BP 19: Membranes and Vesicles

Time: Wednesday 10:00–12:45 Location: H43

BP 19.1 Wed 10:00 H43

Dynamics of endosomal population and cargo trafficking — •Jonathan Edward Dawson[1], Lionel Foret[3], Roberto Villasen[2], Claudio Collinet[2], Yannis Kalaidzidis[2], Marino Zerial[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden — [2]Max Planck Institute for Molecular Cell Biology and Genetics, Dresden — [3]Ecole Normale Supérieure-LPS, Paris

Endosomes are vesicular structures that transport cargo molecules that are internalized into the cell by endocytosis. Endosomes exchange material by fusion and fission and form a cellular compartment in which cargo is sorted. We present a theoretical description of a population of endosomes. In the description we capture the cargo trafficking on a population level and take cargo influx, outflux, fusion and fission into account. Experimentally the cargo distribution in the endosomal population can be determined by fluorescence microscopy. Our theory predicts scaling properties of the network which are observed experimentally. The theory also describes characteristic features of steady state distribution of cargo molecules in Rab5 positive endosomes. We compare our theory to experimental data and determine the kinetic parameters of the early endosomal network in HeLa cells.

BP 19.2 Wed 10:15 H43

Forming vesicles by different methods: the advantages of microfluidic jetting — •Silke Kirchner[1], Alexander Ohlinger[1], Andrey A. Lutich[1], Fernando D. Stefani[2], and Jochen Feldmann[1] — [1]Photonics and Optoelectronics Group, Ludwig-Maximilians-Universität, München, Germany — [2]Departamento de Física Universidad de Buenos Aires, Buenos Aires, Argentina

Phospholipid bilayer vesicles have attracted significant attention during the last decade being a simple model system for cell membranes. The fabrication of vesicles with controlled size distribution, membrane thickness and entire vesicle filling is of particular interest. Among the widely-used methods of vesicle formation are ultrasonification and electroformation. Although these techniques were extensively used and developed they have a number of disadvantages: the low degree of control over and the broad distribution of the vesicles' sizes.

In order to overcome these difficulties the microfluidic jetting technique can be used. The microfluidic jetting method is supposed to increase the degree of control over the vesicles formation process. We will discuss the effect of changing the jet parameters (speed and volume of the jetted liquid) and the membrane properties (combination of different lipids and membrane phase controlled by temperature) on the vesicle fabrication process. Apart from the well-controlled vesicle's size distribution microfluidic jetting offers the possibility to produce vesicles filled with any required solution.

BP 19.3 Wed 10:30 H43

Effective attraction of curved inclusions in membranes — •Thorsten Auth and Gerhard Gompper — Forschungszentrum Jülich, Institut für Festkörperforschung, 52425 Jülich, Germany

Conical inclusions in a lipid bilayer generate an overall spontaneous curvature of the membrane that depends on concentration and geometry of the inclusions. Examples are integral and attached membrane proteins, viruses, and lipid domains. We propose an analytical model to study budding and vesiculation of the lipid bilayer membrane, which is based on the membrane bending energy and the translational entropy of the inclusions. If the inclusions are placed on a membrane with similar curvature radius, their repulsive membrane-mediated interaction is screened. Therefore, for high inclusion density the inclusions aggregate, induce bud formation, and finally vesiculation. Already with the bending energy alone our model allows the prediction of bud radii. However, in case the inclusions induce a single large vesicle to split into two smaller vesicles, bending energy alone predicts that the smaller vesicles have different sizes whereas the translational entropy favors the formation of equal-sized vesicles.

BP 19.4 Wed 10:45 H43

Free energy calculations of the main phase transition in lipid bilayers — •Martin Hömberg and Marcus Müller — Institut für Theoretische Physik, Georg-August-Universität Göttingen, 37077 Göttingen, Germany

In coarse-grained models of lipid bilayers one integrates out local degrees of freedom, so that the study of collective phenomena, like phase transitions, lateral phase separation in heterogeneous bilayers, and self-assembly, becomes feasible in computer simulations. However, the precise calculation of phase diagrams is still a formidable task due to hysteresis effects and metastability in the vicinity of phase transitions.

Here we employ DPD for the simulation of a coarse-grained solvent-free model for single component lipid bilayers. The non-bonded interactions between the lipids are derived from an excess free energy, which takes the form of a weighted density functional. We find a rich phase diagram, study the main phase (liquid-gel) transition, and present a method to calculate the free energy at this transition as a function of an orientational order parameter. We apply a combination of Umbrella Sampling and histogram reweighting techniques for transforming the liquid phase reversibly into a gel phase. We are able to locate the phase transition point precisely from the free energy profile and we obtain a value of the line tension between liquid and gel domains. This value is compared to the value obtained from a spectral analysis of the boundary fluctuations of gel domains in a liquid phase.

15 min. break

BP 19.5 Wed 11:15 H43

Effects of the bulk in a simple model of nonequilibrium formation of lipid domains in biomembranes — Sergio Alonso and •Markus Bär — Physikalisch-Technische Bundesanstalt, Berlin, Germany

Proteins inside the cell strongly interact with biological membranes depending on the lipid composition and the interaction with other proteins. We consider a simple model of membrane organization into domains based on a cyclic binding and unbinding of the MARCKS protein to acidic lipids known as myristo-electrostatic (ME) switch. The model describes the formation of membrane domains under nonequilibrium conditions, because the ME switch consumes ATP and leads to non-vanishing currents of proteins. We study the coarsening dynamics and the effects of the coupling to a three-dimensional bulk in the domain pattern formation. The effect of the bulk is an effective decrease of reaction rates in the ME switch, for which simple expressions can be derived. The predictions are verified by comparison of numerical simulations including the bulk and analytically obtained phase diagrams.

BP 19.6 Wed 11:30 H43

Influence of Additives on the Short-Time Dynamics of the Phospholipid DMPC — •Sebastian Busch and Tobias Unruh — Physik Department E13 and Forschungsneutronenquelle Heinz Maier-Leibnitz (FRM II), Technische Universität München, Lichtenbergstraße 1, 85748 Garching bei München

In nature as well as in industrial applications, phospholipid membranes contain many components which have significant influence on the properties of the membrane. A striking example is the use of sodium glycocholate (NaGC) as co-emulsifier which enhances the stability of phospholipid-stabilized emulsions by orders of magnitude.

In pharmaceutical technology, the term "fast co-emulsifier" was coined to describe the ability of NaGC to even stabilize droplets which undergo a rapid deformation due to crystallization.

On the other hand, the status-quo of the description of phospholipid membrane dynamics, the free volume theory, predicts a decrease of mobility when additives fill up voids within the lipophilic core of the membrane.

We are able to show with quasielastic neutron scattering that the addition of NaGC indeed increases the picosecond dynamics of the phospholipid DMPC. This effect is compared to the influence of lipophilic additives, namely myristic acid, farnesol, and cholesterol.

BP 19.7 Wed 11:45 H43

Exploring the Nanoscale: Dynamics of Lipid Rafts Revealed by STED Fluorescence Fluctuation Spectroscopy — •Veronika Mueller, Christian Ringemann, Rebecca Medda, Christian Eggeling, and Stefan Hell — Max-Planck-Institute for Biophysical Chemistry, Department of NanoBiophotonics, Am Fassberg 11, 37077 Goettingen, Germany

The study of molecular dynamics at the single-molecule level with

fluorescence far-field optics offers new detailed insights into scientific problems, especially in living cells. Unfortunately, the resolution of common far-field techniques is limited to about 200nm in the lateral direction by diffraction. In recent years, several concepts such as stimulated emission depletion microscopy (STED) have been successfully applied to overcome the diffraction barrier. We present the combination of high resolution STED microscopy with different fluorescence fluctuation techniques providing the unique ability to study molecular dynamics with high spatial (<40nm) and temporal resolution (<1ms) in living cells. Using fluorescence correlation spectroscopy (FCS), we were able to explore single-molecule dynamics in up to 70-fold reduced focal volumes on two-dimensional samples such as lipid membranes with excellent signal-to-noise ratios. Special attention is drawn to inhomogeneous lipid diffusion on the plasma membrane of living cells. This new technique provides the possibility to non-invasively record molecular time traces and fluctuation data in continuously tuneable nanoscale focal areas and thus offers a powerful new approach to study the dynamics of biomolecules in living cell membranes.

BP 19.8 Wed 12:00 H43

Response of tethered membranes to pH, ionic strength and temperature variations studied by neutron and x-ray reflectometry — •Samira Hertrich, Joachim Rädler, and Bert Nickel — Ludwig-Maximilians-Universität, Department für Physik und CeNS, Geschwister-Scholl-Platz 1, 80539 München

Lipid membranes chemically grafted to a solid surface provide model systems to study membrane-protein interactions. Here, a multi-step chemical reaction is employed to fabricate tethered membranes on silicon oxide by silane chemistry. Reflectometry measurements show that the lipid bilayer is elevated from the surface through a PEG cushion by 7nm. Fluorescent labeled lipids allow for optical characterization by microscopy confirming homogeneity and mobility of the lipid bilayer. The stability of this system has been tested in a wide pH range from 4 to 11. With x-ray reflectivity (D4, HASYLAB) we observe a reversible contraction of the PEG layer at pH > 9.5, originating from a dehydration of the PEG interlayer as is shown by neutron reflectivity (REFSANS and N-Rex, FRM-2). In contrast, temperature changes and variation of the ionic strength of the buffer did not cause significant changes of the PEG interlayer thickness. The tethered membrane system is now used to test for the binding of neural proteins to the membrane. Initial experiments indicate that the effects of protein binding are a thinning of the lipid bilayer and an increase of water in both the head and the chain region of the membrane. Assistance from Martin Haese-Seiller and Adrian Rühm with the neutron experiments is gratefully acknowledged.

BP 19.9 Wed 12:15 H43

Diffusing proteins on a fluctuating membrane: Analytical theory and simulations — •Ellen Reister, Stefan M. Leitenberger, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

Using both analytical calculations and computer simulations we consider the lateral diffusion of a membrane protein and the fluctuation spectrum of the membrane in which the protein is embedded. The membrane protein interacts with the membrane shape through its spontaneous curvature and bending rigidity. Using a rigorous path-integral approach we derive an analytical expression for the effective lateral diffusion coefficient of the protein in the limit of small ratios of temperature and bending rigidity, which is the biologically relevant limit. Simulation results show good quantitative agreement with our analytical result. The analysis of the correlation functions contributing to the diffusion coefficient reveals that correlations between the stochastic force of the protein and the response in the membrane shape are responsible for the reduction of the diffusion coefficient.

Our quantitative analysis of the membrane height correlation spectrum shows a non negligible influence of the protein-membrane interaction causing a distinctly altered wave-vector dependence compared to a free membrane. Furthermore, the time correlations exhibit the two relevant timescales of the system: that of membrane fluctuations and that of protein diffusion that is typically much longer than the other. We suggest that the long-time decay of height correlations may provide a means to determine effective diffusion coefficients of proteins.

BP 19.10 Wed 12:30 H43

Mesoscopic simulations of membrane protein trafficking and signal transduction across membranes — •Diana Morozova, Gernot Guigas, and Matthias Weiss — DKFZ, Cellular Biophysics Group, Im Neuenheimer Feld 280, D-69120 Heidelberg

Acylation is a frequent posttranslational modification that triggers the membrane association of soluble proteins. Besides those peripheral membrane proteins (PMPs) also many transmembrane proteins are subject to lipid modifications, hence indicating that these membrane anchors may also regulate the trafficking of transmembrane proteins. Using coarse-grained membrane simulations we find that acylation indeed significantly alters the tilting of transmembrane proteins with respect to the bilayer normal. Cluster formation and partitioning behavior due to hydrophobic mismatching with the surrounding lipid bilayer is also altered, therefore allowing for ample possibilities to regulate the trafficking of transmembrane proteins via palmitoylation [1].

Using the same simulation approach, we also have studied the trafficking of peripheral membrane proteins (PMPs). In particular, we have observed a cross-leaflet oligomerization of PMPs due to membrane mediated attraction. The strength of this effect is determined by the radii and membrane anchor lengths of the involved PMPs. Since both of these might be altered, for example by ligand binding, the observed cross-leaflet oligomerization may be the fundamental process by which PMPs can trigger an intracellular signalling cascade without the need for accessory transmembrane factors.

[1] D. Morozova & M. Weiss, Biophys. J., in press