ARTICLE

A STUDY ON IDENTIFICATION OF STATIC AND DYNAMIC PROTEIN COMPLEX AND FUNCTIONAL MODULE IN PPI NETWORK

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ABSTRACT

The availability of large-scale high-throughput experimental data has provided the opportunity of exploring biological networks to reveal complex structure and organization in the cell. Proteins are the main actors to perform cellular functions and majority of them do not carry out their functions in isolation but by interacting together in a complex manner. Protein complexes and functional modules are two important constructs formed by physical interactions among proteins. Identifying protein complexes and functional modules are crucial to understand the principles of cellular organization with important applications in disease diagnosis and therapy. However, experimental detection of protein complexes and functional modules is highly limited in the current state-of-the-art high-throughput experimental techniques. Thus computational approaches for detecting protein complexes and functional modules from protein-protein interaction data are valuable complements to the experimental techniques. From computational viewpoint, mining objects like protein complexes and functional modules from protein-protein interaction data (equivalently from protein-protein interaction networks) is computationally challenging task, since many problems related to determining structural properties of graphs are often NP-hard in nature. In this survey, we review the current state-of-the-art as computational techniques as well as recent emerging techniques for detecting protein complexes and functional modules, and discuss some promising research directions.

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240

241

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