**Parse & Display NCI networks manual**

**Basic concept:**

This tool is intended to display biological pathways taken from NCI-Nature DB, while combining patient’s gene expression information upon the display.

**Main Files:**

* NCI\_UI\_FINAL.m – main code. Run this to start the program. This file contains all the calculations and display options and is where all the “Information required” session’s variables are read to.
* NCI\_UI\_FINAL.fig- main code’s “.fig” file. Built using guide.
* GraphCursorCallback.m- Allows the data tip options (display edge information).

**NOTE- all of the above files are to be saved in the same directory.**

**Information required:**

* The pathways information is taken from NCI-Nature DB. The DB is not available as a whole- each pathway can be downloaded separately as a “.cx” file. The following link contains the pathways: <http://www.ndexbio.org/#/search?searchType=All&searchString=Regulation%2520of%2520nuclear%2520SMAD2%252F3%2520signaling&searchTermExpansion=false>

After choosing a relevant pathway, one should open the cx file using notepad and save the file as “.txt” file. It is now ready to be used within the program.

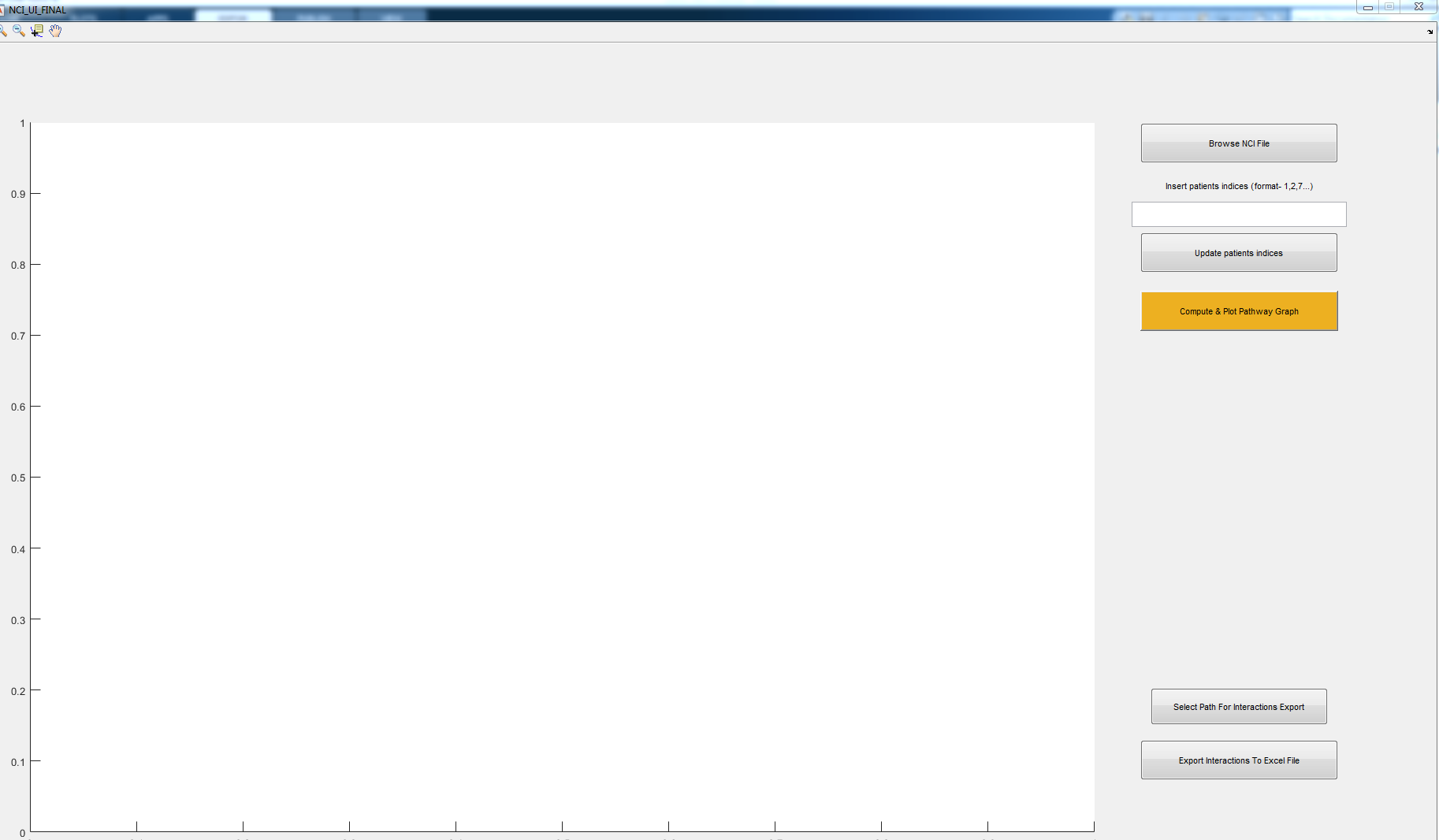
**NOTE- At the moment, when a pathway is to be displayed, one should choose it’s file path using the “browse” button on the UI. We should consider changing it so that if a certain pathway is being examined using the pathifier it will automatically relate it to the proper NCI-Nature pathway file.**

* The patient’s gene expression (variable patients\_data in the code)- contains a structure with the standart gene expression data (data, normals, genes). Currently this data is read from a local copy of such a structure located on my computer and contains data of 50 samples.
* Normal means (variable normals\_means in the code)- contains an array of the normal mean gene expression per gene. The indices are coherent with patients\_data genes indices. This data was calculated using the same local copy of 50 samples that is currently used as patients\_data.
* Normal variances (variable normals\_vars in the code)- contains an array of the normal variance gene expression per gene. The indices are coherent with patients\_data genes indices. This data was calculated using the same local copy of 50 samples that is currently used as patients\_data.

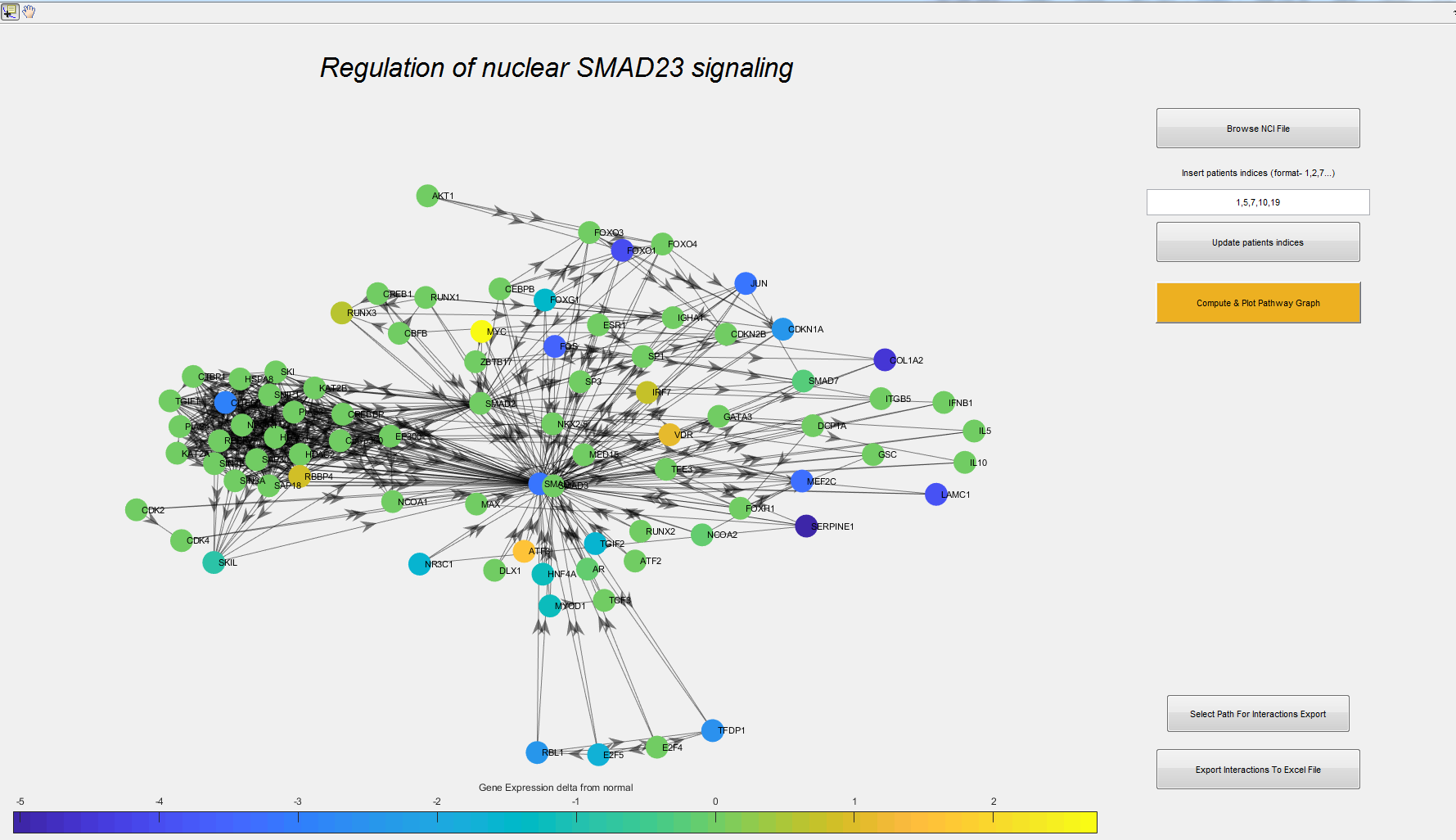
**NOTE- The normal variances and means where calculated based on METABRICK data. It should be calculated based on a larger and/or a more reliable DB if possible. In addition, the variance is currently not being used. It should be discussed with Eytan wither or not to use it to normalize the gene expression delta from normal.**

**Run NCI\_UI\_FINAL.m example:**

* First of all – make sure all the files from the “Information required” session are available and are loaded properly on the code (code lines 117-141). The home – 0/1 was only set this way because I worked on this code from two different computers and read local files in each one of them. The pathway file itself is currently being browsed and loaded using the UI and therefor should not include a code change.
* Run the main code (NCI\_UI\_FINAL.m).
* You will see the next UI pop up:



* Press the “Browse NCI File” button to choose the pathway “.txt” file that you have downloaded from NCI-Nature’s website. Once you chose it there should appear a headline that contains the pathway’s name on the top of the UI window.
* In the “Insert patient’s indices” Edit-text window specify the patient’s indices for the patients you want to check the pathway for (their gene expression data will be used for the display). You can either specify a single index (e.g type “7”) or several indices (e.g type “1,5,7,10,19”). If you choose several indices, then the data that will be used for the display will simply be the mean values of this group of patients.
* Press the “Update Patient’s Indices” button to update it in the code.
* Press “Compute & Plot Pathway Graph”. You should wait a few moments and then see the network representing the pathway:



* Finally, you can choose to export an interaction table (as an “.xls” file) of the pathway using the two buttons on the bottom of the UI. Choose where to save the file using the upper button of the two and then press the lower one to save it. Make sure that a proper excel file had been saved.