

Vasant Honavar

Professor, Artificial Intelligence Research Laboratory,
Department of Computer Science and Graduate Program in
Bioinformatics & Computational Biology
Iowa State University

***Computational Discovery of Protein Sequence-
Structure-Function Relationships***

Proteins are the principal catalytic agents, structural elements, signal transmitters, transporters and molecular machines in cells. Hence, characterization and prediction of protein sequence-structure-function relationships using diverse sources of information (protein sequences, protein structures, different sources of sequence or structural features of proteins, gene expression data, taxonomies that group proteins into functional families based on different criteria, and databases of known protein-protein interactions) is one of the most important problems in functional genomics. This problem presents several challenges as well as opportunities in information integration and data mining from autonomous, heterogeneous, distributed information sources. In this talk, I will briefly describe INDUS - a Protein Bioinformatics Platform which is being developed in our lab to explore some solutions to these problems, motivated by the needs of representative data-driven knowledge discovery tasks in computational molecular biology. I will present some results on two representative applications: (a) assignment of functions to protein sequences and (b) sequence-based prediction of protein-protein interaction residues. I will conclude with a brief outline of some current and future research directions.

**Tuesday, October 15th
4:00 p.m.**

Room 1111
Biotechnology Center/Genetics
425 Henry Mall