

CSC Manual

CSC executable is designed to identify protein complexes from Protein-Protein Interaction data. 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 **CSC_exe** folder, **change** your matlab working directory to one containing this folder.
2. Double click the **gui2.exe**. 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 any PPI dataset in *tab-delimited* form.
5. Once uploaded, you can view the *number of unique proteins* and the *number of interactions* in the dataset next to the command button.
6. Now, upload the organism specific benchmark PPI dataset using the **Load benchmark set** button.
7. The *number of benchmark complexes* is displayed in the box next to the command button.
8. Next, load the semantic similarity score values for the required protein pairs using **Load Semantic similarity** button. The *number of rows uploaded* will be displayed in the box.
9. Now, go to the *Parameter Panel*, although you can *change* the Semantic similarity threshold value, it is kept at 0.4. The Connectivity threshold value is fixed at 0.4.
10. Once the input and parameters are set for CSC, go to the *Output Panel*. Pressing the **Run CSC** button starts the complex finding process.
11. When the complex finding process is over, you can see the *number of clusters* in the box next to the command button.
12. You can save the cluster results into a file "*result.txt*" by pressing **Write to file**.