point, you have a network with some edge mappings. Next, let's create mappings for nodes. The following section demonstrates how to create a new style using a continuous mapping. The goal is to superimpose node statistics (in this example, node degree) onto a network and display it along a color gradient.

1. **Find the property:** In the **Node** tab of the **Style** panel, find the **Fill Color** property. If it is not already visible

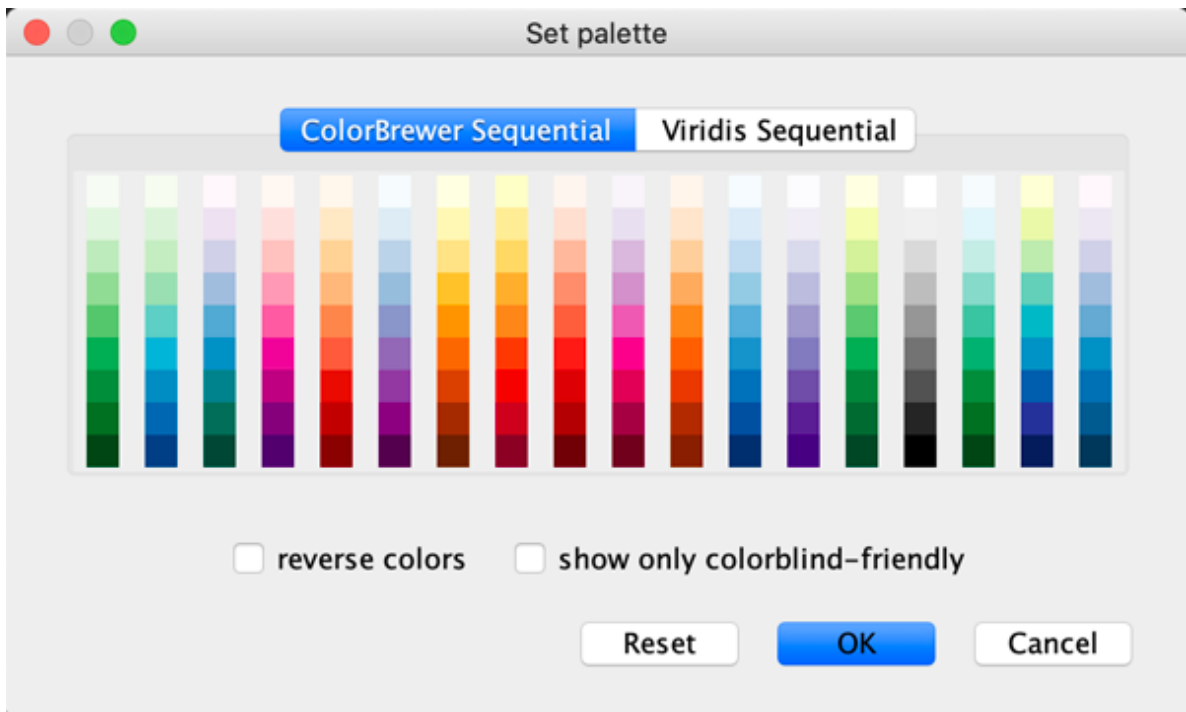
in the properties sheet, add it by selecting the drop-down item **Properties** → **Paint** → **Fill Color**.

2. **Set the node table column:** Expand the entry for **Fill Color** by clicking the arrow icon on the right. Click the **Column** entry and select *Degree* from the drop-down list that appears.
3. **Set the mapping type:** Set the **Continuous Mapping** option as the **Mapping Type**. This automatically creates a default mapping based on the range of values in the *Degree* column.

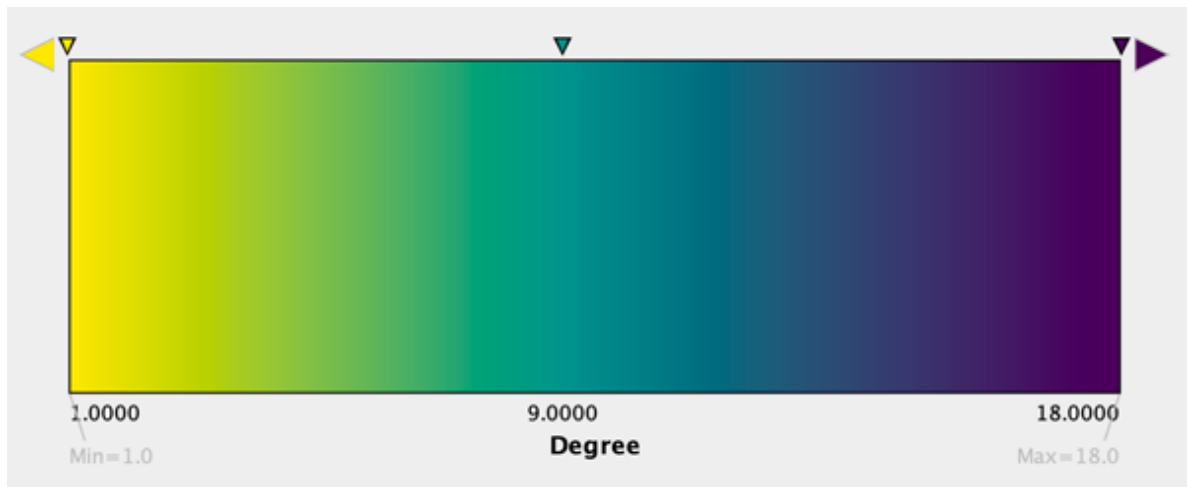


4. **Define a color palette.** We encourage you to choose palette from the existing ones provided, but you can also choose the color states yourself and provide any number of intermediate colors. Both methods are described here.

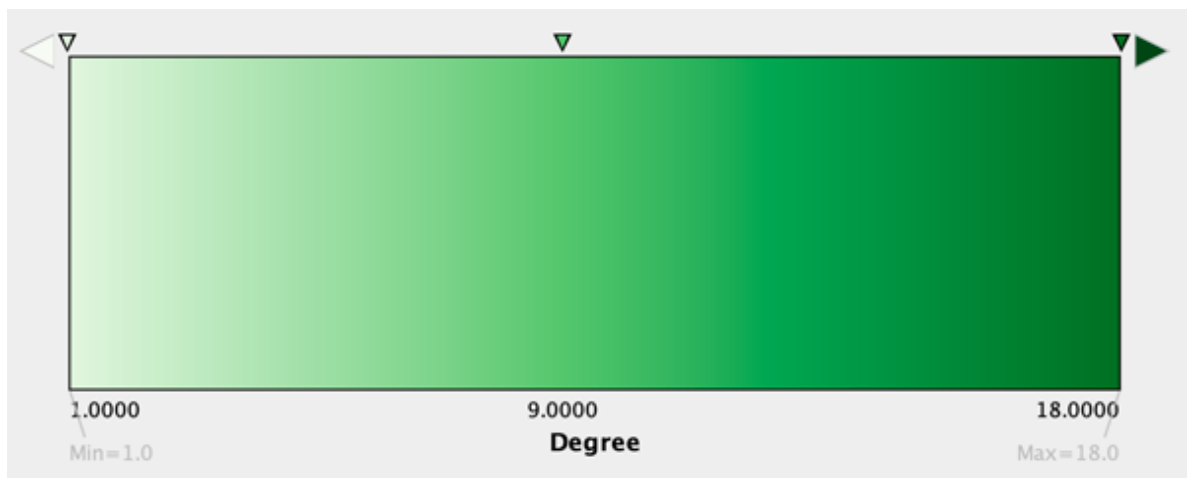
Choose a predefined palette from the Palette picker. These come from published recommendations for choosing colors in scientific and cartographic applications, such as [BrewerColors](#). Click the **Current Palette** button in the top left of the **Continuous Mapping Editor** to choose from a set of palettes. Below shows the **Set Palette** dialog to choose a full palette. For this tutorial, we are choosing the “green shades” palette. Note that any palette can also be reversed by selecting **reverse colors**.



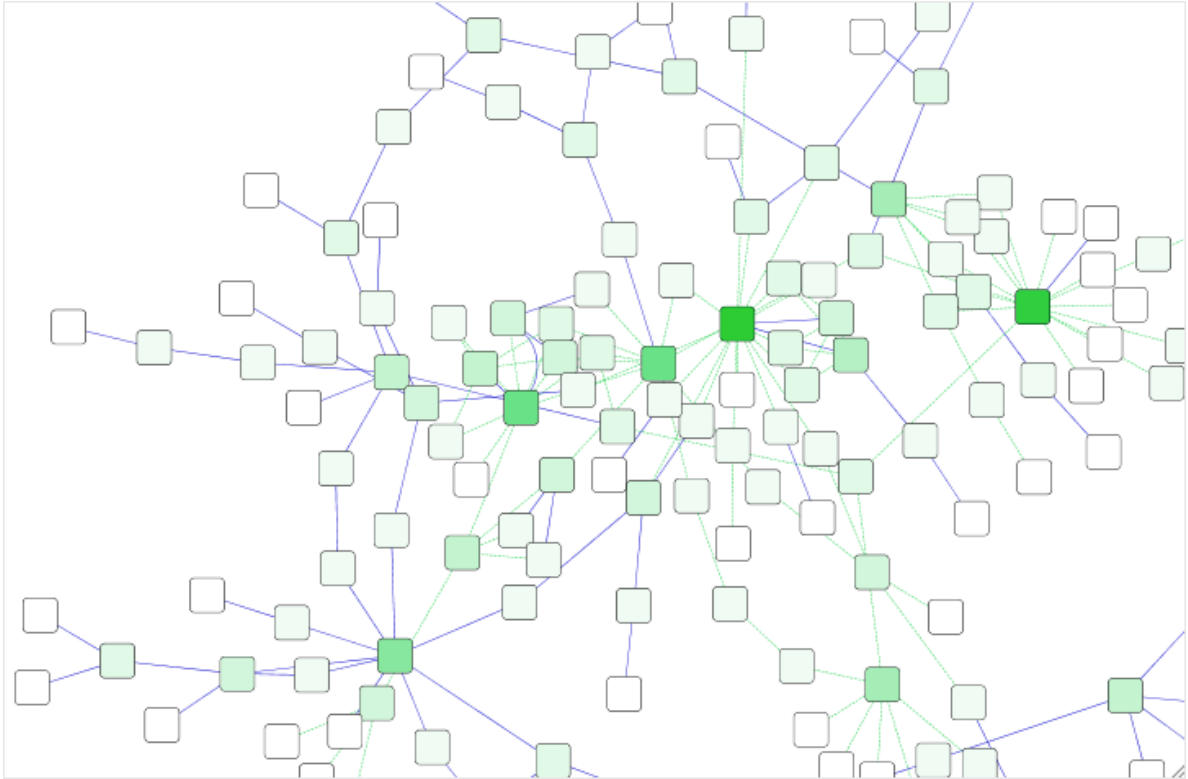
Define the points where colors will change: Double-click on the default gradient rectangle next to **Current Mapping** to open the **Continuous Mapping Editor**. Note the two smaller triangles at the top of the gradient.



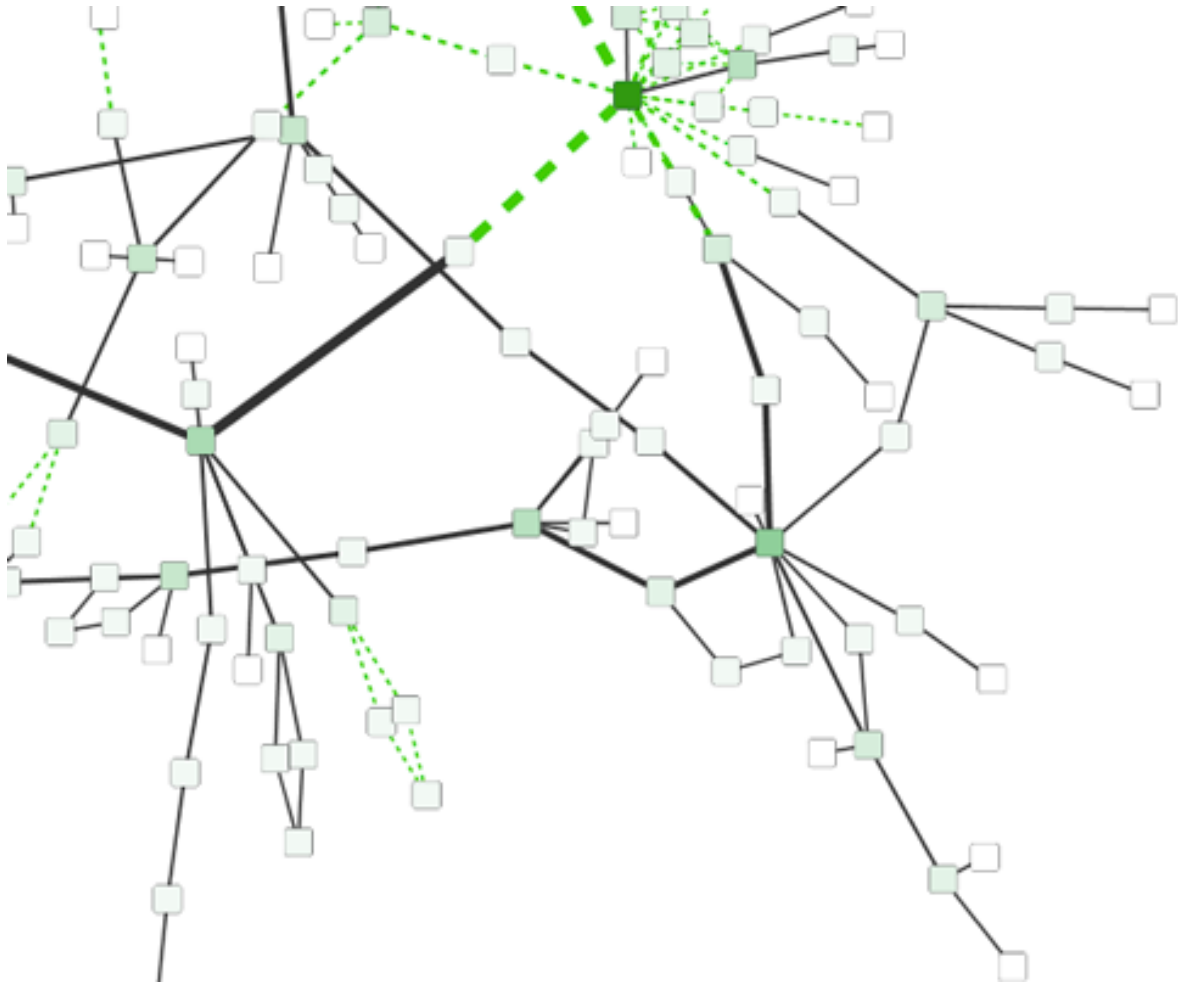
5. **Define the colors between points:** Double-click on the larger leftmost triangle (facing left) and a color palette will appear. Set the color white and repeat for the smaller left-side triangle. For the triangle on the right, set the color green and then choose the same color for the smaller right-side triangle.



The color gradients will immediately appear on the network. All nodes with degree 1 will be set to white, and all values between 1 and 18 will be painted with a white/green color gradient (see the sample screenshot below).



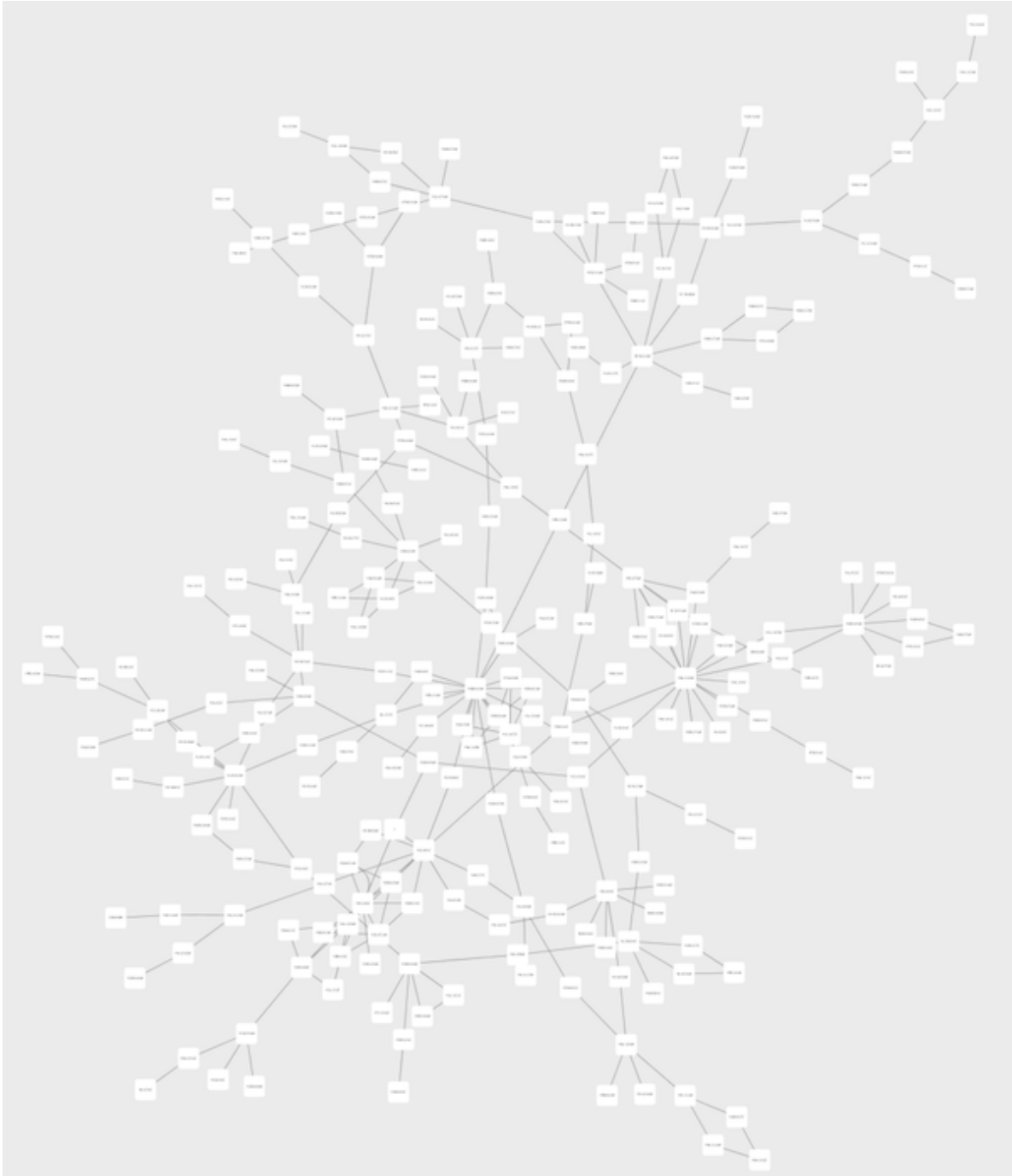
6. **Repeat for other properties:** You can create more continuous mappings for other numeric table data. For example, edge data table column *EdgeBetweenness* is a number, so you can use it for continuous mapping. The following is an example visualization which maps **Edge Width** to *EdgeBetweenness*.



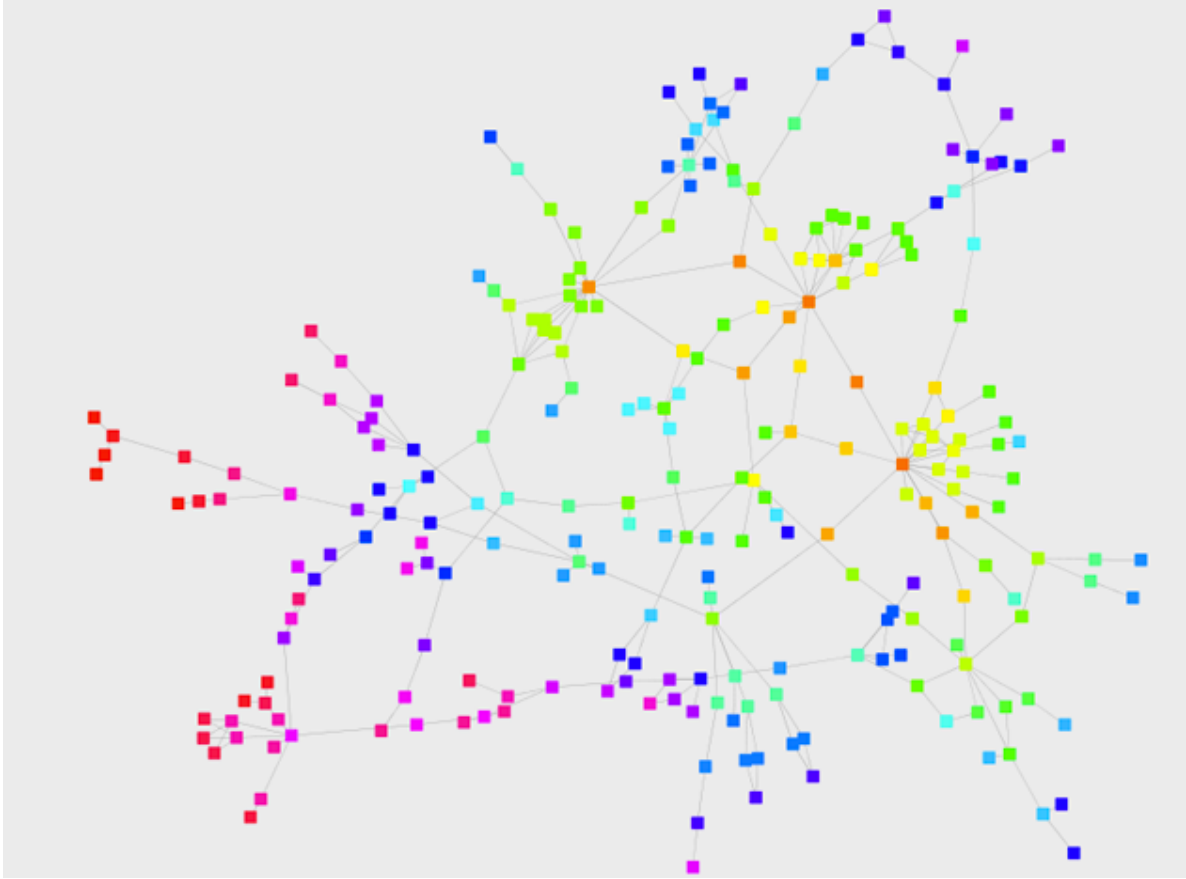
12.5.4 Tutorial 4: Setting Automatic Values to a Discrete Mapping

The goal of this section is to learn how to generate automatic values for discrete mappings.

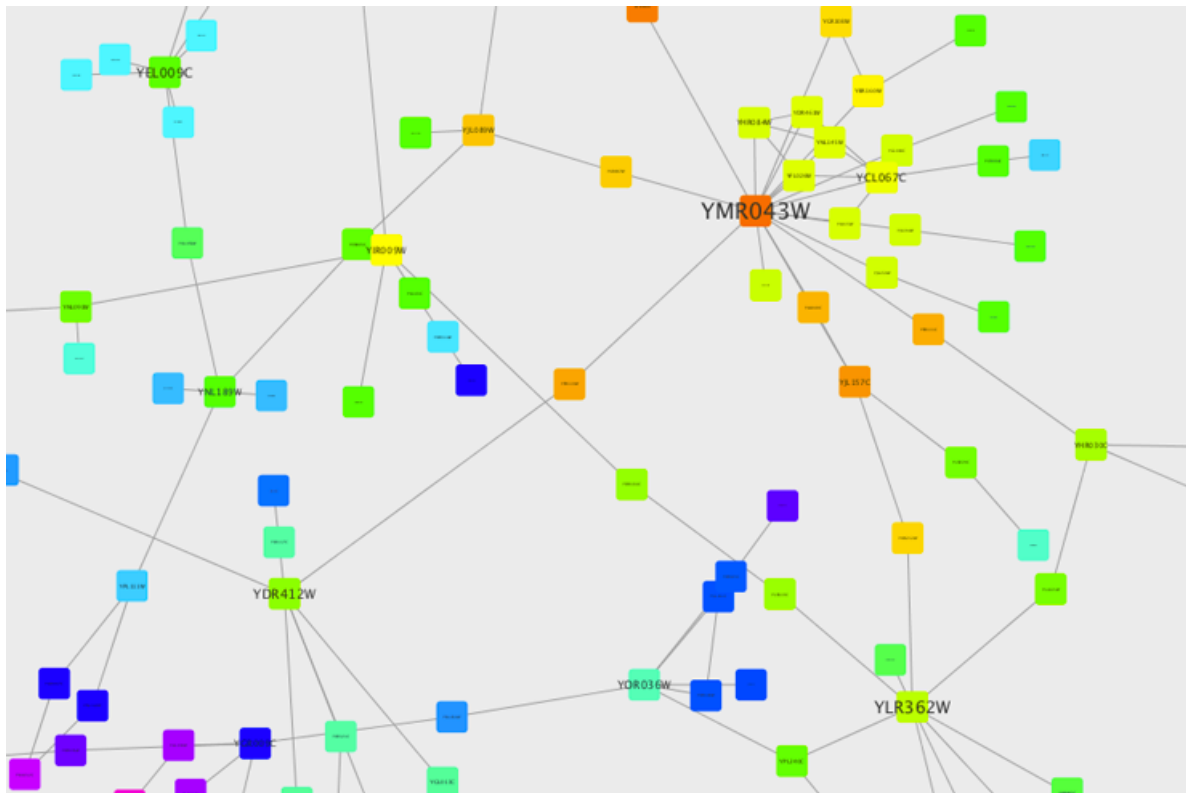
1. Switch the **Current Style** to **Minimal**. Now your network looks like the following:


















2. Create a discrete mapping for **Fill Color**. Select *AverageShortestPathLength* (generated by the **Network Analyzer**) as the controlling property.
3. Right-click the **Fill Color** cell, then select **Mapping Value Generators** → **Rainbow**. Cytoscape will automatically generate different colors for all the property values as shown below:



4. Create a discrete mapping for **Label Font Size**. Select *AverageShortestPathLength* as controlling property (**Column** field).
5. Right-click the **Label Font Size** cell, then select **Mapping Value Generators** → **Number Series**. Type 3 for the first value and click **OK**. Enter 3 for increment.
6. Apply **Layout** → **yFiles Organic Layout**. The final view is shown below:



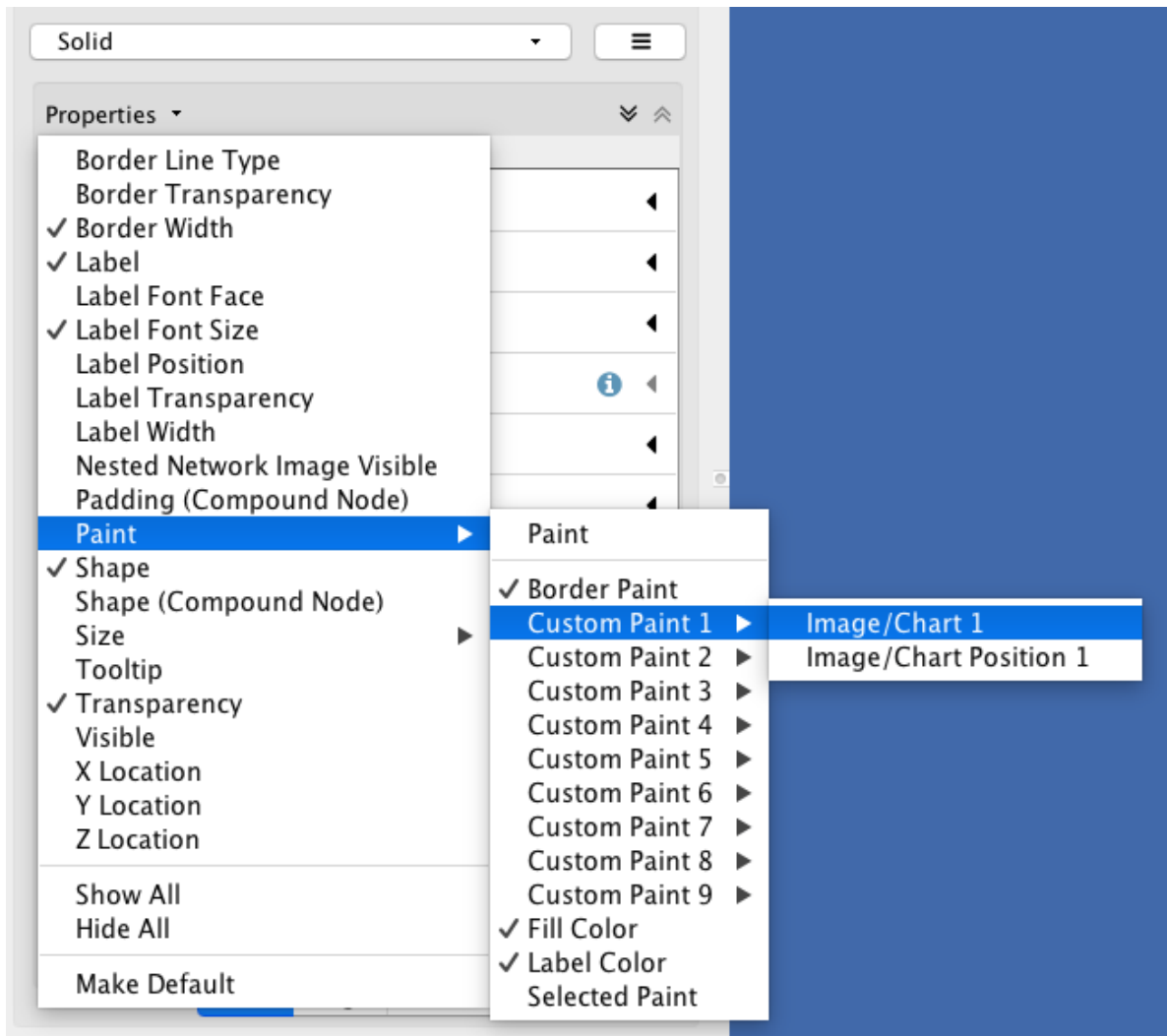
This mapping generator utility is useful for categorical data. The following example shows a discrete mapping that maps the species column to node color.

			Fill Color	▼
Column	Degree			
Mapping Type	Discrete Mapping			
1		R:255 G:128 B:0 - #FF80...		
2		R:255 G:255 B:0 - #FFFF...		
3		R:128 G:255 B:0 - #80FF...		
4		R:0 G:255 B:0 - #00FF00		
5		R:0 G:255 B:128 - #00FF...		
6		R:0 G:255 B:255 - #00FF...		
7		R:0 G:128 B:255 - #008...		
8		R:0 G:0 B:255 - #0000FF		
9		R:127 G:0 B:255 - #7F00...		
11		R:255 G:0 B:255 - #FF00...		
17		R:255 G:0 B:128 - #FF00...		
18		R:255 G:0 B:0 - #FF0000		

12.5.5 Tutorial 5: Using Images in Styles

This tutorial is a quick introduction to the node image feature. You can assign up to nine images per node as a part of a style.

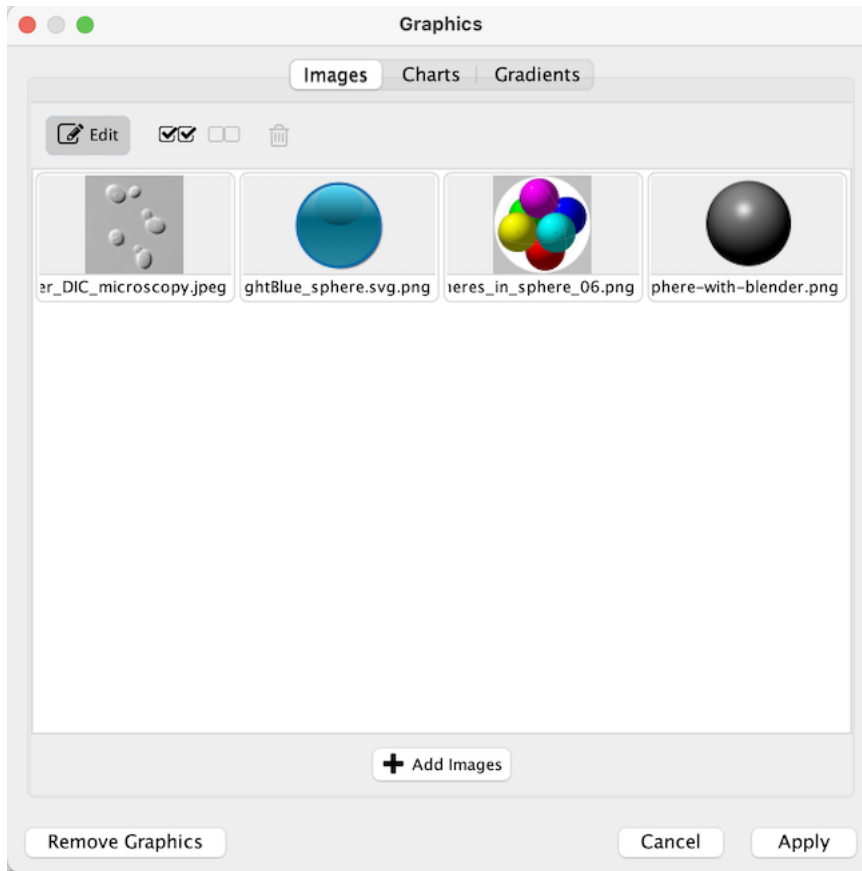
1. In this first example, we will use the presets that Cytoscape 3 has. In general, you can use any type of bitmap graphics. User images should be added to the **Image Manager** before using them in a style.
2. If you are continuing from the previous tutorials, skip to the next step. Otherwise, load a network and run the *Network Analyzer* (**Tools** → **Analyze Network...**). This creates several new table columns (statistics for nodes and edges).
3. Click the **Style** panel in the **Control Panel**, and select the **Solid** style.
4. If the property **Image/Chart 1** is not in the properties sheet yet, add it from the drop-down **Properties** → **Paint** → **Custom Paint 1** → **Image/Chart 1**.



5. Click the **Default Value** cell of the **Image/Chart 1** entry in order to open the **Graphics** dialog.

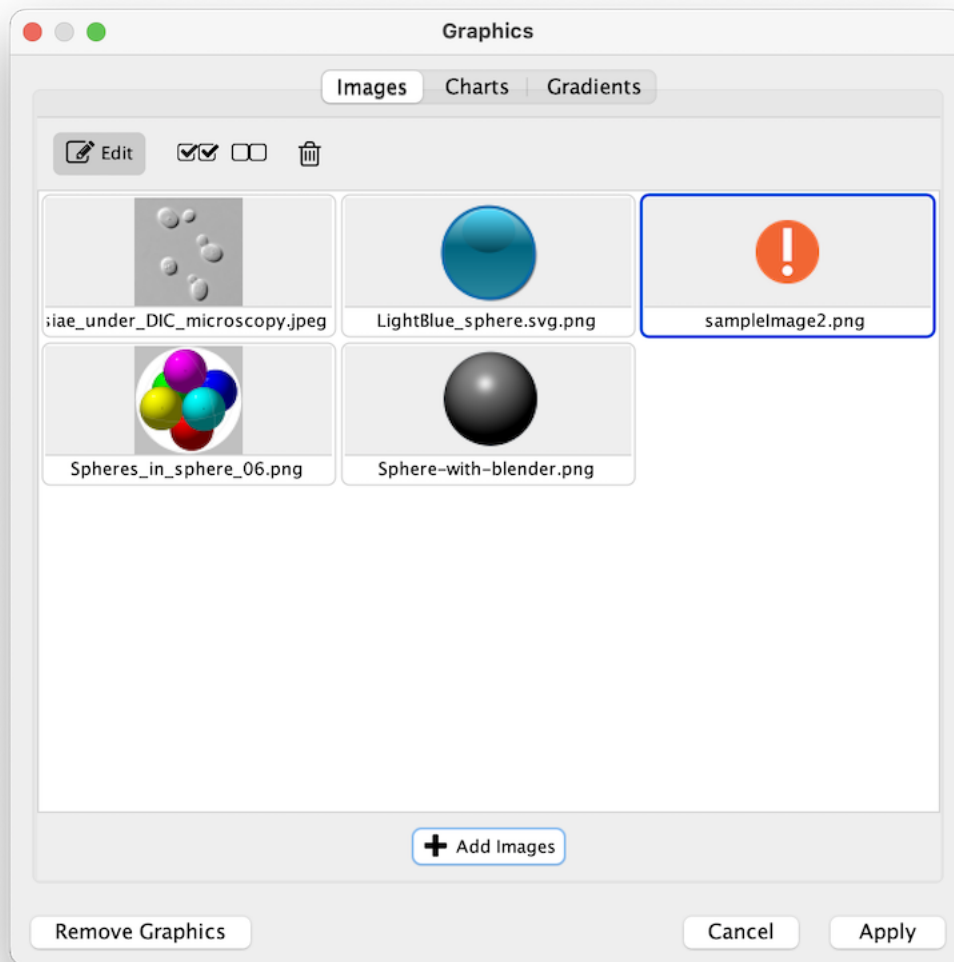


6. Select any of the images from the list and click **Apply**.

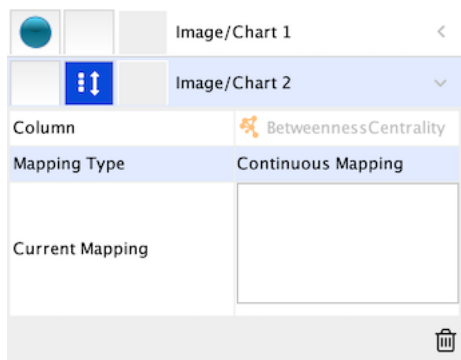


7. Click the **Default Value** cell of node **Transparency** and set the value to *zero*.
8. Set the **Default Value** of node **Size** to *80*.
9. Set the **Default Value** of node **Label Font Size** to *10*, to increase readability.
10. Also change the edge **Width** to *6*. Now your network looks like the following:

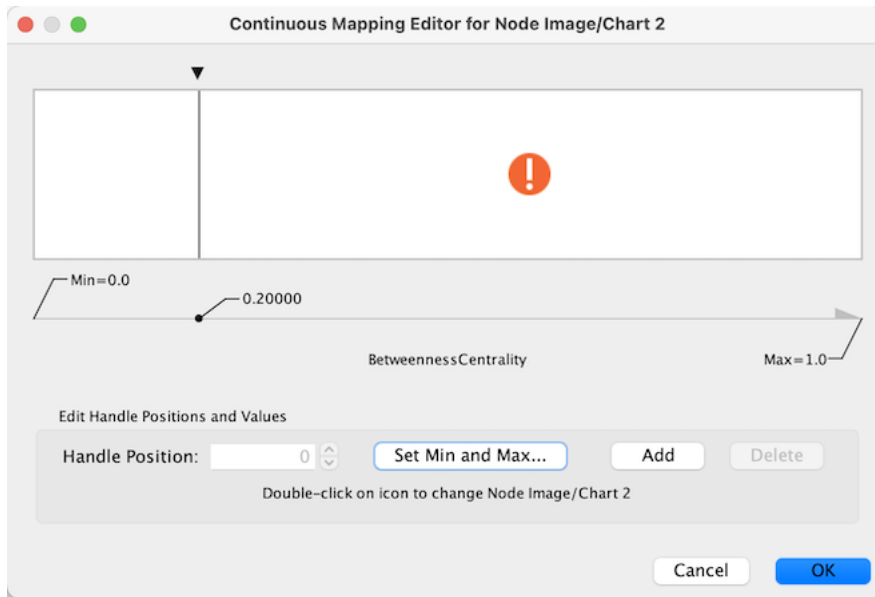




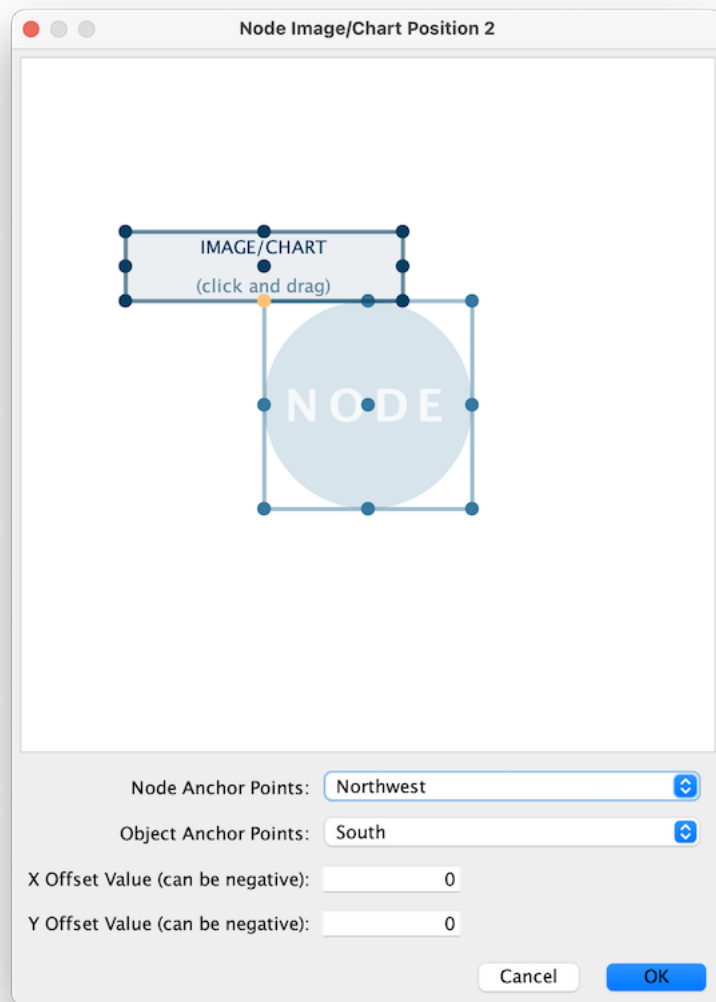
12. Create a Continuous Mapping for **Image/Chart 2** and select *BetweennessCentrality* as its controlling property. Double-click the **Current Mapping** value cell to open the **Continuous Mapping Editor**.



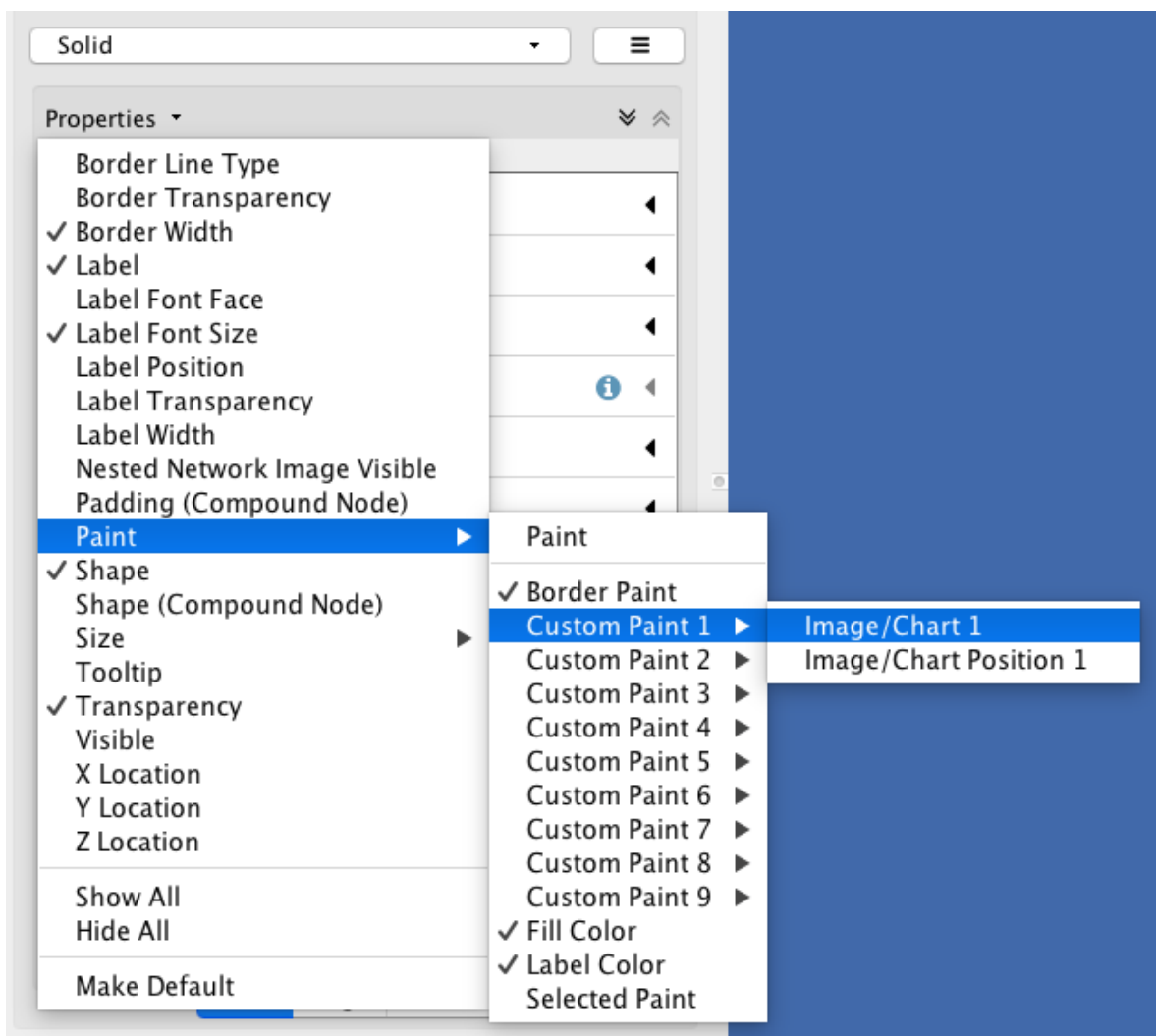
13. In the **Continuous Mapping Editor**, add a handle position by clicking in the **Add** button, and move the handle to 0.2. Double-click the region over **0.2** and set the new icon you have just added in the last step.



14. Add the property **Image/Chart Position 2** from the drop-down option **Properties** → **Paint** → **Custom Paint 2** → **Image/Chart Position 2**. Click its **Default Value** cell to move the position of the graphics to upper left.



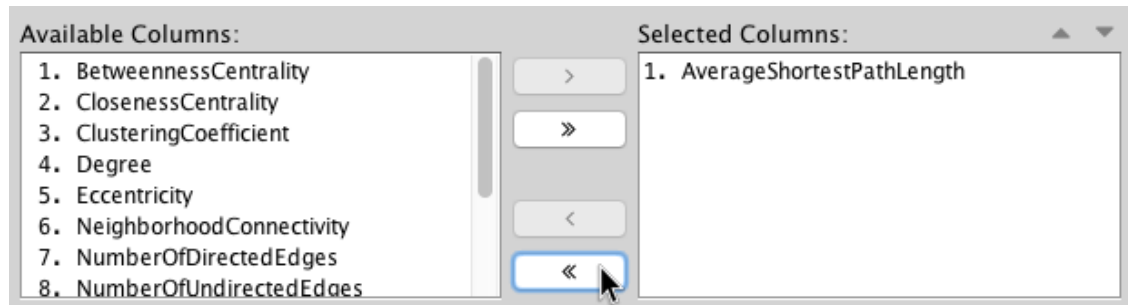
Now the important nodes in the network (nodes with high [betweenness centrality](#)) are annotated with the exclamation mark icon:



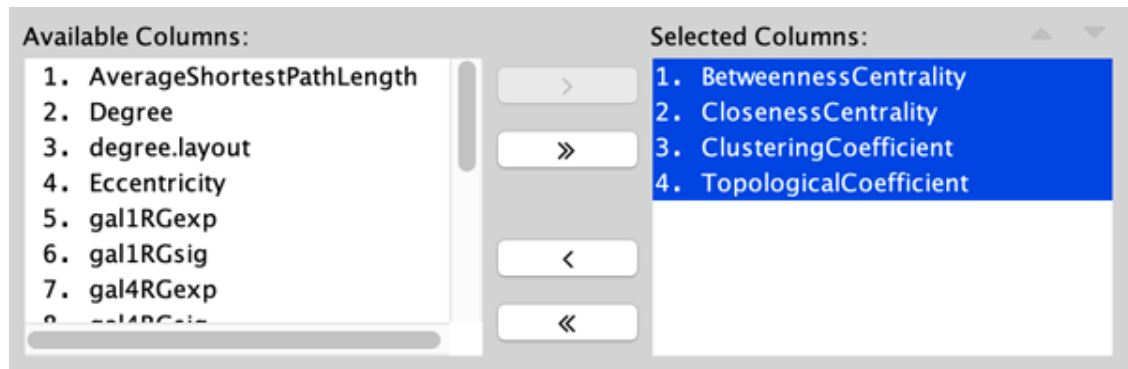
- Click the **Default Value** cell of the **Image/Chart 1** entry in order to open the **Graphics** dialog.



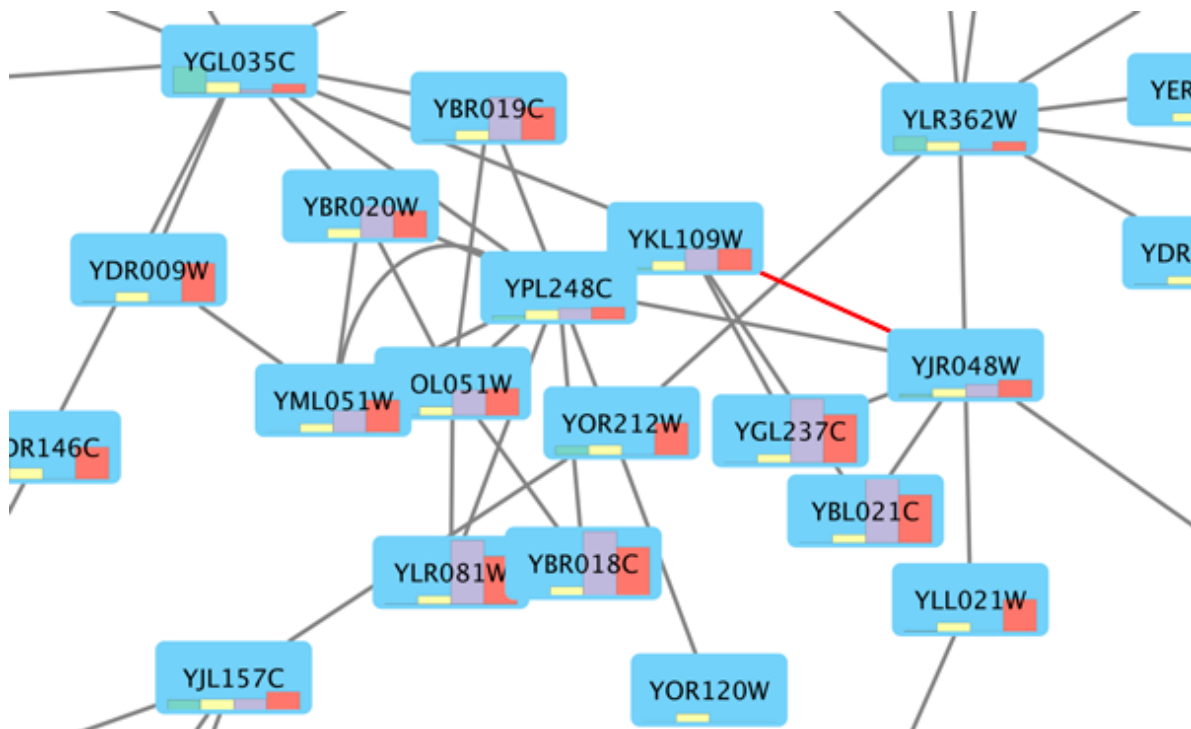
- Click the **Charts** tab and make sure the **Bar Chart** option is selected.
- Select data columns:** Now you have to choose the columns in the Node table that contains the data you want to be displayed as charts. The **Available Columns** list displays all node columns that can be used as chart data (i.e. single or list columns of numerical types).
 - First click the **Remove All** button to remove the current selected columns (by default, Cytoscape selects the first column in the **Available Columns** list).



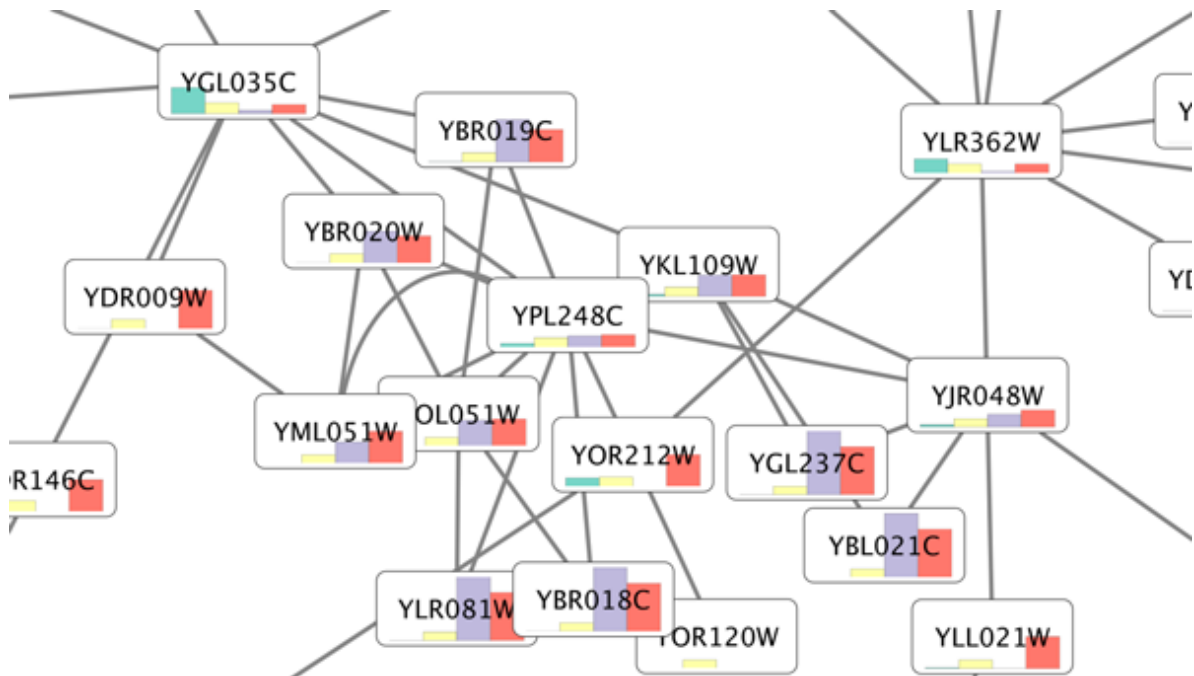
- Now select all *centrality* and *coefficient* columns from **Available Columns** list and click the **Add Selected** button.



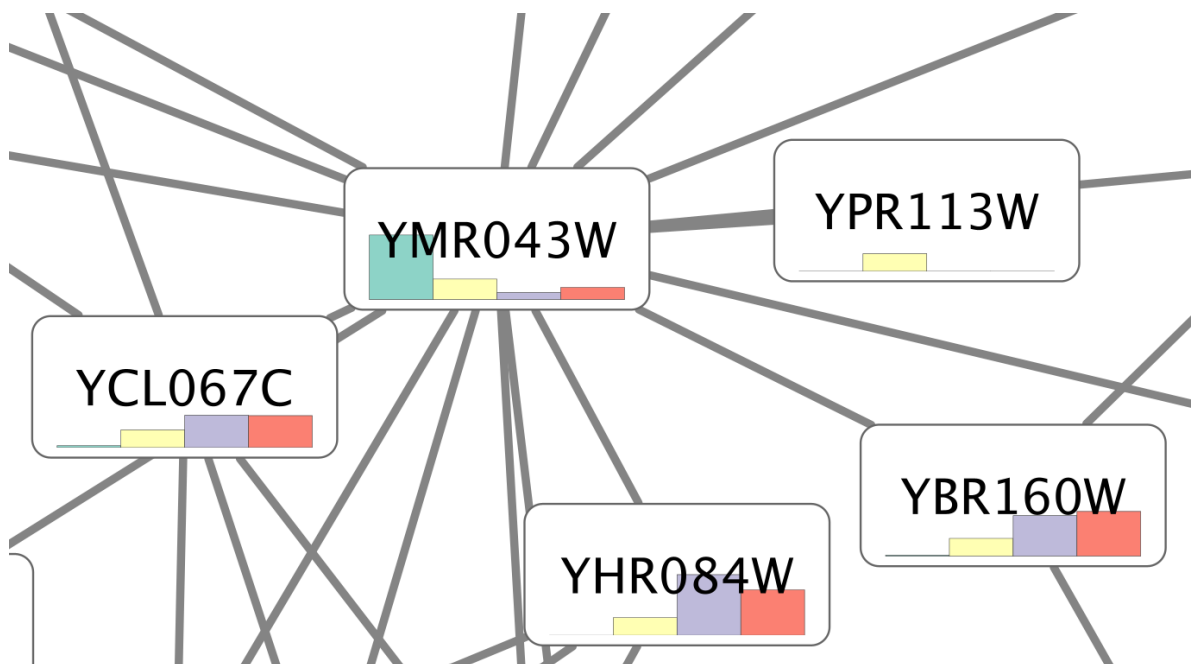
9. Click the **Apply** button to create bar charts with the selected data columns and default options.



10. The network view doesn't look so good yet, so let's make a few changes to its style before we continue. In the example shown below, the node **Shape** is set to *Rectangle*, the node **Fill Color** is set to *white*, the **Node Border** width is set to *1*, and the **Node Border Paint** is a dark grey.



11. Focus on one node to see the chart details. For example search for and then focus on node **YMR043W**.



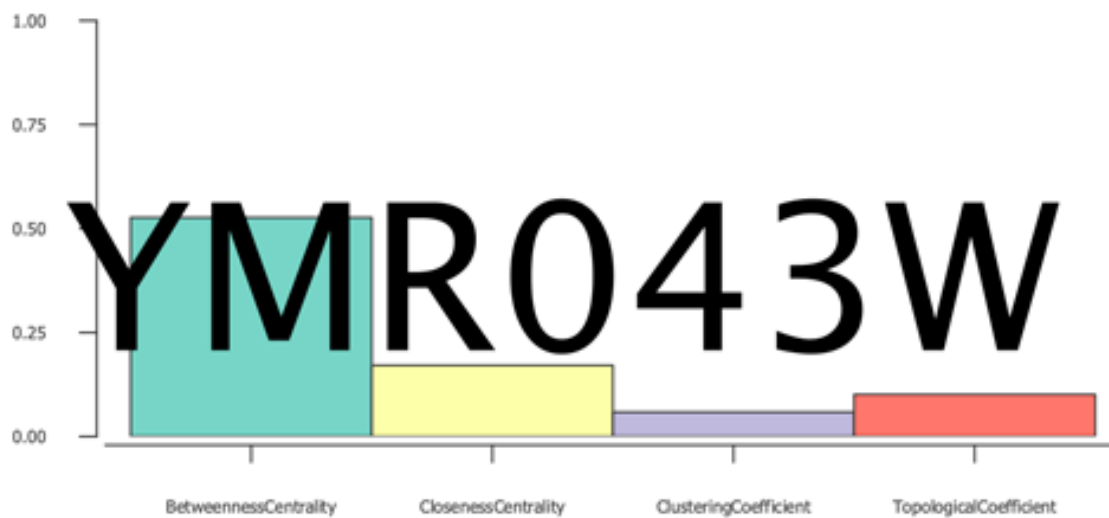
12. **Change other chart options:** Click the **Default Value** cell of the **Image/Chart 1** property again in order to open the **Graphics** dialog, and then expand the **Customize** option in the **Bar Chart** editor.



In this panel, you can:

- Choose another **Color Palette** or set all the colors individually (just click on each color).
- **Show/Hide Value** and **Domain Labels** and also set the **Domain Label Position**.
- Change the chart **Orientation**.
- Show/Hide Axes.
- Change the line width and color for axes and bars.
- Increase or reduce the separation between bars (up to 50% of the total chart width).
- **Note:** Other chart types provide different options.

13. Check both **Show Domain Axis** and **Show Range Axis** and apply the graphics again. Now the node chart should look like this:

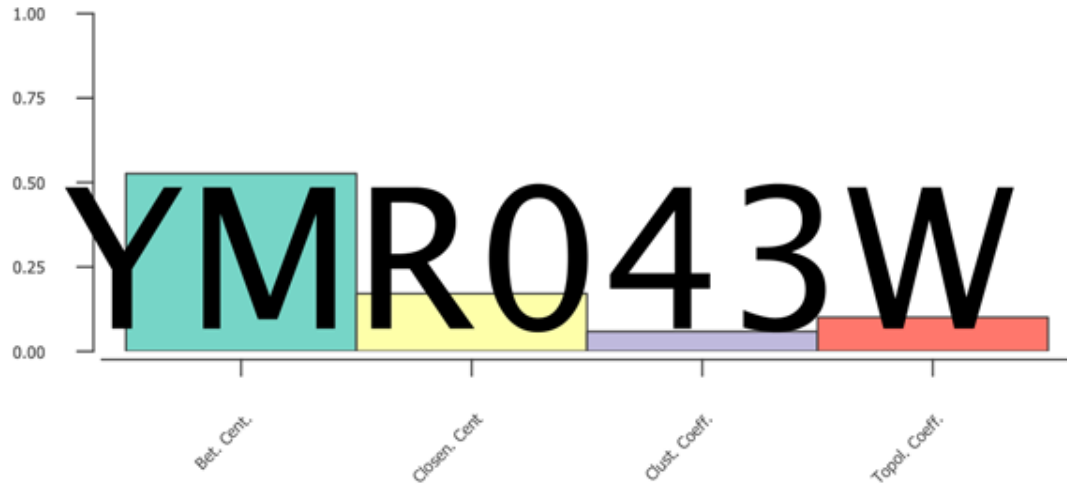


14. The default domain labels are not very useful, so let's set better labels:

- In the **Node Table**, create a new *List Column* of type *String* and name it *domain_labels*.
- Edit any of the cells of the created column (double-click it) and type ["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."].
- Right-click the same cell and select the option **Apply to entire column**.

y	NumberOfDirectedEdges	NumberOfUndirectedEdges	Radiality	TopologicalCoefficient	domain_labels
0	1	0	0.46774...	0.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
7	3	0	0.50462...	0.33333333	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	1	0	0.66666...	0.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	3	0	1.0	0.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	1	0	0.66666...	0.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	2	0	0.83333...	1.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	2	0	0.83333...	1.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	2	0	0.83333...	1.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]
0	1	0	0.66666...	0.0	["Bet. Cent.", "Closen. Cent.", "Clust. Coeff.", "Topol. Coeff."]

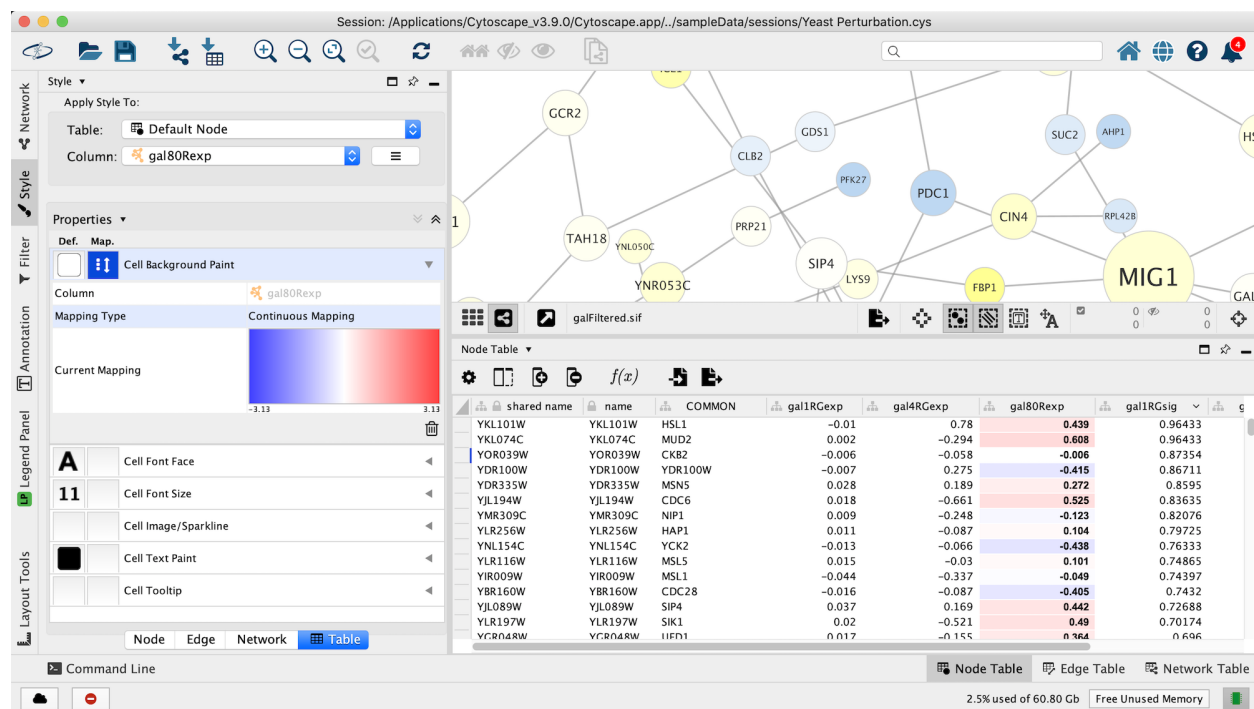
- Open the chart editor again and select the **Options** panel.
- Select *domain_labels* on the **Domain Labels Column** drop-down button.
- Select “Up 45°” on the **Domain Labels Position** drop-down button. The labels should look like this now:



12.5.7 Tutorial 7: Creating a Style for the columns of the Node Table

The goal of this tutorial is to set a style for columns in the **Node Table**. The **Column** tab of the **Style** interface offers default and mapping style options for a set of table cell attributes, for this tutorial we will use **Cell Background Paint** and **Cell Font Face**. There is no **Bypass** option for **Column** styles.

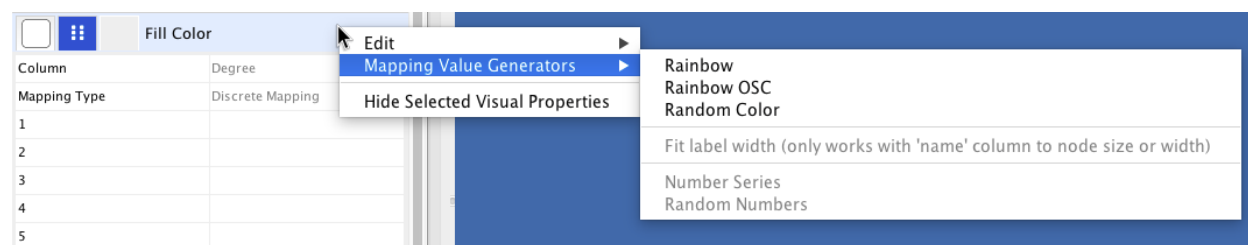
1. Open the **Yeast Perturbation** sample session from **View** → **Show Starter Panel**.
2. At the top of the **Column** tab of the **Style** panel, click the plus sign and select **Node** in the **Table** column.
3. Next, select the data column you want to add the style to under the **Column** drop-down, in this case the **gal80Rexp** column.
4. In the mapping column of **Cell Background Paint** select the **gal80Rexp** column and select a default red-blue continuous mapping. This will color the background of the cells in the corresponding column in the **Node Table**.
5. In the default column of **Cell Font Face**, select **Arial-BoldMT**.



12.6 Advanced Topics

12.6.1 Discrete Mappings
















Several utility functions are available for Discrete Mappings. You can use these functions by right-clicking on any property entry (shown below).



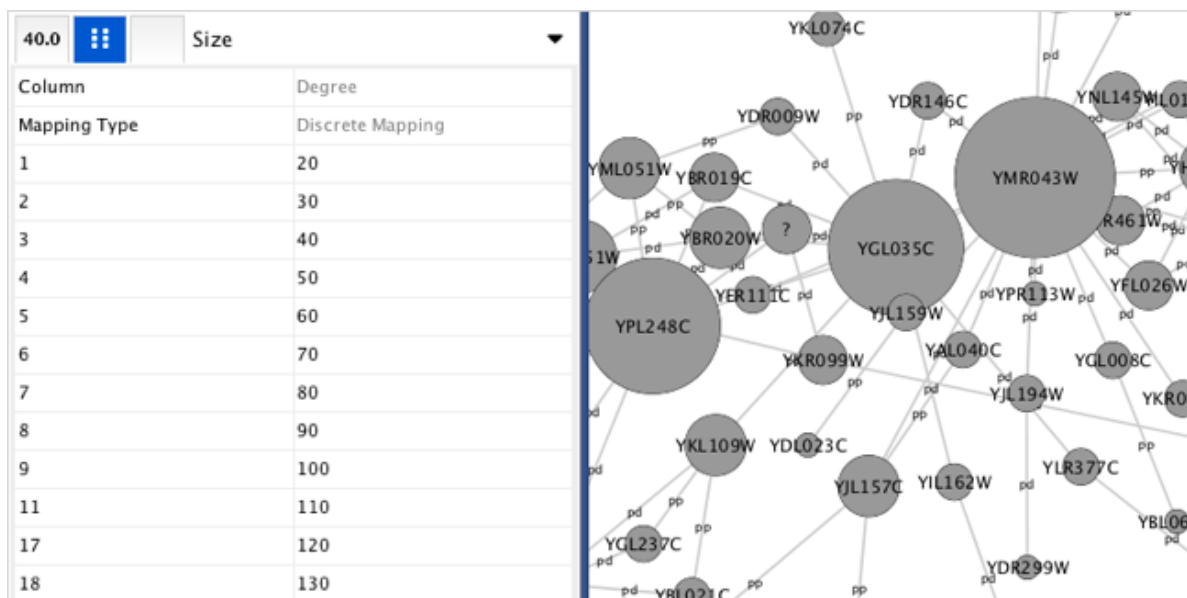
Automatic Value Generators

Mapping Value Generators: Functions in this menu category are value generators for discrete mappings. Users can set values for discrete mappings automatically by selecting these functions.

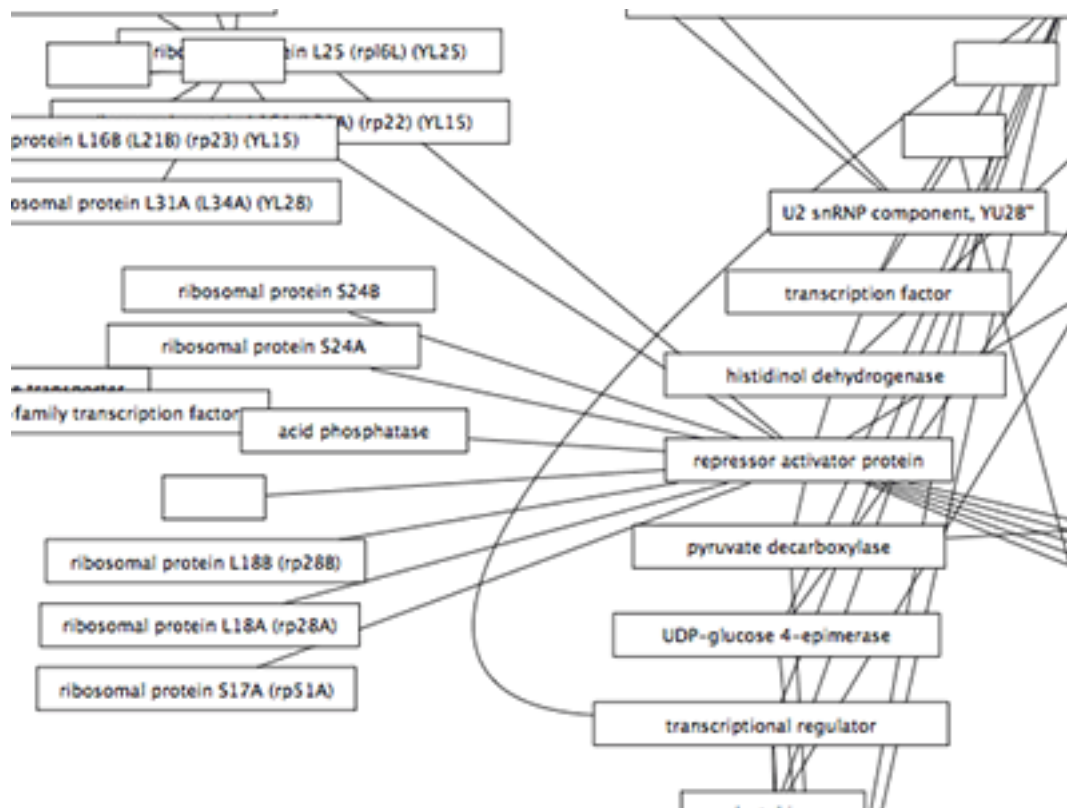
- **Rainbow** and **Rainbow OSC** - These functions try to assign as diverse a set of colors as possible for each data value.

			Fill Color	▼
Column	Degree			
Mapping Type	Discrete Mapping			
1	 R:255 G:128 B:0 - #FF80...			
2	 R:255 G:255 B:0 - #FFFF...			
3	 R:128 G:255 B:0 - #80FF...			
4	 R:0 G:255 B:0 - #00FF00			
5	 R:0 G:255 B:128 - #00FF...			
6	 R:0 G:255 B:255 - #00FF...			
7	 R:0 G:128 B:255 - #008...			
8	 R:0 G:0 B:255 - #0000FF			
9	 R:127 G:0 B:255 - #7F00...			
11	 R:255 G:0 B:255 - #FF00...			
17	 R:255 G:0 B:128 - #FF00...			
18	 R:255 G:0 B:0 - #FF0000			

- **Random Numbers and Random Colors** - Randomized numbers and colors.
- **Number Series** - Set a series of numbers to the specified mapping. Requires a starting number and increment.

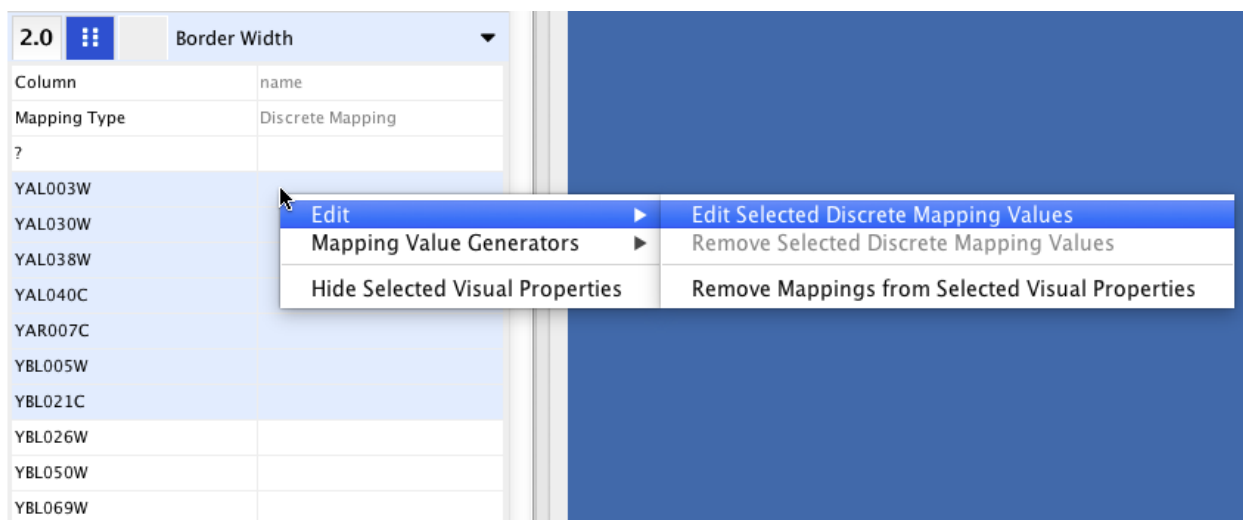


- **Fit label width** - This function is only for node **Width** and **Size**. When a discrete mapping for node **Width** or **Size** is available, you can fit the size of each node to its label automatically by selecting this function. See the example below:



Edit Selected Values at Once

You can set multiple values at once. First, you need to select discrete mapping rows in which you want to change values then right-click and select **Edit** → **Edit Selected Discrete Mapping Values**. A dialog pops up and you can enter the new value for the selected rows.



12.6.2 Working with Continuous Mapping Editors

There are three kinds of **Continuous Mapping Editors**. Each of them are associated with a specific property type:

Range Settings Panel



Each continuous mapping editor has a range settings section (labelled **Edit Handle Positions and Values**) with the following fields and buttons.

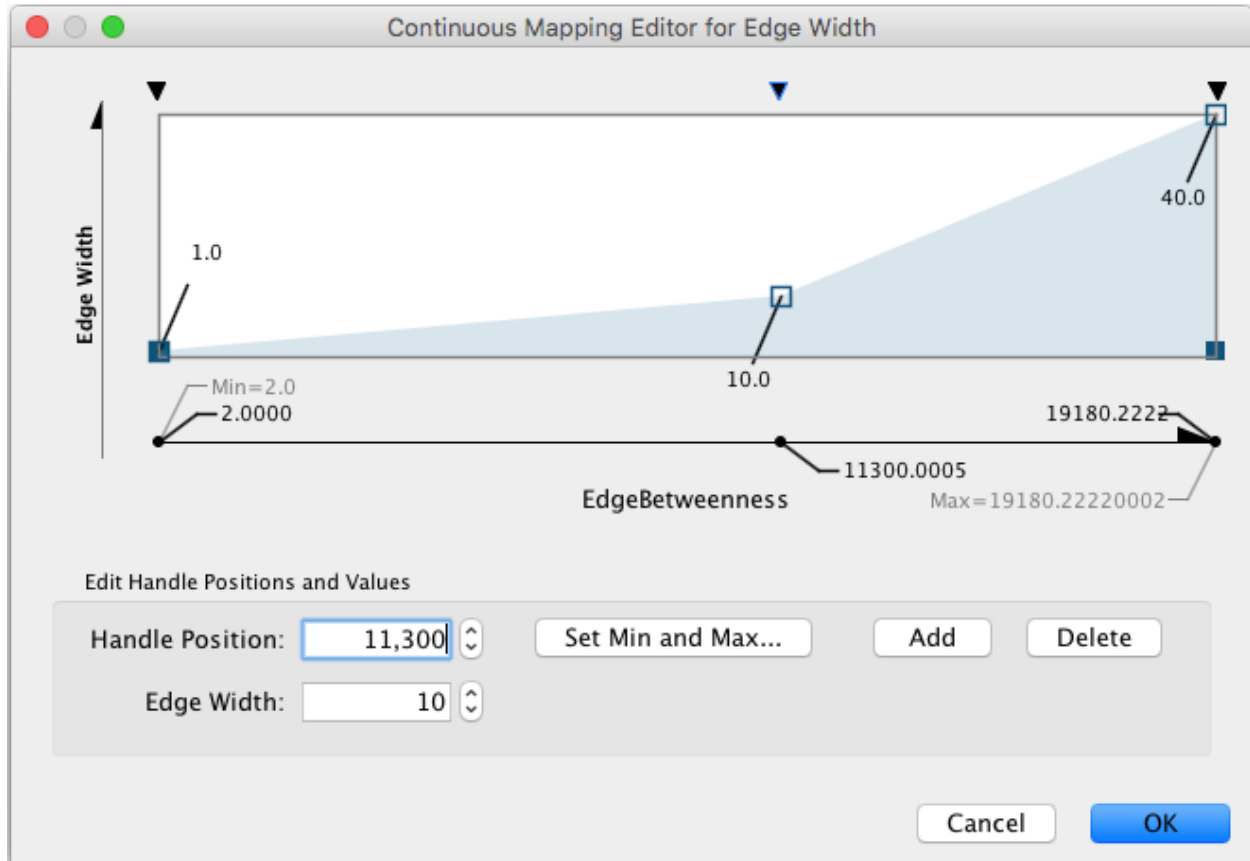
1. **Handle Position** - This box displays the current value for the selected slider handle. You can also directly type the value in this box to move the slider to an exact location.
2. **Set Min and Max...** - Click this button to set the overall range of this editor. The first time you open the editor, the *Min* and *Max* values are set by the range of the data column you selected (i.e. the minimum and maximum values of the mapped column). In the pop-up dialog you can manually enter the **Min** and **Max** values, or they can be set to the current minimum and maximum values of the data column by clicking the **Reset** button.
3. **Add** - Adds a new handle to the editor.
4. **Delete** - Deletes the selected handle from the slider widget.
5. *Handle Value* (e.g. **Node Fill Color**) - Click this button to edit the value (e.g. a color) assigned to the selected handle.

Gradient Editor



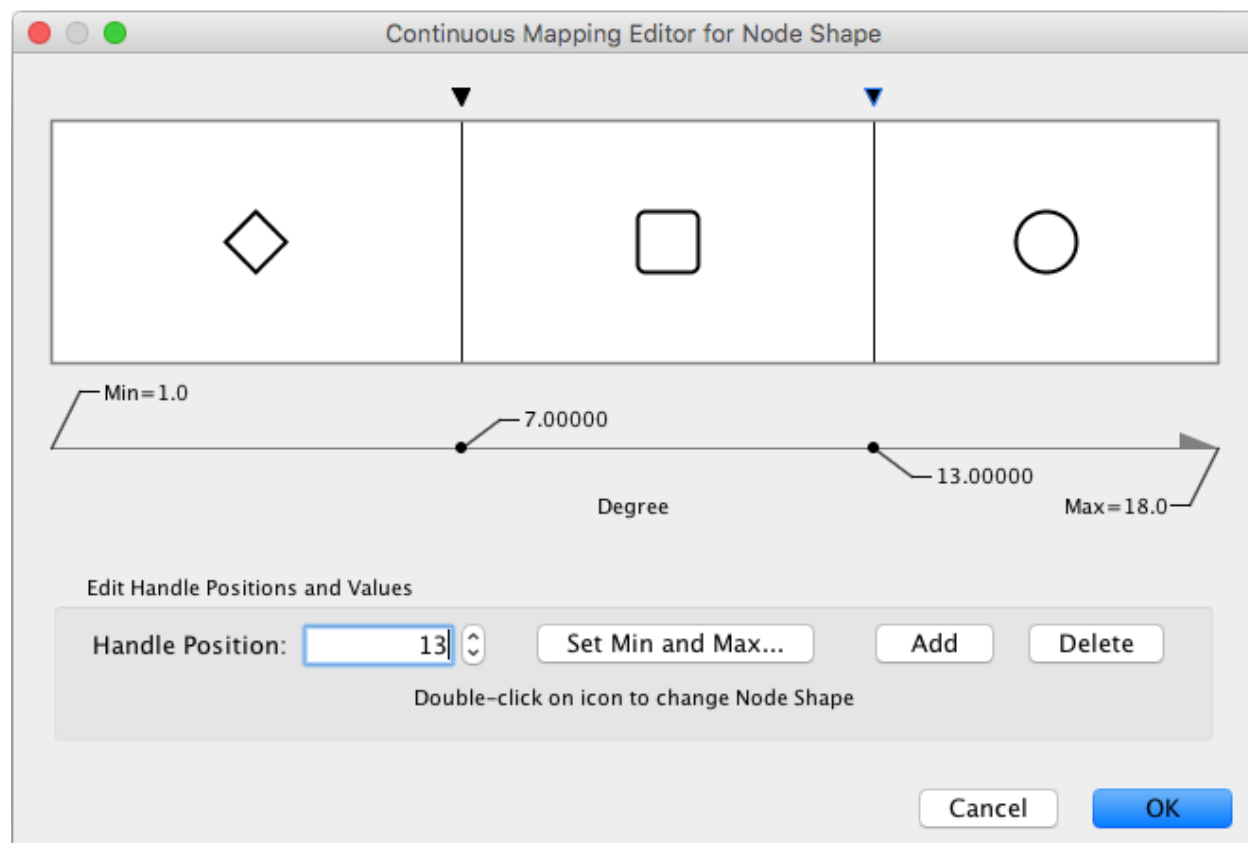
The **Gradient Editor** is an editor for creating continuous mappings for colors. The default palette depends on the range of values in the column used for mapping. To change the palette, click the **Current Palette** button and select a palette. This dialog also includes options to **show only colorblind-friendly** and **reverse colors**, for reversing the colors of the palette. To change the color manually, double-click the handles (small triangles on the top), and choose a single color from any palette. A color gradient will be created only when the editor has two or more handles (see the example below).

Continuous-Continuous Editor



The **Continuous-Continuous Editor** is for creating mappings between numerical data and numerical properties (e.g. size, transparency). To change the value assigned on the Y-axis (the property shown in the example above is edge **Width**), drag the small squares or double-click them to directly type an exact value.

Continuous-Discrete Editor



The **Continuous-Discrete Editor** is used to create mappings from numerical column values to discrete properties, such as fonts, shapes, or line styles. To edit a value for a specific region, double-click the icon on the track.

12.6.3 Enhanced Graphics

Enhanced Graphics provides support for a set of visual style passthrough mappings for use with **Node Custom Graphics**. These mappings are all of the form:

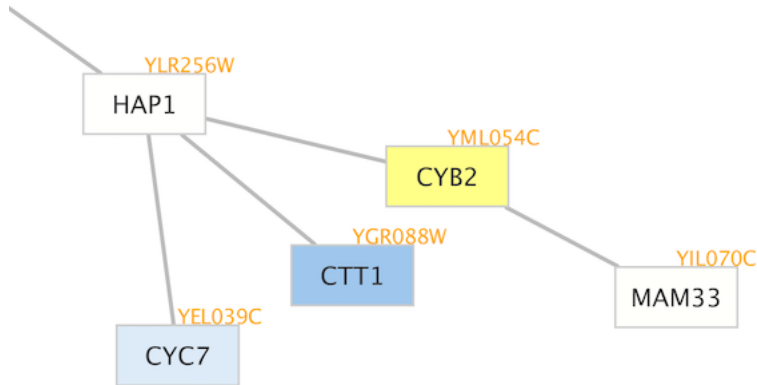
```
type: argument1="val1" argument2="val2"
```

where type is the type of chart or gradient and the arguments are the instructions for constructing that chart or graphic.

To use **Enhanced Graphics**, first add the desired mapping to a new column in the **Node Table**. Then, create a **Style** for one of the **Custom Paint** properties using the new column in a **Passthrough Mapping**. This will add your custom defined chart or graphic to the nodes.

An example of using **Enhanced Graphics** to add a second label to nodes is shown below. In this case, the yeast ORF ID is added as a secondary node label, and offset to the upper right of the node. For the full list of supported graphics types can be found here. The mapping for this is as follows:

```
label: attribute=name labelsize=10 outline=false background=false color=orange
```



label

This chart type provides a mechanism to add text labels to nodes that have more display options than the simple labels provided by Cytoscape visual properties. Arguments:

- **color**: Specify the color of the label
- **attribute**: The attribute to get the label from.
- **background**: A boolean option that causes a translucent background to be painted behind the label and on top of the network.
- **bgcolor**: The color of the background.
- **dropShadow**: Add a drop shadow behind the label.
- **label**: The label to paint.
- **labelfont**: The font family to use for the labels
- **labelsize**: The font size to use for the labels
- **labelstyle**: The font style to use for the labels
- **outline**: Outline the font.
- **outlineColor**: The color of the outline.

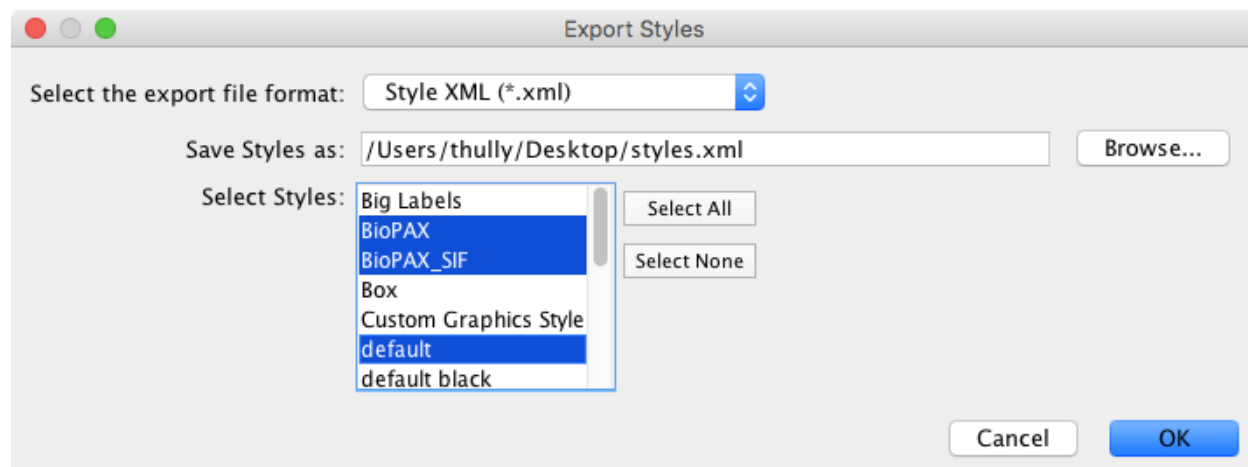
For a more detailed description of the workflow for adding **Enhanced Graphics**, refer to the tutorial.

12.7 Managing Styles

All Cytoscape style settings are initially loaded from a default file that cannot be altered by users. When users make changes to the properties, a `session_syle.xml` file is saved in the session file. This means that if you save your session, you will not lose your properties. No other style files are saved during normal operation.

12.7.1 Saving Styles

Styles are automatically saved with the session they were created in. Before Cytoscape exits, you will be prompted to make sure you save the session before quitting. It is also possible to save your styles in a file separate from the session file. To do this, navigate to the menu option **File** → **Export** → **Styles to File...**, and save the selected styles to a file. This feature can be used to share styles with other users.



You can also change the default list of styles for all future sessions of Cytoscape. To do this, click the **Options**



drop-down in the **Style** section, and select **Make Current Styles Default**. This will save the current styles as a `default_vizmap.xml` file to your `CytoscapeConfiguration` directory (found in your home directory). These styles will then be loaded each time Cytoscape is started.

Style File Formats

The Cytoscape-native style format is **Style XML**. If you want to share style files with other Cytoscape users, you need to export them to this format.

From version 3.1.0 on, Cytoscape can also export [Cytoscape.js](#) compatible JSON file. Since Cytoscape.js is an independent JavaScript library, and there are some differences between Cytoscape and Cytoscape.js, not all properties are mapped to JSON. The following properties are not supported by the exporter:

- Custom Graphics and their locations
- Edge Bends
- Nested Networks
- Network Background (Note: This can be set manually as standard CSS in Cytoscape.js)

The **Continuous-Discrete Editor** is used to create mappings from numerical data values to discrete properties, such as fonts, shapes, or line styles. To edit a value for a specific region, double-click on the icon on the track.

12.7.2 Importing Styles

To import existing styles, navigate to the menu option **File** → **Import** → **Styles from File...** and select a `styles.xml` (Cytoscape 3 format) file. Imported properties will supplement existing properties or override existing ones if the properties have the same name. You can also specify a style file using the `-V` command line option. Properties loaded from the command line will override any default properties. Note that legacy menu, but not by command line.

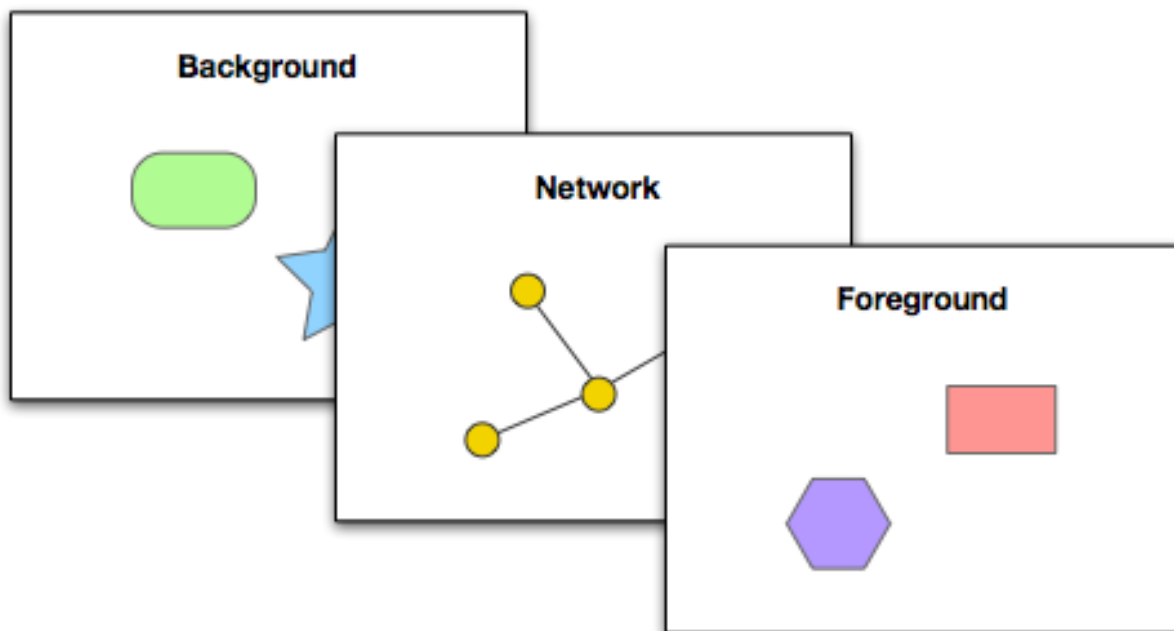
Network Annotations

Annotations in the form of shapes, images or text can be added to the network canvas.

The network canvas is made up of three transparent layers:

- **Foreground Layer**
- **Network Layer**
- **Background Layer**

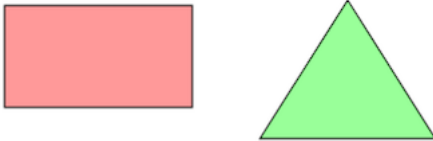
The middle **Network Layer** contains nodes, edges and charts. The **Foreground** and **Background** layers contain annotations.



13.1 Types of Annotations

There are five types of annotations available:

1. Images (loaded from image files)
2. Shapes (rectangles, triangles, etc. . .)



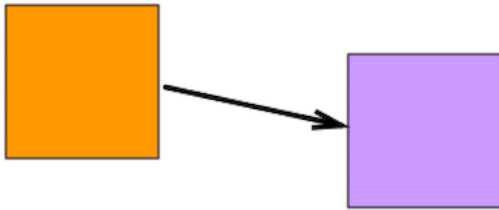
3. Text

My Text Annotation

4. Bounded Text (combines text with a surrounding shape)

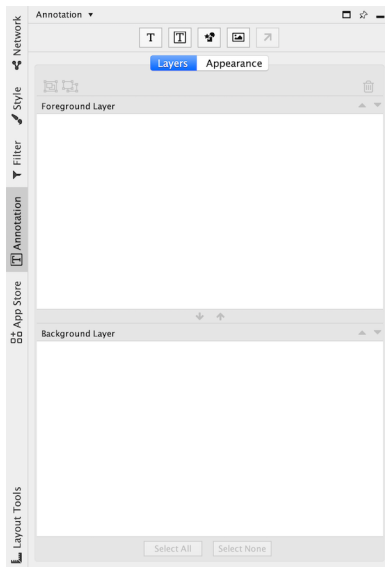


5. Arrows (connects other annotations or nodes)



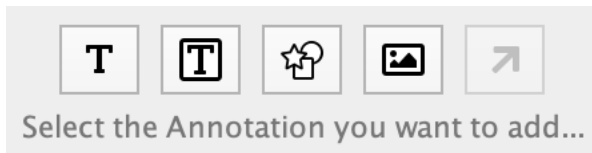
13.2 The Annotation Panel

The **Annotation** panel shows the annotations that are currently present on the foreground and background layers. The panel allows you to create and delete annotations, select annotations, move annotations up and down, move annotations between layers, and group annotations.

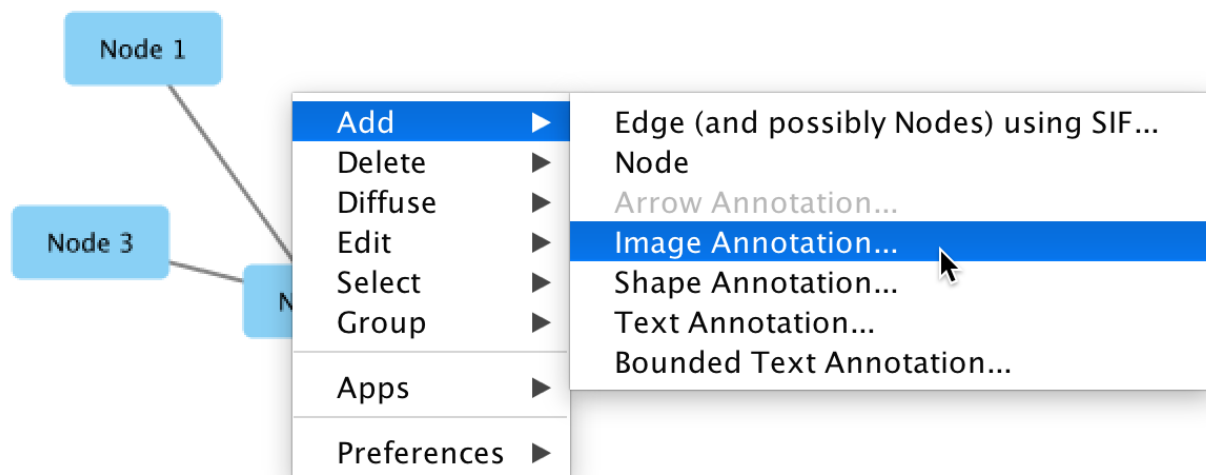


13.3 Creating Annotations

At the top of the **Annotation** panel there are five buttons for creating each type of annotation. Start by clicking the button for the type of annotation you would like to add.



Alternatively, right click on the network canvas and select the annotation type under the **Add** menu.



13.3.1 Shape, Bounded Text, Image, Text

1. Click the button for shape, bounded text or image annotation. For image annotations, a file chooser will appear where you can select an image file.

2. Click the general location on the network canvas where the annotation should be placed. The annotation will appear on the canvas.
3. The annotation properties can be edited in the **Appearance** tab in the **Annotations** panel. The properties can be edited again after the annotation is created by selecting the annotation.
4. To resize the annotation, click on one of the resize handles and move the mouse cursor to resize the annotation. The annotation can be resized again later.
5. Click the mouse again to stop resizing.


13.3.2 Arrow

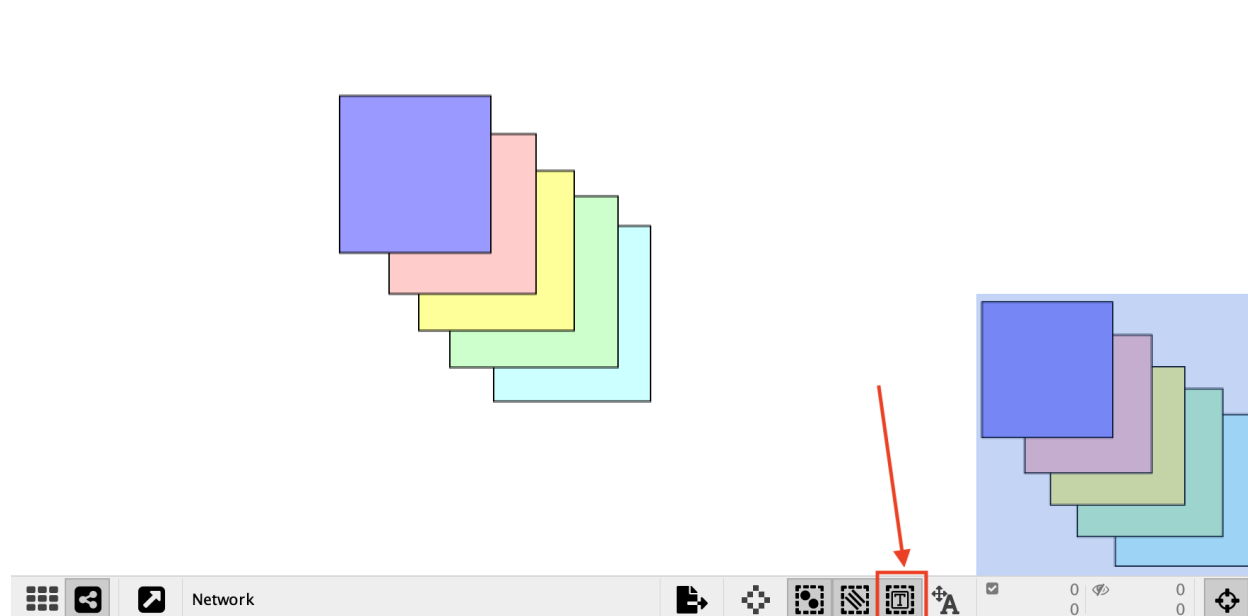
Creating an arrow annotation requires there to be at least one other annotation on the network canvas.

1. Click the button for arrow annotation.
2. Click on an existing annotation on the canvas; this will be the source annotation.
3. Click on another annotation on the canvas or a node; this will be the destination.
4. An arrow annotation appears connecting the source and destination.
5. The arrow properties can be edited in the **Appearance** tab in the **Annotations** panel to select start and end arrow head, color etc.

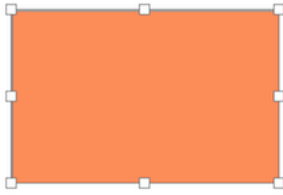
13.4 Selecting Annotations

One or more annotations can be selected in the **Annotations** panel by clicking on them.

To be able to select annotations in the network canvas **Toggle Annotation Selection** must be enabled. Toggle the  button at the bottom of the network view to enable/disable annotation selection mode.

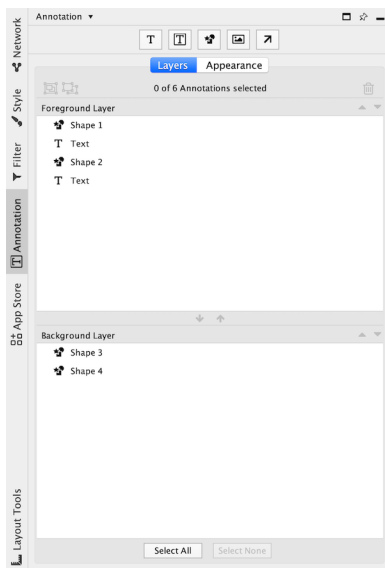


When an annotation is selected, 8 resize handles are visible. The annotation can be moved by clicking on it with the mouse and dragging. The annotation can be resized by clicking and dragging one of the handles.







It is possible to select multiple annotations at the same time. Hold **Ctrl** on Windows, or **Command** on Mac, while clicking on each of the annotations you would like to select. This works both in the **Annotations** panel and on the network canvas. When multiple annotations are selected they can be moved and resized at the same time.

13.5 Moving Annotations Backwards and Forwards



The **Annotation** panel displays a list of annotations on the foreground layer and a list of annotations on the background layer.

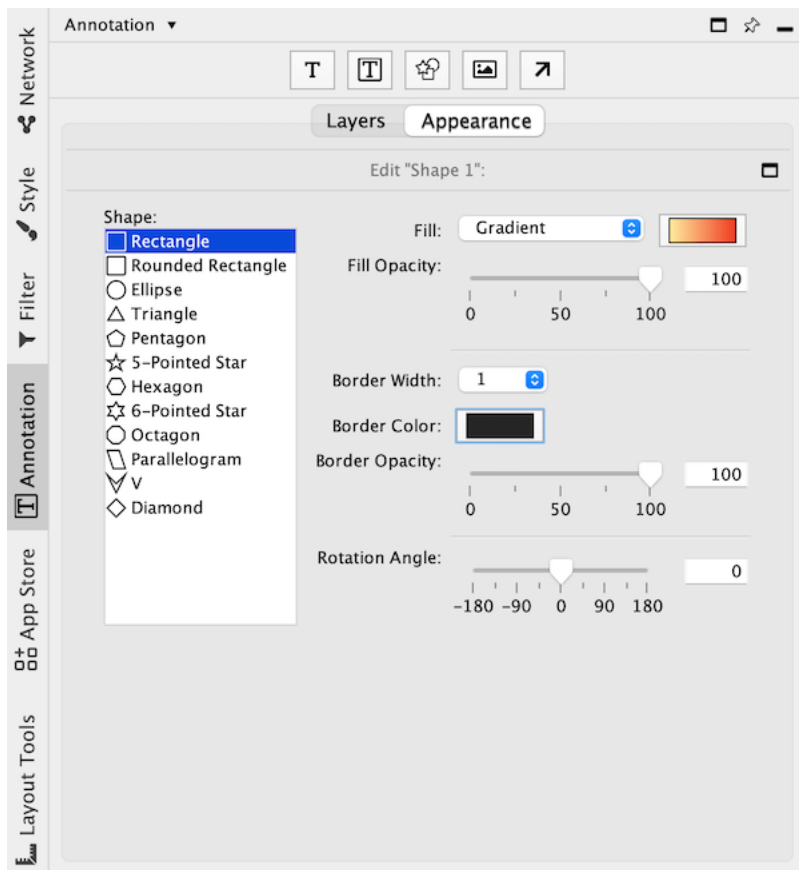
Annotations that are towards the top of a list are drawn above annotations lower in the list. To move an annotation within a layer select it and click the  button to move it forward or the  button to move it backward. To move an annotation between layers select it and click the  to move it to the foreground layer or the  button to move it to the background layer.

13.6 Renaming Annotations

Each annotation has a name that is displayed in the **Annotation** Panel. These names are primarily for organizational purposes and do not affect how the annotation is displayed on the canvas. To rename an annotation double-click the annotation in the **Annotation** panel and enter the new name.

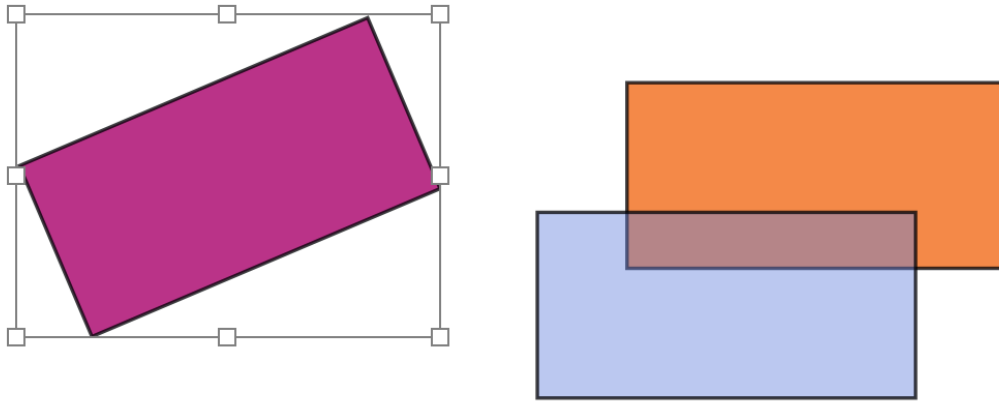
13.7 Editing Annotations

To modify the properties of an annotation (eg, color, text) select the annotation in the **Annotation** panel or in the network, then click the **Appearance** tab. Alternatively, right-click on the annotation in the network and select **Modify Annotation...**




The annotation can now be resized in the network view window. Other aspects of the annotation, like color, font, shape, opacity and rotation, can be edited in the **Appearance** tab.

The below example describes annotations with edited rotation and opacity.

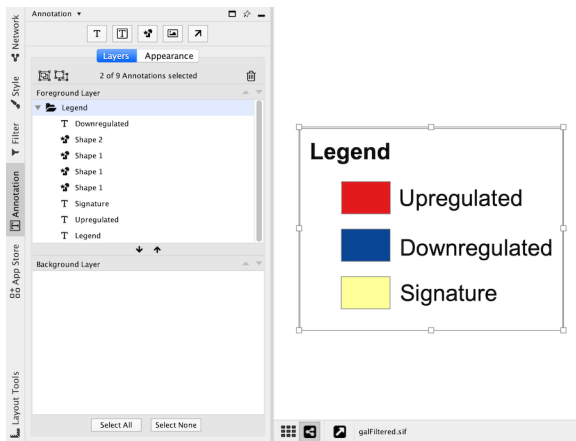




13.8 Deleting Annotations

To delete annotations, select one or more annotations in the **Annotation** panel and click the  button, or select the annotation in the network and click **delete** on the keyboard or right-click an annotation and select **Edit** → **Cut**.

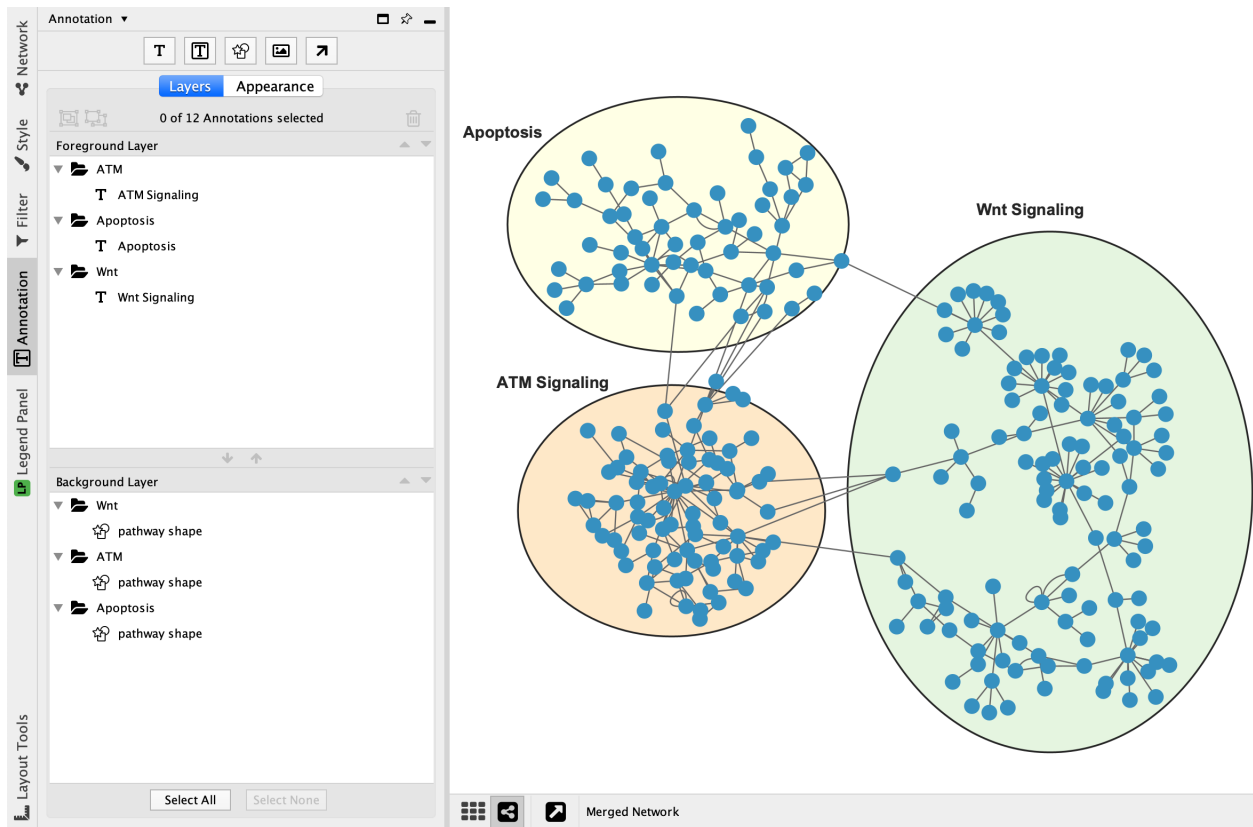
13.9 Grouping Annotations

Two or more annotations can be combined into a group. When grouped the annotations move and resize as if they were a single annotation. Groups may be nested (a group may contain other groups).



To create a group select two or more annotations and click the  button. The group will be given a default name that can be changed after the group is created. To un-group annotations select the group and click the  button.

A group may contain annotations from the foreground and background canvases. The group will show up in both the foreground and background layers in the annotations panel.



Note: Deleting a group will delete all the annotations contained within the group.

CHAPTER 14

Command Panel

The **Command Panel** provides a simple command-line interface to Cytoscape using the **Commands API**. It allows the user to type commands into Cytoscape and see the results in a **Reply Log**.

Any app that registers commands will be available through the **Command Panel**. Commands are part of the more general **Cytoscape Automation** feature, which includes multiple ways of scripting Cytoscape execution.

The **Command Panel** can be opened from **View → Show Command Panel**.



The **Command Panel** can also be used to read and execute script files. Each line in the script file is a command that is sent to an app. Script files may be entered on the Cytoscape command line using the `-S` flag to Cytoscape, or through **Tools → Execute Command File** menu item.

Cytoscape commands consist of three parts: a command class, or namespace; a command within that namespace; and a series of arguments or options provided as a series of **name=value** pairs. For example, to import an XGMML format file from the **Command Line Dialog** or a command script, you would use:

```
network import file filePath="path-to-file"
```

where **network** is the namespace, **import file** is the command, and there is only one argument: `filePath="path-to-file"`. If there were more arguments they would appear on the same line separated by spaces.

The **Command Panel** also uses the Command API to provide help. **help** by itself will list all of the command classes (or namespaces) and **help** followed by a namespace will list all of the commands supported by that namespace. Details of a specific command are available by typing **help** followed by the namespace and command (e.g. **help layout force-directed**). The **Command Panel** registers the **command** namespace and supports a single command: **run**, which takes a file argument. Here is the help for the command **run** command from the command namespace:

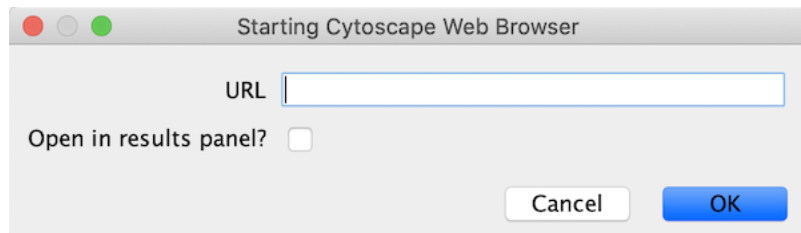
```
help command run
      command run file=<File>
```


Similarly, the help for the **network import file** example from above is:

```
help network import file
network import file arguments:
dataTypeList=<String>: List of column data types ordered by column index
  (e.g. "string,int,long,double,boolean,intlist" or just "s,i,l,d,b,il")
defaultInteraction=<String>: Default interaction type
delimiters=<ListMultipleSelection [,,; ,\t]>: Text Delimiters
delimitersForDataList=<ListSingleSelection (\\|\\|/|,)>:
  Text Delimiters for data list type
file=<File>: Data Table file
firstRowAsColumnNames=true|false: First row used for column names
indexColumnSourceInteraction=<int>: Column for source interaction
indexColumnTargetInteraction=<int>: Column for target interaction
indexColumnTypeInteraction=<int>: Column for interaction type
NetworkViewRendererList=<ListSingleSelection ()>: Network View Renderer
RootNetworkList=<ListSingleSelection (-- Create new network collection
  --|Network)>: Network Collection
startLoadRow=<int>: Start Load Row
TargetColumnList=<ListSingleSelection ()>: Node Identifier Mapping Column
```

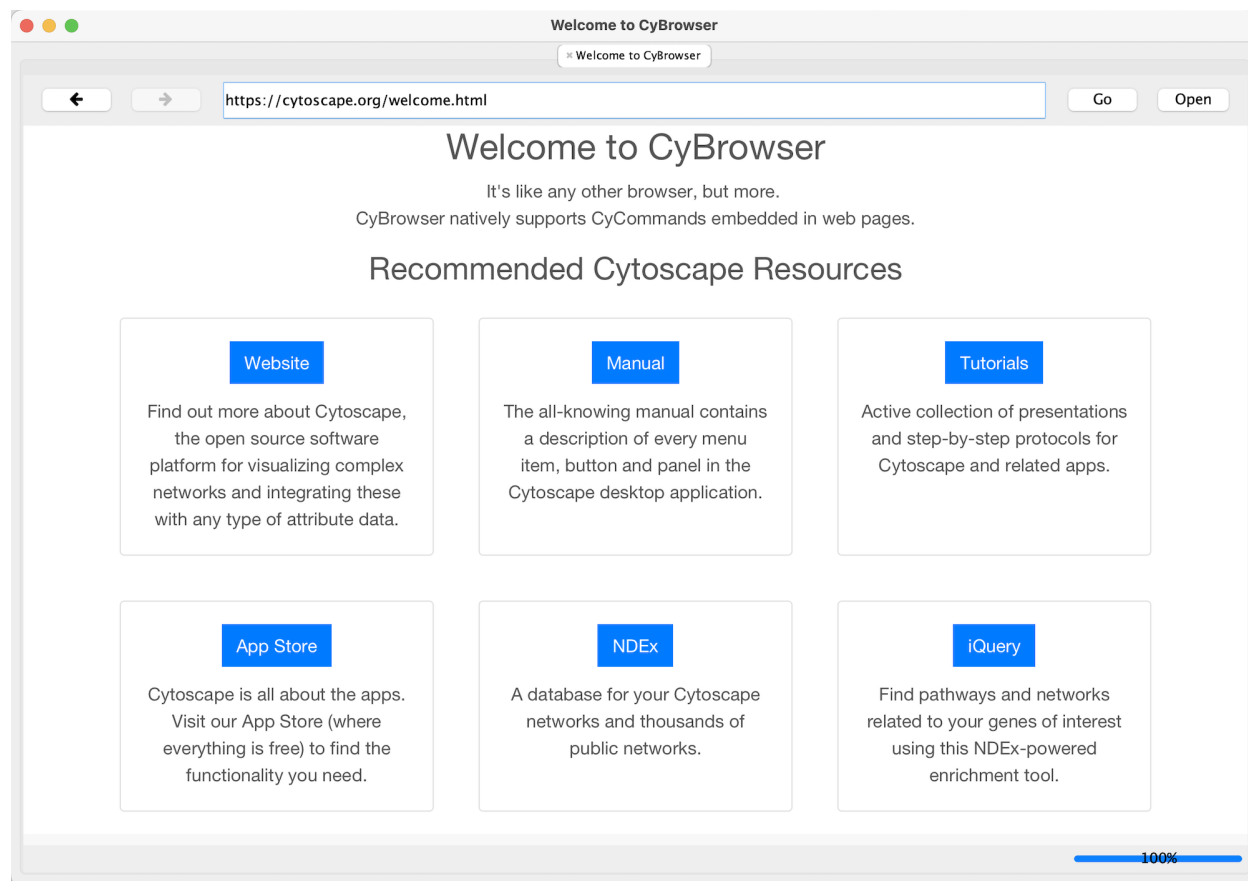
Cytoscape Web Browser

Cytoscape includes a simple web browser that can be used for viewing web sites from within Cytoscape. It is also used by Cytoscape apps, link outs, displaying the user manual, and displaying interactive tutorials. You can bring up a browser window by selecting **Tools** → **Open web page**, which will bring up the initial **Starting Cytoscape Web Browser** dialog. It provides a field to type in a web site address and a checkbox to indicate whether the browser window should be opened in the Cytoscape Results Panel.



You can also access the web browser by clicking on the **Cytoscape Web Browser**  icon in the tool bar, which will bring up the main **Cytoscape Web Browser** with a landing page (see screenshot below) with links to various resources like this manual, tutorials, the Cytoscape website and more.

15.1 Cytoscape Web Browser Window



The main **Cytoscape Web Browser** window provides a rudimentary browsing interface, with forward/back buttons, a text field to enter a new URL, and a **Go** button to move to the new page. In addition, there three context menus:

1. **Selected text:** The selected text menu has just one item, **Copy**, which copies the selected text.
2. **Link:** Using the link menu, users can copy the link location, open the link in a new window or the computer's native browser, or open the link in a new tab. They can also use this to download the link target to a file.

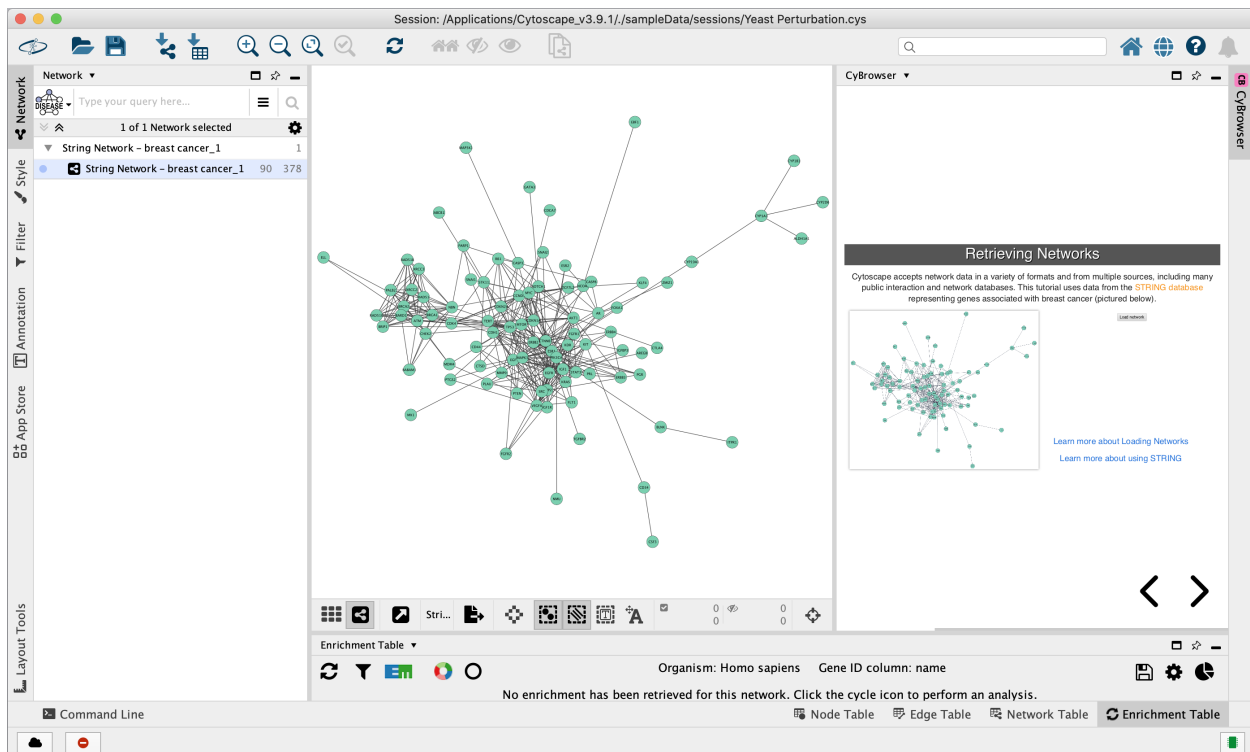
Open link in native browser
Copy link location
Open in new window
Open in new tab
Download to file

1. **Other** If the cursor is not over a link, and no text is selected, the default menu is shown. Using the default menu, users can close their browser or reload the page.

Reload

Close browser

15.2 Cytoscape Web Browser in Results Panel



In addition to being able to open web pages as a separate window, a web page may also be opened in the results panel. This provides many of the same functions as the browser window except that the interface to go forward and backwards is gone, and you can't open links in different tabs.

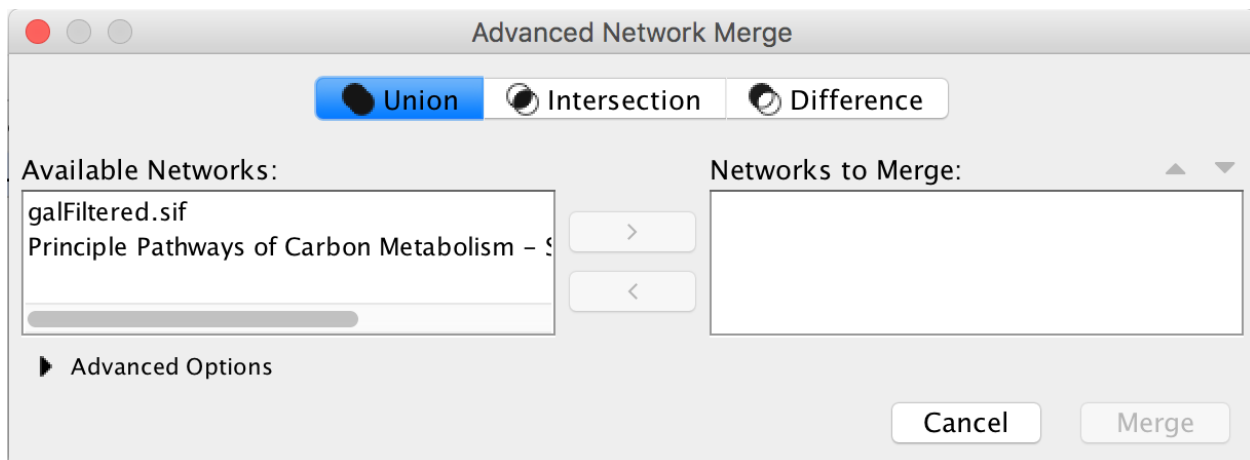
15.3 Why Cytoscape Web Browser?

Cytoscape Web Browser is not a Chrome or Firefox replacement, but it provides a very quick way to view Cytoscape-specific web pages and provides a level of integration with Cytoscape that is more difficult to provide in all of the various browsers provided by all of the platforms Cytoscape runs on. In particular, **Cytoscape Web Browser** supports special links that are actually just Cytoscape commands. For javascript implementers, **Cytoscape Web Browser** also provides hooks to listen to node and edge selection in Cytoscape.

Cytoscape allows for merging of both network and table data, through **Tools** → **Merge**.

16.1 Merge Networks

The **Advanced Network Merge** interface is available from **Tools** → **Merge** → **Networks...** and allows for merging of two or more networks.



16.1.1 Basic Operations

- Select either **Union**, **Intersection** or **Difference**.
- Networks available for merge are listed under **Networks to merge**. Select a network from the list and click the right arrow to transfer the network to **Selected networks**. Click **Merge** to continue. The merged network will be displayed as a separate network.

16.1.2 Advanced Options

The **Advanced Network Merge** interface includes an expandable **Advanced Network Merge** panel, where you can specify the details of how to merge the networks. The options available here are:

- **Matching Columns:** This specifies the network columns that should be used for merging. Typically, the **name** column or some other column containing identifier information is used here.
- **How to merge columns:** A table lets the user specify for each of the individual network columns, what the corresponding column in the merged network should be named and its data type.

▼ Advanced Options

Matching Columns (table columns to match nodes between networks):

galFiltered.sif
name

How to merge columns:

galFiltered.sif	Merged Network	Column type
name	Matching.Attribute	List<String>
AverageShortestPathLength	AverageShortestPathLength	Double
BetweennessCentrality	BetweennessCentrality	Double
COMMON	COMMON	String
ClosenessCentrality	ClosenessCentrality	Double
ClusteringCoefficient	ClusteringCoefficient	Double
Degree	Degree	Integer
Eccentricity	Eccentricity	Integer

Node Edge

☒ Enable merging nodes/edges in the same network

Cancel Merge

16.2 Merge Tables

It is also possible to merge tables, via **Tools** → **Merge** → **Tables...**:

Merge Data Table

Source

Source Table: galFiltered.sif default node

Columns To Merge

Select Columns: AverageShortestPathLength
BetweennessCentrality
ClosenessCentrality
ClusteringCoefficient
COMMON
Degree
Eccentricity

Select All
Select None

Key column to merge: name

Type of merge: Copy Columns

Target

Merge table to: a network collection

Select Network Collection

Network Collection: galFiltered.sif

Merge data in: Node Table Columns

Key column for network: shared name

Cancel OK

Merging of node and edge tables works similarly to network merge, and tables can be merged within or between network collections.

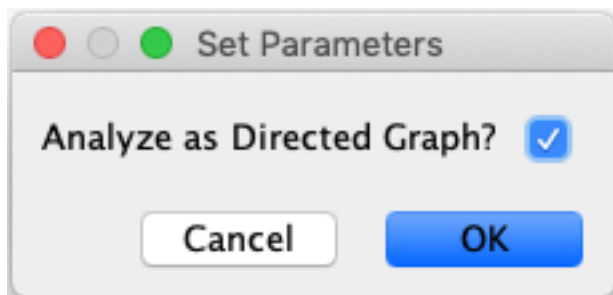
Analyzer computes a comprehensive set of topological metrics for undirected and directed networks, including:

- Number of nodes, edges and connected components.
- Network diameter, radius and clustering coefficient, as well as the characteristic path length.
- Charts for topological coefficients, betweenness, and closeness.
- Distributions of degrees, neighborhood connectiveness, average clustering coefficients, shortest path lengths, number of shared neighbors and stress centrality.

17.1 Network Analysis

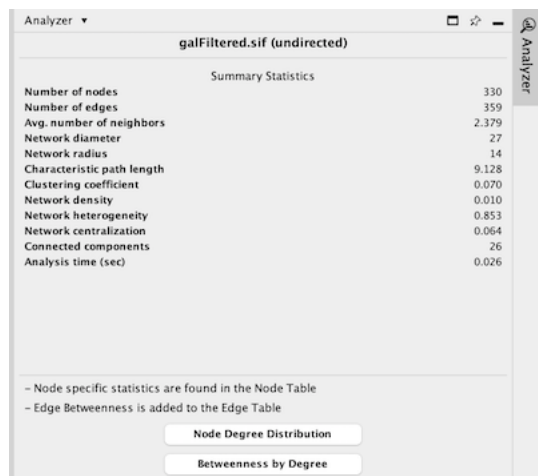
17.1.1 Analyze Network

To run Analyzer, select **Tools** → **Analyze Network**.



Analyzer will run different statistics depending on whether the network is directed or undirected, with the default being undirected. A **Set Parameters** dialog will open where you can specify if the network should be analyzed as a directed graph.

When results are ready, they will appear in the **Results Panel**.



The results have multiple tabs, accessible via the buttons on the bottom of the panel. Details on the network metrics can be found [here](#).

- Simple Metrics
- Node Degree Distribution
- Clustering Coefficient
- Topological Coefficient
- Average Shortest Path Length
- Neighborhood Connectivity
- Betweenness Centrality
- Closeness Centrality
- Stress Centrality

17.1.2 Analyze Subset of Nodes

Prior versions of this tool offered the option of analyzing all nodes or only a selected subset. This is no longer supported directly in the program. Instead, if you want to analyze a subnetwork, you can use the command **File** → **New Network** → **From Selected Nodes, All Edges** in the **Command Panel** to create the desired subnetwork.

17.1.3 Plot Metrics

Once the Analyzer is run, several additional columns are added to the **Node Table** (and an **EdgeBetweenness** column is added to the **Edge Table**). To plot any of these new columns, right-click on the column header and select **Plot Histogram...** for a single parameter distribution, or **Plot Scatter...** for a bivariate plot of the data. Within either of these charts it is possible to select a section of the data, and select the nodes (edges) in the main graph window corresponding to the region selected on the chart.


17.2 NetworkAnalyzerDemo

Comprehensive online documentation and a tutorial for **NetworkAnalyzer** are available at <http://med.bioinf.mpi-inf.mpg.de/networkanalyzer/>.

For additional information see Yassen Assenov, Nadezhda Doncheva, Thomas Lengauer, and Mario Albrecht, DOI: [10.1038/nprot.2012.004](https://doi.org/10.1038/nprot.2012.004).

CHAPTER 18

Enrichment Table

The Enrichment Table core app provides access to functional enrichment analysis for any network loaded into Cytoscape using [g:Profiler's web service](#). Click the **Perform Gene Enrichment** button (reload icon)  in the **Enrichment Table** panel to retrieve enrichment analysis results, or use the menu option **Tools** → **Enrichment Table** → **Perform Gene Enrichment**.

18.1 Organism and Gene ID

Running enrichment analysis requires two mandatory parameters:

- Organism: Organism associated with the query genes
- Gene ID: Node table column containing the gene symbols

Organism: Homo sapiens Gene ID column: Human Readable Label

Both these parameters are predicted by **Enrichment Table** app if enough information is available.

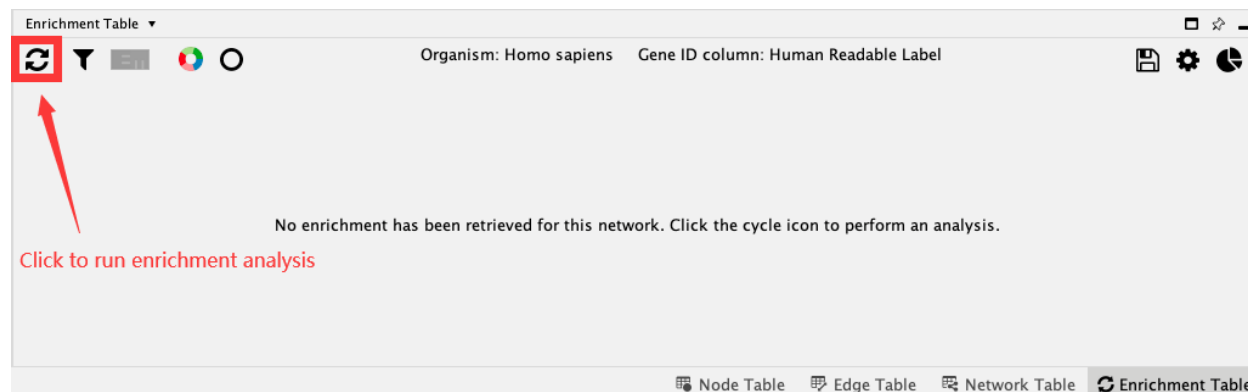
- The possible **organism** is predicted on startup by processing the data from the network in columns `[species,organism,IntAct::species]`
- The **gene id** column is predicted on startup in the following ways:
 1. Retrieves `NODE_LABEL` from style for any generic network
 2. Selects `display name` for `stringapp` networks

If you want to manually set organism and gene ID or the prediction is incorrect, you can change the options in the **Network-specific enrichment panel settings** which can be accessed by clicking the gear icon in the **Enrichment Table** panel.

18.2 Running Enrichment Analysis

There are three ways you can perform enrichment analysis:

- Use the menu option under **Tools** → **Enrichment Table** → **Perform Gene Enrichment**.
- In the Cytoscape **Command Line**, enter `enrichment analysis`, and click enter.
- Click the **Perform Gene Enrichment** button (reload icon) in the **Enrichment Table** panel.



Note: By default, the enrichment analysis is performed on all nodes of the current network using the genome as background. If a subset of nodes are selected, enrichment analysis is performed for just those nodes using the complete network as the background.

Now you get the table containing enrichment results. The results are sorted according to the p-value in a increasing order by default.

18.3 Filter Results

There are couple of parameters based on which you can filter the table by categories and evidence code:

- Click the **Filter enrichment table** button with filter icon to access the filters.
- Select **Gene Ontology Biological Process** in the categories. Click **OK**. You will see a filtered table, and a summary of the number of filtered versus all rows at the top of the table.
- Open the filter panel again and check **Remove redundant terms**. Click ok to see terms with both filters applied.

source	chart color	term id	term name	description	p-value	query size	background...	term size	intersection...	precision	recall	intersection...
Gene Ontol...		GO:0005737	cytoplasm	"The conten...	1.86441E-45	400	21690	12270	358	0.895	0.029	[RNH1, DCA...
Human Prot...		HPA:0160051	endometriu...	endometriu...	2.38792E-27	331	10976	6779	295	0.891	0.044	[DCAF8, GP...
Human Prot...		HPA:0380000	placenta	placenta	4.03451E-27	331	10976	7482	309	0.934	0.041	[RNH1, DCA...
Human Prot...		HPA:0160000	endometriu...	endometriu...	1.4651E-26	331	10976	7017	299	0.903	0.043	[DCAF8, GP...
Gene Ontol...		GO:0044260	cellular mac...	"The chemic...	2.30081E-26	387	21092	3234	150	0.388	0.046	[RNH1, LSM...
KEGG		KEGG:04141	Protein proc...	Protein proc...	4.62761E-26	222	8064	169	41	0.185	0.243	[MEPCE, RN...
Human Prot...		HPA:0351181	pancreas; p...	pancreas; p...	4.1485E-25	331	10976	5596	263	0.795	0.047	[DCAF8, GP...
Human Prot...		HPA:0210000	fallopian tube	fallopian tube	1.01796E-24	331	10976	7432	305	0.921	0.041	[RNH1, DCA...
Human Prot...		HPA:0170051	endometriu...	endometriu...	1.1323E-24	331	10976	6684	289	0.873	0.043	[DCAF8, GP...
Human Prot...		HPA:0180000	epididymis	epididymis	2.25472E-24	331	10976	7306	302	0.912	0.041	[RNH1, DCA...
Human Prot...		HPA:0180051	epididymis; ...	epididymis; ...	2.25472E-24	331	10976	7306	302	0.912	0.041	[RNH1, DCA...
Human Prot...		HPA:0610831	urinary blad...	urinary blad...	3.48588E-24	331	10976	7270	301	0.909	0.041	[RNH1, DCA...
Human Prot...		HPA:0610000	urinary blad...	urinary blad...	3.48588E-24	331	10976	7270	301	0.909	0.041	[RNH1, DCA...

18.4 Charts

Charts provides the ability to visualise a set of terms for each node in the network. By default, a split donut chart is displayed, corresponding to the top 5 terms. You can change the number of terms and type of chart in **Network-specific chart settings** (right-most button).

- Click **Draw chart using default color palette** to create charts with default settings.
- To remove charts, click on **Reset charts**.
- To change charts settings, go to **Network-specific chart settings**.

Enrichment Table

Organism: Homo sapiens Gene ID column: Human Readable Label 953 rows

source	chart color	term id	term name	description	p-value	query size	backgroun...	term size	intersectio...	precision	recall	intersectin...
Gene Ontol...		GO:0005737	cytoplasm	"The conten...	1.86441E-45	400	21690	12270	358	0.895	0.029	[RNH1, DCA...
Human Prot...		HPA:0160051	endometriu...	endometriu...	2.38792E-27	331	10976	6779	295	0.891	0.044	[DCAF8, GP...
Human Prot...		HPA:0380000	placenta	placenta	4.03451E-27	331	10976	7482	309	0.934	0.041	[RNH1, DCA...
Human Prot...		HPA:0160000	endometriu...	endometriu...	1.4651E-26	331	10976	7017	299	0.903	0.043	[DCAF8, GP...
Gene Ontol...		GO:0044260	cellular mac...	"The chemic...	2.30081E-26	387	21092	3234	150	0.388	0.046	[RNH1, LSM...
KEGG		KEGG:04141	Protein proc...	Protein proc...	4.62761E-26	222	8064	169	41	0.185	0.243	[MEPCE, RN...
Human Prot...		HPA:0351181	pancreas; p...	pancreas; p...	4.1485E-25	331	10976	5596	263	0.795	0.047	[DCAF8, GP...
Human Prot...		HPA:0210000	fallopian tube	fallopian tube	1.01796E-24	331	10976	7432	305	0.921	0.041	[RNH1, DCA...
Human Prot...		HPA:0170051	endometriu...	endometriu...	1.1323E-24	331	10976	6684	289	0.873	0.043	[DCAF8, GP...
Human Prot...		HPA:0180000	epididymis	epididymis	2.25472E-24	331	10976	7306	302	0.912	0.041	[RNH1, DCA...
Human Prot...		HPA:0180051	epididymis; ...	epididymis; ...	2.25472E-24	331	10976	7306	302	0.912	0.041	[RNH1, DCA...
Human Prot...		HPA:0610831	urinary blad...	urinary blad...	3.48588E-24	331	10976	7270	301	0.909	0.041	[RNH1, DCA...
Human Prot...		HPA:0610000	urinary blad...	urinary blad...	3.48588E-24	331	10976	7270	301	0.909	0.041	[RNH1, DCA...

Draw ring charts and reset ring charts in the network

Node Table Edge Table Network Table Enrichment Table

18.5 Term Selection

Enrichment Table shows results based on the nodes selected in the network. If no nodes are selected, all terms are shown in the table. When a set of nodes are selected, terms consisting of all the selected nodes are shown. Similarly, to visualize one or more enrichment term, select the rows in the table and the corresponding nodes will be highlighted in the network.

18.6 Optional Settings

In addition to Organism and Gene ID column, there are other parameters that can be changed to obtain a more precise enrichment results. These options are available in the **Network-specific enrichment panel settings** (gear icon). For example, you can remove redundant terms in the table by selecting the appropriate redundancy (Jaccard) cutoff, the default is 0.5.

Enrichment Table

Organism: Homo sapiens Gene ID column: Human Readable Label 953 rows

Manually set species

source	chart color	term id	term name	description	p-value	query size	backgroun...	term size	intersectio...	precision	recall	intersectin...
Gene Ontol...		GO:0005737	cytoplasm	"The conten...	1.86441E-45	400	21690	12270	358	0.895	0.029	[RNH1, DCA...
Human Prot...		HPA:0160051	endometriu...	endometriu...	2.38792E-27	331	10976	6779	295	0.891	0.044	[DCAF8, GP...
Human Prot...		HPA:0380000	placenta	placenta	4.03451E-27	331	10976	7482	309	0.934	0.041	[RNH1, DCA...
Human Prot...		HPA:0160000	endometriu...	endometriu...	1.4651E-26	331	10976	7017	299	0.903	0.043	[DCAF8, GP...
Gene Ontol...		GO:0044260	cellular mac...	"The chemic...	2.30081E-26	387	21092	3234	150	0.388	0.046	[RNH1, LSM...
KEGG		KEGG:04141	Protein proc...	Protein proc...	4.62761E-26	222	8064	169	41	0.185	0.243	[MEPCE, RN...
Human Prot...		HPA:0351181	pancreas; p...	pancreas; p...	4.1485E-25	331	10976	5596	263	0.795	0.047	[DCAF8, GP...
Human Prot...		HPA:0210000	fallopian tube	fallopian tube	1.01796E-24	331	10976	7432	305	0.921	0.041	[RNH1, DCA...
Human Prot...		HPA:0170051	endometriu...	endometriu...	1.1323E-24	331	10976	6684	289	0.873	0.043	[DCAF8, GP...
Human Prot...		HPA:0180000	epididymis	epididymis	2.25472E-24	331	10976	7306	302	0.912	0.041	[RNH1, DCA...
Human Prot...		HPA:0180051	epididymis; ...	epididymis; ...	2.25472E-24	331	10976	7306	302	0.912	0.041	[RNH1, DCA...
Human Prot...		HPA:0610831	urinary blad...	urinary blad...	3.48588E-24	331	10976	7270	301	0.909	0.041	[RNH1, DCA...
Human Prot...		HPA:0610000	urinary blad...	urinary blad...	3.48588E-24	331	10976	7270	301	0.909	0.041	[RNH1, DCA...

Node Table Edge Table Network Table Enrichment Table

18.7 Enrichment Map Generation

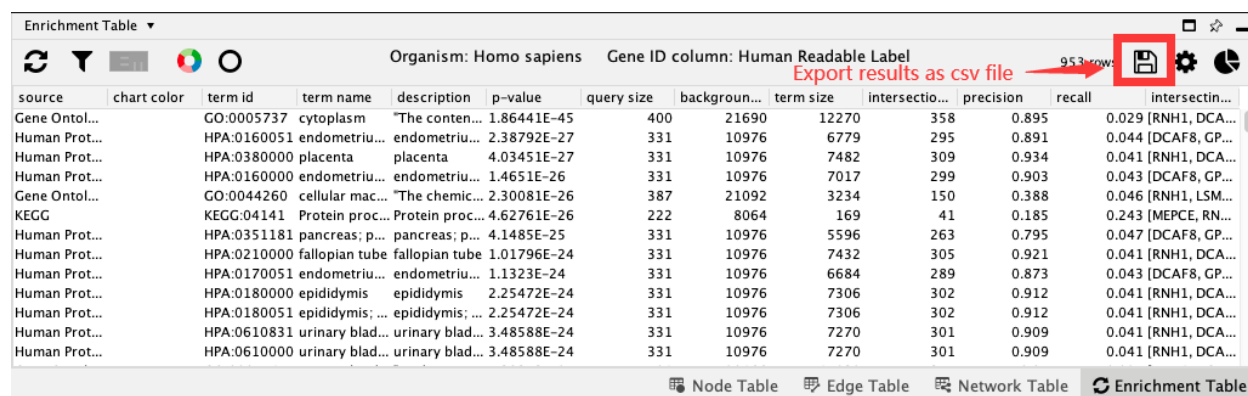
We can generate an [Enrichment Map](#) from the enrichment data generated by the **Enrichment Table** app. This requires the [Enrichment Map](#) app to be installed in Cytoscape. Once enrichment map app is present, click the **Enrichment Map** icon. Specify the output file name and connectivity cutoff and click **OK** to continue.

18.8 Export results

Enrichment Table app provides functionality to export the data as a csv-formatted table:

- Select the **Export enrichment table** icon.
- Select the desired file location and file name for the table.

The default file extension is **.csv**.



18.9 Automation

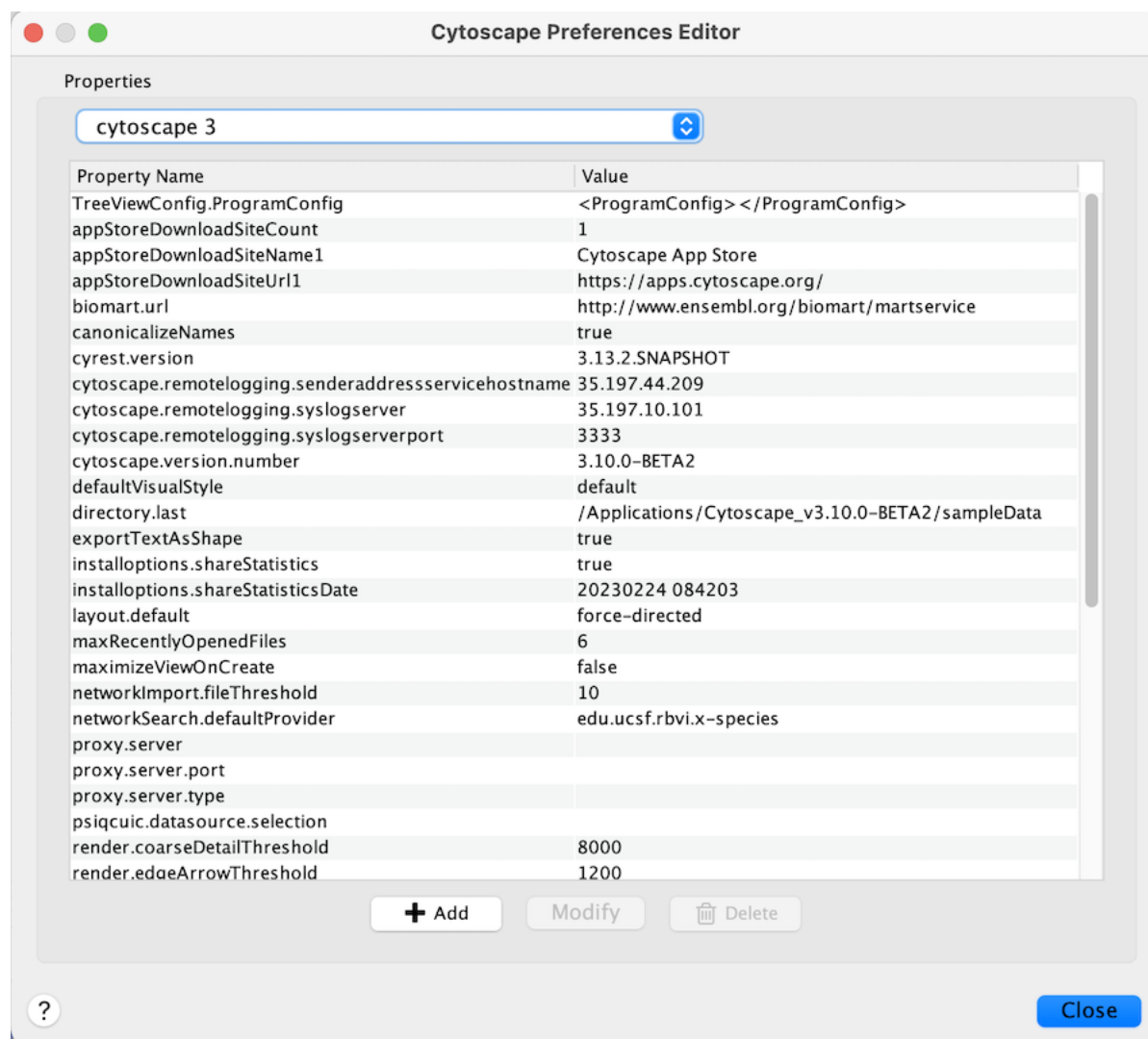
The enrichment analysis is supported in automation use cases as well. The basic command syntax is `enrichment analysis`. You can optionally choose the organism associated with the query genes with the `organism` parameter. You can also optionally select the node table column containing the gene symbols with the `geneID` parameter. All parameters are listed [here](#).

Cytoscape Preferences

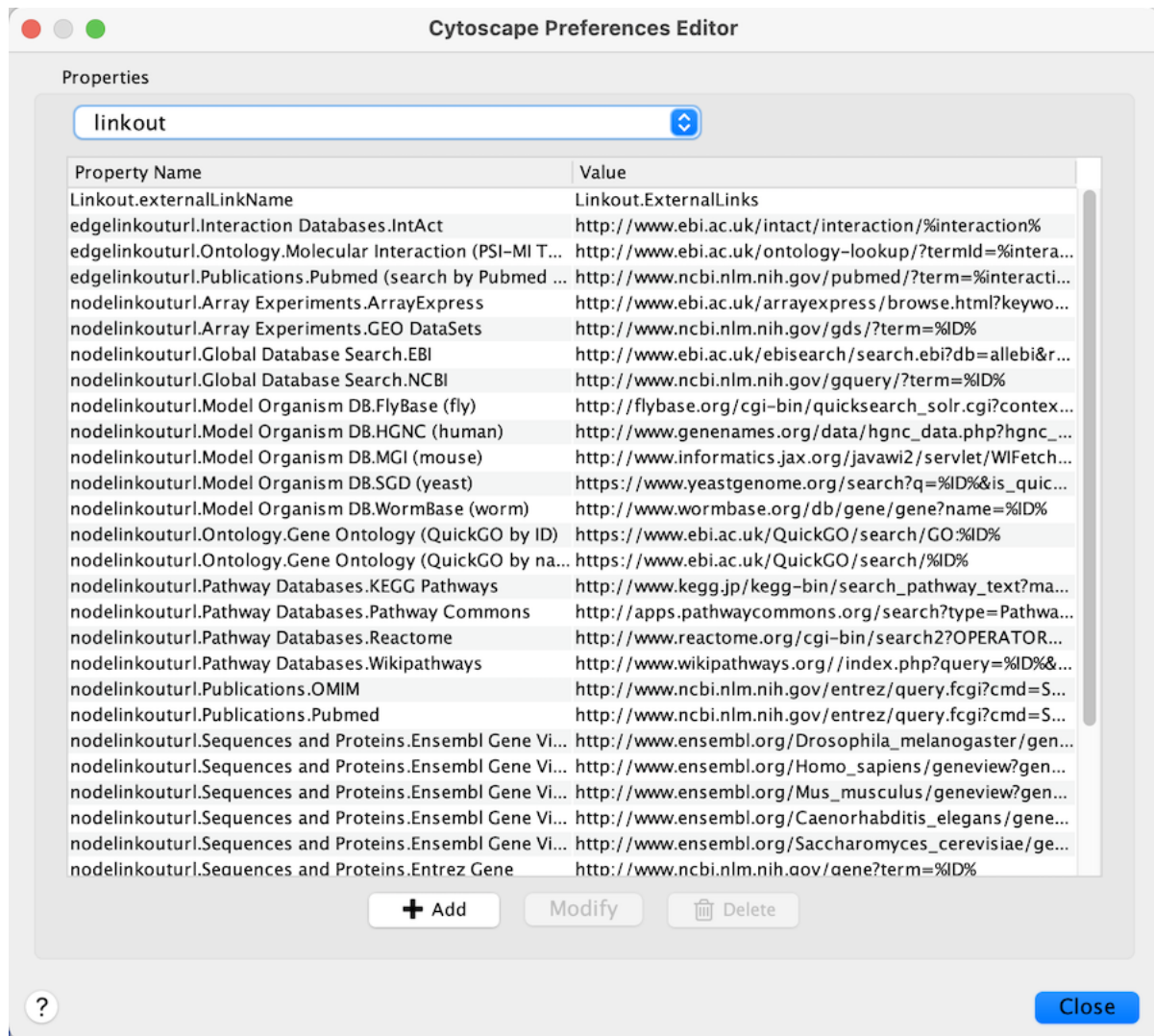
19.1 Managing Properties

The Cytoscape properties editor, accessed via **Edit** → **Preferences** → **Properties...**, is used to specify default properties. Any changes made to these properties will be saved in .props files under the `CytoscapeConfiguration` subdirectory of the user's home directory.

Cytoscape properties are configurable using the **Add**, **Modify** and **Delete** buttons as seen below.

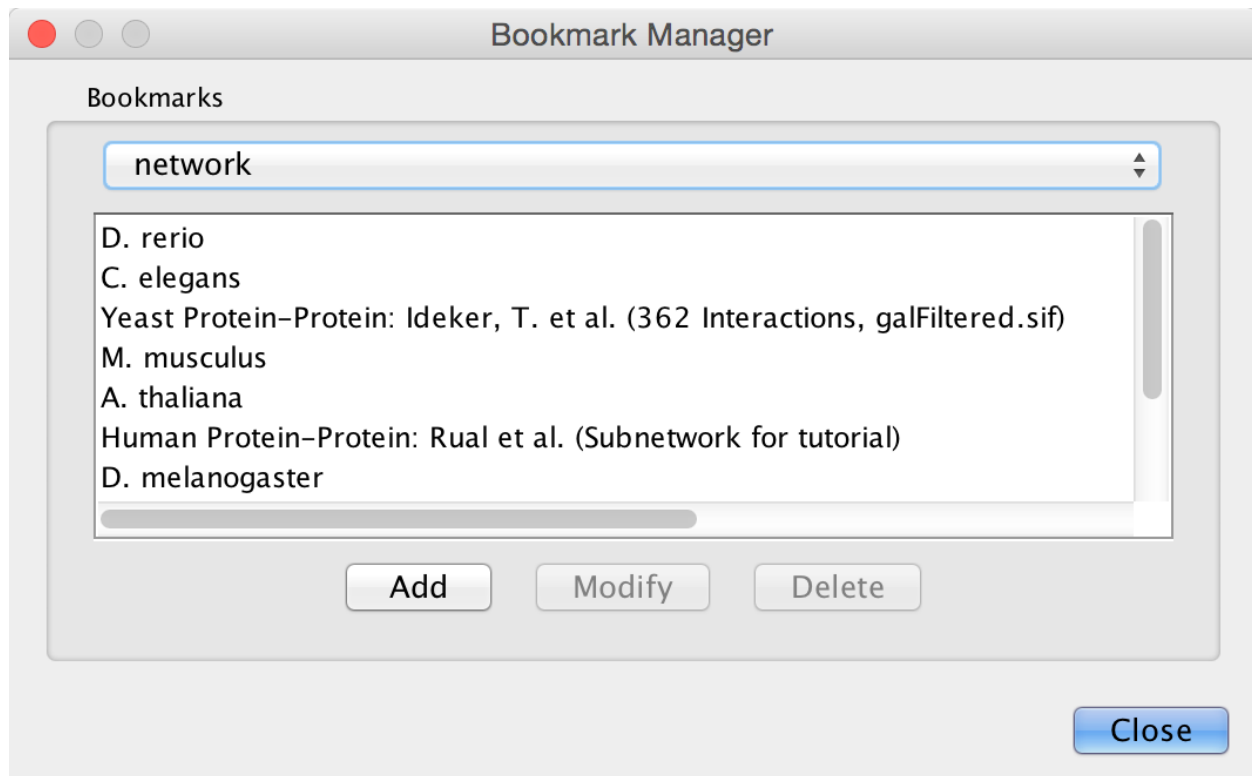


App properties may also be edited in the same way as editing Cytoscape properties. For example, to edit the properties of **Linkout**, select **linkout** from the combobox of the **Preferences Editor**. Some apps may store properties inside session files in addition to (or instead of) storing them in the `CytoscapeConfiguration` directory.



19.2 Managing Bookmarks

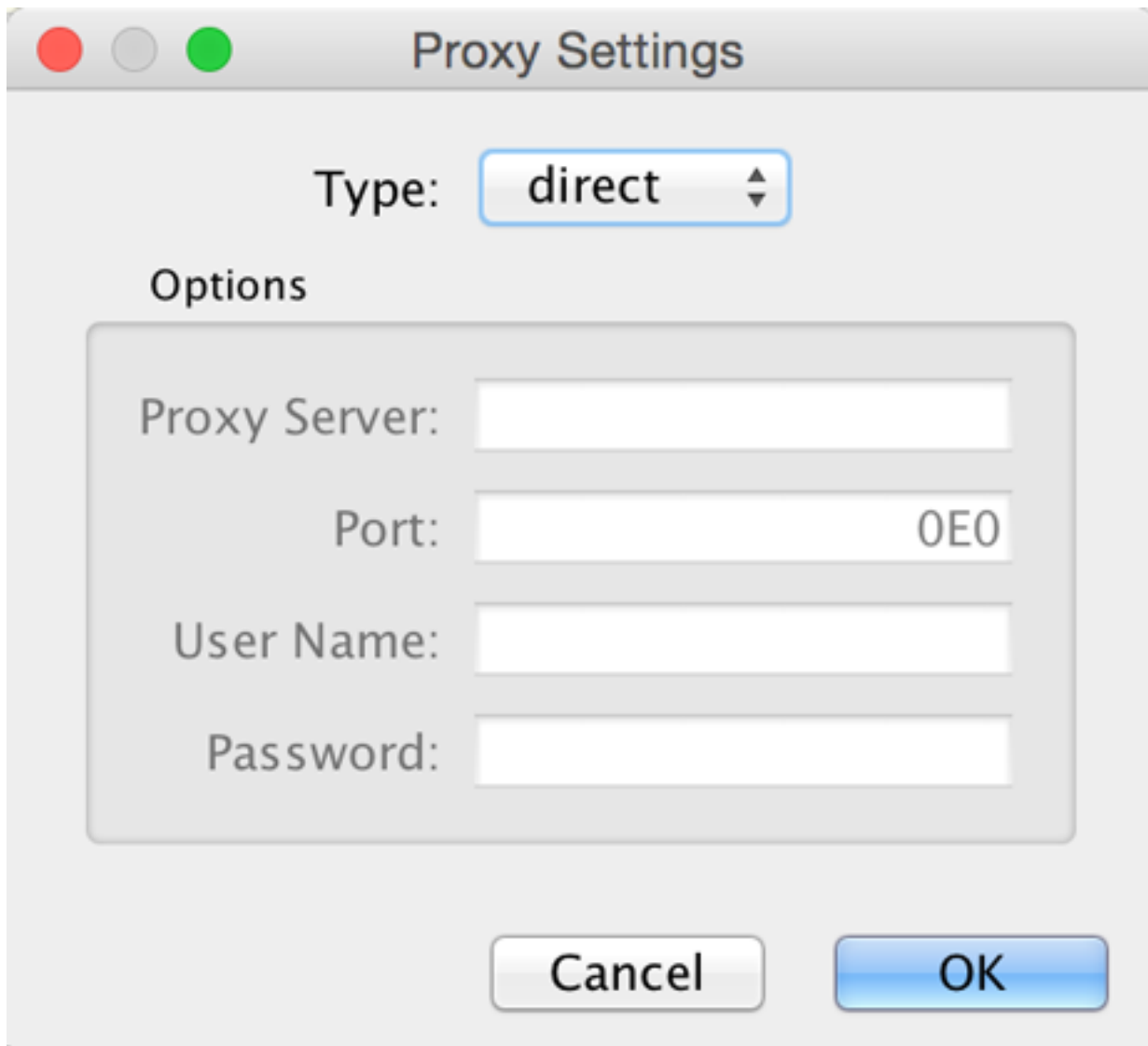
Cytoscape contains a pre-defined list of bookmarks, which point to sample network files located on the Cytoscape web server. Users may add, modify, and delete bookmarks through the Bookmark manager, accessed by going to **Edit** → **Preferences** → **Bookmarks...**



There are currently several types of bookmarks (based on data categories), including network and table. Network bookmarks are URLs pointing to Cytoscape network files. These are normal networks that can be loaded into Cytoscape. Table bookmarks are URLs pointing to data table files.

19.3 Managing Proxy Servers

You can define and configure a proxy server for Cytoscape by going to **Edit** → **Preferences** → **Proxy Settings...**

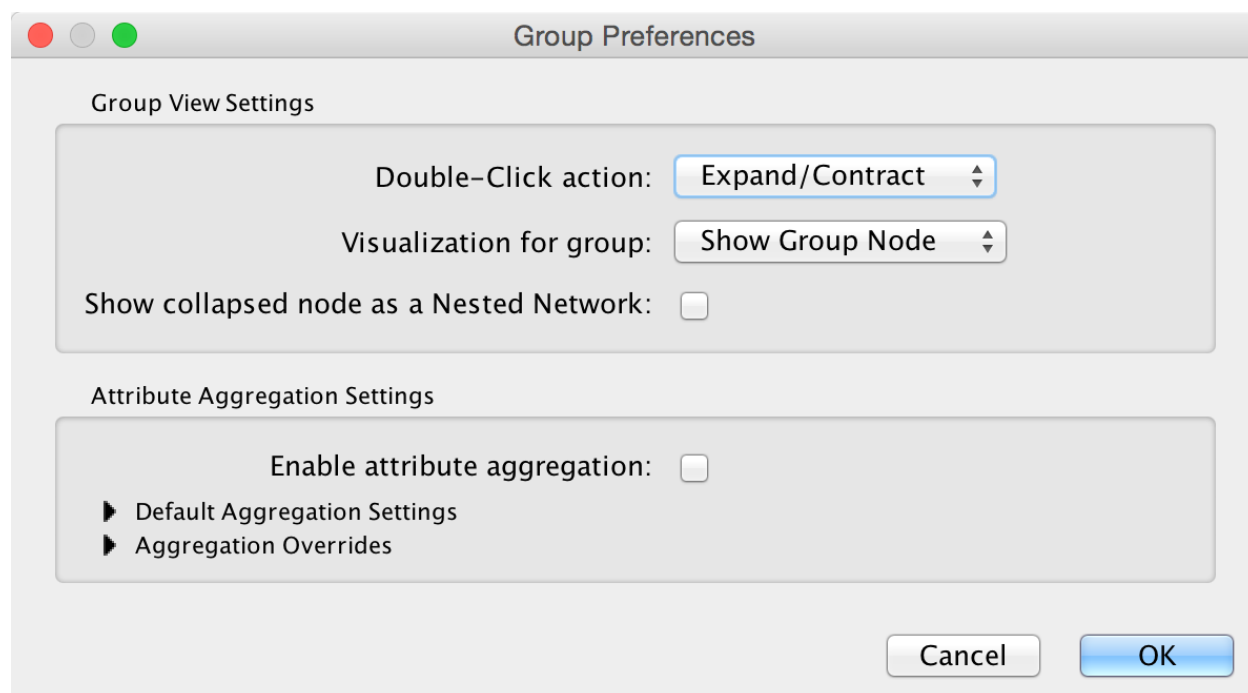


After the proxy server is set, all network traffic related to loading a network from URL will pass through the proxy server. Cytoscape apps use this capability as well. The proxy settings are saved in `cytoscape3.props`. Each time you click the **OK** button after making a change to the proxy settings, an attempt is made to connect to a well known site on the Internet (e.g., google.com) using your settings. For both success and failure you are notified and for failure you are given an opportunity to change your proxy settings.

If you no longer need to use a proxy to connect to the Internet, simply set the Proxy type to *direct* and click the **OK** button.

19.4 Managing Group Settings

The configuration of Cytoscape group view may also be edited through **Edit** → **Preferences** → **Group Preferences...**



Note that **Group Preferences** apply to **node groups** established after the group preferences are set. They do not apply to groups that already exist.

The **Group Preferences** dialog provides access to three **Group View Settings** and all of the **Attribute Aggregation Settings**. There are two interacting settings involved in the group view and group interaction:

- how an expanded group appears
- what happens when a node (group member or group node) is double-clicked
- what appears inside of a group node when it is collapsed

19.4.1 Group View Settings

The following node visualization options are available:

- **None:** No specific visualization – just do expand/contract, but don't treat the expanded group special in any way
- **Compound Node:** Show the group node as an area surrounding the member nodes, but position it behind the member nodes to allow direct selection of each of the members. If you move a node within this area, you may need to resize the area to encompass the newly positioned member node. Moving the group node will cause all member nodes to move with it. There are **visual styles** that allow you to change the color, shape and padding for the compound node.
- **Show Group Node:** When the group is expanded, show the group node as an additional node and add member edges between the group node and each of the member nodes. This is useful, for example, for complexes where it may be important to show a group node (the entire complex) at the same time as group member nodes (each individual protein).
- **Single Node:** Show the group node as an area surrounding the member nodes, but put it in front of the member nodes so that the member nodes can not be selected or moved individually.

If you set the **Double-Click** action to something other than **Expand/Contract**, the groups won't collapse on double-click, which may be appropriate for displaying group nodes that contain other nodes (i.e., the **Compound Node** visualization or **Single Node** visualization).

19.4.2 Attribute Aggregation Settings

Attribute aggregation provides an automated way for a group to aggregate all of the attributes of its children. Since the columns in a Cytoscape network must all be of the same type, a group can't simply create a list of integers to aggregate the integer columns of its members – the right approach to aggregating the attributes of group members will obviously depend on the application. Cytoscape allows you to set the default aggregation approach for each type of column: Integer, Long, Double, String, Boolean, String List, Integer List, Long List, or Double List in the **Default Aggregation Settings** section. In general, the user is provided with a list of some common aggregations. For example, Integer aggregations include Average, Minimum Value, Maximum Value, Median Value or Sum.

In addition, users can indicate that a specific column should use an aggregation approach different from the default by looking at **Aggregation Overrides**.

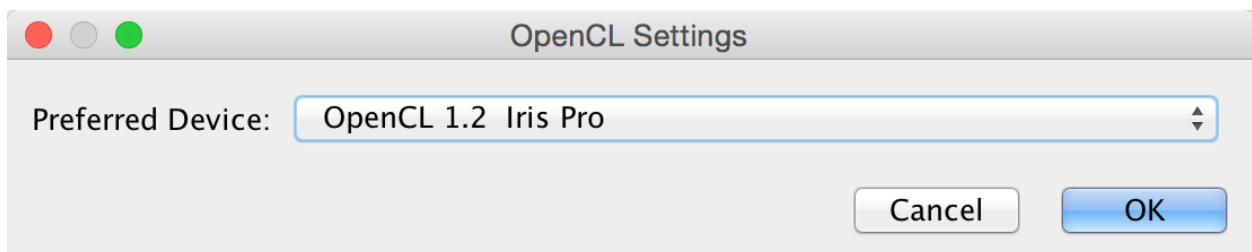
19.4.3 Grouping Tips

The **Show collapsed node as a Nested Network** checkbox determines the contents of a grouping node when its member nodes are hidden. If it is checked, the group node contains a graphic of the laid out member nodes. For the Compound Node visualization, this box should remain unchecked so the grouping node can appear as a background to member nodes.

Attribute aggregation only occurs when the group is collapsed or when the group visualization is changed (e.g., from **Single Node** to **Compound Node**).

19.5 Managing OpenCL Settings

You can choose between one or more OpenCL drivers installed on your system by going to **Edit** → **Preferences** → **OpenCL Settings...**



OpenCL is a library that enables Cytoscape to use your system's graphics processing unit (GPU) to accelerate certain layouts and other calculations. If no choices are presented, consult the support web page for your system's graphics card.

Linkout provides a mechanism to link nodes and edges to external web resources within Cytoscape. Right-clicking on a node or edge in Cytoscape opens a popup menu with a list of web links.

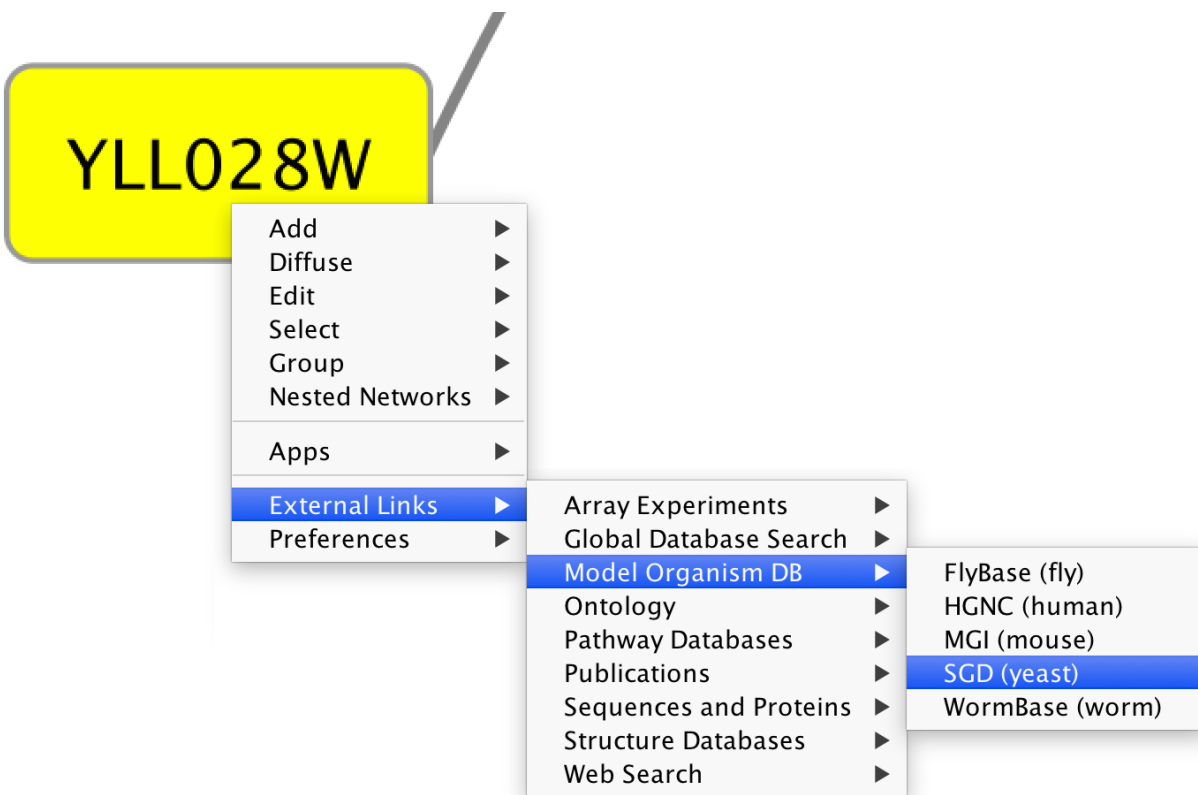
By default, Cytoscape includes a number of links such as Entrez(NCBI), SGD and Google, as well as a number of species-specific links. In addition to the default links, users can customize the **External Links** menu and add (or remove) links by using the Cytoscape Preferences Editor (found under **Edit** → **Preferences** → **Properties...** in the **linkout** group).

External links are listed as **key-value** pairs in the editor where *Property Name* specifies the name of the link and *Value* is the search URL. Linkout menus are organized in a hierarchical structure that is specified as part of the key. Linkout key terms specific to nodes start with the keyword `nodeLinkouturl`; for edges this is `edgeLinkouturl`.

For example, the following entry:

```
nodeLinkouturl.Model Organism DB.SGD (yeast)=http://www.yeastgenome.org/cgi-bin/locus.  
↪fpl?locus=%ID%
```

places the SGD link under the **Model Organism DB** submenu. This link will appear in Cytoscape as:



In a similar fashion one can add new submenus.

The `%ID%` string in the URL is a place-holder for the node label. When the popup menu is generated this marker is substituted with the node label. In the above example, the generated SGD link for the YNL050C protein is:

```
http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YNL050C
```

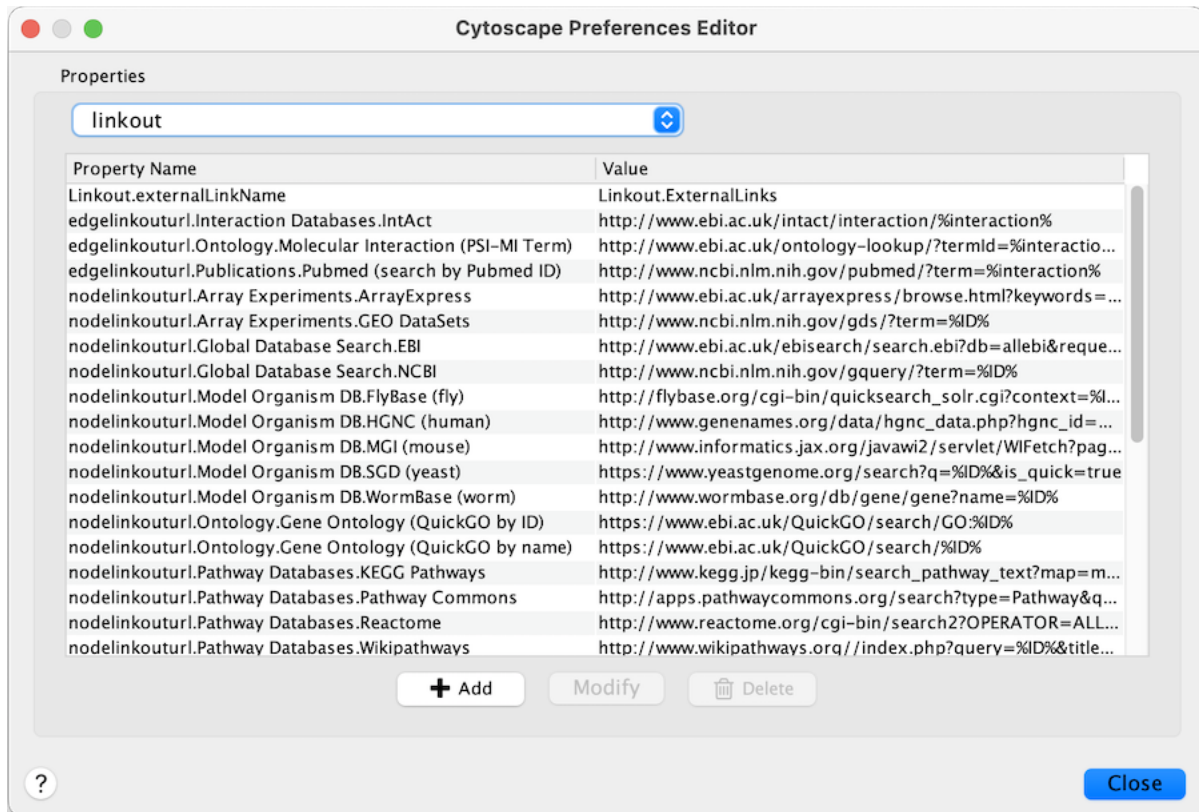
If you want to query based on a different column, you need to specify a different node label using **Styles**.

For edges the mechanism is much the same; however here the placeholders `%ID1%` and `%ID2%` reflect the source and target node label respectively.

Currently there is no mechanism to check whether the constructed URL query is correct and if the node label is meaningful. Similarly, there is no ID mapping between various identifiers. For example, a link to NCBI Entrez from a network that uses Ensembl gene identifiers as node labels will produce a link to Entrez using the Ensembl ID, which results in an incorrect link. It is the user's responsibility to ensure that the node label that is used as the search term in the URL link will result in a meaningful link.

20.1 Adding and Removing Links

The default links are defined in the `linkout.props` file contained in the `CytoscapeConfiguration` directory. These links are normal Java properties and can be edited directly via text editor or by using the Cytoscape Configuration Editor (**Edit** → **Preferences** → **Properties...**) and selecting *linkout* (shown below).

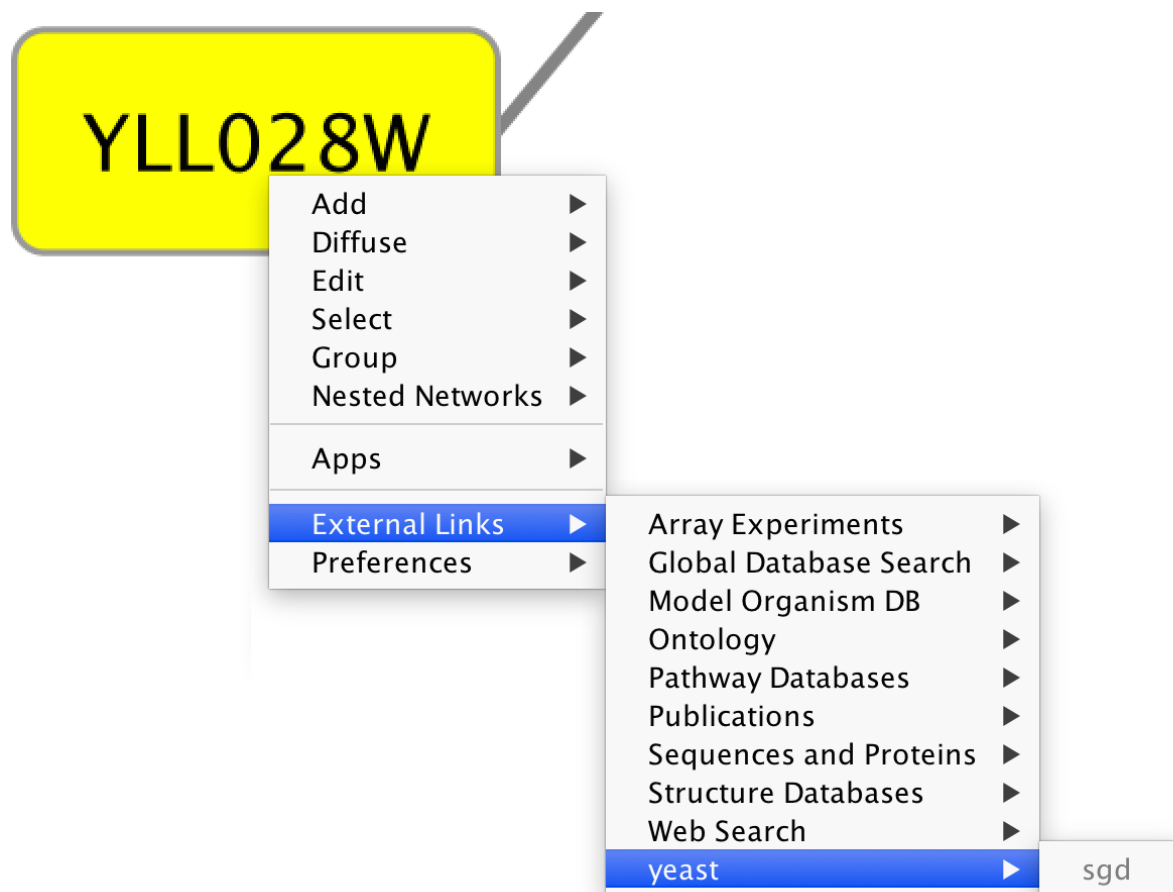


In addition, new links can be defined when starting Cytoscape from command line by specifying individual properties. The formatting of the command is `cytoscape.sh -P [context_menu_definition]=[link]`. *context_menu_definition* specifies the context menu for showing the linkout menu item. The structure of this definition is *nodelinekouturl* or *edgelinekouturl* followed by “.” and followed by the “.”-separated menu hierarchy.

For instance this command:

```
cytoscape.sh -P nodelinekouturl.yeast.SGD=http://db.yeastgenome.org/cgi-bin/locus.pl?
↪ locus\=%ID%
```

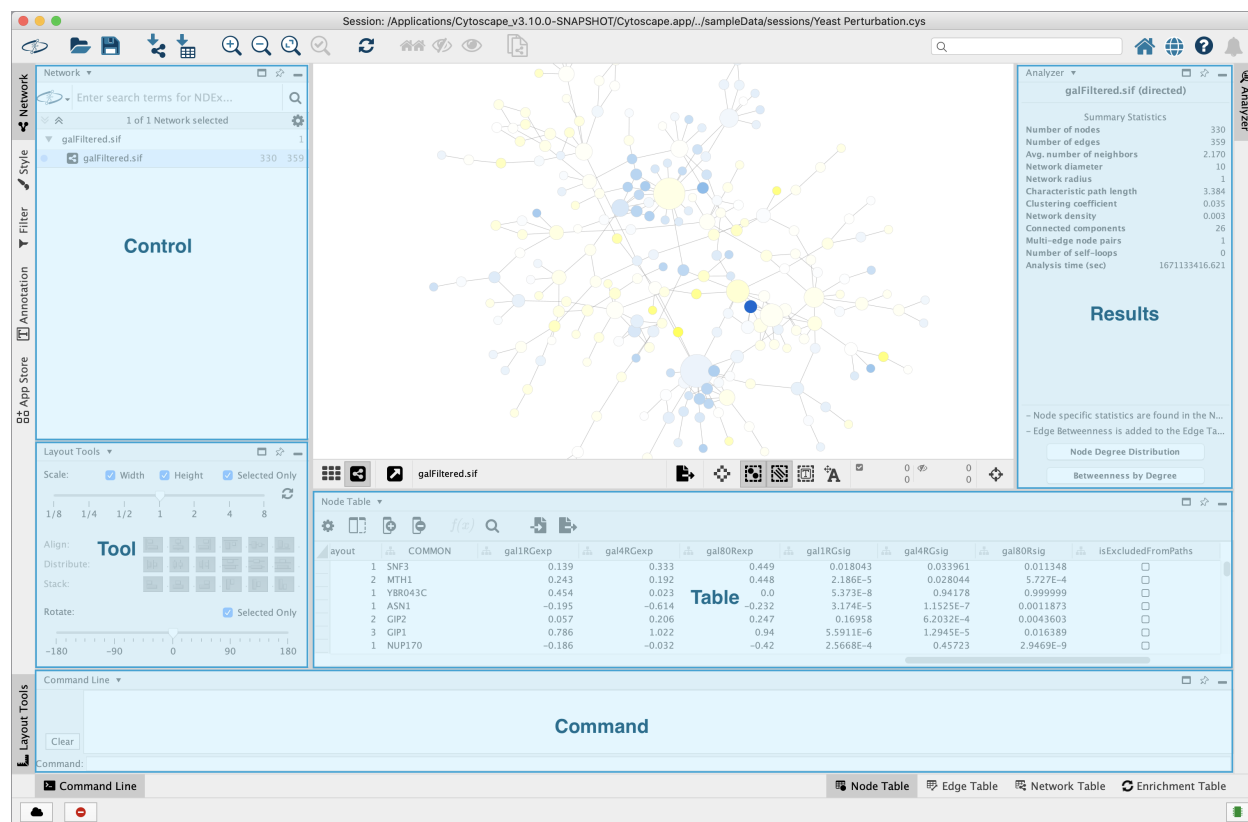
will add this menu item:



To remove a link from the menu, simply delete the property using **Edit** → **Preferences** → **Properties...** and selecting **commandline**. Linkouts added in the command line will be available for the running instance of Cytoscape.

There are five panels that can be visible or hidden:

- **Control Panel** (left)
- **Tool Panel** (bottom left)
- **Table Panel** (bottom right)
- **Results Panel** (right)
- **Command Panel** (bottom)



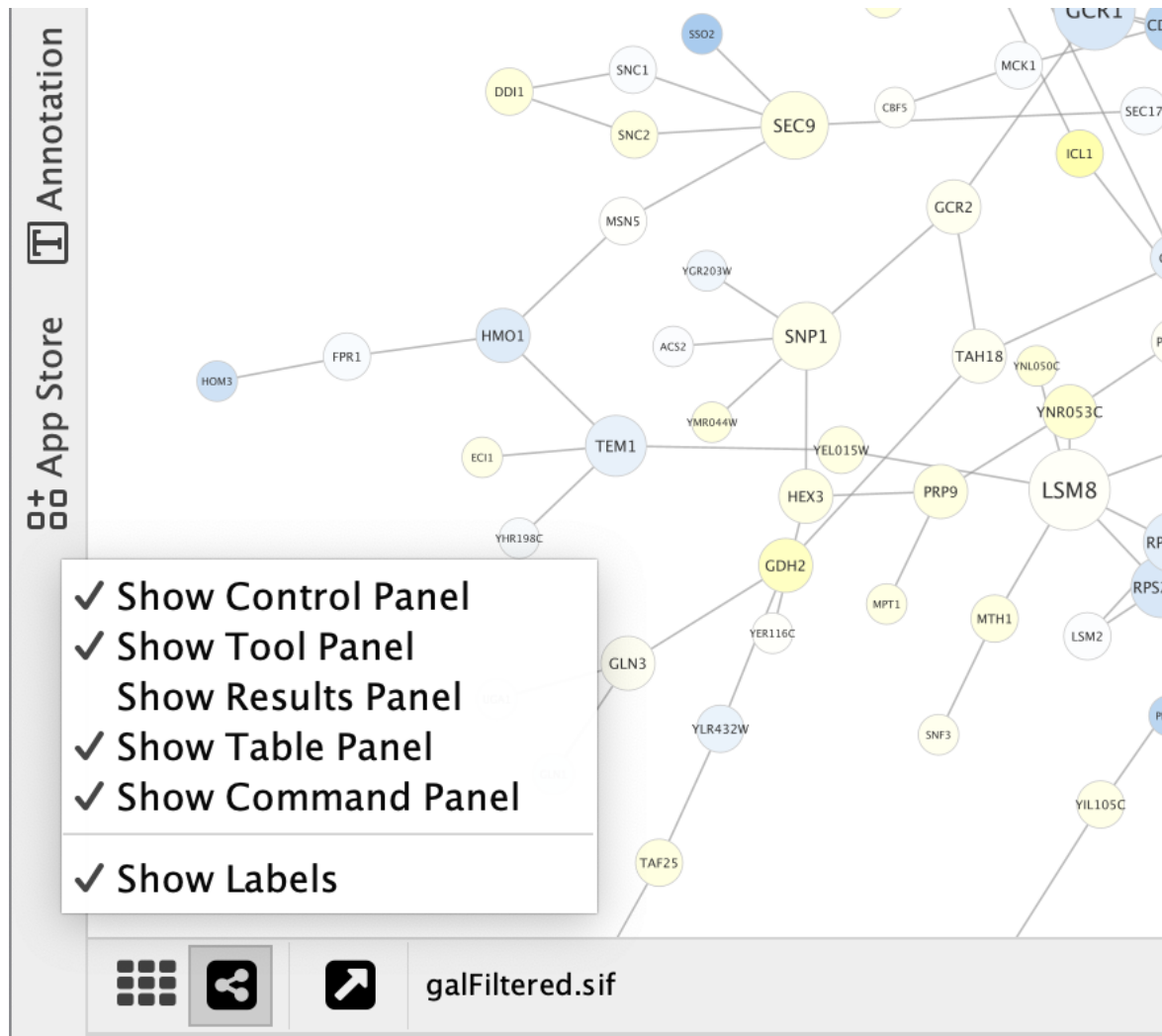
Each panel contains multiple tabs. For example the **Control Panel** contains at a minimum the **Network**, **Style**, **Filter** and **Annotation** tabs. The **Table Panel** contains the **Node Table**, **Edge Table**, **Network Table** and **Enrichment Table** tabs. The **Node** and **Edge** tables contain any data associated with nodes and edges, and the **Network Table** contains network-wide associated data, for example URL or publication links. You can add relevant network-wide information to your network by adding columns in the **Network Table**. Analysis results from **Network Analyzer** (**Tools** → **Analyze Network**) are shown in **Results Panel**. Installed apps may add additional tabs.


21.1 Managing Panels

These panels can compete for valuable screen real-estate (e.g. by making the network view too small), so it is important to manage each panel's state and size properly and according to the user's needs. You can take advantage of these 5 panel states in order to manage the available screen real-estate:

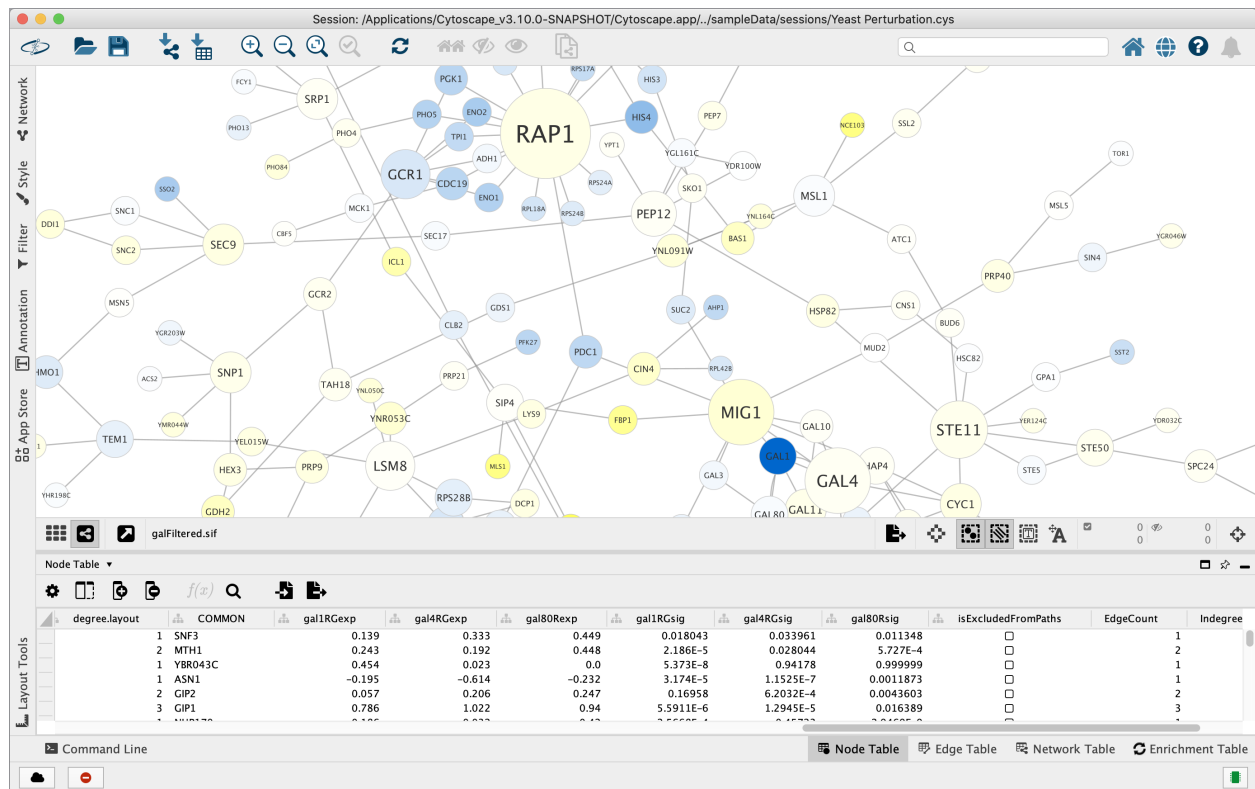
- **Hidden:** A panel can be totally removed from the screen if you find it unnecessary. To do that, uncheck the corresponding option under the **View** menu (e.g. uncheck **View** → **Show Results Panel** to hide the **Results Panel**). When a panel is hidden its tabs no longer appear in the sidebar. In order to show the panel again select the same menu option.

Alternatively, you can right-click an empty space on any sidebar to hide/show a panel:




- **Minimized:** Use the **Minimize** icon  at the top-right corner of a panel to quickly hide it. The tabs from a minimized panel still appear on the sidebar, and by clicking a tab the panel will be shown again as undocked. Some panels (e.g. **Tool Panel**) may be minimized by default.

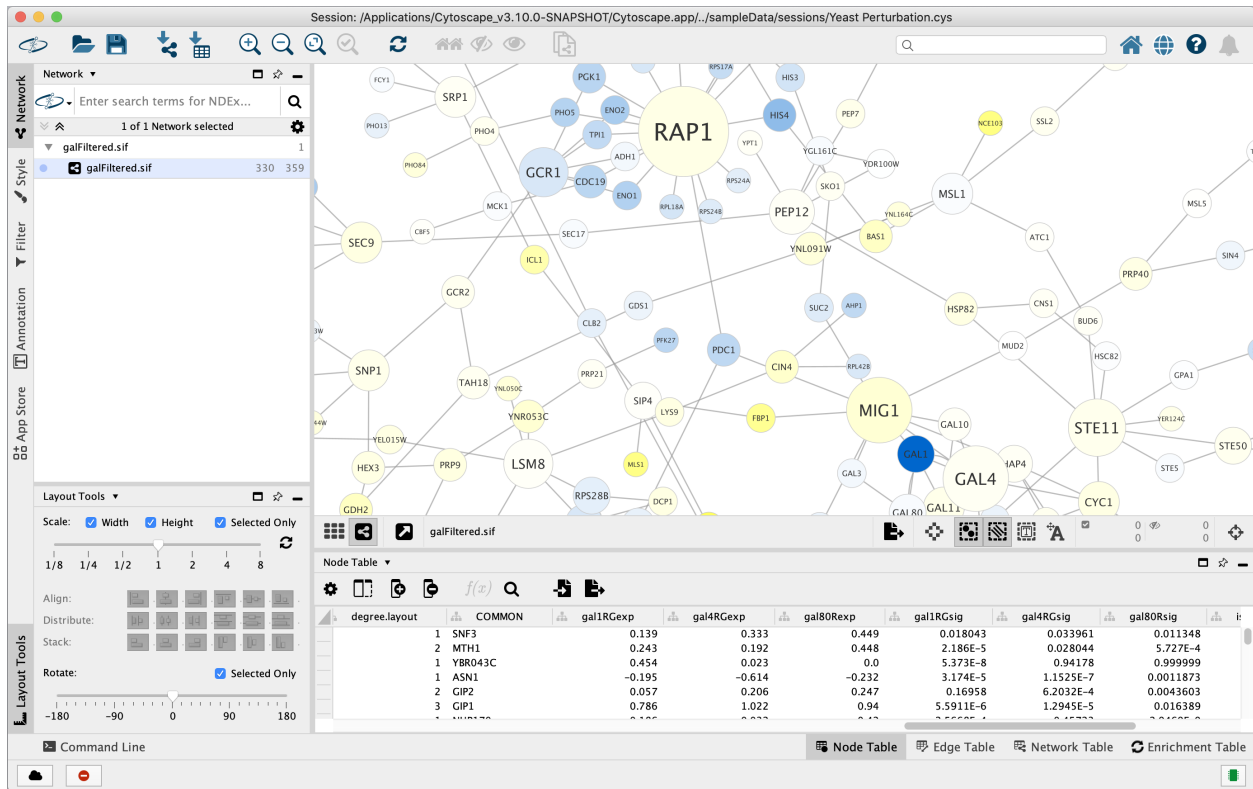
In the example below, the **Control** and **Tool** panels are minimized (**Results** and **Command** are hidden):





- **Docked:** The most used panels (e.g. **Control**, **Table**) are initially docked by default. When docked, a panel takes the space that could be used by its adjacent panels and by resizing it, those adjacent panels are resized as well (e.g. by resizing the **Control Panel** horizontally, the **View Panel** is also resized). If a panel is undocked or

floating, use the **Dock** icon  to make it docked.

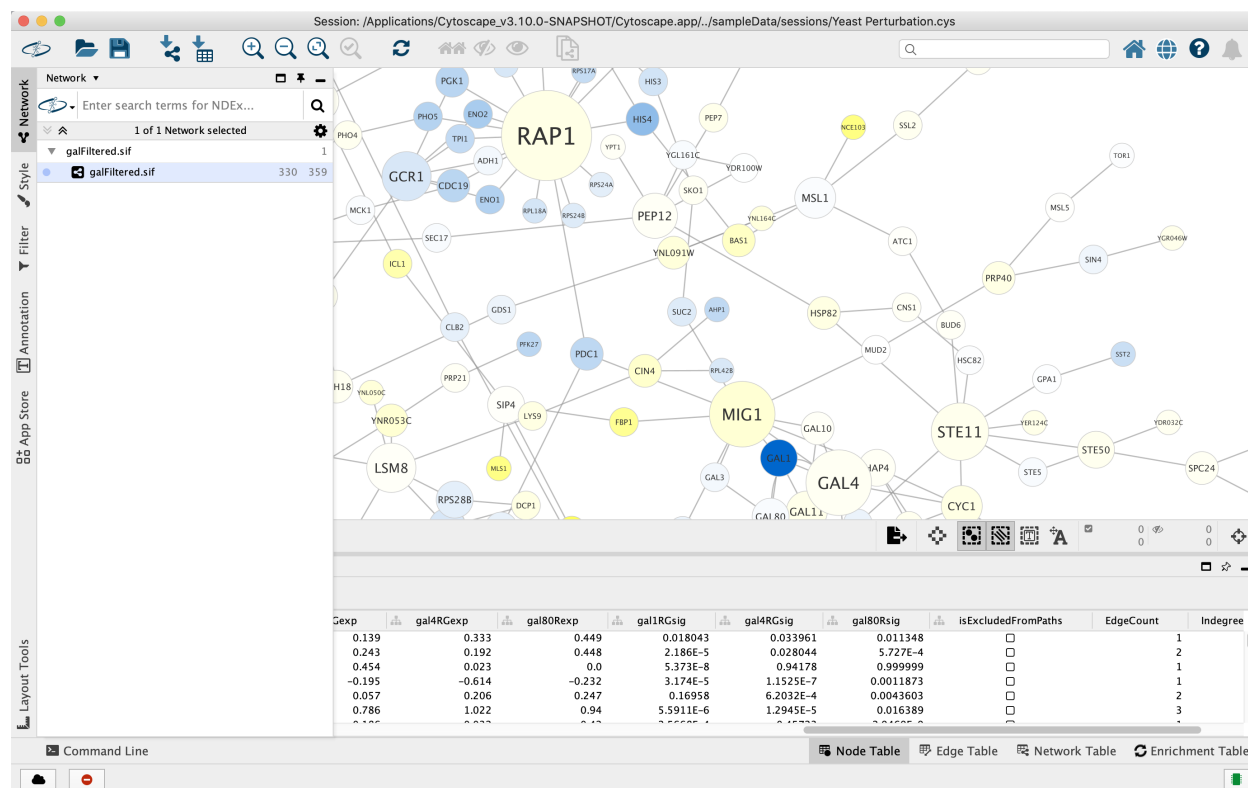
In the screenshot below, all panels are docked, except **Results** and **Command**, which are hidden:




- **Undocked:** A panel is undocked when the **Undock** icon  is clicked or a minimized panel is shown again by clicking one of its tabs on the sidebar. In this state, the panel is displayed over other panels but is still anchored to one of Cytoscape corners. That allows it to be resized more freely (vertically and horizontally) without affecting the size of other panels. You can also double-click the undocked panel's title bar to quickly maximize it. And double-clicking the title bar of a maximized panel again will restore it to its previous size. To

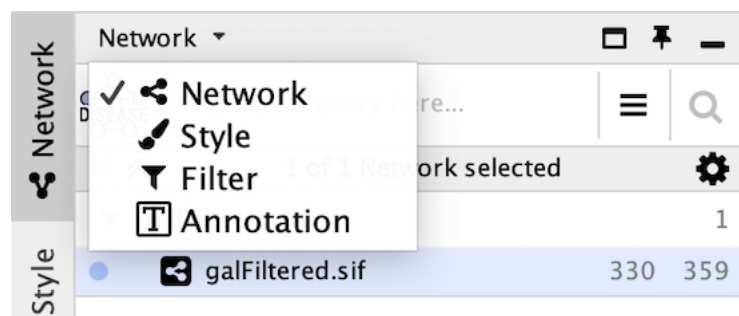
temporarily hide an undocked panel click the **Minimize** icon . An undocked panel will be automatically minimized when other panels or components outside the undocked panel are clicked.

In the example below, the **Control** panel is undocked:

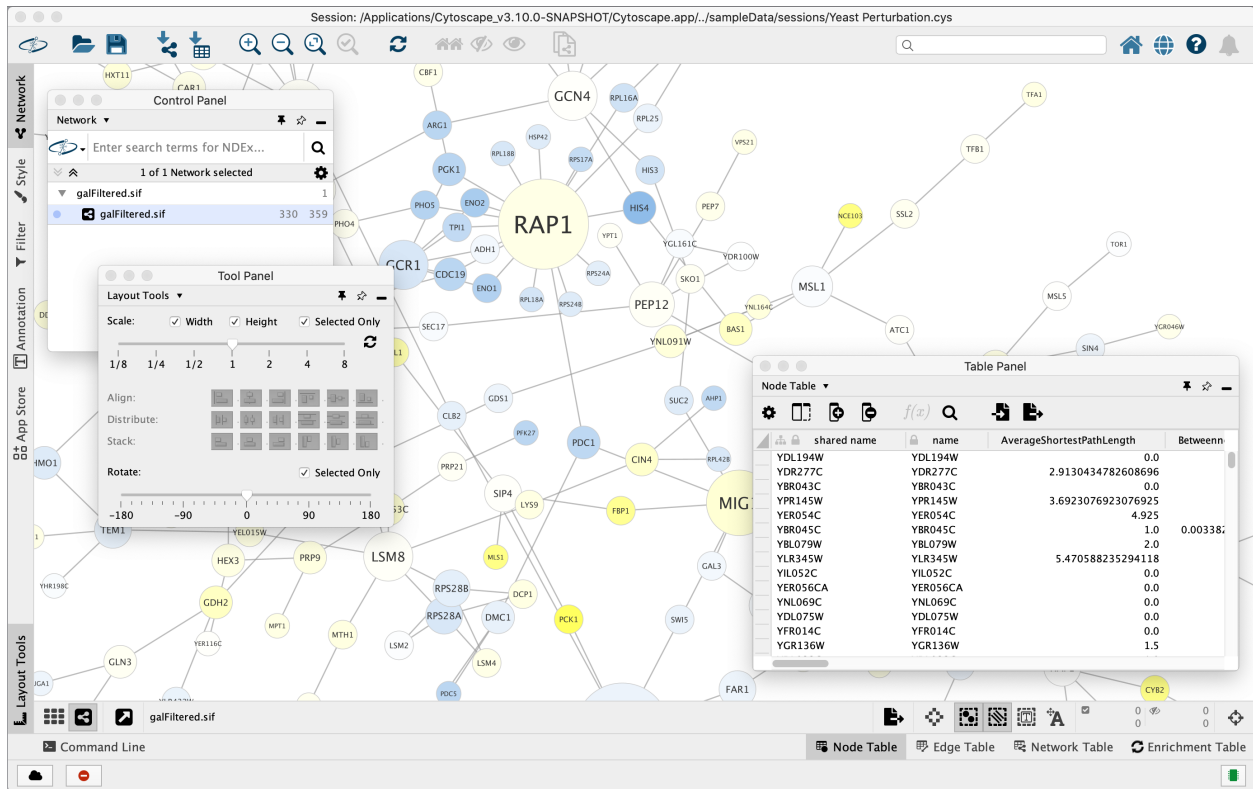


- **Floating:** Use the **Float** icon  to completely detach a panel from the Cytoscape desktop. A floating panel has its own window that can be resized, maximized and minimized like any other application window. It can also be moved to another monitor in a multi-monitor setup.

When a panel is floating, its tabs are not removed from the corresponding sidebar in the main desktop window, but you can also use the drop-down in the floating panel's title bar to show another tab's content:



In the image below, the **Control**, **Table** and **Tool** panels are floating:

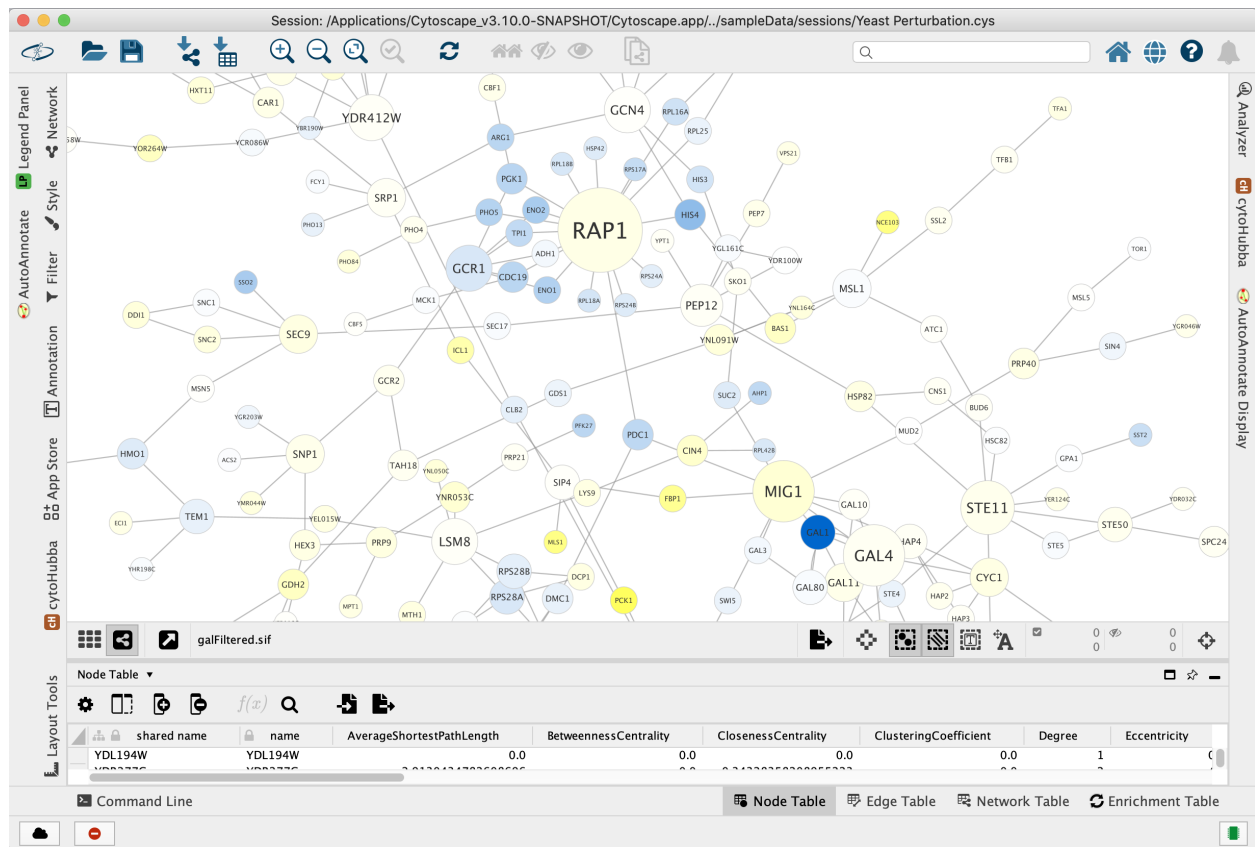


21.2 Other Features

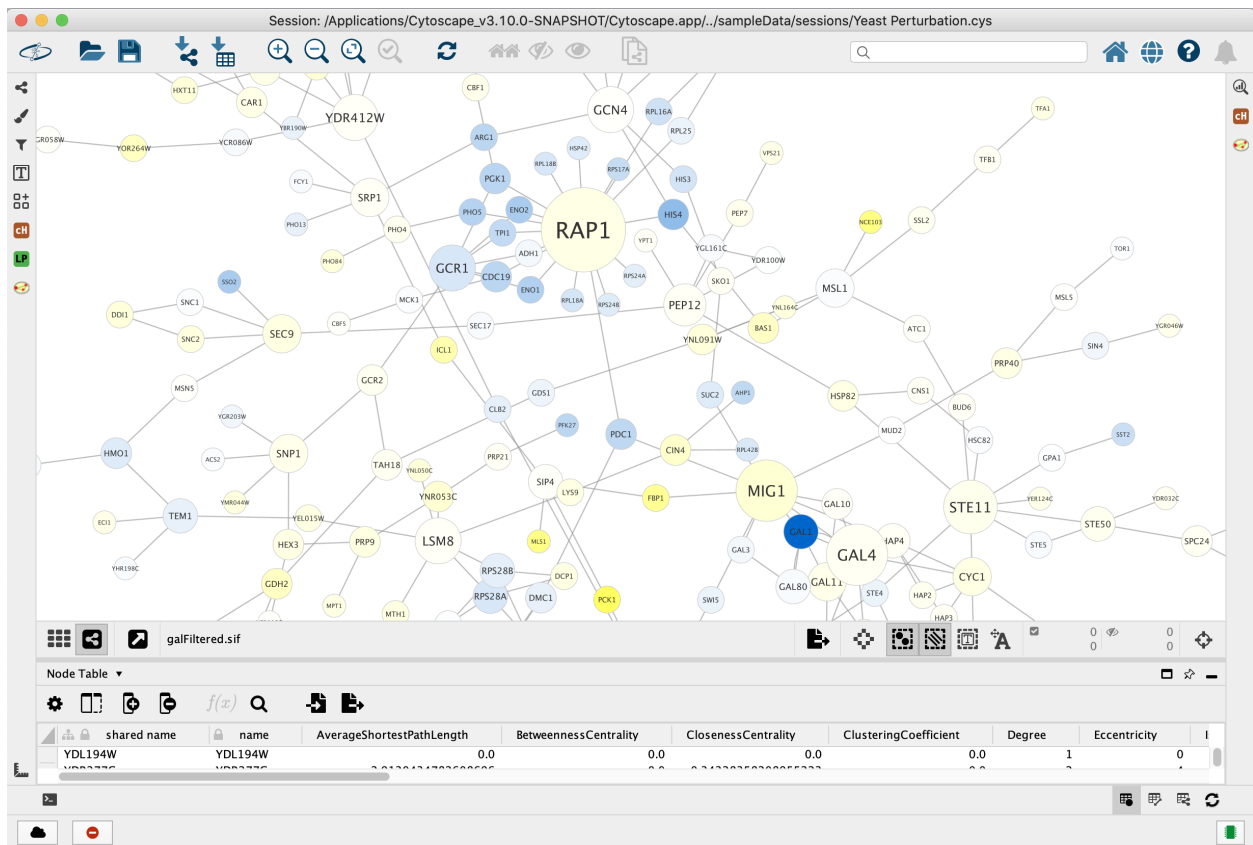
21.2.1 Hide Sidebar Labels

When you install and use Cytoscape apps, those apps may add their own tabs, which can sometimes lead to very busy sidebars. In order to make the sidebars cleaner and easier to use, Cytoscape allows you to hide the tab labels and show only their icons. Right-click anywhere on a sidebar and uncheck the context-menu option **Show Labels**.

In the example below, notice how the left sidebar is crowded with many tabs:



In the next example, the tab labels have been hidden:



22.1 What is Level of Detail (LOD)?


Cytoscape is able to display large networks (> 10,000 nodes) while maintaining interactive speed. To accomplish this goal the **level of detail (LOD)** used to display the network is chosen based on the number of nodes and edges currently being displayed. For example, by default, node labels (if present) are only rendered when less than 200 nodes are visible because drawing text is a relatively expensive operation. This can create some unusual behavior. If the screen currently contains 198 nodes, node labels will be displayed. If you pan across the network, such that now 201 nodes are displayed, the node labels will disappear. As another example, if the sum of rendered edges and rendered nodes is greater than or equal to a default value of 4000, a very coarse level of detail is chosen, where edges are always straight lines, nodes are always rectangles, and no anti-aliasing is done.

Additionally Cytoscape may temporarily lower the **level of detail** even more while the network is being interacted with (eg. panning, zooming, moving a node). For example edges and charts may not be displayed during interaction. When the network is no longer being interacted with it will be displayed again in higher detail.

Low LOD vs High LOD

With low LOD values, all nodes are displayed as square and anti-aliasing is turned off. With high LOD values, anti-aliasing is turned on and nodes are displayed as actual shape user specified in the Style.

22.1.1 Force to Display Detail

If you want to display every detail of the network at all times regardless of LOD values, you can toggle to full details mode by **View** → **Always Show Graphics Details** (or CTR+SHIFT+D on Windows/Linux, Command+SHIFT+D for Mac), or click the **Always Show Graphics Details** button  in the **Network View Tools**. This option forces the display of all graphics details. If the network is large, this option slows down rendering speed. To hide details, unselect the menu item (**View** → **Always Show Graphics Details**).

22.1.2 Parameters for Controlling LOD

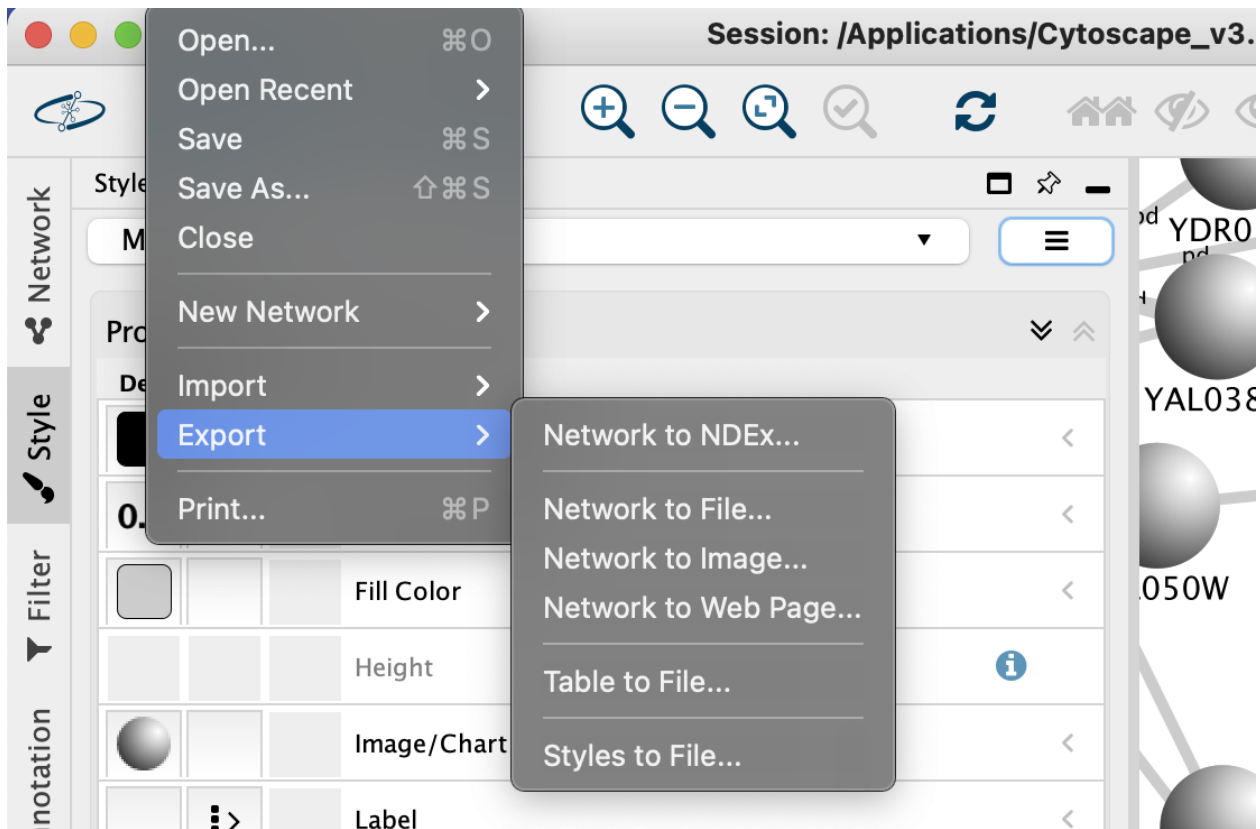
The default values used to determine level of detail can be changed by setting properties under **Edit** → **Preferences** → **Properties...**

NOTE: *The greater these thresholds become, the slower performance will become.* If you work with small networks (a few hundred nodes), this shouldn't be a problem, but for large networks it will produce noticeable slowing. The various thresholds are described below.

NOTE: Since Cytoscape 3.9 interactivity will always be maintained even when a high level of detail is chosen. It is generally safe to increase the level of detail or to force full graphics details even for very large networks.

When printing networks or exporting to formats such as PostScript, the highest level of detail is always chosen, regardless of what is currently being displayed on the screen.

23.1 Raw Data Export



To use data from Cytoscape networks in an external application, the data has to be exported. As a Cytoscape network consists of a number of different types of data, there are options in Cytoscape for each exportable data type. These

options (Network, Table, Styles) can be found on the **File** → **Export** submenu (shown above).

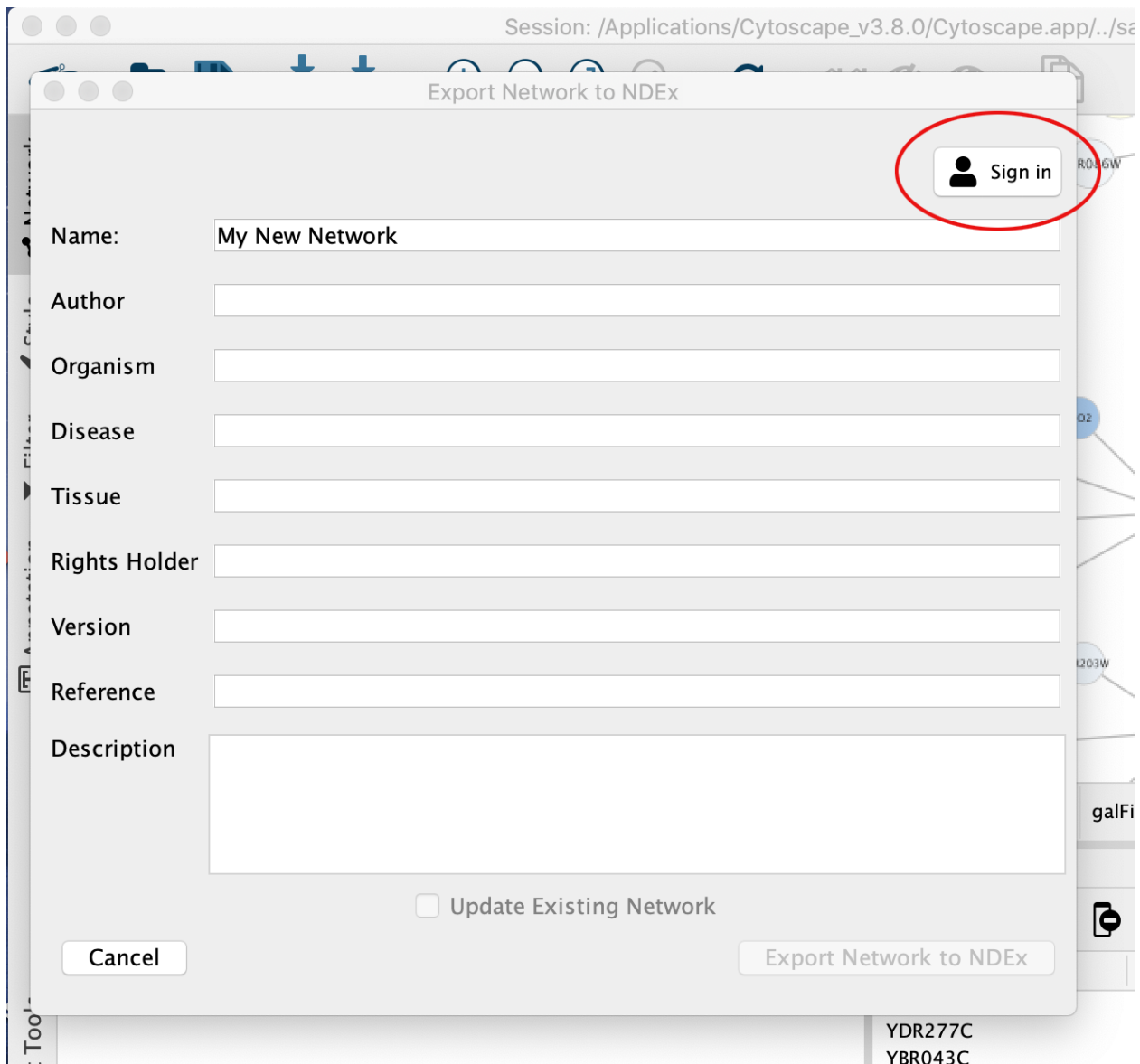
23.1.1 Network Data Exchange (NDEx) Public Database

The **Network to NDEx** option is used to store a network on the public NDEx server. You can use the NDEx public server to store your networks on the cloud, for [sharing networks](#) with collaborators, or to [archive networks](#) for publication. To store a network, you must first create a free NDEx account, which you can easily do by visiting the [NDEx Public Server](#) website.

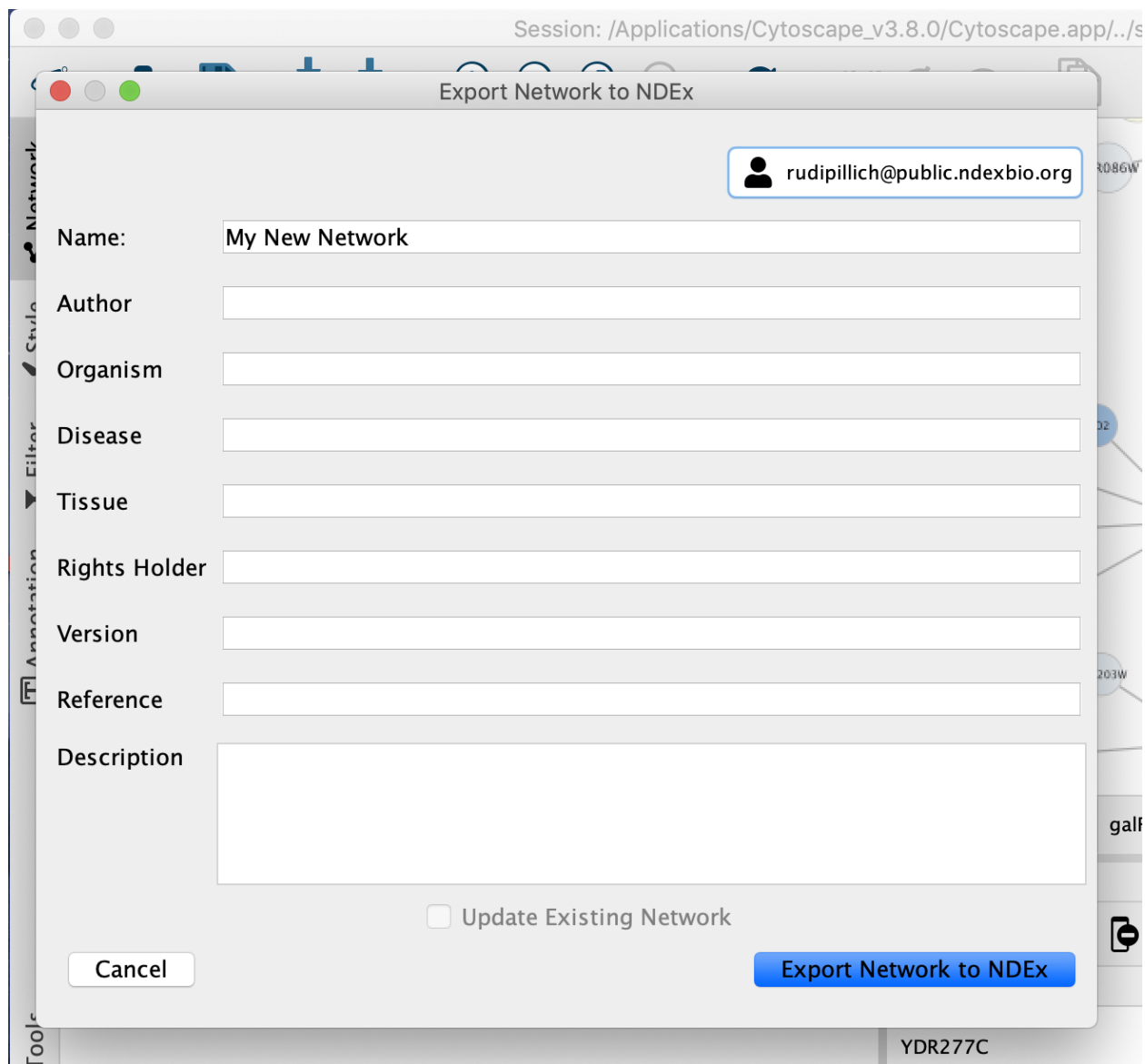
The **Network to NDEx** option saves only the currently selected network to your NDEx account. Such networks are suitable for processing by other applications and web services, as they contain only the nodes and edges in the selected network – other views and the nodes and edges unique to them are not written. If you later re-import this network (using the Cytoscape [Search bar](#)), only the single network you saved will be loaded.

When you select the option, the CyNDEx-2 Browser dialog will appear and enable you to provide various **metadata** to annotate the network and make it findable in subsequent NDEx searches. You can set the name of your network by editing the **Network Name** attribute. The **Update Existing Network** option enables you to overwrite the existing copy of the network (if you have permission to do so). We recommend to provide as much metadata as possible, and always provide at least **Version** and **Description** attributes.

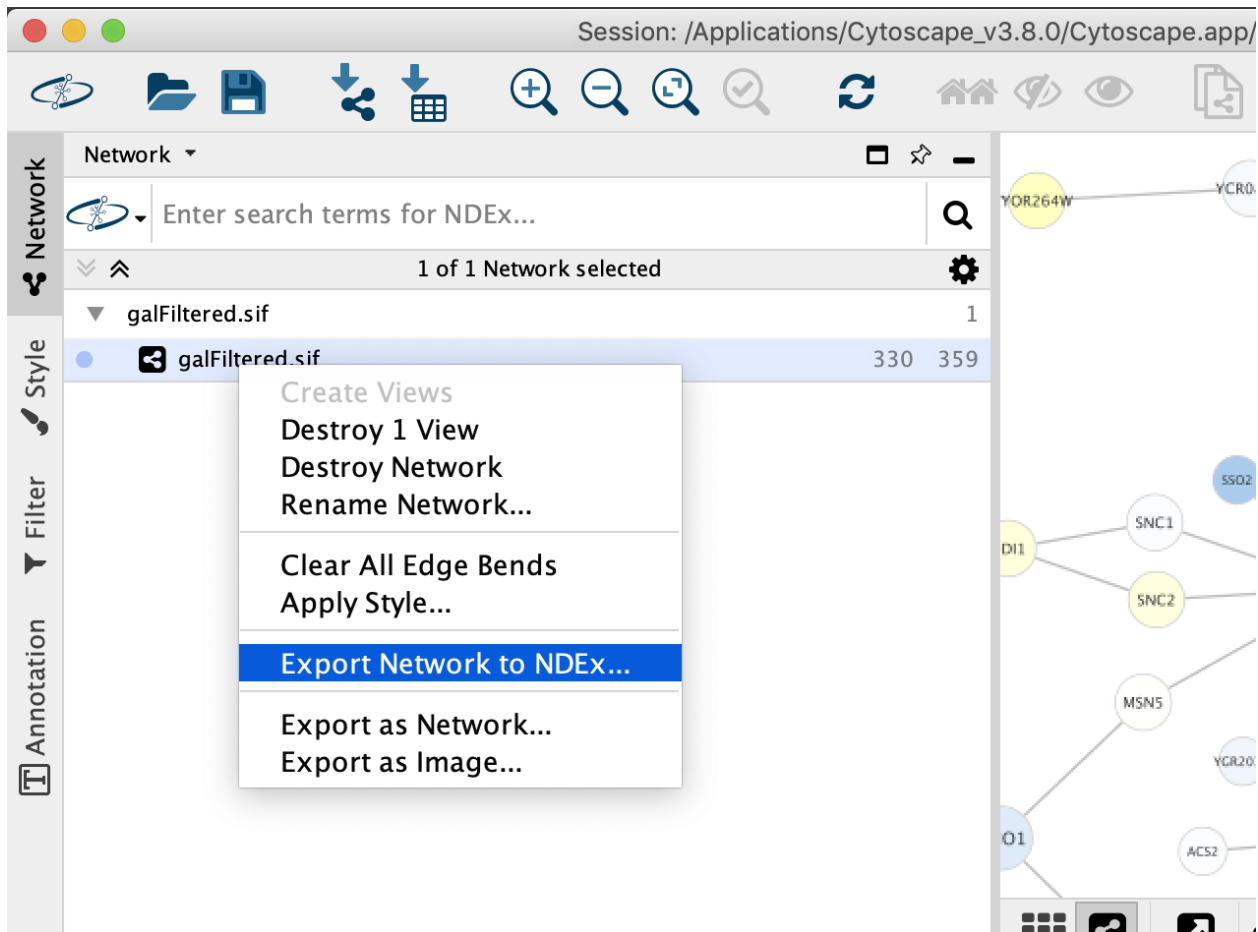
To export your network, you must first associate your NDEx account credentials with the CyNDEx-2 Browser by filling out the profile form (red oval in screenshot below).



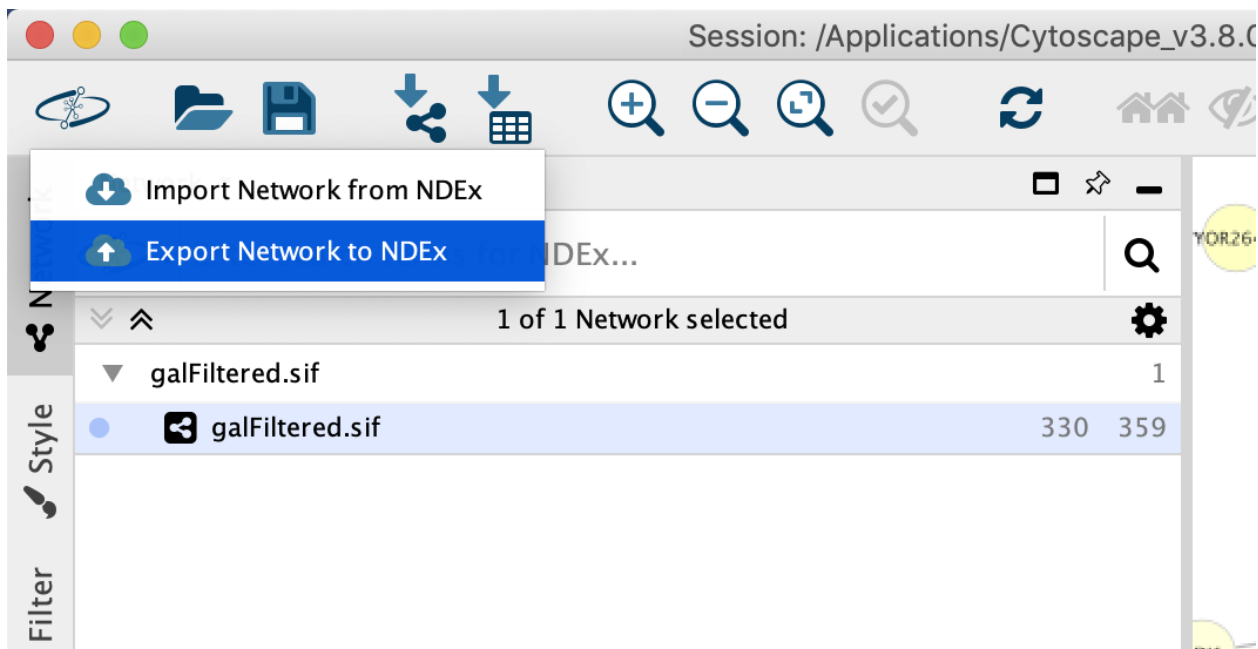
Once the profile is created, you are allowed to export your network to NDEx.



Export commands have also been added to the network and collection context menus in the Cytoscape Network panel, as another method of accessing the network save dialog.

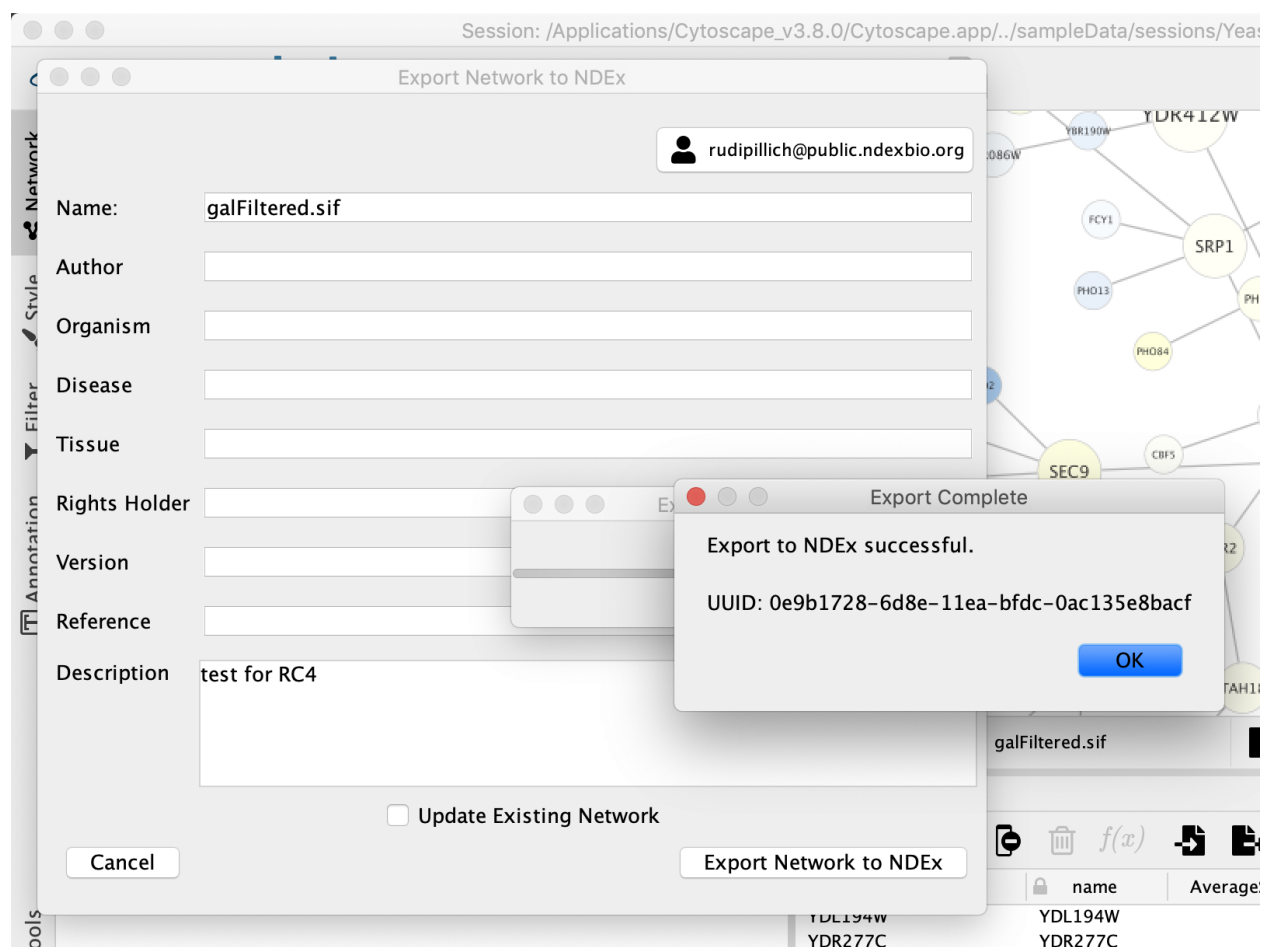


Finally, the NDEx button in the toolbar provides an additional convenient way to both Import and Export to NDEx.



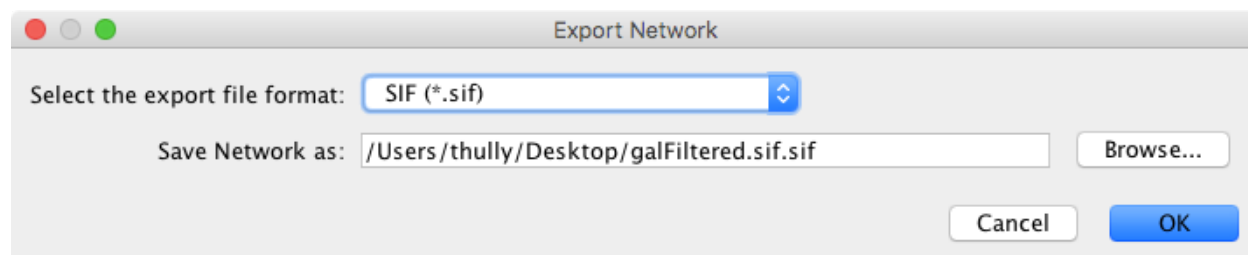
When the export operation is complete, a confirmation dialog will be displayed as shown below. If you want to share your network with external collaborators or for more sharing options, please refer to the guide for [Uploading and](#)

Sharing Networks in NDEx.



Further information on NDEx is available at the [NDEx Informational/Doc website](#).

23.1.2 Network



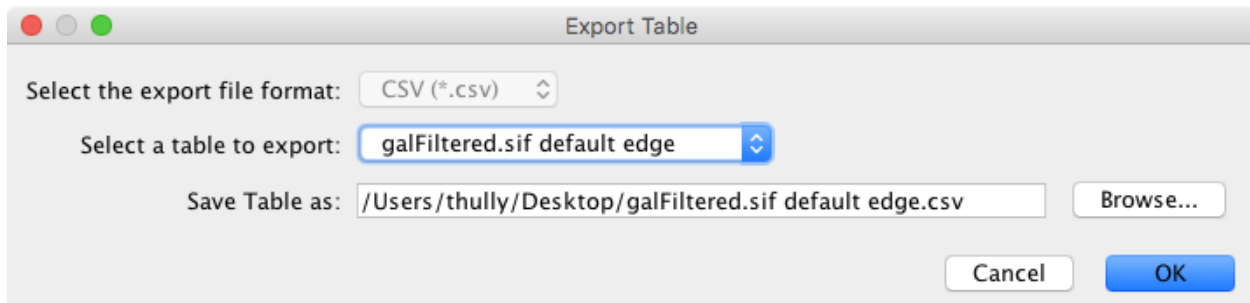
The **Network** option is used to export network data. Network data includes the nodes and edges in the network, and also will include data attributes and visual information if the chosen format supports it (like XGMML). Network data can be exported in a number of formats, including:

- SIF (Simple Interaction Format)
- NNF (Nested Network Format)
- XGMML
- GraphML

- PSI-MI Level 1 and 2.5
- Cytoscape.js JSON (can be used with Cytoscape.js, a tool described in future sections)
- CX JSON (for Cytoscape Cyberinfrastructure network exchange)

The default format is SIF, which is a simple tab-delimited network format that provides node names and edge interactions only. You can choose the format using the dialog drop-down box. A file name is automatically suggested based on the network name and selected format, with the file path defaulting to the current working directory. You can change the suggested file name/path using the text box or Browse button. Press **OK** to export with the selected options.

23.1.3 Table

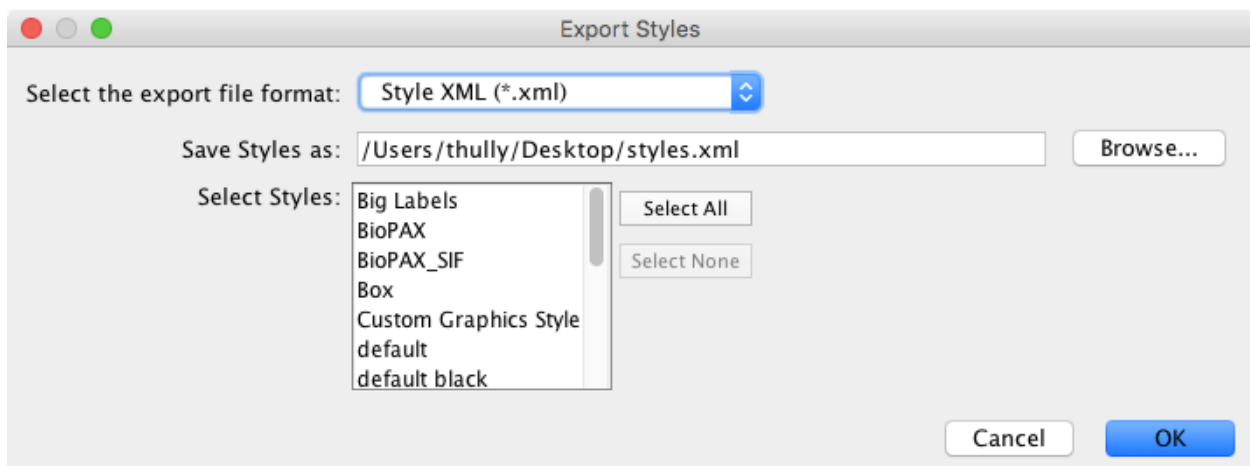


The **Table to File...** export option is used to export any of the data tables that are available in the current Cytoscape session. This includes the node, edge, and network tables that can be seen in the Table Panel, as well as any unassigned tables. The only currently supported file format currently for export is CSV (comma-separated value).

The export dialog for **Table** has only two selectable options - the table to export and the file name (file type is always CSV). A file name is suggested based on the name of the selected table with the path defaulting to the current working directory. As in Network, the suggested file name can be changed using the Browse button or the text field. Press **OK** to export the selected table with the given file name.

A shortcut button for **Export Table to File...** is also available in the **Table Panel** .

23.1.4 Styles



The **Styles** option is used to export one or more styles available in the current Cytoscape session. Supported formats include Style XML (which can be imported by 3.x versions of Cytoscape) or Cytoscape.js JSON (which can be used with Cytoscape.js, described in future sections).

Style export has three options - the export format (as described above), the style(s) to export, and the file name (a suggestion will be made based on the current directory and file type). As in Network → Table, the suggested file name can be changed using the Browse button or the text field. The list of styles is a multiple-selection list - one or more can be selected using Ctrl/Cmd-click (to select multiple discontinuous elements) or Shift-click (to select a contiguous element range). Press **OK** to export all selected styles with the given file path.

23.2 Exporting for Publication

When you finish your data analysis and visualization, you can publish your data to share the results. Cytoscape has several options to do this, with most options suitable for Cytoscape users and other options suitable for programmers wanting to create unusual or complex network viewers. These are further explained below.

- An NDEx network
- A session file
- A static image
- An interactive web application
- [CyNetShare](#)
- Full web application
- Simple network view (for web application developers)

23.2.1 As an NDEx Network

The easiest way to share your results with others is to save your network in the NDEx Public Database by using the [Network to NDEx](#) or [Collection to NDEx](#) options. Then, visit your NDEx account and enable the **Sharable URL** (similar to a Google Doc shared link) so that your private network can be accessed by whoever you send the link to.

NDEx also has additional options that enable you to:

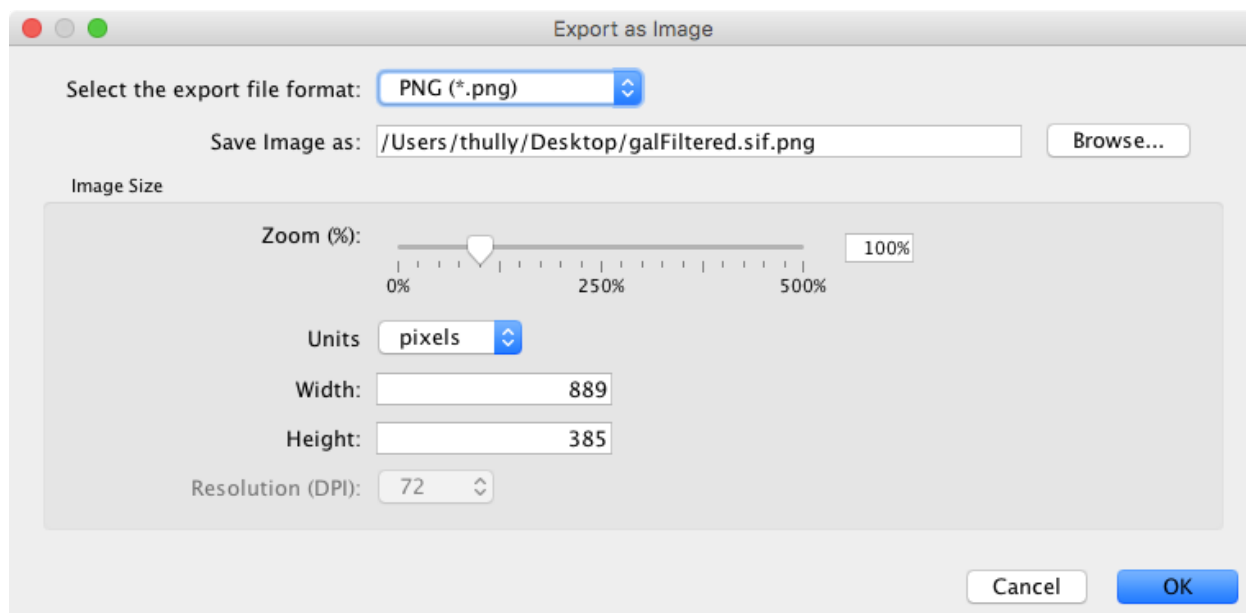
- request a **DOI** suitable for use in publications, grant applications or progress reports
- create working **groups** and specific sharing within NDEx.
- run different types of **queries** on your networks
- perform **enrichment analysis** on a variety of datasets, including curated pathways, large interactomes, drug-target association networks and many more.

For more information on NDEx publishing and sharing features, see the [Publishing in NDEx](#) and [Sharing Networks in NDEx](#) manuals.

23.2.2 As a Session File

Another easy way to share your results with others is simply saving everything as a session file (which is a zipped session archive). You can save your current session by clicking the **Save Session** icon. You can save to a thumb drive, a shared file system, or even a cloud drive directory such as Dropbox. If you save to a shared drive, beware not to have two people work on the same session file with Cytoscape at the same time, as unpredictable results may occur.

23.2.3 As a Static Image



Cytoscape can generate publication-quality images from network views. By selecting **File** → **Export as Image...**, you can export the current network view into the following formats:

- JPG
- PNG
- PS (Post Script)
- SVG
- PDF

The image export dialog has a variable number of options based on the file format selected, with file type and file name always being selectable. PNG and JPEG have options for scaling, while other formats only have a single option, **Export Text as Font**. The file name is suggested based on the name of the selected table with the path defaulting to the current working directory. As in raw data export, the suggested file name can be changed using the **Browse** button or the text field. Press **OK** to export an image with the given file name and parameters.

We recommend using **PDF** for publications because it is a standard vector graphics format, and it is easy to edit in other applications such as Adobe Illustrator.

Known Issues

For PDF export, there is an option to **Export text as font**. **This option does not work for two-byte characters such as Chinese or Japanese**. To avoid corrupted texts in the exported images, please uncheck this option when you publish networks including those non-English characters.

23.2.4 As an Interactive Web Application

The Web is an excellent platform for data sharing and collaboration, and Cytoscape (as of version 3.2.0) provides a number of ways to publish your network on the web, with each choice representing tradeoffs between ease, simplicity, and customization options. All solutions leverage the cytoscape.js drawing library, and so enable not only viewing but also Cytoscape-style interactive browsing of networks and attributes.

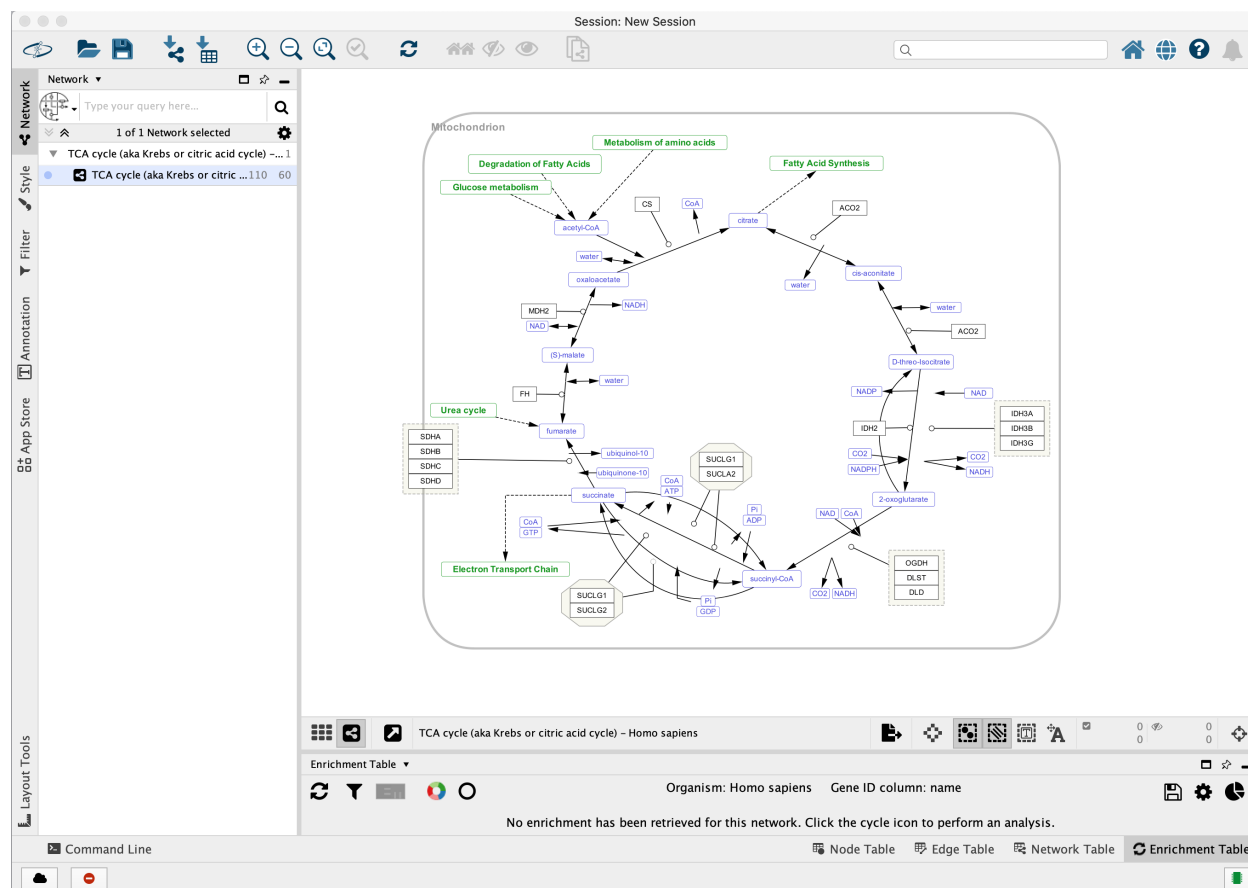
The simplest choice is [CyNetShare](#), where you save your network (and optionally a style) on a public file system, then interactively view the network in a browser. Like Google Maps, you can generate and publish a URL that allows collaborators to also view your network.

Alternatively, Cytoscape can generate an entire web site showing a single page containing the viewer with your network pre-loaded. You can load this directly onto your own web server to become part of your web site.

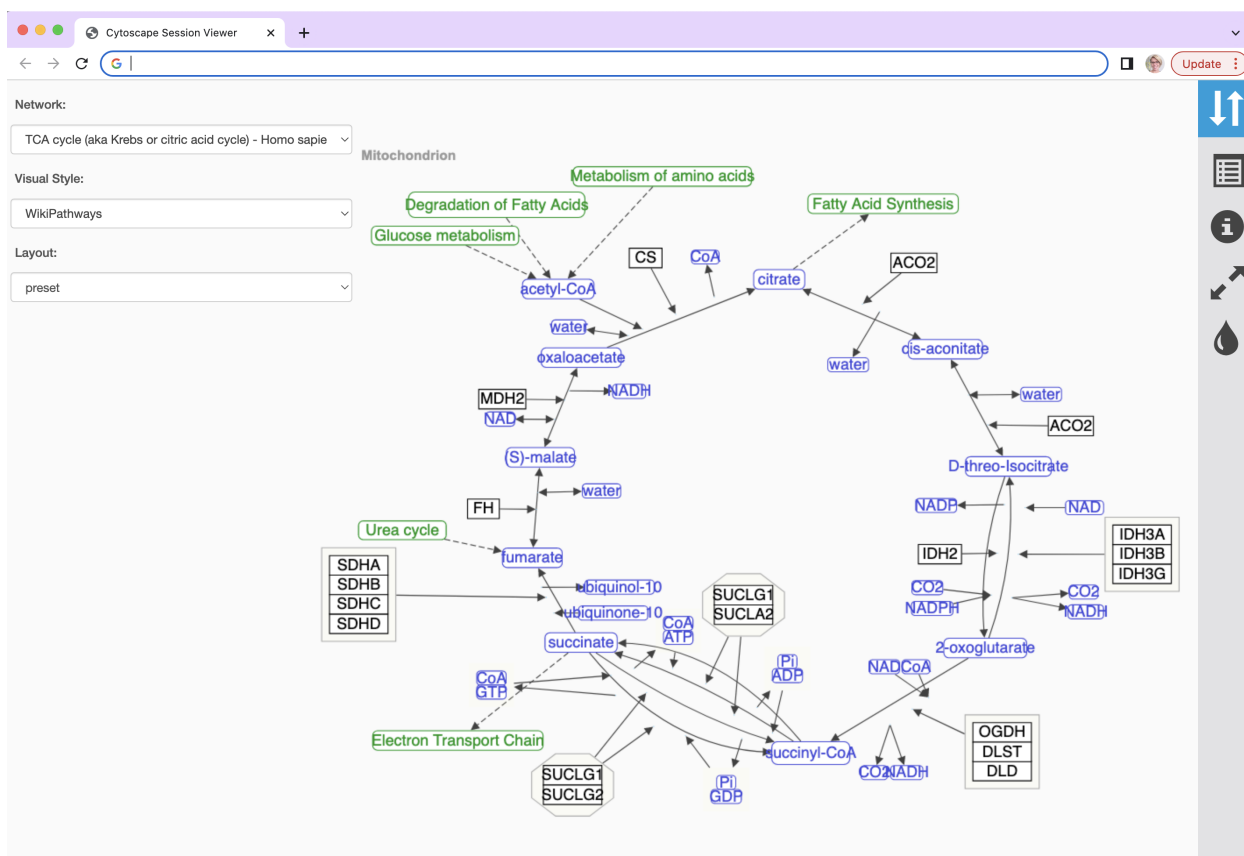
Finally, Cytoscape can generate the skeleton of a web site for further customization by [JavaScript](#) programmers.

These features are available as **Export** menu items under the **File** menu, and are described in sections below.

For example, here is a network in Cytoscape:



Here is the same network as an interactive web visualization:



Note that web browsers can render small networks (e.g., 1000 nodes) quickly and effectively, but attempting to render large ones (e.g., 5000 nodes) will take a very long time.

A word about exporting styles to interactive web applications: Our web applications are based on the `cytoscape.js` display library, which renders a subset of Cytoscape styles. For more information, see the **Export Styles to Cytoscape.js** section below.

Sharing via CyNetShare

CyNetShare is a browser-based web application that renders JSON-formatted networks and attributes saved in public directories. Optionally, you can specify styles that the web application will use to draw your network as it appears in Cytoscape. **CyNetShare** is similar to Google Maps in that once you have loaded your network and have tweaked its appearance to suit your needs, you can have **CyNetShare** generate a new URL that you can e-mail or post as a link on your own web site. That URL will bring up **CyNetShare** preloaded with your network for anyone to see.

To use **CyNetShare**:

1. Select **File** → **Export** → **Network to File...** to export your network to a public directory. Choose the *Cytoscape.js JSON (*.cyjs)* export file format.
2. Optionally, select **File** → **Export** → **Style...** to export your style settings. Choose the *Style for cytoscape.js (*.json)* export file format.
3. Use your public directory system to determine direct URLs for the files you exported.
4. Start **CyNetShare**
5. Enter the network's URL as the **Graph URL**.
6. Optionally, enter the style's URL.

7. Click the **Visualize** button.

The CyNetShare User Guide is provided on the [CyNetShare](#) web page.

Note that if you specify a style URL, the style is added to the list of styles available in [CyNetShare](#)'s Visual Style dropdown, and you can apply the style by selecting it in the list. [CyNetShare](#)'s initial display uses the visual style named **default** – use the Visual Style dropdown to choose the style in effect when Cytoscape generated the .cyjs and .json files.

Note that the mechanics of generating a URL for a file in a public directory system is a fast moving topic. Until recently, systems like Dropbox (and others) allowed users to create a URL that resolved directly to a file – a direct URL would be appropriate for use with [CyNetShare](#). As of this writing, some public directory systems (e.g., Dropbox) generate shareable URLs instead, which resolve to a web page that allows file download – a shareable URL doesn't work with [CyNetShare](#). Systems that offer shareable URLs may offer direct URLs as part of their premium (or Pro) package. To tell if your public directory system generates a direct URL, have it generate a URL for a file, then paste the URL into the address field of a browser and observe whether the browser displays the file itself (good!) or a download page for the file (bad!).

Hint: if Dropbox generates a shareable link that looks like `https://www.dropbox.com/s/w5e7towcchuvdeu/cynetwork.cyjs?dl=0`, you may be able to create a direct link by changing the `dl=0` to `dl=1`: `https://www.dropbox.com/s/w5e7towcchuvdeu/cynetwork.cyjs?dl=1`.

A simple strategy for always getting a direct URL is to store your file in a public directory served up by a web server, if you have access to one – a URL served by a web server might appear as: **`http://myserver.com/~mypublicdir/netstyle.json`**.

Alternately, you can use [Gist](#) to create a shareable document having a “direct” URL. To try this:

1. Use Cytoscape to generate your network as a .cyjs file on your local disk
2. Use an editor to open the file and copy its contents to the clipboard
3. Use a web browser to surf to [Gist](#)
4. Paste the contents into a Gist document
5. Select **Create public Gist**
6. Select **Raw** to place the direct URL into your browser's address field
7. Use that URL with [CyNetShare](#)

Generating a Full Web Application

The full page export option is designed for users who want to publish their network as a complete [single-page application](#). Cytoscape creates a zip archive containing a complete [JavaScript](#)-based web application that works as a basic viewer (like [CyNetShare](#)) for Cytoscape-generated network visualizations. You can unzip the archive onto a web server (or your PC) and view the network via a web browser on PCs and tablets.

The screenshot displays the Cytoscape Session Viewer window. The top toolbar includes icons for navigation and file operations. The main area shows a network diagram with nodes and edges. A sidebar on the right contains icons for showing/hiding the toolbar, table browser, selectors, fitting the network to the window, and setting the background color. The bottom section features a 'Table Browser' with two tabs: 'Node' and 'Edge'. The 'Node' tab is active, showing a table of node data.

Show/hide toolbar

Show/hide table browser

Show/hide selectors

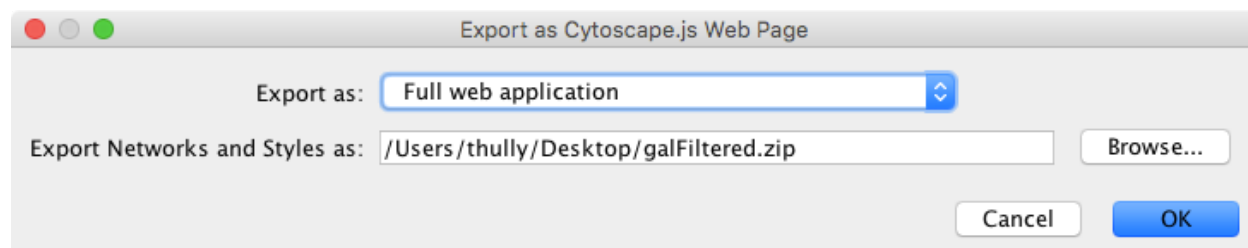
Fit network to window

Set background color

Table Browser

SUID	id	shared_name	selected	SUID	name
422	422	YNL216W	false	422	YNL2
433	433	YOL120C	false	433	YOL1
435	435	YNL301C	false	435	YNL3
439	439	YDR171W	false	439	YDR1
441	441	YBR093C	false	441	YBR0
443	443	YER074W	false	443	YER0

To generate an entire web page for all networks in the session as a zip archive, select **File** → **Export** → **Network to Web Page...** The following dialog will appear:

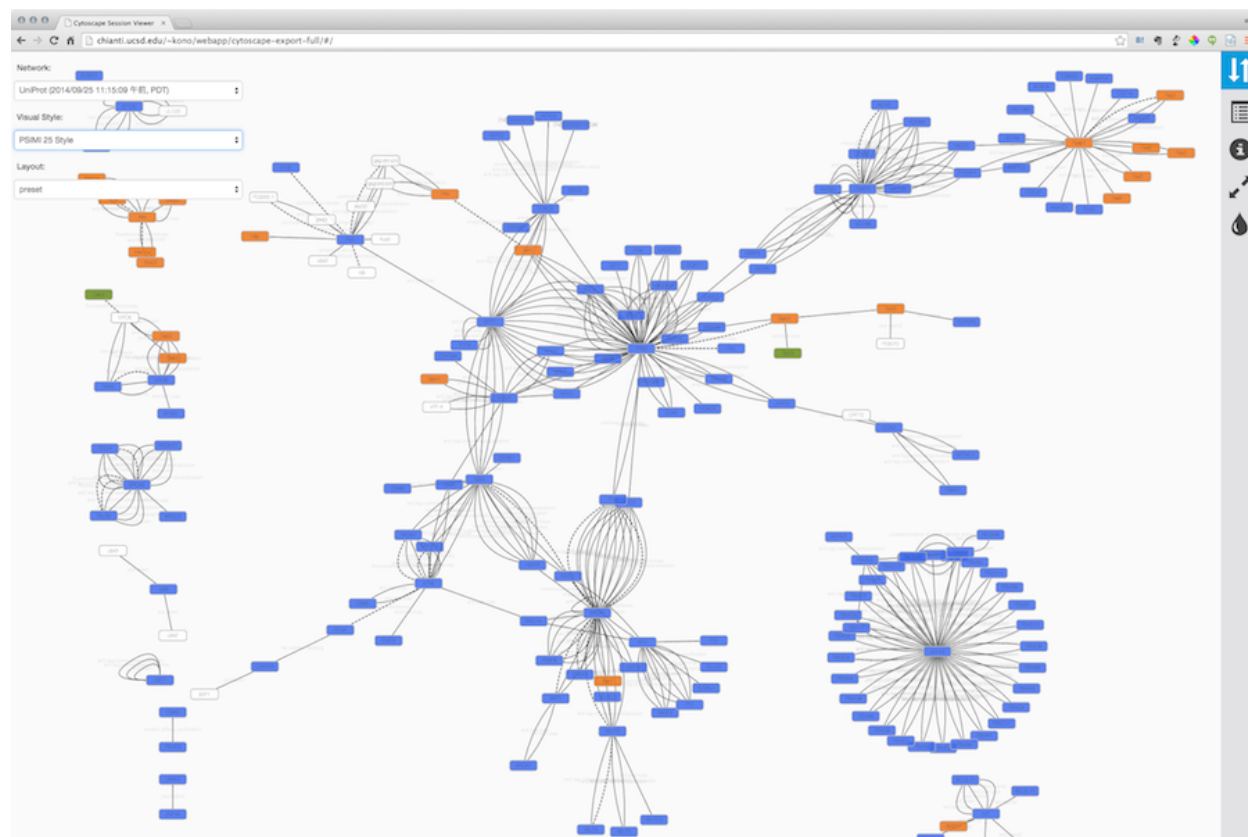


This simple dialog has only two options - the file name and the type of web export (full, simple network view, or JSON). For full web application, we use the default. The file name is suggested based on the name of the selected table with the path defaulting to the current working directory. As in raw data export, the suggested file name can be changed using the **Browse** button or the text field. Press **OK** to export a web archive with the given file name.

To view the web page, unzip the archive into a folder on your PC or web server. The folder will contain an **index.html** file, the network data, and other files. You can open the **index.html** file in your browser (usually from your browser's **File** → **Open** menu item.)

Here is an example exported file from Cytoscape:

- Example full export deployed to web server



Note that because Cytoscape uses the latest HTML5-based web technologies, it cannot support older or non-conformant web browsers such as Internet Explorer. We strongly recommend using the latest version of modern web browsers such as Google Chrome, Mozilla Firefox, or Apple Safari.

Extending the webpage with Cytoscape.JS functionality

As of version 3.6.2 of the JSON Support core app in Cytoscape, the user may add custom [Cytoscape.JS events](#) to the exported webpage. In the `web_session/scripts` directory, a `custom.js` file has been added with a designated spot for custom JS code.

For example, to add linkouts to nodes in the webpage (i.e. opening a URL specified by the `href` node attribute when the user clicks the node), the `custom.js` file should look like:

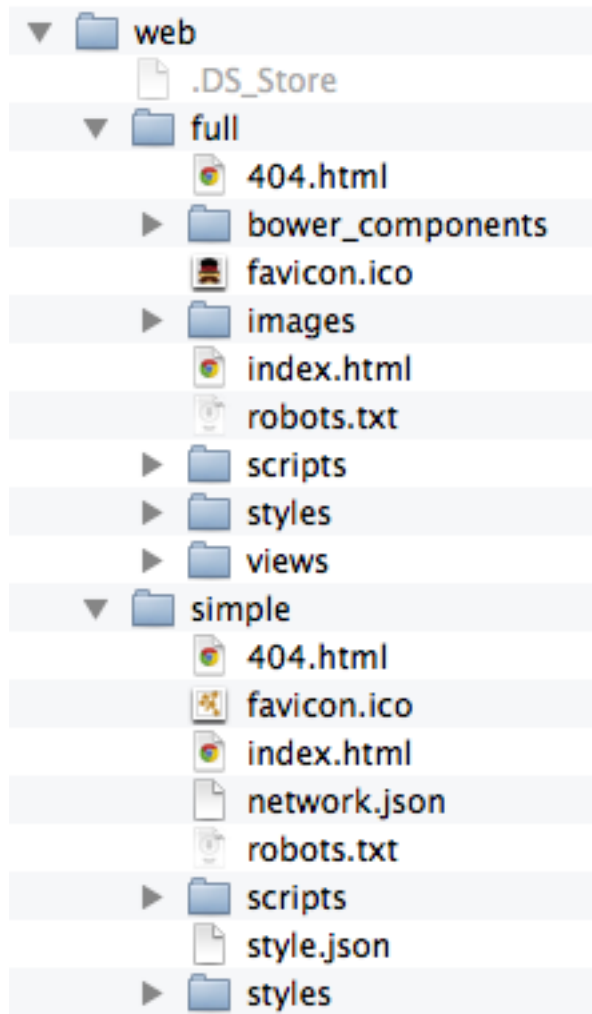
```
// Notice that the `cy` object may only be referenced
// after the document has finished loading.

$( document ).ready(function() {
  cy.on('tap', 'node', function() {
    try { // your browser may block popups
      window.open( this.data('href') );
    } catch(e) { // fall back on url change
      window.location.href = this.data('href');
    }
  });
});
```

This change has to be made each time you export a web page. If you want to change the default export template, refer to the next section.

Customize Export Template (For Web Application Developers)

The code generated by Cytoscape for the Full Web Application and the Simple Network View web applications is minimalistic. While you can directly modify this code yourself to create your own page design or add new features, the modifications will apply to a single exported network. If you are a web application developer, you can change the application code generated for **all** exports by editing HTML5 template code resource files in your `~/CytoscapeConfiguration/web` directory:



In this folder, you can find **full** and **simple** sub directories corresponding to Full Web Application and the Simple Network View described above.

Requirements

To build these project, you need the following tools installed:

- Node.js
- gulp
- grunt

Full Export Template

This is an AngularJS based web application built with grunt (at least for now – we have plans to migrate to gulp). Source code and more documentations are available here:

- <https://github.com/idekerlab/cyjs-full-export>

To build the project into *dist* directory, type:

```
grunt
```

Simple Export Template

This template is generated by a simple `gulp` project. The source code is available here:

- <https://github.com/idekerlab/cyjs-export-simple>

To build the project into *dist* directory, type:

```
gulp
```

Use Your Custom Templates for Export

Once you have your own builds, you can deploy your templates by replacing the contents of *full* and *simple* with your own builds.

Cytoscape and OpenCL (Computing on the GPU)

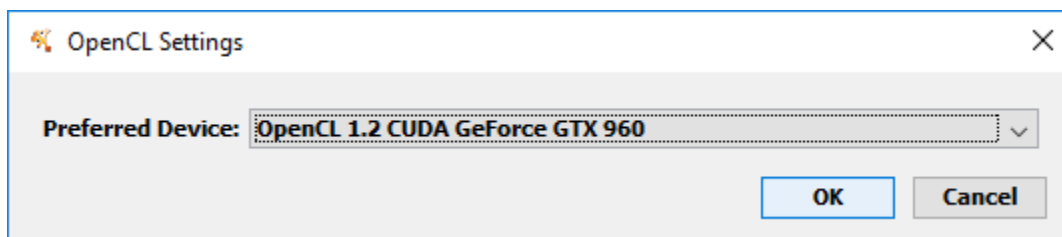
24.1 What it is for?

Cytoscape has basic support for offloading computationally intensive tasks for parallel processing on a GPU, multicore CPU or a multiprocessor card using [OpenCL](#). The OpenCL support in Cytoscape is mostly intended to provide a unifying OpenCL access for third-party Cytoscape Apps, but some core functionality (Prefuse layout) also has OpenCL implementation for increased performance.

As OpenCL can run on almost any device, including desktop computers without dedicated GPUs, you should be able to use OpenCL functionality on any platform where you can run Cytoscape, although you may need to install additional drivers for your device.

24.2 Setup & Configuration

The CyCL core app (should be already part of your Cytoscape distribution) lets you see the available OpenCL devices and configure your preferred device for OpenCL computation. You can see available OpenCL devices and configure your preferred device for OpenCL, select **Edit** → **Preferences** → **OpenCL Settings...**:



In most cases, you want your preferred device to be your GPU (if you have one). If you do not see the device you intend to use (or any device at all) in the configuration window, you may need to install OpenCL drivers. For GPUs from major manufacturers, OpenCL drivers are usually installed with the graphics driver. If you have installed the latest graphics drivers and still do not see your device in the list, check the website of your GPU manufacturer. To use

OpenCL on a CPU (i.e., on any desktop computer) or a Xeon Phi, you need to install the drivers separately from the web page of the manufacturer of your CPU.

Drivers for Intel CPUs can be downloaded at https://software.intel.com/en-us/articles/opencl-drivers#latest_CPU_runtime - look for *runtime-only*. AMD requires you to find drivers per device for older hardware or use ROCm: <https://github.com/RadeonOpenCompute/ROCm/wiki#What-Is-ROCm>.

Warning: After you have just installed drivers for your OpenCL device, Cytoscape may require restarting to be able to see the device.

24.3 OpenCL/GPU Troubleshooting

If any OpenCL app is not working, here are some of the common causes:

24.3.1 No OpenCL devices are available

Diagnosis and treatment: See *Setup and configuration* above.

24.3.2 The Cytoscape console says “Could not find OpenCL.dll”

Treatment: Make sure your Windows OS directory containing OpenCL.dll is listed in the value of the Java system property `java.library.path` (OpenCL.dll can usually be found in `%windir%\SysWOW64%` or `%windir%\system32`). You can modify `java.library.path` by adding a line of the form `-Djava.library.path=path1;path2` to the `Cytoscape.voptions` file. `Cytoscape.voptions` can be found in the Cytoscape installation directory.

24.3.3 The computer is unresponsive for a while and then resets the screen while running OpenCL on the GPU.

Treatment: This problem arises if you run computations on the GPU that also handles your main display and the computation occupies the GPU for too long, preventing the operating system (e.g., Windows) from updating the display. If the operating system detects this, it terminates the GPU computation. You can either try to run smaller chunks of the computation or configure the **Timeout Detection and Recovery** (TDR) to let the computation complete even if the system becomes unresponsive. Further info can be found at [this NVidia thread](#) or [Microsoft webpage](#). Microsoft also has [documentation for the registry keys that need to be changed](#).

24.3.4 My problem is not listed here

Try to install drivers for your CPU and run on the CPU platform (see links above). CPU platforms offer lower performance, but are generally more reliable. If this does not help you, ask for help in a [Cytoscape-tagged StackOverflow post](#).

25.1 What is Cytoscape.js?

The screenshot shows the Cytoscape.js website. The left sidebar contains a table of contents with links to Introduction, Downloads, Roadmap, Notation, Selectors, and Style. The main content area features the title 'Cytoscape.js 2.0.3' and a description: 'A JavaScript graph library for analysis and visualisation (compatible with CommonJS/Node.js, jQuery 1.4+, and plain JavaScript)'. Below this are links to GitHub, Downloads, Live code examples, Twitter, Previous questions, Ask a question, File an issue, and Future version milestones. A paragraph states: 'This is how easy it is to get started with Cytoscape.js (this code creates the instance you see on the bottom-right:'. Below this is a code block showing the initialization code for Cytoscape.js, and a small graph visualization with four nodes: Jerry, Elaine, Kramer, and George, connected by directed edges.

Table of contents [top](#)

- Introduction
 - About
 - Cytoscape.js & Cytoscape
 - Funding
- Downloads
 - 2.0
- Roadmap
- Notation
 - Architecture & API
 - Notation
 - Position
 - Elements JSON
- Selectors
 - Notes & caveats
 - Group, class, & ID
 - Data
 - Compound nodes
 - State
- Style
 - Format
 - Properties
 - Mappers

Cytoscape.js 2.0.3

A JavaScript graph library for analysis and visualisation (compatible with [CommonJS/Node.js](#), [jQuery 1.4+](#), and plain JavaScript)

[GitHub](#) | [Downloads](#) | [Live code examples](#) | [Twitter](#) | [? Previous questions](#) | [Ask a question](#) | [File an issue](#) | [Future version milestones](#)

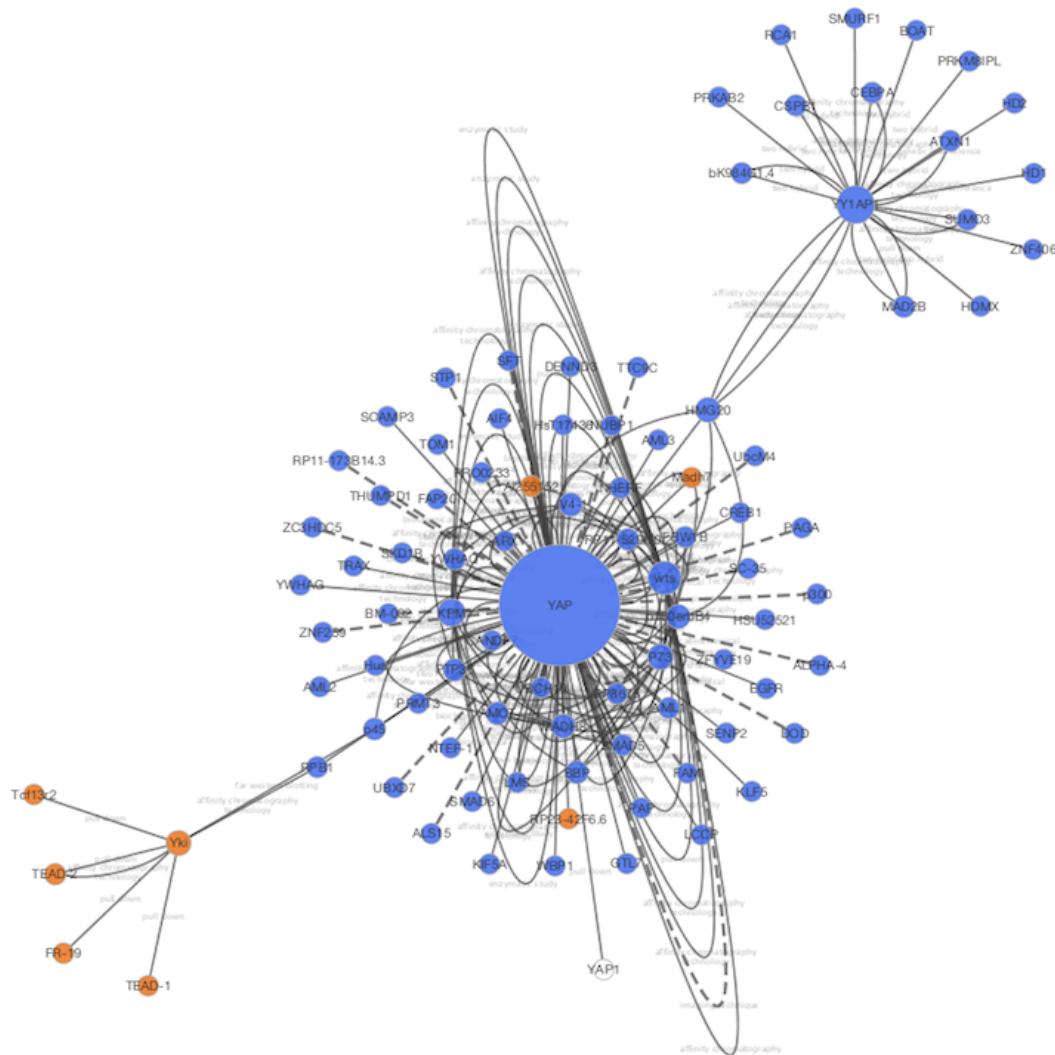
This is how easy it is to get started with Cytoscape.js (this code creates the instance you see on the bottom-right:

```
$(loadCy = function(){  
  
  options = {  
    showOverlay: false,  
    minZoom: 0.5,  
    maxZoom: 2,  
  
    style: cytoscape.stylesheet()  
      .selector('node')  
      .css({  
        'content': 'data(name)',  
        'font-family': 'helvetica',  
        'font-size': 14,  
        'text-outline-width': 3,  
  
      })  
  
  })  
  
  // ...  
  
  // Show all the code...
```

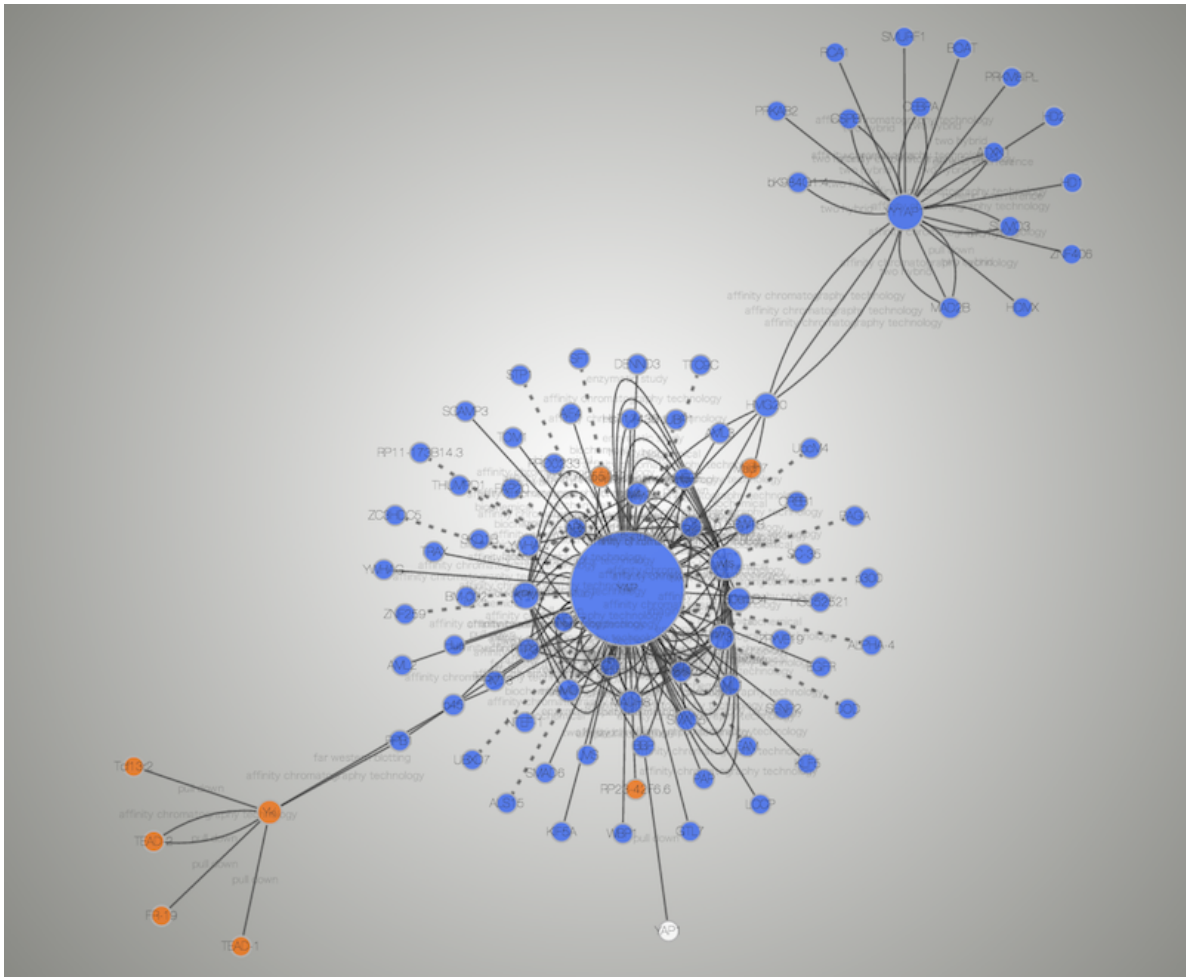
Cytoscape.js is a **JavaScript library** for interactive network visualization. It is a building block for web applications and is **NOT** a complete web application. If you have network data sets and want to share visualizations created with Cytoscape, you can build your own website using Cytoscape.js and this new **Export to Cytoscape.js** feature.

25.1.1 Examples

- A network visualized with Cytoscape 3.1.0



- Same network exported to Cytoscape.js (Rendered with Google Chrome and Cytoscape.js 2.0.3)



25.1.2 Differences and Shared Concepts

Although Cytoscape and Cytoscape.js are two completely independent software packages, they are sharing higher level concepts. The following is the list of similarities and differences between the two:

Cytoscape

- **Desktop application** for network visualization written in [Java programming language](#)
- Needs desktop or laptop computers to run
- Users have to install Java runtime
- High performance application for large scale network analysis and visualization
- Expandable by [Apps](#)
- Use **Styles** to map data to network properties, such as node color, edge width, node shape, etc.

Cytoscape.js

- A [JavaScript library](#) for network visualization, **NOT** a complete web application nor mobile app

- Runs on most of modern web browsers, including tablets and smart phones
- No plugins are required to run. Modern web browser is the only requirement
- Need to write code to set up your web site or web application
- Expandable by [Extensions](#)
- Use **CSS-based Styles** to map data to network properties

In a long term, Cytoscape and Cytoscape.js will be more integrated, and as the first step Cytoscape now supports reading and writing Cytoscape.js network/table JSON files. In addition, Cytoscape can convert *Styles* to Cytoscape.js Style object.

25.2 Data Exchange between Cytoscape and Cytoscape.js

Since Cytoscape.js is a JavaScript library, its basic data exchange format is **JSON (JavaScript Object Notation)**. All of these import/export functions are part of standard Cytoscape user interface, and you can read/write Cytoscape.js JSON files just like other standard files such as SIF.

25.2.1 Export Network and Table to Cytoscape.js

Cytoscape.js stores network data (graph) and its data table in the same object. Cytoscape writes such data complex as JSON, i.e., both network and data tables will be exported as a single JSON file. You can select a network and export it from **File → Export → Network to File...** and select **Cytoscape.js JSON (*.cyjs)** as the file type.

Cytoscape only supports one of the Cytoscape.js supported JSON formats, which is:

```
{
  elements:{
    nodes:[],
    edges:[]
  }
}
```

SUID will be used as unique identifier for nodes and edges in the JSON. For more information about this format, please visit [Cytoscape.js web site](#).

Important Note about Data Compatibility

Cytoscape creates JSON file directly from data table and tries to extract as much data as possible from the original table. However, since table column names will be directly converted into **JavaScript** variable names, invalid characters will be replaced by underscore (_):

- Original Data Table Column Names:

```
Gene Name
KEGG.pathway
```

- The Names above will be replaced to:

```
Gene_Name
KEGG_pathway
```

You should be careful when you plan to use this feature for data roundtrip: from Cytoscape to Cytoscape.js back to Cytoscape. For such use cases, **we strongly recommend to use JavaScript-safe characters only in your table column names**. Naming your columns only with alphanumeric characters and underscore (`_`) is the best practice. (For actual data entries, all characters are allowed. This restriction is only for table column names.)

25.3 Export Styles to Cytoscape.js

Cytoscape and Cytoscape.js are sharing a concept called **Style**. This is a collection of mappings from data point to network property. Cytoscape can export its Styles into CSS-based Cytoscape.js JSON.

You can export all styles into one JSON file from **File → Export → Styles to File...** and select **Style for cytoscape.js (*.json)** as its format.

25.3.1 Limitations

Cytoscape.js does not support all of Cytoscape Network Properties. Those properties will be ignored or simplified when you export to JSON Style file.

Currently, the following Visual Properties will not be exported to Cytoscape.js JSON:

- Custom Graphics and its positions
- Edge Bends
- Tooltips
- Node Label Width
- Node Border Line Type
- Arrow Colors (they are always same as edge color)

25.3.2 Cytoscape.js and Cytoscape Compatibility

Cytoscape's network rendering system is designed for desktop use, while the browser-based renderer incorporates web technologies (e.g., cytoscape.js and Cascading Style Sheets). As a result, most but not all networks will render the same in the browser as in Cytoscape. Cytoscape visual styles not supported in the web browser are ignored. A complete compatibility list is available [here](#).

25.3.3 Import Cytoscape.js data into Cytoscape

Cytoscape.js network JSON files can be loaded from standard Cytoscape file menu: **File → Import → Network ...**. Both File and URL are supported.

25.4 Build Your Own Web Application with Cytoscape.js

Although Cytoscape can export networks, tables, and Style as Cytoscape.js-compatible JSON, users have to write some **JavaScript** code to visualize the data files with Cytoscape.js. Details of web application development with Cytoscape.js is beyond the scope of this document. If you need examples and tutorials about web application development with Cytoscape.js, please visit the following web site:

<https://github.com/cytoscape/cyjs-sample/wiki>

25.4.1 Questions?

If you have questions and comments about web application development with Cytoscape and Cytoscape.js, please send yours to [our mailing list](#).

Cytoscape's intuitive graphical user interface is useful for *interactive* network data integration, analysis, and visualization. It provides great features for exploratory data analysis, but what happens if you have hundreds of data files or need to ask someone to execute your data analysis workflows? It is virtually impossible to apply the same operations to hundreds of networks manually using a GUI. More importantly, although you can save your *results* as session files, you cannot save your *workflows* if you perform your data analysis with point-and-click GUI operations. Cytoscape has several options that support automating your workflows, all under the umbrella of Cytoscape Automation. More tutorials and examples are available at the [Cytoscape Automation web page](http://automation.cytoscape.org) (<http://automation.cytoscape.org>).

26.1 R and Python Packages

If you are already using R or Python, then you're in luck! There are packages available in these languages filled with helper functions to make accessing and controlling Cytoscape quick and intuitive.

The R package is called **RCy3** and is available via Bioconductor, see <https://www.bioconductor.org/packages/release/bioc/html/RCy3.html>. The RCy3 repo offers a nice interface for browsing the documentation and available vignettes (see Articles menu): <http://cytoscape.org/RCy3/index.html>. There are also a collection of video tutorials on the [Cytoscape YouTube channel](#).

The Python package is called **py4cytoscape**.

26.2 Commands

The **Commands** feature allows you to script a sequence of Cytoscape commands and menu items, where commands can have parameter values that would normally be provided by a user via a Cytoscape dialog box. For example:

```
session open file="C:\\myfile.cys"
```

loads a session from a file similarly to the **File** → **Open...** menu item. Commands may resolve to Cytoscape core functions or automation-enabled apps installed in Cytoscape. You can create a command script file that Cytoscape

can execute via the **Tools** → **Execute Command File...** menu item or on the Cytoscape command line at startup.

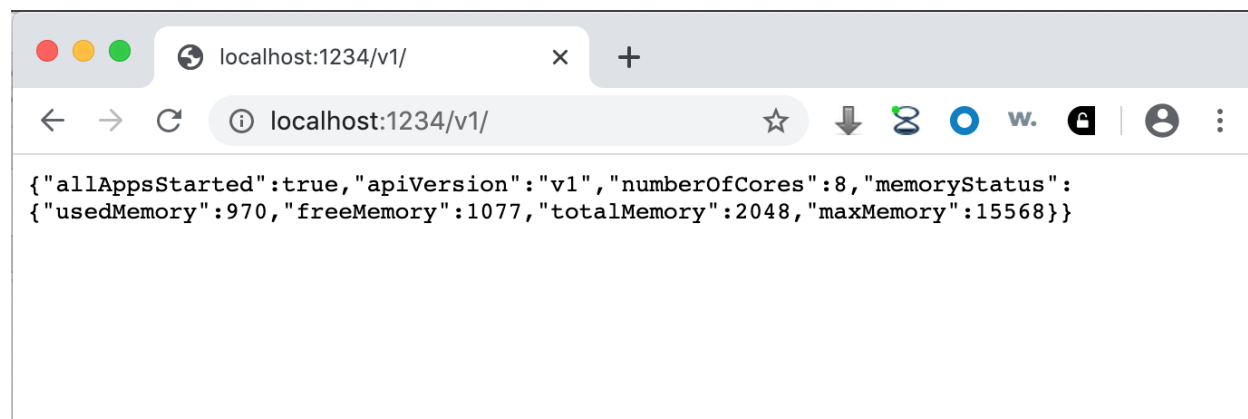


Commands is the built-in Cytoscape feature to automate your workflow as simple script. You can learn more about Commands in the [Command Tool](#) section.

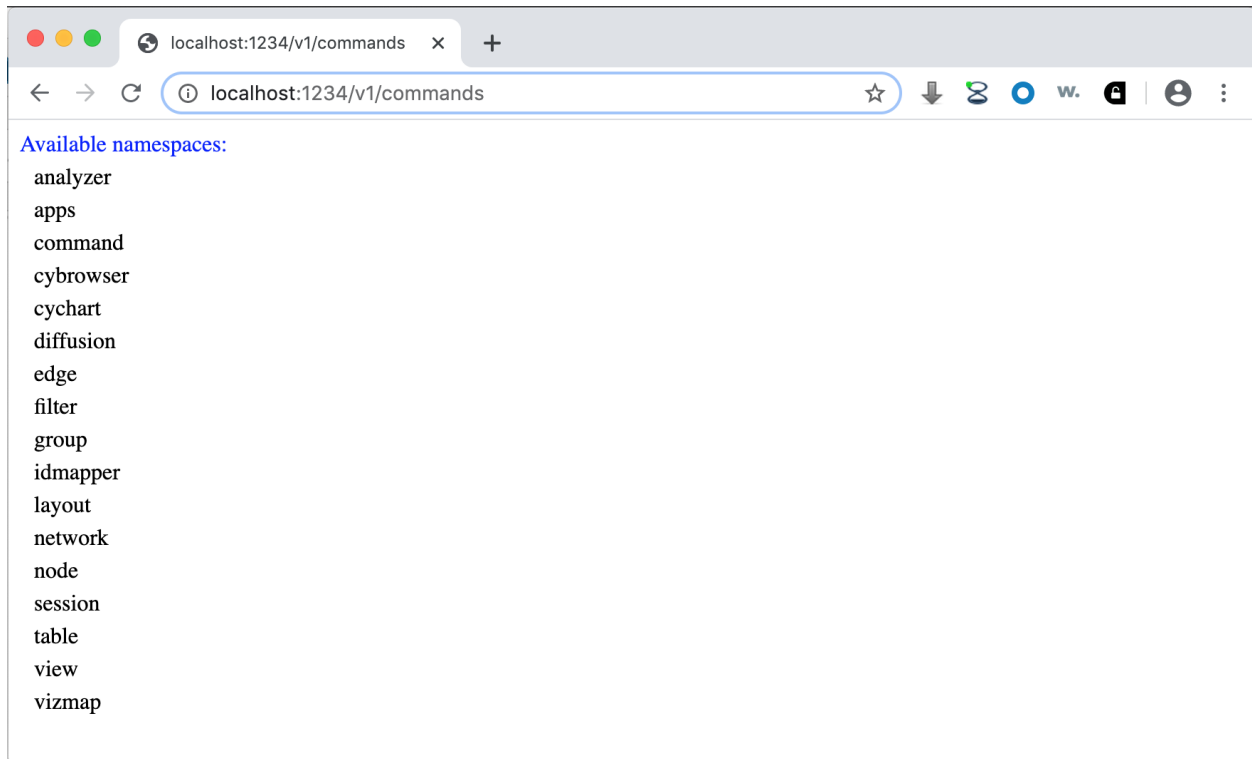
26.3 CyREST Interface Layer

In some cases, you may need to leverage the complex control and data structures available in a fully featured programming language, such as [R](#), [Python](#), [Ruby](#) or [JavaScript](#). Such languages enable complex Cytoscape-centric workflows or the integration of Cytoscape into larger workflows. Cytoscape enables programmatic access to both its Commands and Functions via its CyREST interface.

By default, the CyREST interface is enabled and available on TCP/IP port 1234. To verify this, start a web browser on your Cytoscape workstation and navigate to either **<http://localhost:1234/v1/>** or **<http://localhost:1234/v1/commands>**. The first form is a Function that returns basic Cytoscape information as a JSON object:



The second form is a Command that returns a list of available Command namespaces:



Note that the list of namespaces will vary depending on the apps you install – some apps provide Commands in namespaces of their own.

If your workstation has port 1234 already in use, you can specify a different CyREST port in two ways:

- Use the **Edit** → **Preferences** menu to alter the *rest.port* property to select a different port (e.g., 8888)
- Specify the port on the Cytoscape command line via the *-R* parameter:

```
cytoscape.bat -R 8888 (for Windows)

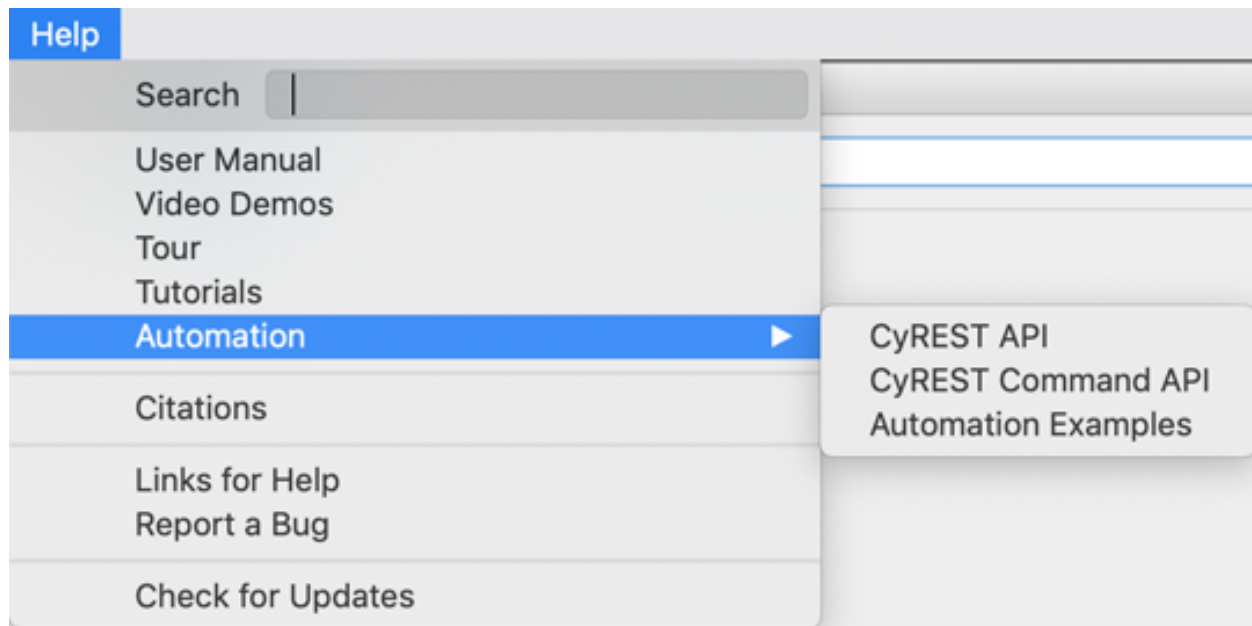
./cytoscape.sh -R 8888 (for Mac or Linux)
```

You can test the new port by using your browser to navigate to **`http://localhost:8888/v1/`**.

Note that if you expect to run more than one instance of Cytoscape on a single workstation, the CyREST port must be unique for each Cytoscape instance. You must use either the property or command line parameter technique to execute each instance with a different CyREST port.

26.3.1 Exploring CyREST Commands and Functions

Cytoscape makes a list of available Commands and Functions available via the **Help** → **Automation** submenus. The **CyREST API** submenu shows available Functions, and **CyREST Command API** shows available Commands. **Automation Examples** leads to a web portal containing the bulk of documentation, samples and tutorials for Cytoscape Automation in general.



Notably, **Automation Examples** contains a tutorial that explains how to explore CyREST Commands and Functions: <https://github.com/cytoscape/cytoscape-automation/wiki/Trying-Automation>.

The **CyREST API** and **CyREST Command API** submenus document CyREST in a Swagger web application, which allows you to explore CyREST endpoints by reading about them and invoking them directly (using a *Try it out!*) button. A sample page matching the **`http://localhost:1234/v1/`** a function is:

Layouts Show/Hide List Operations Expand Operations

PUT /v1/apply/layouts/copycat/{sourceViewSUID}/{targetViewSUID} Copy network view layout to another view

GET /v1/apply/layouts/{algorithmName}/{networkId} Apply a Layout to a Network

GET /v1/apply/layouts Get all available Layout names

GET /v1/apply/layouts/{algorithmName}/parameters Get Layout parameters

Implementation Notes
Returns all editable parameters for the Layout algorithm specified by the `algorithmName` parameter.

Response Class (Status 200)
successful operation

Model Example Value

Inline Model [
 Inline Model 1
]
Inline Model 1 {
 name (*string, optional*): The name of the Parameter,
 value (*object, optional*): The value of this Parameter as a JSON primitive,
 description (*string, optional*): Long-form description of Parameter,
 type (*string, optional*): The type of Parameter, represented as the simple name of its Java class
}

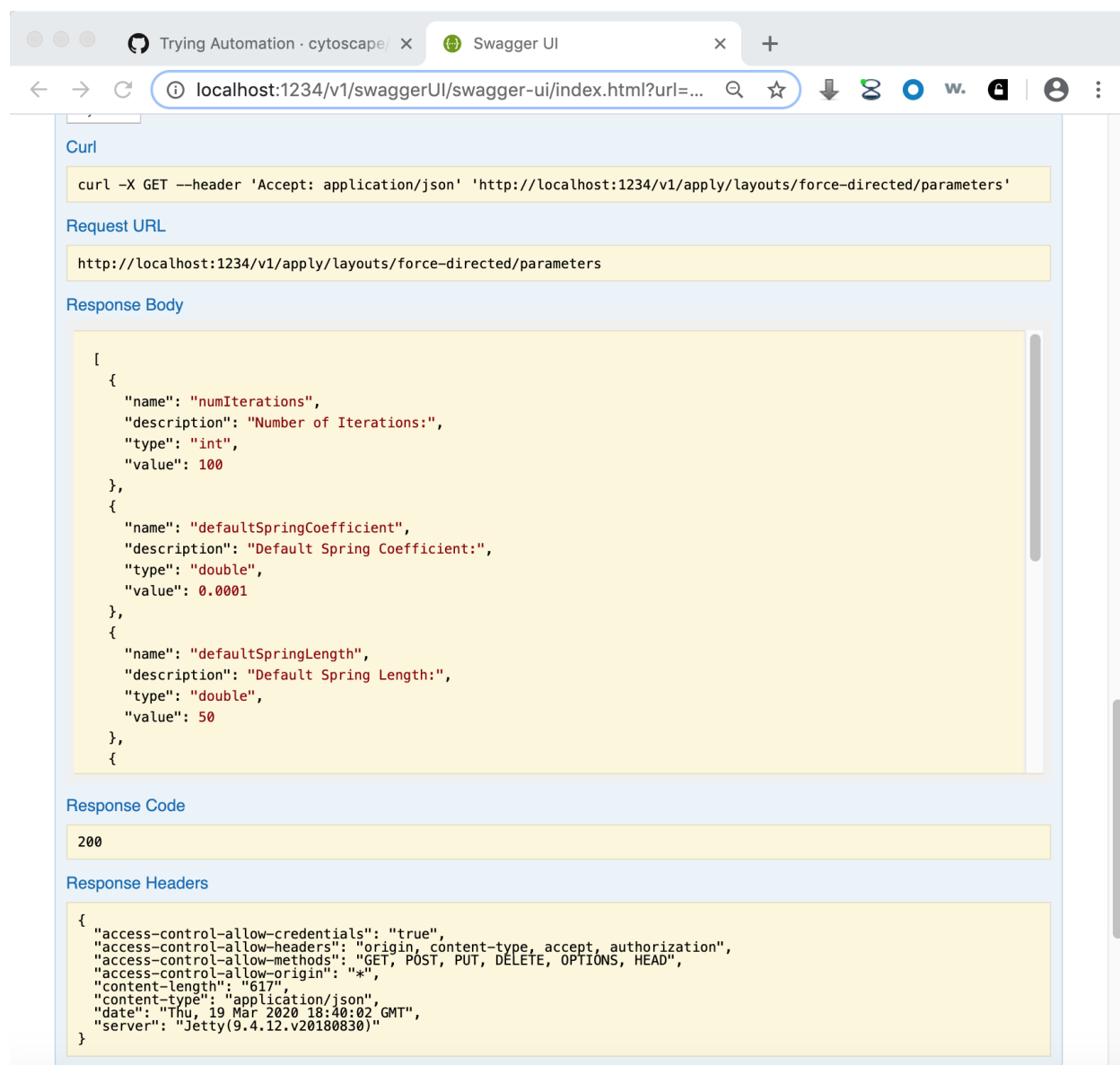
Response Content Type application/json

Parameters

Parameter	Value	Description	Parameter Type	Data Type
algorithmName	(required)	Name of the Layout algorithm	path	string

Try it out!

Note that the page contains a description, input parameters, output values, result code and the *Try it out!* button. Pressing the button executes the Function and shows the actual CyREST call and its results. **Making good use of Swagger as a prototyping tool can greatly reduce code writing and debug time!**



To find out more about how to use CyREST, visit the Cytoscape Automation [tutorial pages](https://github.com/cytoscape/cytoscape-automation/wiki/Trying-Automation) (<https://github.com/cytoscape/cytoscape-automation/wiki/Trying-Automation>).

Note that Swagger pages reflect functionality in Cytoscape at the time it executes, including Commands and Functions contributed by installed apps. To discover CyREST functionality in uninstalled apps, you must first install them, and then use **Help** → **Automation** submenus to generate the Swagger pages (or simply reload your Swagger browser page).

Cytoscape Privacy Policy

We respect the privacy of all Cytoscape users, and we do not collect any information on Cytoscape users except in the situations listed below. In no case do we attempt to tie any of this information back to a user, nor do we give, share, sell, or transfer this information to any third party unless required by law. We use this information only in the aggregate to generate statistics to assist in securing continued funding for Cytoscape.

- On the Cytoscape download web page, we log the date, time, browser signature, and IP address to which we deliver Cytoscape.
- When Cytoscape starts, it fetches news and version information from a Cytoscape server. We log the date, time, and IP address of the workstation running Cytoscape.
- During Cytoscape execution, we log usage statistics tagged with the date, time, and IP address of the workstation running Cytoscape. This logging can be turned off during Cytoscape installation or by setting the **installoptions.shareStatistics** property to false using the Cytoscape **Preferences Editor**.

This policy may change from time to time, and if it does, we will notify you via our normal mass notification media. We will also update this section of the user manual.

Note that some internal Cytoscape Apps and Apps available through the **Cytoscape App Store** connect with third party services via the Internet. Once an App links to such a service, you are subject to the privacy policy of that service.

CHAPTER 28

Basic Expression Analysis Tutorial

The Cytoscape Basic Data Visualization tutorial is now available [here](#).

The complete set of Cytoscape tutorials is available at tutorials.cytoscape.org.