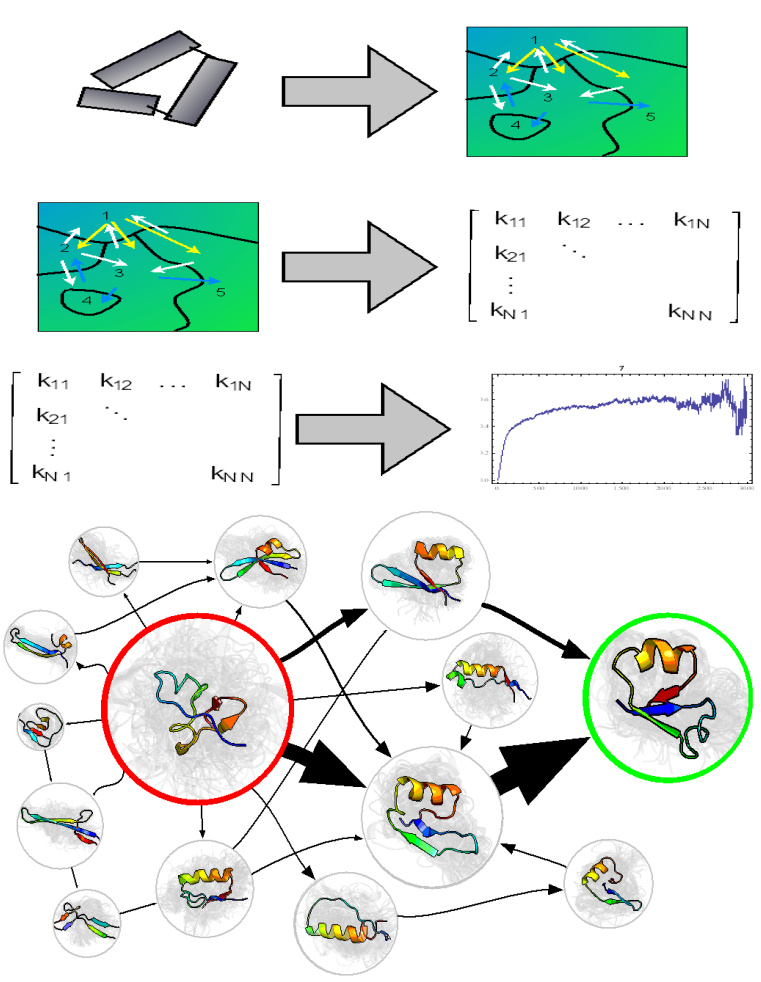
Boston University

Joint Physics and Chemistry Colloquium



Some Surprises in the Biophysics of Protein Dynamics

The self-assembly of proteins ("protein folding") is one of the key steps in the function of proteins, such as enzymes and antibodies. The mechanism by which this assembly occurs has been an outstanding question in molecular biophysics and biophysical chemistry for decades. Also, protein misfolding has been linked to numerous diseases, such as Alzhemier's and Huntington's Disease. Over the last 5 years, there has been tremendous progress in our ability to understand protein dynamics, such as folding in atomic detail. With the latest technology utilizing worldwide distributed computing ("Folding@home"), we can directly simulate the folding of proteins on the 80 residue scale on the 10's of millisecond timescale in all-atom detail. One can also use these methods to study folding in the presence of biological machinery, such as inside chaperonins or the ribosome tunnel. Moreover, a new mechanistic framework has provided a new framework for simulating and conceptualizing protein folding, leading to a new analytic statistical mechanics theory for protein folding kinetics. The picture that is emerging suggests a change in how we conceptualize protein dynamics in general, including protein folding and misfolding, including new roles for non-native interactions, novel mechanisms for folding and misfolding, and new thoughts for the role of water in protein folding in vivo.

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February 8, 2011 (Tuesday) at 3:30pm (Refreshments at 3:15pm)

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