

Exercise 1 – Import/export networks and attributes

In this exercise we will play around with different ways of importing and exporting network, attributes and views to/from Cytoscape.

Create network manually

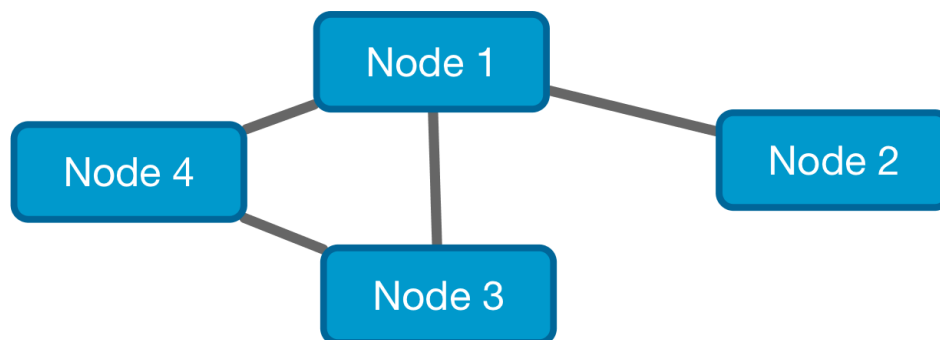
Sometimes, not very often, you might want to create a network from scratch and then add nodes and edges manually.

Create an empty network.

Hint: Menu bar -> File -> New -> Network -> Empty Network

You can add some nodes and edges by right clicking on the canvas.

Add some nodes and edges so your network looks like this:



Nodes and edges can contain additional information (attributes) that is stored in tables. Investigate the tables on the table panel (bottom) and add a column to the edges table called “Similarity” which contains floating-point numbers between 0 and 1 for each of them.

The screenshot shows the 'Table Panel' in Cytoscape. It contains three tabs: 'Node Table', 'Edge Table' (which is selected), and 'Network Table'. The 'Edge Table' displays a list of edges with columns for 'shared...', 'undire...', 'name', 'interac...', and 'Similarity'. The 'Similarity' column contains four floating-point values: 0.324435, 0.657854, 0.987234, and 0.234745.

shared...	undire...	name	interac...	Similarity
Node 1...	undire...	Node 1...	undire...	0.324435
Node 1...	undire...	Node 1...	undire...	0.657854
Node 1...	undire...	Node 1...	undire...	0.987234
Node 3...	undire...	Node 3...	undire...	0.234745

You just created a similarity network.

Importing Network + Attributes

In most of the cases you will have your data in some kind of delimited text format and you will have to map it to Cytoscape. The standard network format for Cytoscape is .sif, which is a tsv (tab-separated value) file where the first and third column represent nodes and the second the relationship between them.

Open on your favourite text editor the presenilin.sif file. Does it make sense to you?

Now look at the attributes files (biopax.xref.UNIPROT.NA and biopax.comment.NA). In both cases, the first column represent a node ID and the second the Uniprot Id or a comment about the gene respectively. These files are old so instead of using a tab they use an equals sign (=) as separator. Also, their first row doesn't belong to the attribute and it's just a header.

Load the network to Cytoscape. As it is in sif format, the mapping should have been done automatically for you.

Hint: File -> Import -> Network > File...

Load the attribute files.

Hint: File -> Import -> Table -> File...

Ensure that you have selected the right network, "presenilin.sif".

The automatic mapping guessed by Cytoscape is incorrect. That is because it is considering a tab as a separator and the file is using "=". Select the correct separator.

Hint: Show Text File Import Options -> Unselect Tab and select Other as "=".

Make sure that the header is considered as a header and not as an attribute.

Hint: Show Text File Import Options -> Transfer first line as column names

Columns name should be unique so it's not a good idea to leave them empty. Make sure that the header is on the correct column and not in the one containing the mapping IDs.

Hint: Right click on columns headers to update their names.

Remember when importing the attributes that the "shared name" column is always string. The mapping column should also be string or the import will fail.

Hint: Right click on the row containing the IDs and select "String"

Inspect the network and the tables. It's all the information from the files contained? Do you think it is more or less manageable than the text files?

Create network from public database

Cytoscape also includes a web service client for PSICQUIC-compliant databases, which allows downloading data from many online databases.

Open the PSICQUIC client.

Hint: File -> Import -> Network > Public databases...

Search for brca1 and brca2 genes

Hint: Just write "brca1 brca2" and click on "Search"

You will see which databases contains relevant data and which databases are down for some reason.

Select IntAct and Mint and click on "Import". After downloading the data and create a network for the result of each database, Cytoscape will ask you if you want to merge the databases. Click on "Yes" and merge the databases you just created. You just got network based on two nodes. This can be extremely helpful when studying specific nodes.

Save session

One of the most useful features of Cytoscape to maintain your analysis and share them is sessions. Every time you click save or open in Cytoscape, you are saving or loading a session.

Cytoscape tends to misbehave over time, especially when dealing with big complex networks. It is important to save often so you can restart if Cytoscape goes crazy or recover in case of failure.

Save your current session.

Hint: Menu bar -> File -> Save As...

Sessions are also a great way of sharing your work with other colleagues.

Start a new session

The easiest way to start clean with Cytoscape without having to restart is to create a new session.

Create a new session and you will see how Cytoscape looks exactly like when you started it.

Hint: Menu bar -> File -> New -> Session

Load an existing session

Load the preseiling.cys session.

Hint: Menu bar -> File -> Open

Have you noticed that the left panel is on the “Style” tab? And the style is a custom style? And the nodes selected on the top-right corner? And the size of the view? And that the table panel now is floating? Everything is saved in the session.

Floating panels is really useful when you have two monitors so you can have one monitor focus on the network view. You can pin it back clicking on the pin icon on the top-right corner. You can also close the panels and manage them from the View menu in the menu bar.

As you can see the network it's the same one that we have before but with some visual style applied. Will see more about visual styles in the next exercises.

Other network formats

There many other standard supported by Cytoscape. Some of them can save only the network data and others the network data and the view.

Export the current network to several formats and open them in your text editor to see how they look like. Try at least Cytoscape.js JSON, XGMML, and one of the PSI-MI formats.

*Hint: File -> Export -> Network
File -> Export -> Network and View*

You can also export you attributes data so the whole network can be reassembled. They are always exported as csv. Export at least your node table and take a look at it in you text editor.

You can also export your style, export your network view as graphics (png, jpg, pdf, ps, ...) or to a web (we will see more about this later).

Grouping nodes

To simplify the networks, Cytoscape also allows for node grouping.

Select a group of nodes and group them.

*Hint: right click on the canvas and go to
Group -> Group Selected Nodes*

Try click on any of the nodes and you will see how the group collapse. Click again to expand it.

This might be really useful when working with network with many independent subnetworks.

Linking to external resources

Cytoscape allows you to automatically perform online searches based on your nodes.

Search for some of your nodes in Entrez

*Hint: right click on the node and go to
External Links -> Sequences and Proteins -> Entrez Gene*

Networks views

Cytoscape works with networks and attribute tables, and the views are just an optional part. In fact, network views are not automatically create for really big network for performance reasons.

Close the current network view. You can see in the network panel (left) that the senilin.sif network still exist but is red. You can still click on it and navigate its attribute tables (bottom). To create a new view just right click on network and Create View. A new view will appear but without any layout applied.

Nested networks

Cytoscape allows nested networks. They can be imported and exported to Nested Network Format (nnf).

Open the nestedNetworks.nnf file and look its content in your text editor and you will see very similar to the sif file but with an extra column that indicate the network.

Load it in Cytoscape.

Hint: File -> Import -> Network > File...

Start on “Overview” and investigate how all the created networks relate.

Hint: You can go to a nested network from its parent by clicking on its node

Root networks

Go to Level2.9, select the node “Node 8” and change its “shared name” it to “OtherNode”.

Now go to Level2.6 and select the node “Node 8”. Its shared name has also been updated to “OtherNode”. That is because all the networks we just created are part of the “Overview” root and they share the network attributes (IDs, interactions, etc.). The same doesn’t happen if you change the name because the name attribute because that is not part of the network but of the attributes.