Tentative Outline
Current Proteomics
Guest Editor(s): Guohua Huang

TITLE: Computational models and methods for predicting protein functions and interactions

Aims & Scope:
Advance in sequencing techniques has resulted in a large body of protein sequences in the last decades. However, the annotation of protein functions lags far behind. It is estimated that almost 1/3 proteins lack annotated functions. Protein is the elemental performer of cellular activities. The knowledge about protein function is vital for us to explore and understand cellular mechanism. Protein performs a specific function not alone, but with other molecules together such as proteins, DNA, RNA. These interactions are also one of concrete manifestations of protein functions. Therefore, identifying protein functions and interactions becomes one of hot topics in the fields of molecular biology and biomedical engineering.

To make up for the low through-put of experiments’ annotating protein functions and interactions, some researchers have pioneered a computational route to annotate functions and interactions. Such methodology has two advantages over physical experiments: high through-put and high efficiency. At theory, the number of proteins to be predicted is not limited. Once obtaining a better computational model, we are able to use it to determine functions and interactions of thousands of proteins within several seconds.

This thematic issue aims to collect up-to-date computational theories and models to explore protein functions and interactions. The utility of machine learning techniques including clustering methods, semi-supervised learning and supervised learning for prediction of functions and interactions are welcome. Application of deep learning to identification of protein functions and interactions were strongly encouraged. We also welcome methods based on heterogeneous network constructed by multi-omics data for predicting protein functions and interactions.

Key words:
Machine Learning, Deep learning, network analysis

Subtopics:
Post-translational modification prediction
Predicting Multi-label functions of proteins
Protein-protein interaction prediction
Protein-drug interaction prediction
Protein-DNA interaction prediction
Protein complex prediction
Protein-RNA interaction prediction

Schedule:
Manuscript submission deadline: June 30, 2017
Peer Review Due: August 30, 2017
Revision Due: October 31, 2017
Notification of acceptance by the Guest Editor: November 30, 2017
Final manuscripts due: December 31, 2017