

Manual

EPIC: Elution Profile-based Inference of Protein Complex Membership

Welcome to the EPIC installation manual, in this document we provide a step-by-step guide on installing and running the EPIC pipeline using Docker. For instructions on installing EPIC directly on your computer, please follow the README.MD file at the root of EPIC's GitHub repository.

1 Installing dependencies

In order to run EPIC locally on your machine, docker needs to be installed, and for easy installation of the EPIC docker image we recommend installing kitematic, as well as creating a docker hub login. Additionally to the docker software suite, we also recommend installing the current version of Cytoscape.

Docker:

For mac OS X follow instructions from (<https://docs.docker.com/docker-for-mac/>)

Kitematic:

The current version of Kitematic can be downloaded and installed from (<https://kitematic.com/>).

Cytoscape:

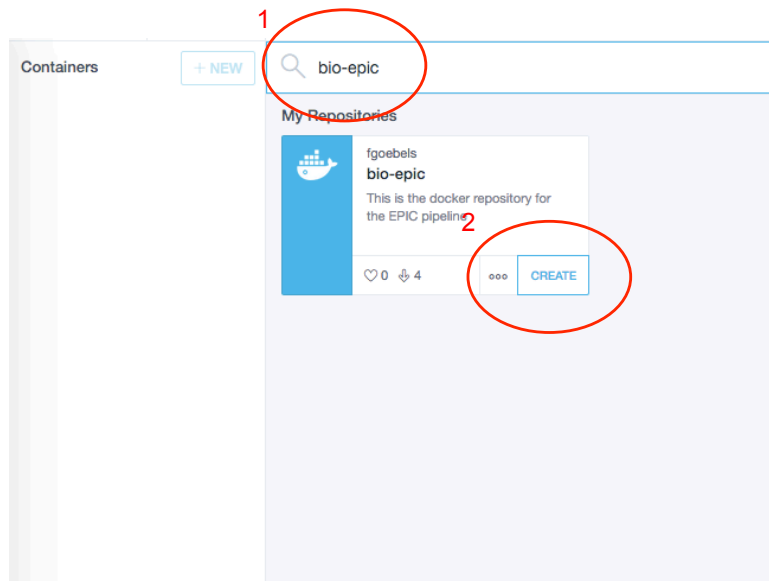
Cytoscape is available from (<http://www.cytoscape.org/>).

2 Building the docker image

The docker EPIC image is online available and can be easily installed by running the following command line in the Terminal/shell (this is recommended):

```
docker pull baderlab/bio-epic
```

Alternatively the docker can also be installed using the Kitematic user interface as follows:



1. First starting Kitematic and enter bio-epic into the search mask
2. Clicking on the CREATE button on the Repository selection

3 Input files

EPIC accepts three types of input files:

3.1 Elution profile files

This is a tab separated file containing the elution profile for all the proteins in one distinct co-fractionation experiment, thus in case of multiple experiments each experiment has its own elution profile file. The first line of the elution profile file is the header line where the first column is ignored, and each subsequent column contains the name of the fraction. Each following line of the elution profile file contains the elution profile for one protein, where the first column contains the protein ID and the following columns each contain the MS value (either spectral counts or intensity) of the protein in each distinct fraction. Examples of the elution profile file can be found in EPIC GitHub

(https://github.com/BaderLab/EPIC/tree/master/test_data/elution_profiles/).

3.2 Reference protein complexes (optional)

This file can be optionally supplied as protein complex reference set, instead of having them automatically generated from CORUM, IntAct, and GO. This file does not have a header line, and each row of the file describes one protein complex by concatenating all its members with tab characters. An example of this file can be found in EPIC GitHub

(https://github.com/BaderLab/EPIC/tree/master/test_data/Worm_reference_complexes.txt).

3.3 Functional annotation network (optional)

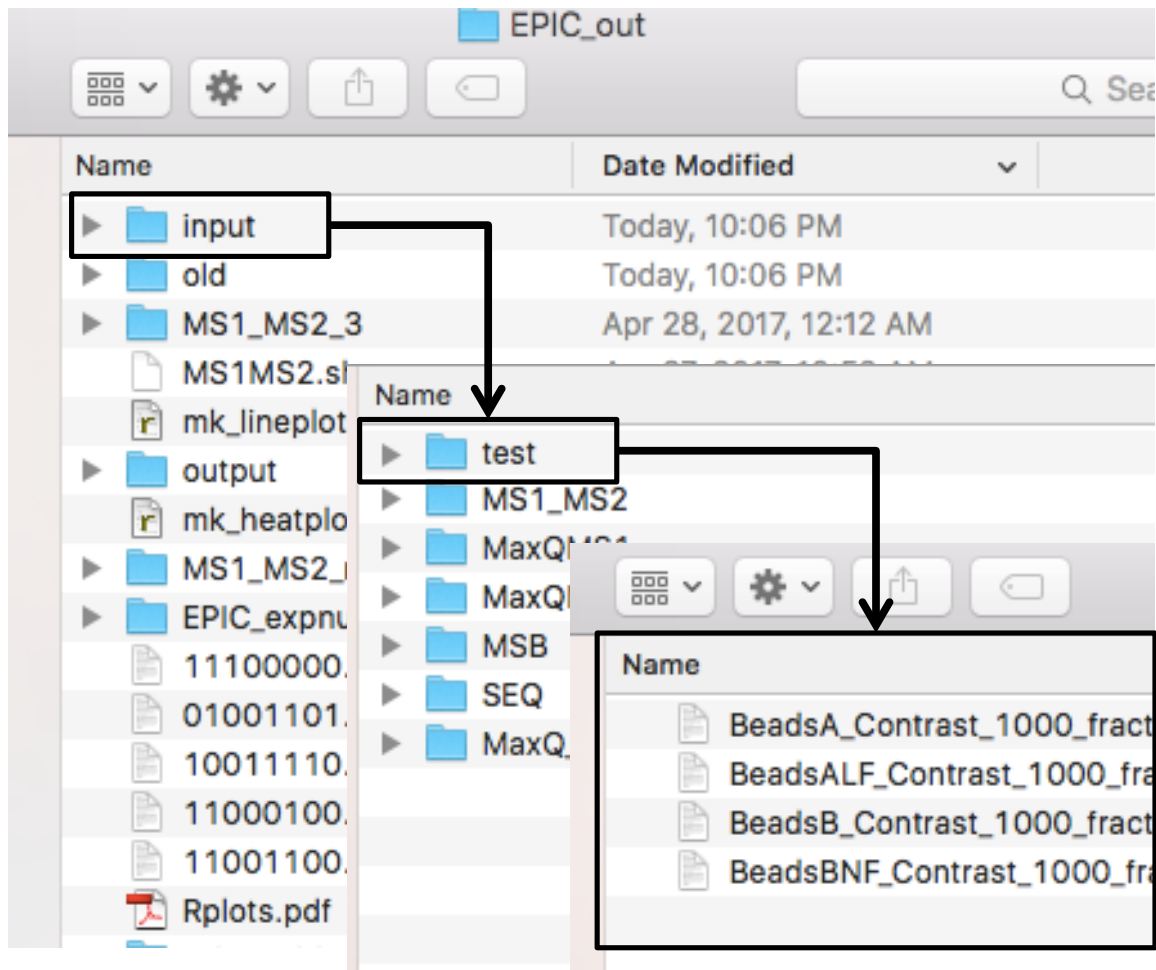
This file can be supplied as an alternative source for functional annotation data that should be used by the EPIC pipeline. This file is also tab separated and has a header line that contains the name of each supplied functional annotation score. Each row contains the scores for each protein pair, where the first two columns contain the protein IDs, and the following columns contain the annotation scores for the protein interaction. An example of functional annotation network file can be found in EPIC GitHub

(https://github.com/BaderLab/EPIC/blob/master/test_data/WormNetV3_noZeros_no_physical_interactions.txt).

4 Input folder structure

For EPIC to properly run the user needs to create a folder that will be linked with the docker image, from which the docker can read and write data from the user. This folder should contain a sub-folder for each elution file the user wants to process, and this folder stores all the elution profile files for the given project. In turn EPIC will read in the data and once done will create an output folder in the same directory that contains all the output files and has the suffix “inputfolder_out”. Note that before running, this folder should only contain elution profile files. This file folder shouldn’t have any other unnecessary files. If you want to run EPIC again, make sure remove the output files/folders first.

For example, here we created a folder named input, which contains a folder named test, which in turn contains 4 elution profile files.



5 Starting EPIC

We recommend setting 6.0 GiB for Memory and 3.0 GiB for Swap. Make sure you restart Docker after updating from our Docker repository.

Before starting EPIC, if you want to see the output results in Cytoscape, Cytoscape should be running on your computer before you run EPIC.

For mac OS X, Jupyter EPIC can be started by opening a terminal window. First copy the start-EPIC.sh file from `.../src/` folder (if you've cloned the EPIC GitHub repository) or copy the file from <https://github.com/BaderLab/EPIC/tree/master/src> to **the directory containing**

the input folder (see 4). After cd to the directory containing the input folder (see 4).

Use the following command:

```
bash start-EPIC.sh
```

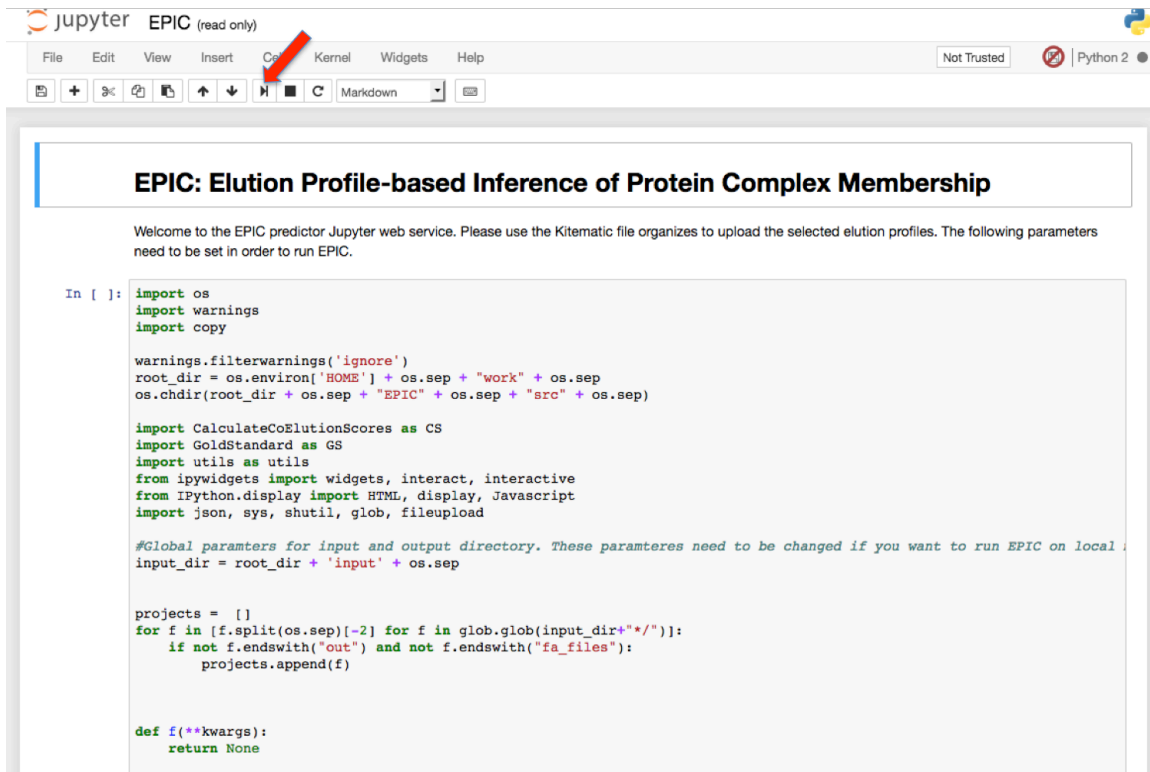
After starting the EPIC container several messages will appear and one of the messages will be the Jupyter token that will allow you to connect to the Jupyter notebook.

```
[I 14:32:32.024 NotebookApp] JupyterLab alpha preview extension loaded from /opt/conda/lib/python3.5/site-packa
rllab
[I 14:32:32.034 NotebookApp] Serving notebooks from local directory: /home/jovyan/work
[I 14:32:32.035 NotebookApp] 0 active kernels
[I 14:32:32.035 NotebookApp] The Jupyter Notebook is running at: http://[all ip addresses on your system]:8888/
[I 14:32:32.035 NotebookApp] Use Control-C to stop this server and shut down all kernels (twice to skip confirm
[I 14:32:45.875 NotebookApp] 302 GET / (172.17.0.1) 0.90ms
[I 14:32:49.576 NotebookApp] Writing notebook-signing key to /home/jovyan/.local/share/jupyter/notebook_secret
```

The highlighted part can be modified to “http://localhost:8888/”, after typing this into a web browser, you will see this:



From here, after clicking EPIC.ipynb the EPIC notebook will be started and you will see:



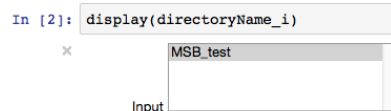
You can click the run button (red arrow) to process each cell. Jupyter is easy to use, as there are plenty of online tutorials available. If you are interested into this, you should definitely check them.

Note: There are a couple of steps that require user input parameters to be set, which we highlight below. You need to keep clicking the run button to run each notebook cell until the notebook asks for parameters, then set the required parameter and continue clicking run to run each notebook cell.

Make sure you go back to re-click to run the cell after you typing your own input!

Input directory

When starting the docker you linked one of your local folders with this docker image. This pipeline considers this folder as the input and output folder. In this folder EPIC expects a folder for each project, where each project folder contains one elution profile file for each co-fractionation experiment. The elution profile file is a tab separated file where the first column contains a protein ID and each subsequent column contains protein value for each fraction, and the file has one row for each protein. Additionally the file has an header line which contains the name of each fraction.



In the input box shown above, you should see the file folder containing all your elution profile files, and you should click it and then click run to process to the next cell/step.

Feature selection:

Please select which co-elution features should be used to generate the co-elution network. We recommend using MI, Bayes, PCCN, and Apex.

```
In [4]: display(features_i)
```

✕

PCCN ☒

Jaccard ☒

Apex ☒

MI ☒

Euclidean ☒

WCC ☒

Bayes ☒

PCC ☒

In the input box shown above, you should click the correlation scores you want to use. You should make your own decision. Ideally, you can benchmark all possible combinations using a super computing platform, or use the score combinations we optimized in the EPIC paper.

Num cores

Number of cores that can be used to calculate co-elution scores. Increasing this number reduces run time if the docher and the machine has multiple cores.

```
In [7]: display(num_cores_i)
```

✕

num_cores

In the input box shown above, you should specify the number of cores you want to use for running EPIC. In general, the more cores used, the faster the EPIC will be, but the optimal number of cores to specify is dependent on your computer hardware.

Classifier:

Here you can select the classifier used to generate the co-elution profiles. EPIC supports both SVM and random forest. We recommend to use random forest.

```
In [8]: display(clf_i)
```

✕

Classifier ☒ Random forest

☐ SVM

In the input box shown above, you see the two machine learning algorithms used in EPIC. You can select the one you want to use.

Reference data:

Here you can either supply an taxid for automatic generation of a reference, or upload a selected set of reference complexes. Please note automatic reference data generation is only supported by Uniprot IDs, and the format for the supplied reference complexes is one complex per line, in which the line contains all the cluster's member IDs separated by tabs.

```
In [10]: display(target_species_i)
display(ref_file)
```

× target_species

In the input box shown above, you should type the taxonomy identifier for the species you want to study. EPIC helps you automatically download all the data from public databases: CORUM, GO and IntAct. The reference protein complexes file was generated after merging all the redundant protein complexes.

```
In [9]: display(target_species_i)
display(ref_file)
```

× target_species

Uploaded to `~/tmp/All.complexes.txt` (16.00 kB)

Or you can supply a reference file you want to use from your own collection. An example of this reference file can be found at GitHub (https://github.com/BaderLab/EPIC/blob/master/test_data/Worm_reference_complexes.txt). In this case, you should not touch your “target_species” input box. And browse the reference complexes file. When you see the “Uploaded to ...” message, this tells you the local functional evidence data is uploaded successfully and you can safely move to the next step.

Mode:

The mode which EPIC should be run with. The supported modes are: experiment only (exp), 1
experiment only when wanting to run EPIC without introducing functional annotation bias into

```
In [12]: display(mode_i)
```

Mode ☒ exp
☐ comb

In the input box shown above, you can select, if you want to incorporate functional evidence or not. “exp” means purely based on functional evidence, and “comb” means the data is based on both experimental data and functional evidence.

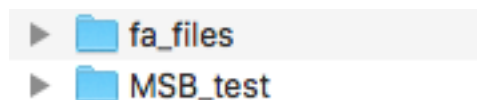
Functional annotation data

Please select which source for functional annotation to use. The user can either automatically generate functional annotation from GeneMania (GM), or STRING. Alternatively, the user can supply his own functional annotation data as a file. In case the mode is experimental only (exp, in mode selection), then this step can be skipped.

```
In [13]: display(fa_source_i)  
display(fa_file)
```

FA source ☒ GM
☐ STRING
☐ FILE
No File
FA File select

In the input box shown above, you can select the resource of functional evidence you want to incorporate. If you select “exp” in the Mode section, this step can be skipped and left as default.



You can also supply your own functional evidence file. An example of functional evidence file can be found in GitHub as mentioned before (https://github.com/BaderLab/EPIC/blob/master/test_data/WormNetV3_noZeros_no_physical_interactions.txt). If you want to use your own functional evidence data, you should create a file folder named “fa_files” in your input directory and put your functional evidence data into this file folder (as below). In the input directory, there should be two file folders, one has elution files (MSB_test) and one has functional

evidence data (fa_files). It is noted that the elution file folder name can be anything you want, but the functional evidence data file folder is fixed. In general, it is best to place these files in their required locations before starting the Docker container.

```
In [17]: display(fa_source_i)
display(fa_file)
```

×

FA source ☐ GM

☐ STRING

☒ FILE

FA File select

No File

WormNetV3_noZeros_no_physical

Then to use functional evidence data, you will select the “FILE” and the selected functional evidence data file as shown below.

Calculating co-elution scores

This is the most time intensive step of EPIC and on average take 20 min per co-elution score per experiment.

```
In [*]: # Calculating scores
scoreCalc = CS.CalculateCoElutionScores(this_scores, elution_datas, output_dir + ".scores.txt", num_cores=num_cores)
scoreCalc.calculate_coelutionDatas(all_gs)
# For debug readin precalculated co-elution scores
#scoreCalc.readTable(output_dir + ".scores.txt", all_gs)

all_gs.positive = set(all_gs.positive) | set(scoreCalc.ppiToIndex.keys())
all_gs.negative = set(all_gs.negative) | set(scoreCalc.ppiToIndex.keys())
all_gs.rebalance()

Filtering: all_6mg.txt
Before filtering 8679861 PPis
filtering
After filtering 2883171 PPis
Num of PPis across all data sets after filtering 2883171
100000
200000
300000
400000
500000
```

This is the most time-consuming step in EPIC. It might take hours, depending on the size of your input data. The star pointed by red arrow means this cell/step is currently running.

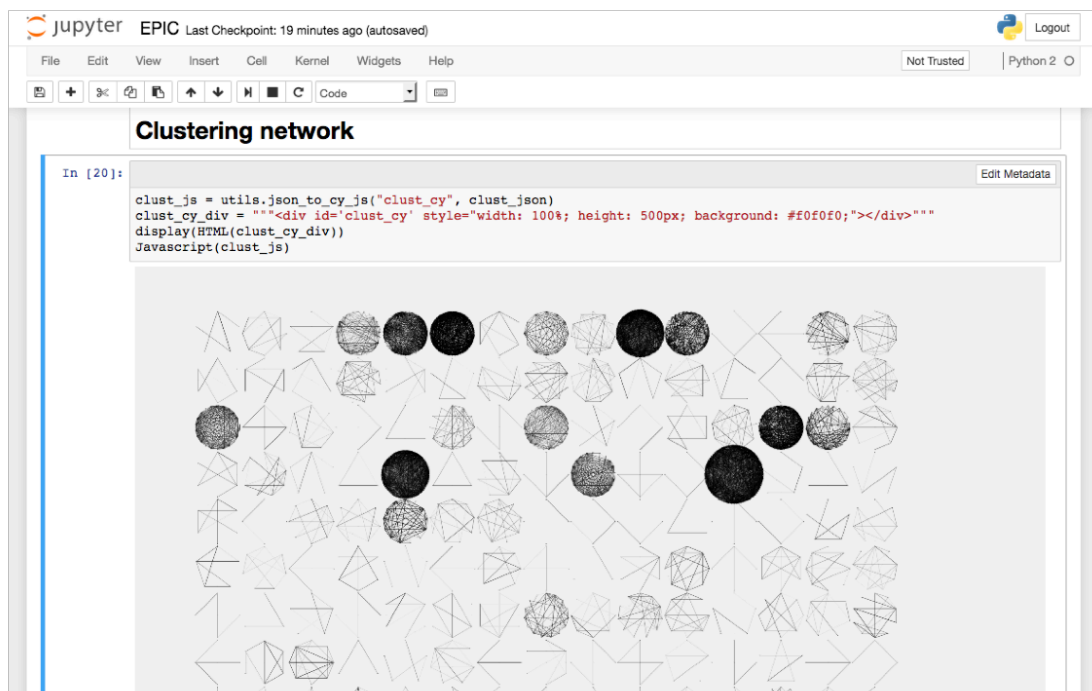
6 EPIC output

After following the prompts of the Jupyter notebook several output files and plots will be generated as well as Cytoscape network will be generated in a running Cytoscape instance.

7 EPIC output

After following the prompts of the Jupyter notebook several output files and plots will be generated as well as a Cytoscape network will be generated in a running Cytoscape instance.

7.1 Cytoscape visualization within the browser

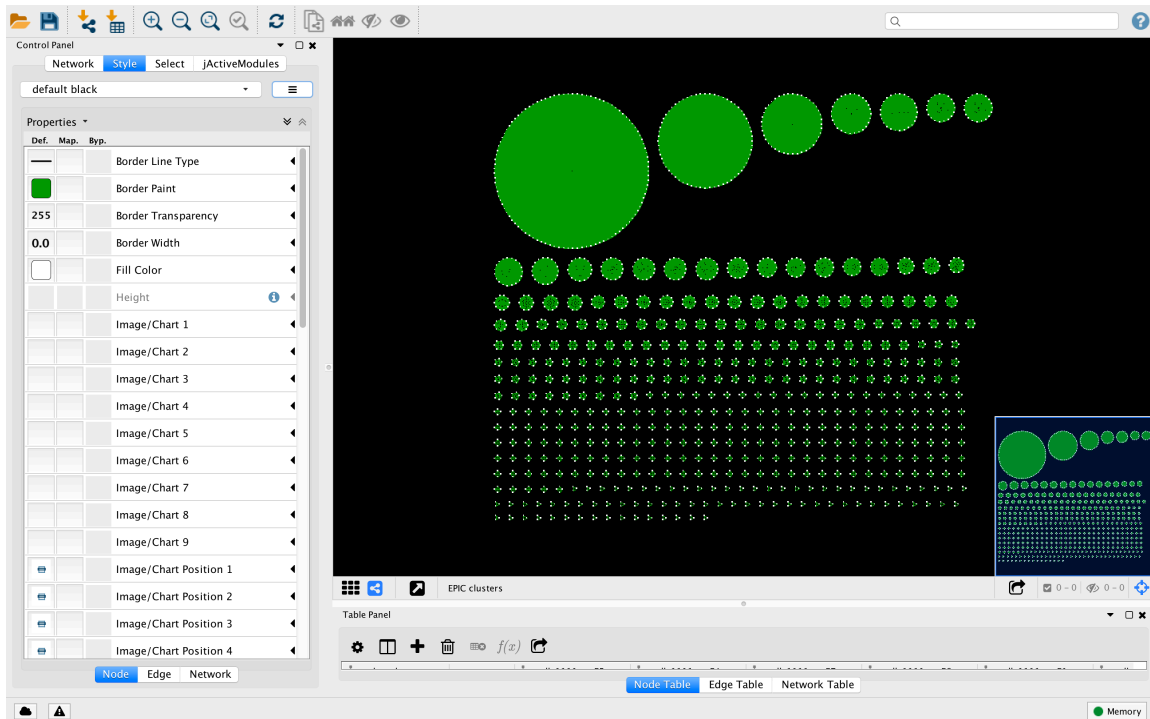


The next figure shows the interactive cytoscape.js widget that visualizes the generated protein complexes, and the user can zoom in and out as well move clusters in side this widget. This allows users to have an initial glance at their created protein complexes, and can always be generated even if the user does not have Cytoscape locally installed.

7.2 Cytoscape

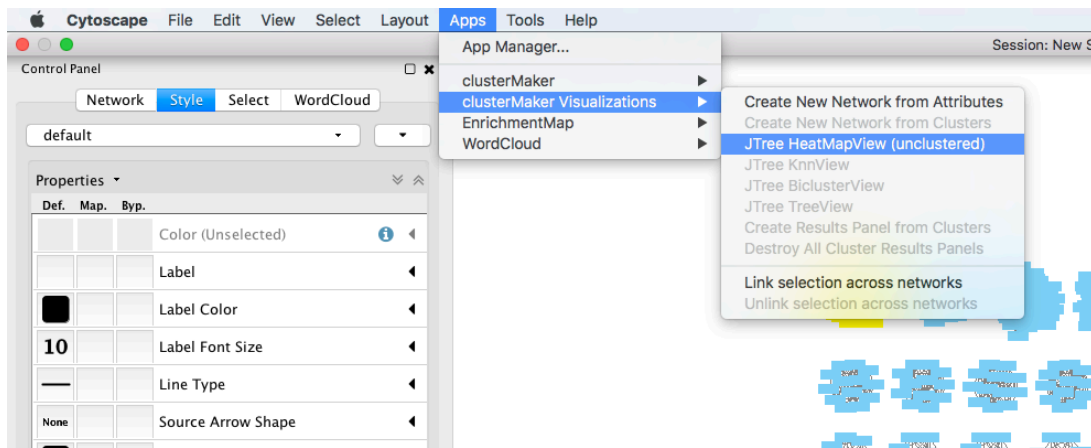
(Make sure your Cytoscape is running before running the Jupyter Notebook, if you want to process this step.)

Running the last cell in the EPIC Jupyter script will send the created clusters to a running Cytoscape instance and generate a new network named “EPIC clusters”, and once selecting the running Cytoscape session the user is prompted to create the view. Once the view has been created the user will see a network that contains a connected component for each predicted cluster. (Make sure to run the layout to see the map!)

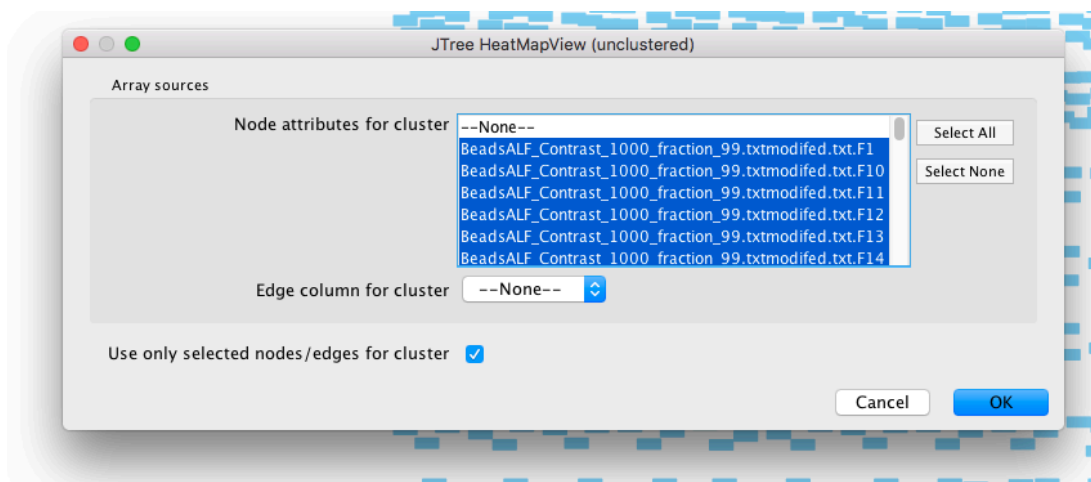


If the user has installed the clustermaker2 app from the Cytoscape app store he can visualize the elution profile for any selected protein as follows (Note, this app is not functional in Cytoscape 3.6.0+, but we are working on fixing it):

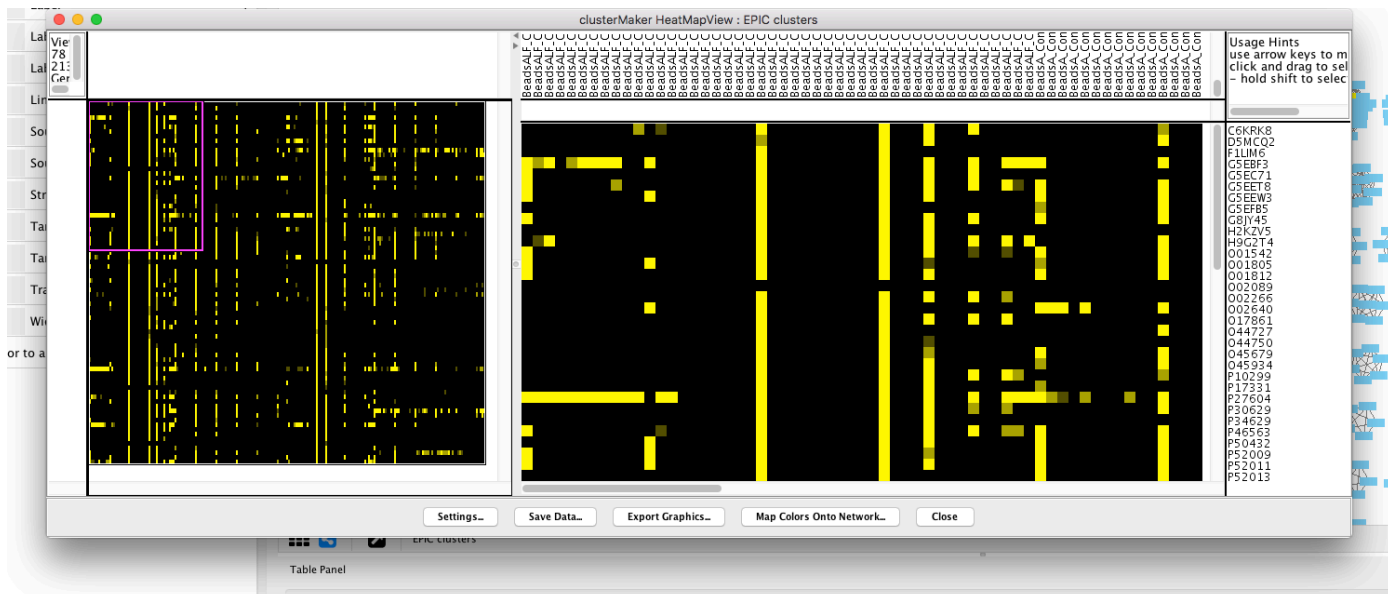
First select the JTree heatMapView from Apps:



This will open the following window, in which the user should select all elution score Node attributes, and check the lower box that says “Use only selected nodes/edges for clustering”:



This will result in opening another window in which the user can freely browse the elution profiles of the selected proteins:



8 Collecting the output

EPIC will create an output directory in the shared folder that contains the project folder and stores several output files in it. Each file has a prefix consisting of the used classifier method and the mode in which EPIC was run with (modes are EXP, or COMB). For example if EPIC was run with a random forest classifier and experiment only each file will have the prefix “Out.rf.exp”. The most important files are as follows:

***.scores.txt**

contains the raw co-elution score.

***.pred.txt**

This tab-separated file contains the generated binary protein interaction network, where the first two columns store the protein ids and the third column is the classifier confidence score.

***.comp.txt**

This is the predicted protein complex file, where each line describes one protein complex.