

CPL: Detecting protein Complexes in protein-protein networks by Propagating Labels

Qiguo Dai, Maozu Guo, Xiaoyan Liu, Zhixia Teng

Email: qiguo_dai@hit.edu.cn

School of Computer Science and Technology, Harbin Institute of Technology, Harbin
150001, P.R. China.

Introduction:

CPL is a graph clustering software, which is designed to detect protein complexes in protein-protein network (PPI). It detects the complexes by label propagation, which is to simulate the interacting activities of proteins.

The paper in the following which describes the CPL method has been submitted.

[1] Qiguo Dai, Maozu Guo, Xiaoyan Liu, Zhixia Teng. CPL: Detecting protein Complexes in protein-protein networks by Propagating Labels. Submitted.

Usage:

The CPL.jar can be run either Window or Linux System, with a JAVA **version of 1.6 or higher**.

The basic command of running CPL is as

```
java -cp CPL.jar CPL -f ppi_file
```

where the *ppi_file* is the file name of a PPI network. In the file, each line is an interaction of a pair of proteins, which are spitted by a tab char. It is strongly recommended that the file should not contain any blank line and the protein name must not contain any blank char.

Options:

In addition to the basic command, you can also choose other parameter to get different detecting results. Such as,

1. `-th <value>`. `<value>` is the parameter of max-based threshold, which is a real value in (0,1]. If not type the `-th`, the average-based threshold is used default.
2. `-u <t>`. `<t>` denotes the updating order of proteins, which is a integer value of 0,1 or 2.
 - 0: the ascending order of the node weight;
 - 1: the descending order;
 - 2: the shuffle order.
3. `-h`. For help.