

# PROCEDURE User Manual

**PROCEDURE** is a graph-based tool which can detect protein complexes from any Protein-Protein Interaction (PPI) Network. The tool is validated using three real-life yeast PPI network datasets. The tool is written in Java. The interface is user-friendly. To operate the tool, you need to follow the steps given below.

1. First, you have to select a PPI network file in **.sif** format. You can browse for the input file by clicking the **"Browse"** button.
2. Second, after loading the PPI network file, click on the **"Find Protein Complexes"** button. It will take few minutes to complete the task.
3. When the task will be completed, the textbox below the above mentioned button will contain the **"path of the final output"** i.e., the predicted protein complexes in a text file. Each line in the file will represent a protein complex.
4. Finally, you can view the output file by just clicking the **"View Predicted Complexes"** button.

**Note:** If you apply minimize and maximize operations, the screen may turn black. You need not worry, just wait for a while.

Authors