AKB 4 Membranes: Phase Behavior and Dynamics

Time: Monday 12:00–13:15 Room: ZEU 260

AKB 4.1 Mon 12:00 ZEU 260

Dynamic simulations of lateral diffusion in fluctuating membranes — •Ellen Reister-Gottfried and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart

When regarding lateral diffusion it is important to remember, that the membrane is flexible and subject to thermal fluctuations. Therefore the Langevin (or Smolouchovski) equation governing the dynamics of a protein diffusing in the membrane becomes a function of the membrane shape. In our novel simulation algorithm we combine the simulation of the membrane dynamics with the simulation of the protein movement. The membrane dynamics follows from the membrane Hamiltonian and a hydrodynamic coupling of the membrane to the surrounding fluid. The movement of the inclusion is calculated by numerically integrating the appropriate Langevin equation, that uses the instantaneous membrane shape. This simulation method allows for studies on large length and time scales and is easily extendable to include various protein-membrane interactions or external potentials acting on the membrane. We use this scheme to calculate diffusion coefficients projected on a flat plane, because this is the quantity, that is typically measured in experiments. In previous work we analytically calculated the difference between the projected and the actual intramembrane diffusion coefficient in the limit that membrane fluctuations are faster than protein diffusion. These results are compared with results achieved with the new simulation method.

AKB 4.2 Mon 12:15 ZEU 260

Coarse-grained simulations of internal phases in lipid membranes — •Friederike Schmid and Olaf Lenz — Universität Bielefeld

We study internal membrane phase transitions by Monte Carlo simulation of a simple coarse-grained model system. Lipids are modeled as single spring-bead chains. They are forced to self-assemble by a surrounding fluid of "phantom" solvents, which only interact with the lipids, but not with one another. The solvent is thus very cheap from a computational point of view, and the model can be simulated very efficiently. Depending on the model parameters, it exhibits a fluid state, tilted and untilted gel states, and an interdigitated state. In the "pretransition" region between the tilted gel state and the fluid state, two types of undulated rippled structures are observed: an asymmetric structure with a sawtooth profile and a period of roughly 15-20 lipid diameters, and a symmetric structure with a period twice as long. Both structures have been reported in experiments, and their molecular structure is still under debate. The structure of our asymmetric ripple state agrees with that found recently by de Vries et al (PNAS 102, 5392, 2005) in an atomistic simulation of a Lecithin bilayer. Moreover, our simulations suggest a structural model for the structure of the symmetric ripple state.

AKB 4.3 Mon 12:30 ZEU 260

Alternative mechanisms of structuring biomembranes — •Markus Bär [1] and Karin John[2] — [1]Physikalisch-Technische Bundesanstalt, Abbestr. 2-12, 10587 Berlin — [2]Max-Planck-Institut für Physik komplexer Systeme, Noethnitzer Str. 38, 01187 Dresden

Cell membranes are composed of a mixture of lipids. Many biological processes re-quire the formation of spatial domains in the lipid distribution of the plasma membrane. In a first step, we study two mechanisms for the formation of protein patterns near membranes of living cells by mathematical modelling. Self-assembly of protein domains by electrostatic lipid-protein interactions is contrasted with self-organization due to a nonequilibrium biochemical reaction cycle of proteins near the membrane. While both processes lead eventually to quite similar patterns, their evolution occurs on very different length and time scales. Self-assembly produces periodic protein patterns on a spatial scale below 0.1 μm in a few seconds followed by extremely slow coarsening, whereas self-organization results in a pattern wavelength comparable to the typical cell size of 100 μm within a few minutes [1].

[1] K. John and M. Bär, Phys. Rev. Lett. 95, 198101 (2005).

AKB 4.4 Mon 12:45 ZEU 260

Ordered domains control membrane diffusion in model membranes — •Carsten Selle, Florian Rückerl, and Josef Käs — University of Leipzig, Insitute for Experimental Physics I, Soft Matter Physics, Linnestr 5, 04103 Leipzig, Germany

We investigate the diffusion properties of biological membrane components by a Single-Particle-Tracking (SPT) technique employing monolayers at the air/water interface as two-dimensional membrane mimetics. Protein diffusion within inhomogeneous membranes was mimicked by motion of surface-charged fluorescent polystyrene beads in monolayers where two differently ordered phases coexist. Associated to ordered liquid-condensed (LC) domains, dimensionally reduced motion of the model proteins in the liquid-expanded (LE) phase was observed. We assume that dipole-dipole interactions between the diffusing beads and LC domains give rise to an attractive potential resulting in a strikingly modified bead diffusion in the LC domain neighborhood. This view point is supported by suitable Monte-Carlo simulations. The simulations demonstrate that model protein diffusion can be strongly affected by both potential depth and also by the domain size. It seems conceivable that living cells could make use of diffusion control accomplished by similar mechanisms in order to enhance kinetics of bimolecular enzyme reactions occuring in the membrane. In recent experiments performed in our lab, giant unilamellar vesicles interacting with fluorescent polystyrene beads have been employed to study the behavior of model proteins at curved sufaces. First results are presented.

AKB 4.5 Mon 13:00 ZEU 260

Phase transition induced morphological changes in lipid vesicles — •Christian Leirer, Achim Wixforth , and Matthias Schneider — Institut für Physik (Biophysik), Universtät Augsburg, Universitätsstraße 1, D-86159 Augsburg

Phase transition in lipid membranes are accompanied by dramatic changes in the area per molecule and their elastic properties. Using Micropipett aspiration, AFM, fluorescence and light microscopy we studied basic phenomena in membranes, that depend strongly on the phase state and explain them in the theoretical framework of membrane elasticity. A variety of effects showing strong similarities to biological systems are dicussed.