

Abstract

In this proteomic era with the availability of bulk information on protein protein interactions from the various advanced proteomic technologies, identification of protein complexes has emerged as a new challenge for researchers in the area of bioinformatics, as it give an insight to the understanding of biological process, functions and structures. The study of protein complexes from the computational approach gives a new perspective to view at biological systems and helps in understanding the underlying mechanisms at the cellular level.

In this report we give a description of the protein complexes inside a protein protein interactions network and discussed various methods and approaches to identify protein complexes.

Based on the core-attachment approach we first give a method to identify protein complexes incorporating gene expression profile. Next, we also give a method to identify protein complexes that uses topological information of the proteins and the Gene Expression Profile information to weight the protein interaction pairs.

Experiment results and analysis supports that our methods can identify protein complexes effectively and can detect overlapping complexes. Validations by biological information such as Gene Ontology similarity scores supports that our methods can predict high biologically significant protein complexes.

We also developed the software implementations for both our proposed methods.