

ComFiR EXECUTABLE

ComFiR executable is designed to identify protein complexes from Protein-Protein Interaction data. It is used for **prioritizing complexes associated with certain human diseases**. It has been implemented in MATLAB 7.6.0(R2008a). We have taken special care to make it a user-friendly tool so that the user can make changes in the parameter as his requirement.

USER'S MANUAL

1. Unzip the ComFiR_exe folder, **change** your matlab working directory to one containing this folder.
2. Type **mainForm** in the matlab console to start the executable. A window pops up.
3. This executable is divided into three parts- *Input Panel*, *Parameter Setting Panel* and finally the *Output Panel*.
4. In the *Input Panel*, click on **Load PPI Dataset** button. Here, you can upload human PPI dataset in **tab-delimited** form.
5. Once uploaded, you can view the *number of interactions* and the *number of unique proteins* in the dataset.
6. Now, upload a benchmark human PPI dataset using the **Load benchmark complex set** button.
7. The number of benchmark complexes is displayed in the *#complexes* box.
8. Next, load the semantic similarity score values for the required protein pairs using **Load SS score button**. The number of rows uploaded will be displayed in the box.
9. Now, go to the *Parameter Panel*, here you can change the **SsT** value. The Connectivity threshold value is fixed at 0.4.
10. Once the input and parameters are set for ComFiR, go to the *Output Panel*. Pressing the **Complex Finding** button, the complex finding process starts.
11. When the complex finding process is over, you can see the *number of clusters* in the box.
12. You can save the cluster results into a file "*ClusterFile.txt*" by pressing **Write cluster to a file**.
13. Once, the complexes are available, you can rank them as per your disease query.
14. Using **Load Disease information**, load a file containing disease genes along with their relevance scores.
15. By pressing **Complex Ranking** button, you can rank the available complexes. The ranked complexes along with their scores and member proteins are written to a file "*DiseasedcomplexFile.txt*".