

THE SPRING 2007 CONDENSED MATTER SEMINAR SERIES PRESENTS

Prof. Don Jacobs
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*“Understanding Protein Stability, Flexibility
and Molecular Cooperativity: Addressing
Non-additivity of Entropy in Free Energy
Decomposition Schemes”*

Abstract:

Proteins are large macromolecules consisting of many noncovalent interactions that determine their three-dimensional structure and stability. Manipulating protein stability and/or function is desired in protein engineering and the pharmaceutical industry. The importance of conformational flexibility to function is well known. For example, enzymes must be flexible enough to mediate a reaction pathway, yet rigid enough to achieve molecular recognition. Consequently, conformational flexibility is a critical link between structure, stability and function. A difficult challenge in biophysical modeling is to develop methods that accurately predict protein flexibility and stability under given thermodynamic and solvent conditions in computing times fast enough for high throughput computational biology applications. After a brief introduction on key features of protein chemistry, I will discuss a promising new paradigm that combines constraint theory with free energy decomposition schemes. Merging these two concepts leads to a Distance Constraint Model (DCM) that is computationally tractable using fast graph-rigidity algorithms. After an overview of the theoretical approach, computational results are presented on the folding/unfolding transitions in the beta hairpin turn and in proteins using mean field approximations, and in the alpha-helix using exact transfer matrix methods.

04.04.07 304 Robeson Hall
4:00 P.M.