

Exercise 5 – Cytoscape as a Service

Publishing our network as a website

The latest versions of Cytoscape allow exporting Cytoscape networks and styles to Cytoscape.js, a JavaScript network visualization framework.

In this part of the exercise we are going to use Cytoscape to create a whole website exposing your network.

Open the galFiltered.cys file in Cytoscape, which is a really elaborated visualization of the galFiltered dataset from the previous exercise.

Hint: Menu bar -> File -> Open...

Export it as a website

Hint: Menu bar -> File -> Export Network View(s) as a website

Uncompressed the generate zip and open the index.html file in your browser.

Cytoscape.js is still a quite immature technology and has some cross-browser compatibility issues. If nothing seems to load on your browser try a different browser.

You just created a full-blown website where the user can interact with your network.

Play a bit with the different styles and layouts.

Hint: If the website start misbehaving just refresh it.

Note that on the right you have some options. One of them allows displaying the attribute tables similarly to the ones in Cytoscape.

This website is based on the <http://cynetshare.ucsd.edu/> project which is open source so feel free to take a look at their source.

Scripting Cytoscape using commands

In this part of the exercise we will script Cytoscape to load a network, apply some style to it and export it as a nice pdf.

Open the “workflow.cycmd” file with your text editor and replace the three occurrences of “[folder]” by the full path to the folder where this exercise is located. It should seem pretty obvious what the commands do.

Open a command line terminal and go to the folder where Cytoscape is installed.

Hint: \$ cd /Applications/Cytoscape_v3.2.1

Run `./cytoscape.sh -h` (or `./cytoscape.bat -h` if you use Windows) and you will see the different options to start Cytoscape. You can load Cytoscape preloading a session, network or visual style, you can run scripts or you can run Cytoscape enabling it's REST api.

Run “workflow.cycmd”.

*Hint: \$./cytoscape.sh -S <full_path_to_this_exercise>/workflow.cycmd
It will take few seconds after Cytoscape open to actually run the script.*

If you check this exercise folder there should be a pdf containing the network view you just generated.

Cytoscape's command line should be open now. You can open it at any time from the Tools menu at the menu bar.

Run “`layout attribute-circle`” and you should see how the network layout changes. Run “`vizmap apply styles=default`” and you should see how the default visual style is applied.

Run “`help`” and you will see the different available commands. You can dig into specific commands using the help command. For example, “`help layout`” will show you the different options of the layout command.

Have you noticed the cluster and clusterviz command? Those are not part of Cytoscape but are added by the clusterMaker app. Apps can expose commands or endpoints to be user by Cytoscape itself or by other apps.

Hit `<ctrl-d>` or `osgi:shutdown` to shutdown Cytoscape.

Scripting Cytoscape using REST API

Cytoscape can also be scripted over the network using its REST API and the cyREST plugin.

Run Cytoscape listening to the port 8888 for its REST API

Hint: `$./cytoscape.sh -R 8888`

You can navigate the commands going to

<http://localhost:8888/cytoscape/commands>

As you can see the commands are exactly the same ones than in the command line. You can also navigate deeper in the specific commands like

<http://localhost:8888/cytoscape/commands/network> or

<http://localhost:8888/cytoscape/commands/network/import%20file>

cyREST offer more possibilities and the guys developing it have taken the time to publish plenty of examples for different programming languages.

<https://github.com/idekerlab/cy-rest-node>

<https://github.com/idekerlab/cy-rest-python>

<https://github.com/idekerlab/cy-rest-R>