The Chair of Applied Dynamics at the Friedrich-Alexander-University Erlangen-Nuremberg has an immediate offer for a

Master's thesis

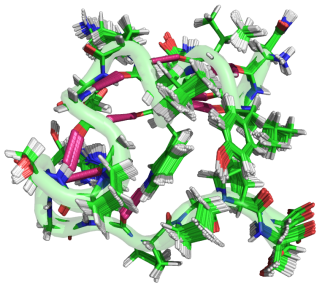
on

Molecular Dynamics and Kinematic Sampling: Validating Protein Motions and Conformations

Molecular Dynamics (MD) simulations are a valuable tool to computationally study conformational dynamics of proteins. Integrating the equations of motion based on sophisticated force-fields can lead to very accurate predictions of protein folding, native state dynamics, conformational changes, or interactions with binding partners. Although tremendous advances over the last decades in hard- and software have increased spatial and temporal scales accessible via MD by several orders of magnitude, limitations regarding very slow conformational changes with high energetic barriers, data interpretation, or force-field inaccuracies remain. This has paved the way for several variants such as steered MD, conformational flooding, or kinematic sampling. While those methods are usually faster, resulting motions and molecular conformations need to be carefully validated due to the reduced accuracy of these methods.
Here, we aim to compare a kinematic sampling procedure with traditional MD. The software framework Kino-Geometric Sampling (KGS) uses only torsional degrees of freedom that are subject to non-covalent constraints such as hydrogen bonds and a hard-sphere steric potential. It has been used to obtain insights into conformational transitions and dynamically coupled residue networks. The goal of this thesis is to analyze to which extent this limited force-field can reproduce accurate conformational changes by comparing it to motions from MD. KGS could be a valuable tool to generate starting conformations for shorter MD simulations, potentially revealing hidden substates that are difficult to observe from traditional MD alone.
The thesis is based on existing software tools (Gromacs for MD and KGS) and includes data preparation, performing simulations, and post-processing (with existing and self-written scripts). The thesis will be jointly advised between Prof. Dr. Sigrid Leyendecker's group at the Chair of Applied Dynamics and Prof. Dr. Rainer Böckmann's group at the Chair of Computational Biology.

Necessary qualifications

- previous programming experience
  (**basic Unix**, Shell, C++, Python, R, ...)
- lecture 'Dynamics of rigid bodies' or similar
- interest in computational biology
- basic knowledge in biochemistry (not mandatory)



KGS ensemble of Trp-Cage Miniprotein Construct TC5b (PDB code 1l2y).

If you are interested, please contact Dominik Budday via e-mail at dominik.budday@fau.de.