BP 25: Membranes

Time: Friday 10:15–13:15 Location: HÜL 186

Invited Talk BP 25.1 Fri 10:15 HÜL 186

Role of membrane curvature in membrane trafficking — •Patricia Bassereau, Benoit Sorre, Andrew Callan-Jones, Gerbrand Koster, Aurélien Roux, Martin Lenz, Jean-François Joanny, and Jacques Prost — Institut Curie, Lab. PhysicoChimie Curie, Paris, France

Similar to proteins, most membrane lipids are transported by carriers (vesicles or tubules) with typical 50-100nm diameters that bud off from a donor membrane. During budding, sorting occurs: some lipids and proteins are selectively incorporated into these transport intermediates. It has been proposed that components can be dynamically sorted due to membrane curving during coat formation. In order to test this hypothesis, we have pulled membrane nanotubes with controlled diameters (15-500 nm) from Giant Vesicles (GUV). We will show that curvature-induced lipid sorting only occurs if the membrane is close to a demixing point. In addition, for these compositions, lipid sorting is further amplified when even a low fraction of lipids is clustered upon cholera toxin binding, suggesting that lipid-clustering proteins may play an important role in curvature-induced sorting in biological membranes. Another aspect of the role of curvature in membrane trafficking can be studied with these nanotubes. Dynamin is a protein, which assembles in helicoidal structures around the neck of vesicles during budding and induces fission upon GTP hydrolysis. We will show that dynamin assembly can occur only when the neck diameter is below a threshold value. This curvature-dependent polymerization mechanism guaranties a correct timing for carrier budding.

BP 25.2 Fri 10:45 HÜL 186

Multi-Parameter Analysis of Inter-Membrane Adhesion Using Simultaneous Fluorescence and Reflection Interference Contrast Microscopy (RICM) — •Susanne Fenz[1], Rudolph Merkel[1], and Kheya Sengupta[2] — [1]Institute of Bio- and Nanosystems (IBN), Research Centre Jülich, 52425 Jülich, Germany — [2]Centre Interdisciplinaire de Nanosciences de Marseille (CINAM/CNRS-UPR3118), Luminy, Marseille Cedex 9, France

We present a biomimetic model system for cell-cell adhesion consisting of a giant unilamellar vesicle (GUV) adhering via specific biotin-neutravidin interaction to a supported lipid bilayer (SLB). Based on a standard fluorescence microscope, a new set-up was developed that enables simultaneous imaging in RICM and fluorescence microscopy as well as determination of molecular diffusion by continuous photobleaching. GUVs adhering to SLBs were characterized with respect to their inter-membrane distance, adhesion energy density and fluctuation amplitude. Fluorescent imaging and recovery after photobleaching of receptors yielded their distribution, concentration and diffusion constant. We present both static and dynamic analysis of the intermembrane distance and bond ordering for the limiting cases of dense and dilute bonds.

BP 25.3 Fri 11:00 HÜL 186

Specific adhesion of membranes: the role of membrane fluctuations — •Ellen Reister, Ana-Sunčana Smith, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart, Germany

We analyse adhesion of a membrane to a flat surface via receptor-ligand pairs both in equilibrium and during the adhesion process. The membrane is modeled with the Helfrich energy, while the ligands in the membrane may react with receptors attached to the substrate via springs. The corresponding reaction rate depends on the distance between membrane and substrate. The positions of the ligands in the membrane and the tethers attached to the substrate are kept fixed. For the two coupled dynamic processes in the system - membrane fluctuations and receptor-ligand reactions – we derive equations of motion that are numerically integrated in our novel simulation scheme. To study the influence of thermal membrane shape fluctuations we compare results for a stiff membrane with simulation results. In equilibrium we find that fluctuations make the transition from a bound to an unbound membrane more continuous and that higher binding energies are necessary to maintain the same degree of adhesion. During the dynamic process of adhesion membrane fluctuations are found to increase the adhesion speed. Both in equilibrium and during adhesion observed spatial correlations between bonds indicate that the fluctuating membrane mediates an attractive force between neighboring bonds.

BP 25.4 Fri 11:15 HÜL 186

A solvent-free coarse-grained model for amphiphilic bilayers — •Martin Hömberg and Marcus Müller — Institut für Theoretische Physik, Georg-August-Universität, 37077 Göttingen, Germany

In recent years collective phenomena like membrane fusion or self-assembly of bilayers have attracted tremendous interest. However, atomistic simulations still cannot reach the corresponding time and length scales. Frequently coarse-grained models are employed to save computation time, among them are the solvent-free models, which reduce the amount of interactions to be computed considerably.

Here we present a flexible and computationally efficient bead-spring-model for simulating coarse-grained membranes without explicit solvent. We use a third-order expansion of a free energy functional in the density to describe non-bonded soft interactions, which include the interactions with the solvent implicitly. The expansion coefficients can be related to material properties, such as the molecular density, the compressibility or the incompatibility between the amphiphilic units.

We use DPD simulations with density-dependent forces to investigate the mechanical properties of amphiphilic bilayers, such as the bending rigidity, the area per lipid and diffusion coefficients. These results are compared to experimental data.

BP 25.5 Fri 11:30 HÜL 186

A simulation study of protein-mediated membrane deformations — •Diana Morozova and Matthias Weiss — German Cancer Research Center, Cellular Biophysics Group (BIOMS), Im Neuenheimer Feld 280, D-69120 Heidelberg

Biomembranes assume a variety of function-related shapes, e.g. spherical buds, membrane necks, or tubular protrusions. In virtually all cases membrane proteins are responsible for inducing these shapes. Using dissipative particle dynamics (DPD), a coarse-grained membrane simulation method, we have studied the influence of cone-shaped transmembrane proteins on the shape of a tensionless membrane and the associated membrane-mediated (i.e. bending-induced) interactions between the proteins. We find a clustering of proteins at high densities that is accompanied by a bud formation. The observed clustering not only depends on the protein density but also on the cone angle of the inclusions and the hydrophobic mismatch between the protein's transmembrane portion and the core of the bilayer.

15 min. break

BP 25.6 Fri 12:00 HÜL 186

Pattern formation in membranes by a translocation-diffusion mechanism — Sergio Alonso, •Sebastian Curth, and Markus Baer — Physikalisch-Technische Bundesanstalt, Berlin, Germany

We study the formation of protein patterns in the membranes of living cells by mathematical modelling. The formation of protein domains by electrostatic lipid-protein interactions and the nonequilibrium biochemical reaction cycle of proteins near the membrane give rise to complex dynamics. Here we consider an initially homogeneous membranes where the proteins self-organize into domains due to the competition between their attraction to the membrane and the interaction with different types of enzymes, which translocate the proteins from the membrane to the bulk. We incorporate also the regulation by calcium of the enzymes in the model.

BP 25.7 Fri 12:15 HÜL 186

Interaction of charged colloids and actin filaments with inhomogeneous lipid membranes — •Florian Rückerl, Lydia Woiterski, Josef Käs, and Carsten Selle — Universität Leipzig, Inst. Exp. Phys. I

Lipid bilayers are simple and controllable mimics of cell membranes. The model membranes used in the experiments are composed of ternary mixtures of lipids (DOPC, cholesterol and DPPC or Sphingomyelin). These compositions can form liquid membranes and exhibit an ordered-disordered phase coexistence.

In giant unilamellar lipid vesicles, electrostatic interactions are screened by the surrounding polar liquid and relatively short-ranged. However, even for supposedly neutral membranes, positively charged

colloids show a much higher binding affinity to the bilayer than negatively charged colloids. Further, we see a strong influence of the phase boundary on the diffusional properties of the tracer particle, namely a switch from two- to one-dimensional diffusion. This observation is similar to our previous experiments on monolayer systems [1,2].

The negatively charged semiflexible polymer actin readily binds to lipid membranes containing 10% of the cationic DOTAP. There is an interesting interplay between the size of the domains in which the DOTAP partitions into, and the length of the filaments. Our experiments indicate a lower limit for the domain size below which the binding of the filaments does not occur.

[1] Rückerl et al., Langmuir 2008, 24 (7)
[2] Forstner et al., Phys Rev E 2008, 77

BP 25.8 Fri 12:30 HÜL 186

***In vitro* characterization of vinculin's lipid membrane-interacting domain, helix 3** — •Volker Wirth[1], Felix List[2], Gerold Diez[1], Wolfgang H. Ziegler[3], and Wolfgang H. Goldmann[1] — [1]Center for Medical Physics and Technology, Friedrich-Alexander-University of Erlangen-Nuremberg, Germany — [2]Institute of Biophysics and Physical Biochemistry, University of Regensburg, Germany — [3]IZKF, University of Leipzig, Germany

The focal adhesion protein vinculin plays an important role in cell migration and adhesion. Binding of vinculin to lipid membranes ensures these processes. Helix 3 (residues 944 – 972) is one of three potential membrane interaction sites that has been reported on the tail domain. In pull-down assays using artificial lipid membranes it was demonstrated that, when helix 3 is mutated on position K952, K956, R963, R966 to Q, its interaction with acidic phospholipid vesicles is impaired. To date, no data exist on the nature of the interaction.

Using differential scanning calorimetry on wildtype helix 3 we could show that it inserts into lipid vesicles consisting of dimyristoyl-L-a-phosphatidylcholine (DMPC) and negatively-charged dimyristoyl-L-a-phosphatidylserine (DMPS). However, when mutating the four basic residues on helix 3, the insertion into lipid vesicles was reduced. Examining the secondary structure of wildtype helix 3 in the presence and absence of DMPC/DMPS lipid vesicles by CD-spectroscopy showed a conformational shift. These observations indicate that the electrostatic interaction of the basic residues on helix 3 induce the insertion into the hydrophobic core.

BP 25.9 Fri 12:45 HÜL 186

Long-Range Motion of Phospholipids on a Picosecond Timescale as Seen with Quasielastic Neutron Scattering — •Sebastian Busch[1], Christoph Smuda[1], Luis Carlos Pardo Soto[2], and Tobias Unruh[1] — [1]Physik Department E13 and Forschungsneutronenquelle Heinz Maier-Leibnitz (FRM II), Technische Universität München, Lichtenbergstraße 1, D-85747 Garching bei München — [2]Grup de Caracterització de Materials, ETSEIB, Universitat Politècnica de Catalunya, E-08028 Barcelona

Phospholipids are not only interesting because of their ubiquity and importance for every living being, but also because they can be used in a variety of technological applications, e.g. as stabilizers of lipid nanoparticles for drug delivery. We aim to understand the diffusional dynamics of phospholipids on a molecular scale, the difference in dynamics of monolayers compared to bilayers, the influence of coemulsifiers, and the correlation of these microscopic parameters to macroscopic physicochemical quantities.

On a long timescale, the free volume theory can describe the long-range diffusive motions of phospholipids satisfactorily. Molecular dynamics simulations have observed that on a short time scale, collective, flow-like motions become important.

We studied liquid crystals, vesicles, and emulsions with DMPC using quasielastic neutron scattering at the time-of-flight spectrometer TOFTOF at FRM II. Experimental evidence was found that the long-range motion on a picosecond time range indeed has a flow-like character.

BP 25.10 Fri 13:00 HÜL 186

Radial density profile and size distribution of synaptic vesicles determined by small angle x-ray scattering — •Simon Castorph[1], Matthew Holt[2], Michael Sztucki[3], Reinhard Jahn[2], and Tim Salditt[1] — [1]Institute for X-ray Physics, Göttingen, Germany — [2]Max Planck Institute for Biophysical Chemistry, Göttingen, Germany — [3]European Synchrotron Radiation Facility, Grenoble, France

The release of neurotransmitters from neurons, in response to stimulation, forms the basis of communication in the nervous system. Neurotransmitters are stored in small membraneous organelles, synaptic vesicles, within the presynaptic terminal. These vesicles undergo an elaborate cycle of fusion with the plasma membrane (releasing neurotransmitter), followed by retrieval and reformation and transport back to the plasma membrane for further rounds of fusion.

In recent years there has been enormous progress in our knowledge of the molecular composition and structure of synaptic vesicles. However, we still lack a detailed view of the physical properties of this trafficking organelle as it proceeds through its life-cycle.

Small angle x-ray scattering is used to find the average structural properties of synaptic vesicles form rat brain. Quantitative fitting of the x-ray scattering curves reveals the width of the size distribution and details of the radial scattering length profile of the vesicle structure. We obtain representative values for the inner and outer radii and the size polydispersity, as well as the density and width of the inner and outer protein layers.