East Carolina University®
Department of Physics

Colloquium

Friday, September 20th, Room N109, Howell Science Complex
3:15 p.m. (Refreshments at 3:00 p.m.)

Professor Donald Jacobs
University of North Carolina - Charlotte

Computational Models for Thermodynamic Stability and Functional Dynamics of Proteins

My talk explores the relationship between the dynamic processes driving protein function and the underlying thermodynamic forces that give rise to conformational ensembles. Various computational frameworks are employed to investigate these ensembles. First, I consider molecular dynamics (MD) simulations based on classical all-atom force fields. While this brute-force approach is robust, it presents two major challenges: the high computational cost required to capture long timescales and large system sizes, as well as the substantial volume of data generated. This data is analyzed using a novel machine learning method to facilitate large-scale comparative analysis and identify functional dynamics. To address the inefficiencies of brute-force MD, I describe a free energy decomposition method that captures the non-additivity of conformational entropy. This phenomenological model expressed either as a mean field theory, or self-consistent mean field theory, but also analogous to Landau theory in its simpler form, accurately predicts the heat capacity of proteins, reflecting the temperature sensitivity observed in experiments. Finally, integrating this thermodynamic model with geometrical simulation yields an efficient kinetic Monte Carlo algorithm, providing a more computationally viable alternative for studying the conformational ensembles of proteins.

Webex link: https://ecu.webex.com/ecu/j.php?MTID=m597b61dec85df5a0e1e21138fe56cd86