Current Computational Models for Prediction of the Varied Interactions Related to Protein-PART 2

Aims & Scope:

Proteins are the principal catalytic agents, structural elements, signal transmitters, transporters and molecular machines in cells. But individual proteins do not function alone; they must interact with other molecules, such as proteins, RNAs, DNAs and small molecule compounds, to carry out their cellular roles. Interactions of proteins are in general identified and characterized through many biochemical or biophysical experimental methods. These experiments are extremely valuable and have contributed greatly to our knowledge of protein interaction mechanisms. However, technical challenges make such experiments both labor-intensive and time-consuming. Reliable computational approaches to identify the interactions of proteins are especially valuable. In recent years, computational techniques have been successfully applied to predict the interactions between protein and various kind of molecules. Especially, protein–protein interactions prediction, protein–RNA interactions prediction and protein–drug interactions prediction based on heterogeneous biological data have become critical topics in the search of functions of proteins and therapeutic targets for various diseases. With the development and application of many new computational techniques, such as machine learning, deep learning, new feature extraction methods and network methods, a great progress has been made in the field of protein interactions prediction.

We will invite investigators to contribute reviews and research articles to describe recent findings which use computational techniques for the research of protein interactions.

Subtopics

Potential topics include, but are not limited to:

- Protein–RNA interaction prediction
- Protein–protein interaction prediction
- Protein–DNA interaction prediction
- Protein–ncRNA interaction prediction
- Protein–drug interaction prediction
- Protein structure prediction
- Protein function prediction
- Protein subcellular localization prediction

Keywords: Protein, Computational approaches, Interaction prediction

Schedule:

Manuscript submission deadline: April 30th, 2019
Peer review due: May 31st, 2019
Revisions due: June 30th, 2019
Notification of acceptance: July 31st, 2019
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