

'Machine Learning and Graph Algorithms for Analysis and Prediction of Protein Structures, Functions and Interactions', a new thematic series from *Algorithms for Molecular Biology* is now accepting [submissions](#).

Analysis of proteins' structures, functions and interactions and their predictions is an important task for understanding how the proteins work. Due to the increasing amount of experimental data with new sequencing technologies, it has been essential to devise computational methodologies for automated analysis and prediction of protein structures, functions and interactions.

In recent years, developing new machine learning techniques has become an active area of research for computer scientists and bioinformaticians for analysis and prediction of protein structures, functions and interactions based on experimental data. Machine learning is a field of computer science dealing with the design and development of algorithms for intelligent analysis of empirical data. Multiobjective versions of the traditional search techniques have also become popular as most of the real-life optimization problems are multiobjective in nature. In addition to the machine learning techniques, graph-theoretic methods for analyzing biological networks like Protein-protein interaction networks have gained popularity. Graph algorithms for dense subgraph identification, maximal clique/quasi-clique and biclique/quasi-biclique discovery, computing shortest paths, cycle finding, graph partitioning, graph clustering etc. are finding a handful of applications in biological network analysis. In many cases, hybridization of methods from the three major fields of machine learning and graph algorithms lead to improved solutions for the biological problems in hand.

Guest edited by Dr A Mukhopadhyay, Dr U Maulik and Dr S Bandyopadhyay, the main focus of this thematic series will be on new applications and developments of machine learning techniques and graph algorithms to address the contemporary problems in prediction and analysis of protein structures, functions and interactions. It will focus on the novel and advanced design of machine learning and graph algorithms as well as state-of-the-art reviews in this area. This thematic series will serve as a platform for researchers having expertise in machine learning, graph theory and systems biology. **We encourage the submission of high-quality theoretical and empirical contributions that discuss novel application of machine learning and graph algorithms which include but are not limited to:**

- Protein structure prediction
- Protein classification
- Molecular design and docking
- Protein function prediction
- Protein functional site prediction
- Analysis and prediction of protein-protein interactions
- Prediction of host-pathogen interactions
- Interactions of proteins and other biomolecules
- Protein complex predictions

Submissions will be handled directly by AMB as explained here: <http://www.almob.org/info/instructions/>

Please submit your manuscript via your [online submission system](#), and state clearly in your covering letter that you are submitting for the thematic series on 'Machine Learning and Graph Algorithms for Analysis and Prediction of Protein Structures, Functions and Interactions'.

Submission deadline: September 30, 2014

For further clarification, please contact the guest editors through the following emails.

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