Modeling Conformational Dynamics of Macromolecules from Simulations and Experiments

by Frank Noé

Computational Molecular Biology
FU Berlin

Abstract:

Obtaining a mechanistic understanding of complex macromolecular arrangements such as protein folding is notoriously difficult for both simulation and experimental approaches. Here we introduce an approach to model conformational dynamics using Markov models that describe the jump process between the different conformations of macromolecules. These models can be obtained from either molecular dynamics simulations or single molecule measurements. While good Markov models are not trivial to construct, they have a great deal of advantages over traditional analyses, such as:

- They allow to identify these low conformational processes and calculate associated rates or timescales
- They do not require global equilibrium information, thus mitigating the MD sampling problem and allowing to access longer timescales than one can directly simulate
- Stationary properties such as free energy differences and kinetic properties such as transition pathways can be easily calculated
- They can be used to directly interpret kinetic experiments, such as T-jump, FCS, dynamical neutron scattering
- Statistical and modeling errors can be calculated and controlled

We will illustrate our approaches on protein and RNA folding processes.

Friday, July 16th 2010, 13:00

Room PH 127

Contact:

Prof. Roland Netz, netz@ph.tum.de , phone: 089 289-12394