

lab notes

Introductory ppt

Overview of topics and aims of lab sessions: [see the pdf](#)

Introduction to cytoscape

For Cytoscape's documentation, see the [List of Tutorials](#) or the [Manual](#)

(You will only need the parts that we cover during the lab sessions, but feel free to explore, since we won't cover all parts of cytoscape)

High-level overview of Cytoscape's UI

- toolbar at top
- large network view area (contains small sub-windows for each network)
- data panel at bottom -- showing edge and node attributes
- Left hand panel -- contains multiple tabs:
 - list of networks, with a "birds eye view" of the current network underneath it
 - vizmapper
 - other panels (for example, Editor)

Manually editing networks

Create empty network (File -> New -> network -> empty network) add nodes and edges by selecting 'Add' from the right click menu. To add edges, right-click on a node. (see http://manual.cytoscape.org/en/stable/Creating_Networks.html#create-a-new-network-or-edit-one-manually.)

Data Panel

(Also known as Attribute Browser) Shows a table of edge attributes on one tab and node attributes on another tab. Only attributes belonging to the selected nodes / edges are shown in the table. Selecting in the table will select the given objects in the network view (with a secondary color). Columns can be sorted, and values can be edited. Sorting and selecting objects that have a given attribute value is one way to filter the network based on the attributes.

Import & Export

For saving or loading a single network, you need to use the Import or Export menu points (also under the File menu) Some tips:

- When exporting, to preserve all data, use xgmml (Other formats might be more appropriate when exporting a network so that you can load it in some other program), and also make sure to use File -> Export -> Network and View... if you want to save the graphical settings, layout, etc. as well: File -> Export -> Network will only save the nodes and the edges, and nodes will appear on top of each other when loading.
- For importing, as one usually imports from various sources, the features for importing from a table or csv file can be very useful (see http://manual.cytoscape.org/en/stable/Creating_Networks.html#creating-networks)

Import & Export vs. Open & Save

The "Open" and "Save" features of cytoscape are for saving and reloading session files. These preserve the full state of a cytoscape session, including the networks that are loaded, the visualizations that are configured, even the placement of dialog windows and panels. They use .cys files. For managing individual networks or datasets, use Import/Export instead.

Saving an image of the network

Use File -> Export -> Current Network View as Graphics menu entry.

About image file formats: there are two large groups: vector graphics (pdf, svg, eps) and bitmap formats (jpeg, png). Vector graphics:

- can be zoomed and resized without loss of image quality
- less widespread, need vector graphics editor (for example, inkscape) to edit

Bitmap formats:

- more programs can handle them, thus might be easier to insert into a ppt or a document.
- image quality degrades when zoomed or resized (which might be needed when inserting into a document to match the resolution of that document)

Of the vector graphics formats, svg should be more standard. Of the bitmap formats: jpeg is lossy due to compression, png is a losslessly compressed format so should be the ideal choice.

Placement of nodes (layout)

When opening a network, cytoscape will place nodes on top of each other. This is pretty useless for showing the structure of the network. Some guidelines we might want to follow when re-arranging the nodes:

- make sure nodes don't overlap
- make sure nodes are not on edges which don't start/end at that edge
- make sure edges don't cross: this might not be possible. If it is, the network is a *planar graph*. If it is not, the best we can do is minimize the number of edge crossings.

- place "more important" nodes at the center and "less important" nodes at the periphery
- place nodes that are connected close to each other, and nodes that are not connected farther away from each other
- place "leaves" around a hub node evenly around the hub
- arrange triangles so that nodes are placed in a symmetrical manner
- etc.

Obviously, we won't be able to satisfy all of these in each case, (for example whether we can place the nodes on a 2d plane without having edges cross is a property of the graph, we won't be able to do that for non-planar graphs), and in fact we will have to accept not following some of them so that others can be more closely followed (i.e. accept a small number of edge crossings so that we can place connected nodes closer together). For small networks, (for example the [network of business links between 15th century Florentine families](#)) we might be able to arrange the nodes by hand. But for networks of non-trivial size (for example the [network of possible structures of a protein](#)), we will have to use some automatic method to place the nodes since we won't want to do it by hand. Cytoscape has a bunch of such algorithms, available under the 'Layout' menu. Some guidelines for selecting the layout algorithm to use:

- There is no silver bullet: the right layout will depend on the network feature we want to emphasize. Also, some layouts are going to be slow, others will be fast but result in less-pleasing results, thus the size of the network will constrain which layouts we can experiment with.
- deterministic vs. stochastic: some algorithms are deterministic, i.e. running them many times will give the same result. Others are stochastic, i.e. running them over and over again will give different (although generally similar) results every time.
- Using or not using network attributes: some algorithms focus on using the edges to guide the layout, others focus on using attributes. (For example, some layouts will group strongly connected nodes together, while others might group nodes having similar or the same attribute values together, even if they are not connected.)

Suggested layouts to use:

- Compound Spring Embedder (CoSE)
- Cytoscape -> Force Directed is also quite good, and it also allows specifying the edge weight or strength attribute.
- yFiles Organic is also pretty good

Showing node and edge attributes on the network

Cytoscape has a very powerful framework for visualizing node and edge attributes: The vizmapper (see [the section in cytoscape's manual](#))

Important points:

- Visual Styles collect the settings used for a given visualization. They can be exported / imported (as vizmap property files) and switched quickly.
- Vizmapper allows modifying the default settings of visual properties, like node size, node color, shape, edge width, etc.
- Various mappers can be used for computing visual properties based on node and edge attributes (Discrete mapper where one specifies each value, Continuous Mapper where a function is used for the mapper)

Generating a legend for the visualization

Cytoscape can automatically generate a visual legend for the visual style set in the visual mapper. Click on the options button at the top of the 'vizmapper' tab, and select the 'create legend from current Visual Style' menu-entry. This will open a window which will also allow saving the legend as an image.