BP 9: Poster II

Cytoskeletal Filaments (BP 9.1 – BP 9.14); Membranes and Vesicles (BP 9.15 – BP 9.27)

Time: Monday 17:30–19:30 Location: P2/2OG

BP 9.1 Mon 17:30 P2/2OG

Vimentin intermediate filaments stabilize dynamic microtubules — •Charlotta Lorenz, Laura Schaedel, and Sarah Köster — Institute for X-Ray Physics, Georg-August-Universität, Göttingen, Germany

Many cellular functions such as cell shape, mechanics and intracellular transport rely on the organization and interaction of actin filaments, microtubules (MTs) and intermediate filaments (IFs), which are the main constituents of the eukaryotic cytoskeleton. We study the interaction between vimentin IFs and dynamic MTs in a minimal in vitro system and show that MTs are stabilized against depolymerization by the presence of vimentin IFs. To explore the electrostatic and hydrophobic contributions to this attraction, we measure interactions between individual MTs and vimentin IFs under different buffer conditions. We theoretically model the interaction to understand the energy landscape of the attraction. Taken together, our results suggest that there is an attractive interaction between MTs and vimentin IFs that supports increased MT stability.

BP 9.2 Mon 17:30 P2/2OG

Influence of Ions on the Assembly of Vimentin Intermediate Filaments — •Manuela Denz[1], Harald Herrmann[2], and Sarah Köster[1] — [1]Institute of X-ray physics, University of Göttingen, Göttingen, Germany — [2]Institute of Neuropathology, University Hospital Erlangen, Erlangen, Germany

The cytoskeleton is mainly composed of intermediate filaments (IFs), microfilaments and microtubules. In contrast to the conserved proteins actin and tubulin, IF proteins vary between different cell types. Despite the many different types, all IF proteins share the same secondary structure of a helical rod domain and intrinsically disordered head and tail domains. The assembly of IFs follows a hierarchical pathway. The assembly of the charged monomers into filaments can be triggered by ions. Here, we focus on the assembly of the IF protein vimentin using different ions. We test the influence of several ions with varying valencies, sizes and concentrations by small angle x-ray scattering (SAXS) and fluorescence microscopy (FM). SAXS probes primarily the lateral assembly of vimentin monomers into so-called unit-length filaments, while with FM the extended filaments are directly imaged. Vimentin assembled with monovalent ions forms single filaments. On the contrary, vimentin forms networks when assembled with multivalent ions. For those ions, vimentin filaments aggregate after exceeding a threshold concentration. With increasing valency of the ion, the threshold for aggregation of vimentin filaments is lowered. However, also differences between divalent ions can be observed, which can be explained by the Hofmeister effect.

BP 9.3 Mon 17:30 P2/2OG

Comparison of mechanisms of kinetochore capture with varying number of spindle microtubules — •Indrani Nayak, Dibyendu Das, and Amitabha Nandi — Department of Physics, Indian Institute of Technology Bombay, Powai, Mumbai 400076, India

The capture of kinetochores by spindle microtubules is crucial for cell division. Earlier experimental studies have shown that dynamical instability driven search-and-capture of a kinetochore by spindle microtubules is a dominant mechanism in eukaryotes. A different mechanism has been reported in *Schizosaccharomyces pombe*, where spindle microtubules being pivoted at the spindle pole body search for the kinetochores. Our work compares these two mechanisms by studying the first passage times of kinetochore capture as a function of microtubule number N. In addition to the *mean* times, we also estimate a more robust measure, namely the *characteristic* times associated with the rare events of capture. We find upon varying N, one mechanism may be preferred over the other. While for fewer N (as in *S. pombe*), the *characteristic* capture times due to pivoting are lesser than those for search-and-capture, the behavior reverses at larger N. Our study provides a physical basis for the selection of one mechanism over another depending upon microtubule number. The *characteristic* timescales are obtained either by computing the survival probability of a kinetochore to high precision or using the statistics of extremes.

BP 9.4 Mon 17:30 P2/2OG

Force Generation by Contractile Actomyosin in Elastic Frames — •Johannes Flommersfeld[1], David Brückner[1], Haiyang Jia[2], Petra Schwille[2], and Chase Broedersz[1] — [1]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, LMU Munich — [2]Max Planck Institute for Biochemistry, Martinsried

Contractile actomyosin gels are crucial for the mechanical properties of cells. Here, we study how the active contraction behavior of actomyosin networks responds to the elasticity of their surroundings. To this end, we design an experimental setup, which couples reconstituted actomyosin networks to 3D-printed elastic structures. Specifically, we use a micropillar array as a force and velocity sensor. These micropillar arrays can be deformed by the activity of the network, which allows for quantitative studies of the static and dynamic properties of contractile actomyosin networks. To understand the observed dynamical behavior of this contractile active gel, we introduce a phenomenological model, which highlights the role of the force-dependent myosin kinetics. Finally, we explore the potential of this setup to perform viscosity measurements of the actomyosin gel.

BP 9.5 Mon 17:30 P2/2OG

Filament Sensor - A tool for near real-time analysis of stress fiber formation in stem cells — •Lara Hauke[1], Benjamin Eltzner[2], Carina Wollnik[1], Stephan Huckemann[2], and Florian Rehfeldt[1] — [1]University of Göttingen, Third Institute of Physics - Biophysics, Germany — [2]University of Göttingen, Institute for Mathematical Stochastics, Germany

Mechanically induced differentiation of hMSC is dependent on Young's elastic modulus E of the microenvironment. While changes in lineage-specific protein expression occur over a period of days to weeks, the pattern formation of the cytoskeleton shows significant differences within the first 24 hours after seeding, therefore, quantified by an order parameter S, being an early morphological marker for mechano-induced differentiation [1]. We use a massively parallel live-cell imaging set-up to record cells under physiological conditions over a period of 24-48 hours to obtain a large, statistically sufficient data set. We aim for a full representation of filament processes over time and space. In contrast to the classification of stress fibers based on their location, we use an unbiased classification due to their temporal and spatial persistence. For this task we developed the 'Filament Sensor' [2, 3], a freely available tool for near real-time analysis of stress fibers. We present experimental data where we can distinguish the cytoskeletal structures of hMSCs on various elastic substrates with 99 % confidence. We are working on single filament tracking, 3D filament tracing, and correlation of focal adhesions and stress fibers. [1]A. Zemel, et al., Nat. Phys., 2010 [2]filament-sensor.de [3]B. Eltzner, et al., PLoS One, 2015

BP 9.6 Mon 17:30 P2/2OG

Modeling Interactions of Molecular Motors with Microtubule Lattice — •William Lecompte[1], Sarah Triclin[2], Laurent Blanchoin[2], Manuel Théry[3], and Karin John[1] — [1]Univ. Grenoble-Alpes, CNRS, Laboratoire Interdisciplinaire de Physique, 38000 Grenoble, France — [2]Univ. Grenoble-Alpes, CEA, CNRS, INRA, Biosciences & Biotechnology Institute of Grenoble, Laboiratoire de Physiologie Cellulaire & Végétale, CytoMorpho Lab, 38054 Grenoble, France — [3]Univ. Paris Diderot, INSERM, CEA, Hôpital Saint Louis, Institut Universitaire d'Hématologie, UMRS1160, CytoMorpho Lab, 75010 Paris, France

Microtubules and their associated molecular motors are ubiquitous in eukaryotic cells. On the one hand, short lived dynamic microtubules are essential for important cellular processes, such as mitotic spindle positioning during mitosis. On the other hand, long lived microtubules are important structural elements, for example as transport tracks for intracellular traffic. Over the past three decades the dynamic instability at the microtubule tip has been the subject of intensive research, however little is known about the dynamics of the microtubule shaft lattice. Recently it has been shown, that structural lattice defects or severing enzymes such as katanin or spastin may trigger a lattice turnover in the shaft. Here we explore with a kinetic Monte Carlo

model the possibility, that the lattice strain induced by molecular motors, such as kinesin motors, may induce a localized lattice turnover. We compare our results with recent in vitro experimental observations on lattice turnover triggered by kinesin motors.

BP 9.7 Mon 17:30 P2/2OG

Length distributions of microtubules with a multistep catastrophe mechanism — •Felix Schwietert, Lina Heydenreich, and Jan Kierfeld — TU Dortmund University, 44221 Dortmund, Germany

Regarding the experimental observation that microtubule catastrophe can be described as a multistep process, we extend the Dogterom-Leibler model for dynamic instability in order to discuss the effect that such a multistep catastrophe mechanism has on the distribution of microtubule lengths in the two regimes of bounded and unbounded growth. We show that in the former case the steady state length distribution is non-exponential and has a lighter tail if multiple steps are required to undergo a catastrophe. If rescue events are possible, we detect a maximum in the distribution, i.e., the microtubule has a most probable length greater than zero. In the regime of unbounded growth, the length distribution converges to a Gaussian distribution whose variance decreases with the number of catastrophe steps. All results are verified by stochastic simulations.

BP 9.8 Mon 17:30 P2/2OG

Stochastic modeling of the tug-of-war between kinesin-1 and mammalian dynein motor proteins in intracellular transport — •Gina Antonieta Monzon[1], Lara Scharrel[2], Ashwin DSouza[2], Stefan Diez[2,3], and Ludger Santen[1] — [1]Center for Biophysics, Department of Physics, Saarland University, 66123 Saarbrücken, Germany — [2]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [3]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

Intracellular transport is a bidirectional, biased stochastic motion performed by teams of kinesin and dynein motors walking in opposite directions along microtubules. A tug-of-war between kinesin and dynein occurs since both motors are involved in the transport. Therfore, it is intringuingly to understand this tug-of-war in order to know how the cell manages targeted cargo transport. In our stochastic kinesin and dynein models [1] we include all known motor properties and a mechanical dynein activation. Studying bidirectional transport we see a blocked state, where forces between kinesin and dynein are balanced and the motors are strongly localized. Investigating the influence of ATP concentration, we see the blocked state remains stable as long as the forces are constant. Moreover, hindering roadblocks does not influence the blocked state neither because of the motor localization.

[1]: G.A. Monzon, L. Scharrel, L. Santen, S. Diez, Activation of mammalian cytoplasmic dynein in multi-motor motility assays, Journal of Cell Science, 2019.

BP 9.9 Mon 17:30 P2/2OG

Investigation and manipulation of the bacterial cell wall synthesis with super-resolution microscopy and optical tweezers — •Franziska Moos, Julian Roth, and Alexander Rohrbach — Department of Microsystems Engineering, Laboratory for Bio- and Nano-Photonics, University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

So far the process of the bacterial cell wall synthesis is not understood, in particular the geometric arrangement. The filamentous protein MreB, which is an actin homolog, plays an essential role in the bacterial cell wall. It is suggested that multiple cell wall synthesis motors couple to MreB filaments, which presumably synthesize the peptidoglycan (PG) strands of the cell wall. Therefore, the MreB filament traces reveal the trajectories of the motors and the position of the PG strands, which are usually invisible with existing technology.

We investigate the cell wall synthesis in Bacillus subtilis indirectly by measuring the motions of fluorescently labeled MreB proteins using total internal reflection fluorescent microscopy. Furthermore we exert mechanical pressure to the bacteria resulting in curvature changes of the cell wall to investigate the influence on the cell wall synthesis. This bending process is achieved by optical tweezers, where microbeads are pressed against the bacteria.

We show preliminary results of the effects of bending bacteria on the cell wall synthesis. The results are used to further strengthen the hypothesis that MreB is transported by several PG synthesis motors.

BP 9.10 Mon 17:30 P2/2OG

Investigation of transport behavior of multiple kinesin-3 motors coupled directly to membranous cargo — Ashwin D'souza[1], •Rahul Grover[1], and Stefan Diez[1,2] — [1]B CUBE, Center for Molecular Bioengineering, TU Dresden, Germany — [2]Cluster of Excellence Physics of Life, TU Dresden, Germany

KIF16B, a kinesin-3 family motor protein, can bind directly to phosphatidylinositols (PI3P) containing organelles such as early endosome and transport them, on microtubules, towards cell periphery. Recently, it was shown that the motor-membrane coupling can influence the transport efficiency of the cargo, dependent on the motor density and membrane fluidity. However, these studies were performed on a planar solid supported lipid bilayer, thus the influence of the cargo shape and size on the transport behavior were not determined. Here, we explore the behavior of ensembles of KIF16B motors transporting spherical liposomes of varying membrane fluidity and size, with a range of surface motor densities. We found that liposomes transported by multiple KIF16Bs have lower velocities compared to the stepping velocity of single KIF16B motors. Moreover, liposomes exhibited higher velocities at lower surface densities of KIF16B, compared to when being carried by higher motor densities. Liposomes driven by ensembles of KIF16B motors also exhibited stop-and-go motion, i.e. processive runs interrupted by pauses which could be an outcome of asynchronous stepping of individual KIF16B motors within an ensemble. This behavior appears to be an emergent property of multi-motor transport as the frequency of pauses for single KIF16B motors is much lower than the liposomes.

BP 9.11 Mon 17:30 P2/2OG

Active self-organization and division in nematic droplets — •Fabian Jan Schwarzendahl and Kinjal Dasbiswas — University of California, Merced, 5200 N. Lake Road, Merced, California 95343, USA

Self-organized droplets of biomaterial that grow and divide are potential models for cell behavior as well as novel realizations of active matter. Recent experiments which reconstitute actin filaments into elongated nematic droplets (tactoids) show that myosin motors self-organize at the tactoid center and subsequently deform and divide the tactoid. This recapitulates aspects of cell division in an in vitro model. We present a minimal continuum model that incorporates the nonequilibrium binding and sliding kinetics of myosin motors on the actin filaments that form a nematic droplet at equilibrium. Using simulations, we demonstrate how our model captures the essential dynamics and morphology observed in experiments. First a single tactoid is formed, then myosin motors bind and accumulate within the tactoid. The myosin motors organize actin filaments according to their polarity to from an aster in the tactoids center, which causes the tactoid to deform into two tactoids with myosin motors at their connecting center. We predict how the organization of filaments and timescales involved should differ from potential equilibrium mechanisms that drive myosin motor centering.

BP 9.12 Mon 17:30 P2/2OG

Functionalizing the microtubule lumen — •Foram Joshi[1], Hauke Drechsler[1], and Stefan Diez[1,2] — [1]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [2]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

Microtubules are hollow tubular protein assemblies of the cytoskeleton, which serve as tracks for motor proteins for the translocation of intracellular cargo. Motors proteins, when bound to a substrate surface in vitro, can be employed to propel reconstituted microtubules for nanodevice applications in molecular sorting, bio-diagnostics and nanometric surface imaging. Conventionally, in these assays the outer microtubule surface is used for cargo attachment via functionalization with biomolecules and/or nanoprobes. The resulting drawbacks are (i) 'roadblock effects', as the attached cargo can severely impede motor stepping, and (ii) varying distances between cargo and substrate surface, as microtubules while gliding, often rotate along their longitudinal axes. To overcome these limitations, we aim to encapsulate the cargo inside the microtubule lumen (15 nm). We will report on strategies to functionalize the lumen with gold-nanoparticles conjugated to lumen-targeting components such as (i) antibodies against acetylated alpha-tubulin, (ii) peptides derived from tau protein, and (iii) microtubule-inner proteins (FAP85). The resulting lumen-functionalized microtubules shall be applied for optimizing motility assays and for fabricating conductive nanowires by the directed growth of encapsulated

inorganic nanoparticles along the microtubule lumen.

BP 9.13 Mon 17:30 P2/2OG

Profilin regulating the polymerisation velocity of Actin — •Lina Heydenreich and Jan Kierfeld — TU Dortmund

F-Actin, as a part of the cytoskeleton, drives crucial biological processes like cell motility, where the control of the polymerisation speed is essential. Experiments in [1] show a maximal polymerisation speed of F-actin at high concentrations of profilin and actin.

We present a kinetic model of F-actin growth in the presence of profilin and obtain an exact result for the mean growth velocity which is in agreement with stochastic simulations and explains the experimental data. The maximal growth speed is limited by the release rate of profilin from filamentous actin. In the limit where nearly all actin monomers are bound to profilin the polymerisation speed follows the Michaelis-Menten kinetics.

[1] Johanna Funk et al. "Profilin and formin constitute a pacemaker system for robust actin filament growth". eLife 8 (2019), e50963

BP 9.14 Mon 17:30 P2/2OG

Hydrodynamics of a compressible film of active gel — •Li-Shing Lin[1] and Hsuan-Yi Chen[1,2] — [1]Department of Physics, National Central University, Zhongli, Taiwan — [2]Institute of Physics, Academia Sinica, Nankang, Taiwan

We construct the hydrodynamic equations for compressible soft active matters forming a film above a solid substrate. This serves as a generic model describing biological systems such as a growing tissue or the lamellipodium of an adherent cell. First, we characterize the hydrodynamic modes of our model and its passive counterpart. Next, we analyze the steady state and linearized dynamics close to it. The relation between the surface relaxation rates and bulk hydrodynamic modes are discussed, and crossover from bulklike (short-wavelength limit) to thin-film-like (long-wavelength limit) behavior is revealed.

BP 9.15 Mon 17:30 P2/2OG

Simultaneous measurement of surface and bilayer tension in a microfluidic chip — •Navid Khangholi, Ralf Seemann, and Jean-Baptiste Fleury — Experimental Physics and Center for Biophysics, Saarland University, 66123 Saarbrücken, Germany

Free-standing lipid bilayers are one of the most used model systems to mimic biological cell membranes. To form an unsupported bilayer, we employ two aqueous fingers in a microfluidic chip surrounded by an oily phase that contains lipids. Upon pushing two aqueous fingers forward, their interface gets decorated with a lipid monolayer and eventually zip to form a bilayer when the monolayers get in nanoscopic contact to each other. Using this straight forward approach, the easy and fast bilayer formation is facilitated by oil draining into the microfluidic device material consisting of PDMS. On the other hand, the oil drainage limits the lifetime of a bilayer to about one hour. We demonstrate that this drainage can be managed resulting in superior bilayer stability and to an increased lifetime of several hours when using a pressure controlled system. Applying different pressures to the aqueous fingers in the microfluidic chip, the formed bilayer can even be bent with a desired curvature. Extracting the contact angle and the resulting curvature of the bilayer region, for a given applied pressure difference, both the bilayer tension and the surface tension of each lipid monolayers can be derived from a single experiment using Young Laplace pressure equation.

BP 9.16 Mon 17:30 P2/2OG

Isolation of Plasma Membrane Lipids from Immobilized Trypanosomes for Model Membrane Studies — •Nicolas Hagedorn and Susanne Fenz — Department for Cell and Developmental Biology, Biocenter, University of Würzburg, Germany

The unicellular parasite Trypanosoma brucei exhibits a dense, but dynamic, homogeneous surface coat of GPI-anchored variant surface glycoproteins (VSGs). However, its plasma membrane is compartmentalized in three structural and functional distinct domains. In contrast to the homogeneous distribution of VSG, proteins with a GPI anchor have been reported to associate with membrane domains. For trypanosomes, the lipid composition of the plasma membrane is still unknown. We propose plasma membrane vesicles (PMVs) to enrich our understanding of the membrane composition and organization. PMVs were prepared by an approach that combines hypotonic swelling followed by hypertonic cell shrinkage. The effects and mechanisms of vesiculation were studied using light-, and electron microscopy. Microscopic evidence suggests that the main vesiculation site was the flagellum. Moreover, the occurrence of VSGs in PMVs was validated by preparation from trypanosomes exhibiting a fluorescently tagged VSG coat. In the future, formation of solid supported lipid bilayers from PMVs will enable us to address the lipid organization as well as distribution and dynamics of VSGs in a model membrane with natural composition using single-molecule fluorescence microscopy.

BP 9.17 Mon 17:30 P2/2OG

Phase Separation and Mechanics of Biomimetic Membranes — •Valeska Rathe and Cornelia Monzel — Heinrich Heine University Duesseldorf, 40225 Duesseldorf, Germany

Under certain conditions, biological membranes are able to phase separate into liquid ordered and liquid disordered domains. To further understand, how this phenomenon affects cell processes, such as molecular aggregation during adhesion or signalling, it is important to examine changes in mechanical and thermodynamic properties of the membrane. Lipid phase coexistence can be induced via temperature change, osmotic shock or other influences. During this process, for example, the bending rigidity of the membrane changes. Liquid ordered domains display an increased bending rigidity compared to the liquid disordered domain and the pre-phase separation state. In this work, the membrane mechanical parameters are studied with giant unilamellar vesicles (GUVs) as they undergo phase separation. GUVs are lipid bilayer spheres, which serve as biomimetic models of the cell membrane. A ternary mixture consisting of DOPC, DPPC lipids and cholesterol is stimulated to phase separate under different conditions. Using the method of fluorescence flicker spectroscopy, changes in the membrane mechanical parameters are derived.

BP 9.18 Mon 17:30 P2/2OG

Is the swimming behavior of Paramecium controlled by the thermodynamic state of its membrane? — •Anne Paeger and Matthias Schneider — TU Dortmund, Deutschland

The transition of native lipid membranes appears to be tied to its growth conditions. How and why seems to be an open debate. Here we study the swimming velocity of Paramecium caudatum, which changes for different variables. Temperature-velocity curves are different for paramecia cultured at different temperatures, i.e. the living system adapts to its growth condition. In this project, we test the hypothesis that adaptation of the swimming behavior of the organism origins in the adaptation of the thermodynamic state of the membrane.

BP 9.19 Mon 17:30 P2/2OG

Influence of viscoelastic properties on the speed of sound in lipid membranes — Matthias F. Schneider and •Gregor Haider — Med. & Biol. Physik, TU Dortmund, Dortmund, Germany

There is an ongoing controversy on the physical origin of nerve pulse propagation. Besides the standard model of Hodgkin and Huxley a physical theory based on momentum conservation and thermodynamics in which density pulses form the basis of action potentials is proposed. In order to test the latter we study the velocity variation of density pulses both in theory and experiment. Indeed the velocity variation of action potentials by at least five orders of magnitude across different species and even up to 3 orders of magnitude within the same system represents an excellent test against theories for pulse propagation in biology and can hence presumably provide new clues to the current debate on the origin of the action potentials. We here explore the predictions of a thermodynamic theory of pulses and study the role of viscoelastic properties of the membrane as well as the surrounding medium on pulse propagation. We show experimentally that an increased shear viscosity of the subphase decreases the velocity of acoustic pulses in lipid monolayers in accordance with theoretical prediction. Finally, the influence of the 2-dimensional dilational surface viscosity on pulse propagation is investigated theoretically and experimentally.

BP 9.20 Mon 17:30 P2/2OG

Fusogenic Liposomes are Intrinsically Tensed — •Laura Schmitt, Rudolf Merkel, and Agnes Cziszár — Insitute of Complex Systems 7: Biomechanics, Forschungszentrum Jülich, Germany

Liposomes are popular carriers for drug molecules, which enter cells either by endocytosis or by fusion of membranes. The former process is slow and significant drug degradation occurs, the latter is most often mediated by fusogenic proteins and is thus costly and complex.

Spurred by this dilemma, fusogenic liposomes were introduced by the last author of this contribution. These liposomes are formed from a ternary lipid mixture and fuse rapidly with cell membranes. Here, we explored basic physical properties of fusogenic membranes.

Therefore, GUVs (giant unilamellar vesicles) were prepared from the fusogenic lipid mixture. We examined their elastic properties using fluorescence microscopy and micropipet aspiration. Additionally, AFM compression was used.

Contrary to control GUVs, fusogenic GUVs showed no thermal fluctuations. Hence, we focused on tension-induced area dilation. We found that very high suction pressures are necessary to deform fusogenic GUVs, the resulting apparent area increases were exceptionally high. Furthermore, fusogenic GUVs could withstand much larger forces than control GUVs when compressed between parallel plates.

This behavior was attributed to an intrinsic membrane tension. We assume that this tension is caused by a coexistence of a non-lamellar lipid phase with the usual lipid bilayer. This non-lamellar phase presumably acts as a membrane reservoir.

BP 9.21 Mon 17:30 P2/2OG

Cooperativity among multiple types of receptor-ligand bonds in membrane adhesion — •Long Li[1,2] and Ana-Sunčana Smith[1,3] — [1]PULS Group, Institute for Theoretical Physics, FAU Erlangen-Nürnberg, Erlangen 91058, Germany — [2]Key Laboratory of Mechanics on Disaster and Environment in Western China, Ministry of Education, College of Civil Engineering and Mechanics, Lanzhou University, Lanzhou, Gansu 730000, China — [3]Division of Physical Chemistry, Ruder Bošković Institute, Bijenička 54, Zagreb 10000, Croatia

In biological system, receptor-ligand bonds rarely work alone and are often embedded into larger macromolecular structures involving more than one pair type. However, the effect of multiple types of receptor-ligand bonds on formation dynamics of adhesion domain is still elusive. We combine theoretical modelling and effective Monte Carlo simulations to investigate the nucleation dynamics of adhesion domains. Typically we find that in during pre-nucleating one or both types of bonds may transiently appear, in the bulk of the parameter space, only one bond type will appear in the stable nucleus of the adhesion domain. The other pair, on the other hand, has catalytic or anti-catalytic effects on the nucleating adhesions. These results not only shed light on the biophysical mechanism of cooperativity between multiple types of bonds in membrane adhesion and but also are interesting in the context of complex functionalisation of functional interfaces in biomedical engineering.

BP 9.22 Mon 17:30 P2/2OG

Optical characterization of thermodynamic states in biological systems — •Carina Fedosejevs and Matthias F. Schneider — Medical and Biological Physics, TU Dortmund

The biological function (permeability, fusion, fission, nerve puls propagation etc.) of membranes has often been hypothesized to be controlled by the thermodynamic state of the membrane rather than to be a sole property of the individual constituents. Phase transitions represent a highly non-linear change in state and are therefore very potent candidates for changes in function. Importantly, phase transitions have not only extensively been demonstrated in lipid membranes, but also in cells.

But how to detect phase states/transitions in biological systems? Incorporating fluorescence dyes into cell membranes as local reporters of state, by analyzing their optical properties (e.g. spectrum and lifetime) with high resolution, will allow us to create a map of the thermodynamic state of the cell. These state-maps, will be compared with biological processes observable with the system.

BP 9.23 Mon 17:30 P2/2OG

Simulation of biological vesicles using a phase-field approach — •Thomas Nevolianis[1], Erik Wittemeier[1], and Dmitry Chigrin[2] — [1]Dept. of Physics, RWTH Aachen University, Otto-Blumenthal-Strasse 18, 52074 Aachen, Germany — [2]DWI - Leibniz Institute for Interactive Materials, Forckenbeckstrasse 50, 52074 Aachen, Germany

The understanding of shape transformations and dynamic behavior of biomembrane vesicles is of fundamental importance in biological and physical sciences. In this study, the three-dimensional deformations of biological vesicles with prescribed volume and surface area, are numerically investigated using a phase-field approach. Interactions of a vesicle with other vesicles, substrate, and fluid flow are incorporated into the theoretical and numerical model. The developed phase-field model is applied to systematically study constraint and unconstraint shape evolution of growing prebiotic vesicles.

BP 9.24 Mon 17:30 P2/2OG

Ellipsometric study of DPPC Supported Lipid bilayer formation evaporated by a solvent-free process on silicon substrates — Marcelo A. Cisternas[1], Francisca Palacios-Coddou[1], Sebastian Molina[1], Maria Jose Retamal[2], Nicolas Moraga[1], Hugo Zelada[1], Marco A. Soto-Arriaza[2], Tomas P. Corrales[3], and •Ulrich G. Volkmann[1] — [1]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]Department of Physics, UTFSM, Valparaiso, Chile

Recent interdisciplinary studies of biological molecules with physical techniques have opened an emerging field for applications in bionanotechnology. The new techniques of preparation and characterization of supported lipid bilayers (SLB) contribute to the creation of new silicon-based nanodevices, which are an important input to the field of bionanotechnology. In this research, we report the novel formation process of supported Dipalmitoylphosphatidylcholine (DPPC) bilayers evaporated directly on bare silicon surfaces by means of physical vapor deposition, without the use of a polymer cushions or solvents, i.e. in a completely dry process. High-resolution ellipsometry measurements in air, without further hydration, detect the characteristic phase transitions of DPPC bilayers: gel to ripple 311.5 +/- 0.9 K, ripple to liquid crystalline 323.8 +/- 2.5 K, liquid crystalline to fluid disordered 330.4 +/- 0.9 K. Acknowledgments: FONDECYT 1180939 (UGV), 1171047 (MS-A), FONDECYT postdoctoral 3160803 (MJR), FONDECYT Iniciacion 11160664 (TPC), PhD. scholarship CONICYT (MAC).

BP 9.25 Mon 17:30 P2/2OG

Verification of evaporated dry phospholipid bilayer formation with AFM — •Maria Jose Retamal[2], Marcelo A. Cisternas[1], Francisca Palacios-Coddou[1], Sebastian Molina[1], Nicolas Moraga[1], Hugo Zelada[1], Marco A. Soto-Arriaza[2], Tomas P. Corrales[3], and Ulrich G. Volkmann[1] — [1]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]Department of Physics, UTFSM, Valparaiso, Chile

Phospholipids are the main components of the cell membrane, and it is of great interest to study their behavior and phase transitions during temperature changes. In particular, we study bilayer systems on silicon surfaces covered with its native silicon oxide layer (Supported Lipid Bilayers or SLB) using Atomic Force Microscopy in air. For the first time the SLB were formed from their gas phase by a totally dry process and without further hydration. In these SLB it was possible to identify with AFM significant changes in the sample topography at the transition temperatures reported in the literature. The cantilever break through forces for single, double and triple bilayers have been measured. It was also found that the AFM tip is capable to modify at room temperature the -otherwise long time stable- SLB structures. These modifications are directly related to the force exerted by the tip on the SLB. Acknowledgments: FONDECYT 1180939 (UGV), 1171047 (MS-A), FONDECYT postdoctoral 3160803 (MJR), FONDECYT Iniciacion 11160664 (TPC), PhD. scholarship CONICYT (MAC).

BP 9.26 Mon 17:30 P2/2OG

Ordering of n-alkanes in lipid bilayers — •Anika Wurl and Tiago Mendes Ferreira — Inst. f. Physik - NMR, Martin-Luther Univ. Halle-Wittenberg, Halle (Saale), Germany

In this work we probe the organisation of n-alkanes in different phospholipid bilayers by determination of C-H order parameters. Though short n-alkanes have been shown to incorporate into lipid membranes [1], the dependency of alkane solubility on chain-length and volume fraction has not been investigated in detail.

Order parameters for both alkanes and lipid tails were measured by 2H NMR and proton-detected local field NMR [2]. Results from both methods agreed and showed increased ordering of the lipid bilayers upon addition of n-alkanes. Experimental order parameters were compared to order parameters calculated from molecular dynamics simulations. Using the CHARMM36 forcefield [3], simulations captured experimentally observed trends and suggested a preferred accumulation of n-alkanes between bilayer leaflets. Our results further showed that at constant volume fraction, n-alkane solubility and ordering decreased with increasing chain length. In addition, alkane organisation within the lipid bilayer was strongly dependent on bilayer hydration and the melting temperatures of both alkane and lipid.

[1] J.M. Pope et al., Biochim. Biophys. Acta 1989, 980, 69 [2] X. Zhao et al., Chem. Phys. Lett. 2001, 342, 353 [3] J. B. Klauda et al., J. Phys. Chem. B 2010, 114, 7830.

BP 9.27 Mon 17:30 P2/2OG

Comparison of Cholesterol and Ergosterol in Binary Bilayer Membranes: Insights from Molecular Dynamics Simulations — •Azadeh Alavizargar, Fabian Keller, Marc Lütgehermöller, and Andreas Heuer — University of Muenster

Cholesterol and Ergosterol are two dominant sterols in the membrane of eukaryotic cells and yeast cells, respectively. Although their chemical structure is very similar, with the exception of two extra double bonds and one methyl group for Ergosterol, their impact on the structure and dynamics of membranes differs. In this work, we have explored different points in the binary phase diagram of the mixtures of these sterols molecules with 1,2-Dipalnitoyl-sn- glycerol-3-phosphocholine (DPPC) lipid bilayer system, employing molecular dynamics simulations. The simulations revealed that Cholesterol has a stronger impact on ordering of the lipids chains with respect to Ergosterol, which likely arise from a more planar structure of the ring part as well as lower tilt angle of this sterol with respect to Ergosterol. Both sterols slightly decrease the order parameter of the pure bilayer system in gel phase and considerably increase it in liquid- ordered phase. From the dynamics point of view, addition of the two sterols leads to faster dynamics of lipids in gel phase with the opposite effect above phase transition temperature. Furthermore, Cholesterol apparently has a stronger influence on the dynamics than Ergosterol in accordance with available experimental data. These results may shed new lights on the impact of sterols on the binary mixtures of membranes.