# Network Coherence Calculator Instructions

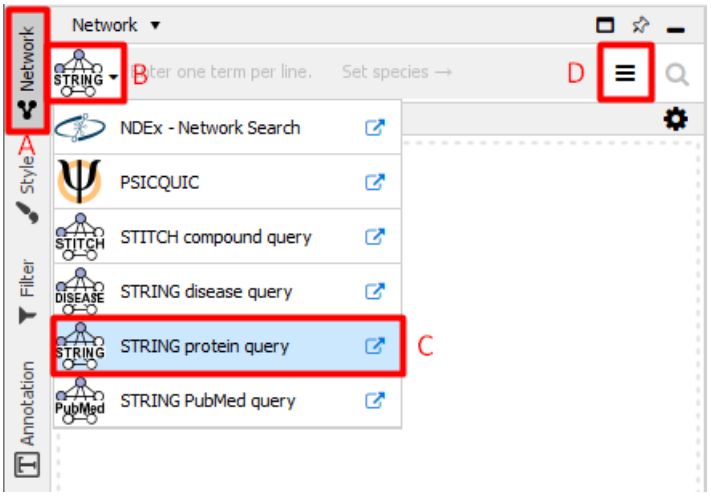
## 1 Prerequisites

- Cytoscape software
- STRING App for Cytoscape
- Network Coherence Calculator App for Cytoscape

## 2 Loading a Protein Interaction Network

Network Coherence Calculator is capable of using any network loaded into Cytoscape, but for the purpose of this tutorial, we will be using the STRING App to import one.

### 2.1 Opening STRING

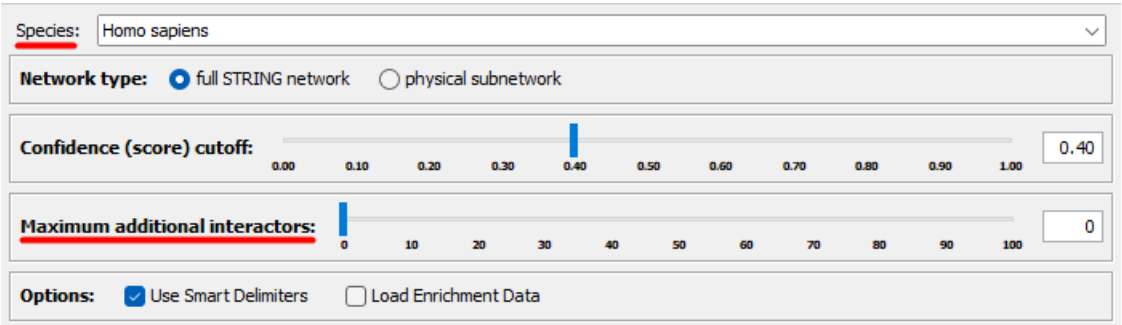



First click the network tab to open the network control panel.

Then click the network app drop-down and select ”STRING protein query”. If you do not see this option you have not installed the STRING App and should do so now.

Then click the button with the three lines to open the STRING App options menu.

### 2.2 Configuring STRING



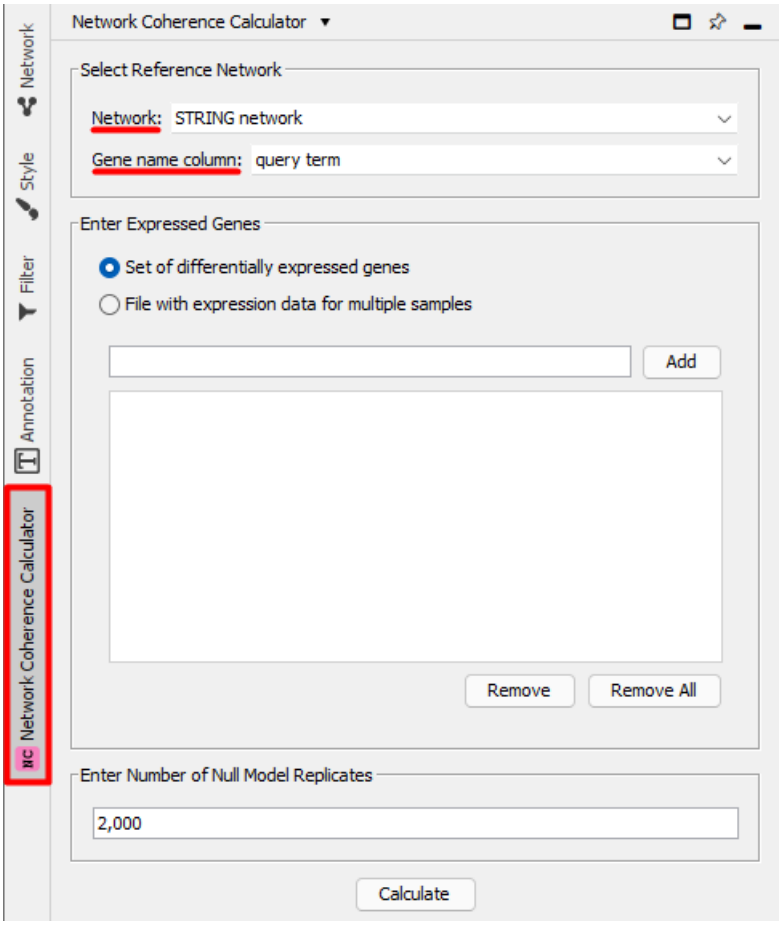
In the options menu, set the species and make sure the ”Maximum additional interactors” is set to 0.

### 2.3 Searching with STRING


Then in the text field enter the subset of gene names that pertain to your calculation and click the search button. For large sets of genes, this will take a while and will sometimes fail. If the STRING App fails to load the network, resubmit the search to try again.

## 3 Configuring the App’s Input

### 3.1 Network




Click on the Network Coherence Calculator tab to open its control panel. Then use the drop down menu to select the network. The network should be the one created in the last section by the STRING app.

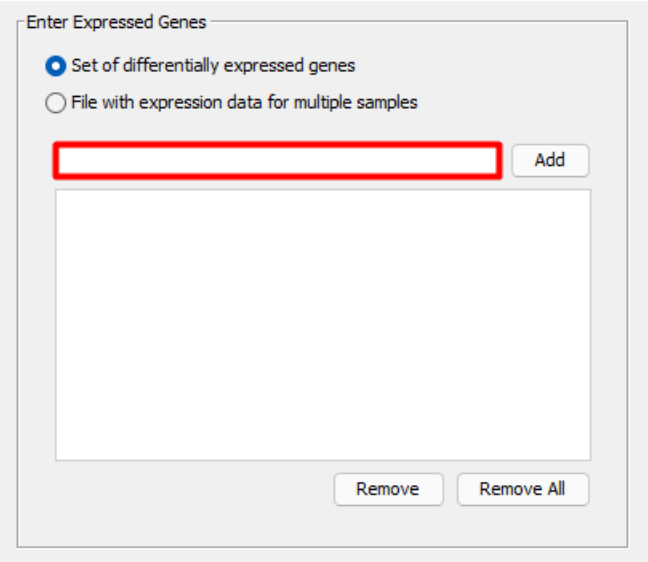
Next use the second drop down menu to select the gene name column. This column designates which column in the node table will be used to try and match with the ex-

pressed gene names that will be entered in the next step. When using the STRING app to generate the network, you should use the ”query term”.

## 3.2 Expressed Genes

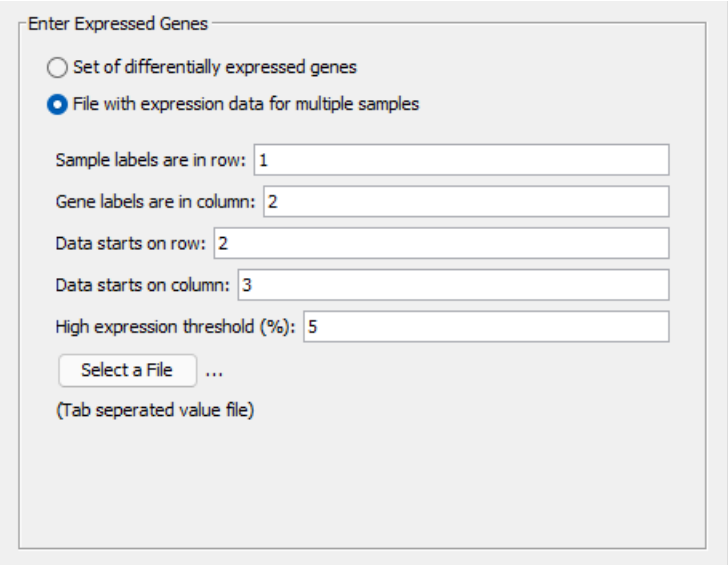
This step will vary based on whether you intend on entering a set of differentially expressed genes or you intend on selecting a file that contains gene expression data for multiple samples. Follow the appropriate sub-step.

### 3.2.1 Set of differentially expressed genes

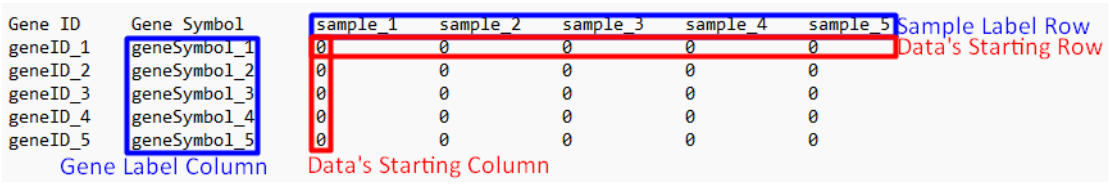



After selecting the ”Set of differentially expressed genes” option, enter each of the gene names in the text field. Following each name, hit return or click the add button. The added genes should appear on there own lines in the field below.

### 3.2.2 File with expression data for multiple samples



Fill in the first four text fields with the row and column values that correspond to the expression data file you plan on using. An example of these values can be seen in the below image of a sample input file.

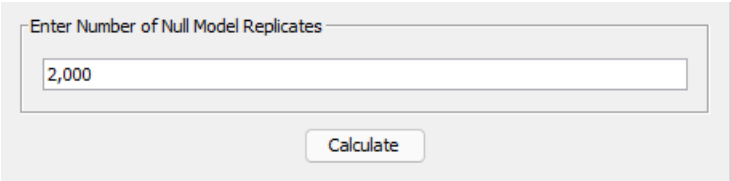



You can see that for this sample file a value of 1 or 2 could be inputed as the gene label column to use either the gene ID or the gene symbol as the gene's name. The values in the chosen column should match those in the Cytoscape node table column that was selected as the "Gene name column" in step 3.1.

Next enter the "High expression threshold". The samples who's expression value for a given gene is in the top x% relative to the other samples will be considered to highly express this gene. Where x is the threshold.

The last portion of this step is to select the file by clicking the "Select a File" button. The file must be a tab separated value file with each row representing a gene and each column representing a sample. This is illustrated in the image above.

### 3.3 Number of Null Model Replicates



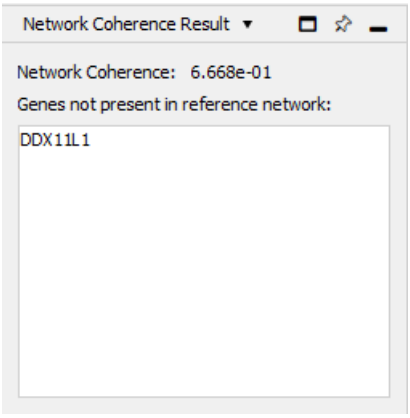

Next enter the number of null model replicates. The network coherence is presented as a z-score, which requires a set of random samples to form a null model for its calculation. Raising this value increases the accuracy of the result, but adds computation time.

Finally click the calculate button to begin the calculation.

## 4 Viewing and Saving the Results

The calculated results will appear in the results panel on the right side of the Cytoscape window and will be formatted in one of two ways. The first if you entered a set of differentially expressed genes and the second if you selected a file with expression data. Proceed to the appropriate subsection.

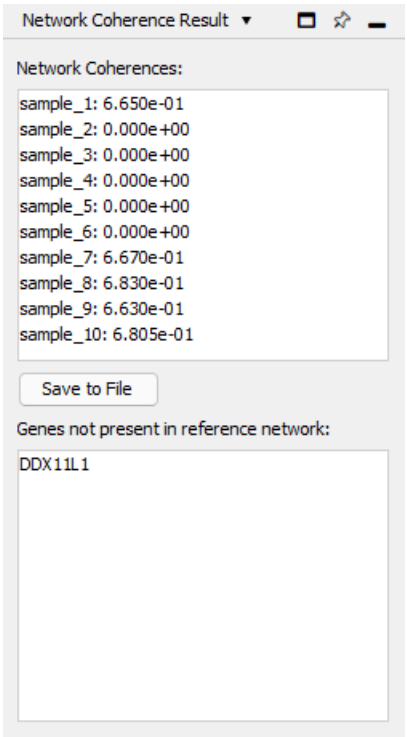
## 4.1 Set of differentially expressed genes




The network coherence is listed at the top of the panel.

The bottom portion is a list of all of the gene names that couldn't be found in the networks "Gene name column" which was selected in step 3.1. These genes were ignored for all aspects of the network coherence computation as if they were not passed as input.

## 4.2 File with expression data for multiple samples




The upper list shows the network coherence for each of the samples that were contained in the input file. To save these coherences, the "Save to File" button can be used to save each of sample's labels and the respective network coherences to a CSV file (comma separated value file).

The bottom list is a list of all of the gene names that couldn't be found in the networks "Gene name column" which was selected in step 3.1. These genes were ignored for all aspects of the network coherence computation as if they were not passed as input.