# CPP 22: Data-driven Methods in Molecular Simulations of Soft-Matter Systems

Time: Tuesday 9:30–10:30 Location: C 230

CPP 22.1 Tue 9:30 C 230

**Consistent interpretation of protein simulation kinetics using Markov state models biased with external information** — •Joseph Rudzinski, Kurt Kremer, and Tristan Bereau — Max Planck Institute for Polymer Research, Ackermannweg 10, 55128 Mainz

Molecular simulation models are often required to provide a microscopically-detailed interpretation of observations from, e.g., single-molecule spectroscopy experiments of proteins. In general, model errors may lead to inconsistencies between simulated and experimentally-measured observables. For static properties, well-established reweighting methods exist for adjusting the simulated ensemble with minimum bias in order to attain consistency for observables of interest. This work presents an analogous reweighting framework that adjusts the ensemble of dynamical paths sampled in a molecular simulation in order to ensure consistency with kinetic observables. The proposed methodology leverages Markov state modeling techniques to efficiently treat the simulated dynamical paths, while employing a Bayesian scheme to reweight these paths with minimum bias according to external reference data. Using small peptide systems as a proof of concept, we demonstrate how biasing a Markov state model significantly improves the kinetic description of the system, while refining the static equilibrium properties. Our conclusions highlight the potential of the methodology for providing consistent interpretations of kinetic protein experiments.

CPP 22.2 Tue 9:45 C 230

**A complete map between amphiphilic sequences and polymer transport through biological barriers: A massively parallel Rosenbluth study.** — •Marco Werner[1], Yachong Guo[2], and Vladimir Baulin[1] — [1]Universitat Rovira i Virgili, Tarragona, Spain — [2]National Laboratory of Solid State Microstructure, Department of Physics, Nanjing University, China

We investigate the relation between the monomer sequence of a polymer composed from hydrophilic and hydrophobic units and its diffusive transport through a lipid membrane. We employ the Rosenbluth method in order to generate random polymer conformations within a given mean fueld potential that represents a membrane or more complex morphologies. Thanks to the massively parallel generation of $1.5 \times 10^7$ independent conformations per sequence on graphics processing units (GPU), we obtain the free energy of the polymer with respect to a given reaction coordinate for all sequence combinations with a length $N \leq 16$ in reasonable time. For the prototypical example of the passive transport of polymers through lipid membranes, our results confirm earlier predictions that an overall balance of hydrophilic / hydrophobic units as well as sequences with short blocks lead to a minimal first escape time of the polymer through the membrane.

CPP 22.3 Tue 10:00 C 230

**Multiscale approach to conformational sampling: solute insertion in a lipid membrane** — •Roberto Menichetti, Kurt Kremer, and Tristan Bereau — Max Planck Institute for Polymer Research, Mainz, Germany

The accurate determination of the thermodynamic properties of soft matter by means of classical atomistic molecular dynamics simulations is often hampered by sampling issues. Coarse-grained models, which describe the system at a lower resolution, provide an efficient tool for addressing this problem. Indeed, coarse-graining smoothens the rough atomistic energy (and consequently free-energy) landscape, thus reducing some of the difficulties of an adequate conformational sampling. In this work, we present a multiscale method which aims at accelerating the exploration of the complex atomistic conformational space by leveraging the one generated by coarse-grained simulations, and apply it to the determination of the potential of mean force for the insertion of a small molecule in a lipid membrane environment. The method offers accurate results with a gain in computational time of roughly one order of magnitude with respect to conventional all-atom umbrella sampling simulations. We further show how the method can be efficiently employed in the framework of computational high-throughput drug screening.

R. Menichetti, K. Kremer and T. Bereau, Biochem. Biophys. Res. Commun. (in press), doi: https://doi.org/10.1016/j.bbrc.2017.08.095 (2017).

CPP 22.4 Tue 10:15 C 230

**Intermolecular interactions in complex liquid systems studied by MD simulations** — •Nebojša Zec[1], Abdenacer Idrissi[2], Slobodan Gadžurić[3], and Milan Vraneš[3] — [1]GEMS at Heinz Maier-Leibnitz Zentrum (MLZ), Helmholtz-Zentrum Geesthacht, Garching bei München, Germany — [2]Université des Sciences et Technologies de Lille 1, Villeneuve d'Ascq, France — [3]University of Novi Sad, Department of Chemistry, Biochemistry and Environmental Protection, Novi Sad, Serbia

We used molecular dynamics (MD) simulations to quantify the intermolecular interactions in pure molecular solvents ($\gamma$-butyrolactone, $\gamma$-valerolactone, propylene carbonate) and their binary mixtures with imidazolium based ionic liquids. The intermolecular interaction potentials were adjusted to reproduce the experimentally measured density of the pure substances as well as the mixtures over the whole range of mixing ratios. Hydrogen bonds, dipole-dipole and stacking interactions are the main interactions in these systems. Comparison of the hydrogen bond geometries with literature values indicates clearly that the hydrogen bond interactions in these systems are comparatively weak. Orientational correlations were characterized by several combined angular and distance distribution functions between first neighbour molecules: The position and tilt of the ring planes with respect to each other indicate ring stacking; and the relative orientation of the C=O bonds shows the relative orientation of molecular dipoles.