

Public Abstract

First Name:Debswapna

Middle Name:

Last Name:Bhattacharya

Adviser's First Name:Jianlin

Adviser's Last Name:Cheng

Co-Adviser's First Name:

Co-Adviser's Last Name:

Graduation Term:SS 2016

Department:Computer Science

Degree:PhD

Title:Probabilistic Graphical Models for Protein Structure Prediction

Computationally predicting the folded and functional three-dimensional structure of a protein molecule from its amino acid sequence with high degree of accuracy is critically important in structural bioinformatics and has huge implications in understanding and curing numerous diseases caused by protein misfolding, including CJD and type II diabetes, as well as neurodegenerative diseases like Alzheimer's, Parkinson's, Huntington's, and amyotrophic lateral sclerosis. Existing computational approaches for protein structure prediction faces two key challenges: (1) difficulty in efficiently navigating the enormous conformational space accessible to proteins and (2) difficulty in accurately capturing energetics of the complex interactions of thousand of atoms in a protein molecule in silico.

This dissertation attempts to address these challenges by (1) developing novel probabilistic graphical models and experimentally motivated probabilistic sampling techniques to fully capture and efficiently explore proteins' conformational space in various granularities and (2) integrating knowledge-based information into existing energy functions in order to improve their ability to discriminate correctly folded protein structures from decoys. We show that our methods outperform many traditional and state-of-the-art protein structure prediction approaches in terms of accuracy, speed and robustness. All of these methods are freely available to the scientific community.