

Manual

Step wise instructions to use the tool:

1. Download the zipped folder containing executable.
2. The zipped folder contains following file
 - executable file(go_mode.exe)
 - Gene Ontology file(go.txt)
 - ppi data file(ppi.txt, Collins dataset is used here)
 - details of true complex(truecomplex.txt)
3. Extract the zipped folder somewhere in your computer and run the go_mode.exe file.
4. The results will be written in results.txt file.