BP 32: Physics of Cells III

Time: Friday 9:30–13:00   Location: H 1028

BP 32.1   Fri 9:30   H 1028

Margination of white blood cells in microvessels — •Dmitry A. Fedosov, Julia Fornleitner, and Gerhard Gompper — Institute of Complex Systems, Forschungszentrum Juelich, Juelich, Germany

Margination of white blood cells (WBCs) towards microvessel walls is an essential pre-condition for their efficient adhesion to the vascular endothelium, which is a crucial step in the organism's immune response. WBC margination depends on hydrodynamic interactions of blood cells with the vessel walls as well as on their collective behavior and deformability. Numerical simulations with 2D and 3D blood flow models using the Dissipative Particle Dynamics method reveal a non-trivial dependence of WBC margination on blood hematocrit, flow rate, WBC deformability, and red blood cell (RBC) aggregation properties. In particular, WBC margination appears to be optimal within certain intermediate ranges of hematocrit and flow rate values, while beyond these ranges WBC margination is substantially attenuated. Moreover, RBC aggregation is found to enhance WBC margination in microvessels. We will present margination state diagrams, which identify WBC margination behavior for a wide range of flow and cell suspension conditions. These findings will help us better understand WBC margination and adhesion in microcirculation.

BP 32.2   Fri 9:45   H 1028

Insights into equilibrium shape from in-silico modeling of red blood cells — •Ulf Schiller[1,2] and Anthony Ladd[2] — [1]Theoretical Soft Matter and Biophysics, Institute of Complex Systems, Forschungszentrum Jülich, 52425 Jülich, Germany — [2]Department of Chemical Engineering, University of Florida, Gainesville FL 32611-6005, USA

We present a novel computational model for deformable particles such as red blood cells. It is based on a finite-element like model of an elastic membrane with director degrees of freedom. The model resembles a two-dimensional liquid crystal coupled to an elastic network. We outline the connection to Helfrich's curvature model, and demonstrate how a coarse-grained worm-like chain model can account for the spectrin network elasticity. One of the advantages of our model is that we have full control over the reference state of the elastic surface. This allows us to probe its influence on the equilibrium shape of RBCs, which in most other models is implicitly built in via the parametric shape function put forward by Evans and Fung. We show simulation results that indicate that the Evans-Fung shape is not a strain-free minimum if a spherical reference configuration is used. The remaining strains drive the RBC away from the discocyte shape and into the stomatocyte shape. The discocyte shape thus requires a-priori assumptions to be stabilized, which is to be contrasted with the relaxation of remaining strains due to dynamic reorganization of the spectrin network. We discuss the relevance of these findings with respect to possible extensions of computational RBC models.

BP 32.3   Fri 10:00   H 1028

Quantification of Depletion Induced Adhesion of Red Blood Cells — •Patrick Steffen[1], Claude Verdier[2], and Christian Wagner[1] — [1]Universität des Saarlandes, Sarbrücken, Germany — [2]CNRS - Universite de Grenoble I, Laboratoire Interdisciplinaire de Physique

Under physiological conditions, red blood cells are known to form aggregates in the forms of rouleaux due to the presence of plasma proteins. Roleaux formation can be also induced in vitro by the adddition of macromolecules to washed red blood cells. Current data on the adhesion strength between red blood cells in their natural discocyte shapes are limited. Here we present measurements on the dextran induced aggregation of red blood cells by use of atomic force microscopy based single cell force spectroscopy (SCFS). The effects of dextran concentration and molecular weight on the interaction energy of adhering RBCs was determined. The results are in excellent agreement with a model based on the depletion effect and former experimental studies.

BP 32.4   Fri 10:15   H 1028

'Wound Healing in vitro': Blood Platelets on Structured Substrates — •Rabea Sandmann[1], Sarah Schwarz G. Henriques[1], Florian Rehfeldt[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics & CRC Physics, University of Göttingen, Germany — [2]Third

Institute of Physics, University of Göttingen, Germany

Blood platelets are anuclear, adherent cells primarily responsible for blood clotting and their activation can be triggered by, e.g., soluble factors like thrombin. Whenever a wound arises, the endothelial cell layer inside blood vessels is disrupted and underlying proteins become exposed, which creates a micro- and nanostructured surface. It is therefore important to understand how platelets react to micro- and nanostructured surfaces. Our results show that isotropic structures in the μm-range do not have an influence on the orientation of cells or the ordering of the stress fibers. However, the degree of surface coating determines the size of the platelets. Furthermore, platelets build distinct geometrical shapes on unstructured glass. Quite similar shapes can be observed on microstructured PDMS substrates. Therefore, the process of shape formation may be governed by underlying nanostructures. We examine the effect of such nanostructured substrates, which have the potential to alter the ordering of stress fibers by confinement of the focal adhesions' positions. Our experiments contribute to the fundamental understanding of cell behavior in general, and may have direct applications in medicine due to the importance of platelets in wound healing.

BP 32.5   Fri 10:30   H 1028

Active fluctuations of the red blood cell membrane violate the fluctuation dissipation theorem — •Timo Betz, Hervé Turlier, Jean-François Joanny, and Cécile Sykes — Institut Curie, UMR 168, 11 rue Pierre et Marie Curie, 75005 Paris, France

Red blood cells are extremely elastic objects, able to recover their shape even after large deformation as when passing through tight capillaries. Despite many decades of intensive research, the influence of active mechanical of red blood cells is still under debate. Here we present direct evidence that the red blood cell fluctuations violate the fluctuation dissipation theorem (FTD). We directly measure the mechanical response function using optical tweezers, and compare it to the thermal fluctuation spectrum represented by the power spectral density (PSD). In equilibrium thermodynamics, the dissipative part of the response function and the PSD are related by the fundamental relation of the fluctuation-dissipation theorem, which we directly tested with our measurements. The experimental investigation of the FDT shows a violation at the low frequency range (f<10Hz), while at higher frequencies the FDT is confirmed. This has important implications for the analysis of red blood cell mechanics, as the FDT is commonly used to extract mechanical parameters from membrane fluctuations. Using classical equilibrium membrane theory, we can show that the effect of the active fluctuations is manifested in an apparent lower membrane tension as compared to the direct measurement using the response function. Our results suggest that the active fluctuations help the RBC to pass through capillaries and to prevent adhesion.

BP 32.6   Fri 10:45   H 1028

Towards the understanding of bond organization in adhesion domains: Coexistence of the dilute and the dense packing — •Daniel Schmidt[1], Timo Bihr[1], Udo Seifert[1], and Ana-Sunčana Smith[2] — [1]II. Institut für Theoretische Physik, Universität Stuttgart — [2]Institut für Theoretische Physik and Excellence Cluster: Engineering of Advanced Materials, Universität Erlangen-Nürnberg

We study the optimal arrangement of ligand-receptor bonds in microdomains that form during the adhesion of biological membranes. In our model-domains, the bonds are placed on a regular lattice and described by harmonic springs. The membrane also interacts with the substrate by a nonspecific potential. Additionally, we explicitly consider the effects of fluctuations of both the membrane and the bonds as well as the membrane tension. The stability of domains emerges from the analysis of the appropriate free energy density. We determine the phase diagram of the system as a function of key parameters such as the stiffness of the bonds, the ligand-receptor binding affinity, and the distance between the bonds.

In a parameter range typical for experiments, we find the commonly observed densely packed domains and a regime in which the bonds are sparsely distributed. The two regimes are separated by an energy barrier, which may signify unstable specific adhesion at intermediate densities, if one of the binding partners is immobile. If both ligands and receptors can freely diffuse through the opposing membranes, we

predict a coexistence between the two domain types, which agrees with recent experimental observations.

BP 32.7 Fri 11:00 H 1028

Direct observation of catch-bonds in focal adhesions of living cells — •Navid Bonakdar, Achim Schilling, Claus Metzner, Michael Kuhn, Richard Gerum, and Ben Fabry — Biophysics Group, University of Erlangen, Germany

Single molecule force spectroscopy data have demonstrated that the chemical bonds between extracellular matrix proteins, integrins, and several proteins of the focal adhesion complex show catch-bond behavior: the binding strength increases under mechanical load. It remains unknown, however, whether catch-bond mechanisms are of any relevance for stabilizing matrix adhesions in living cells. To measure adhesion strength, we bind RGD-coated magnetic beads to integrin adhesion receptors of living cells and apply forces of up to 80 nN with a magnetic tweezer. In the case of a pulling force that increases linearly with time, the characteristic bead detachment force is expected to increase logarithmically with the loading rate for thermally activated Bell-type molecular bonds. We find that the detachment force tends to increase faster than logarithmically, demonstrating that the adhesion bonds strengthen under force. This may be indicative of catch bonds, but could also arise from a complex binding energy landscape. To distinguish between these two possibilities, we applied a staircase-like mechanical load with the same average loading rate but with forces that at all times exceeded those of the linear ramp protocol. We find significantly increased detachment forces under a staircase-like loading protocol compared to a linear force ramp, which rules out other mechanisms except catch-bond behavior.

15 min break

BP 32.8 Fri 11:30 H 1028

The Hair Bundle's Viscous Losses in Response to Tip-Link Forces — •Johannes Baumgart — Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden

The ear can sense air vibrations smaller than the Bohr radius. One important step of this highly sensitive process is the mechanotransduction, which takes place in the hair bundle. Therein active forces along the tip links can amplify the motion. Here we investigate which viscous forces counteract this active forces.

One individual bundle consists of closely apposed stereocilia surrounded by a viscous liquid, which are coupled by stiff horizontal top connectors and softer tip links. This configuration ensures a highly coherent motion over broad frequency ranges, as was shown by experimental data in conjunction with a detailed three-dimensional finite-element model incorporating the fluid-structure interaction[1].

We investigate with the same numerical model how the bundle responds to a force at all tip links with the same phase and amplitude. This forces can displace the free standing bundle coherently, if the stiff horizontal top connectors below the tip links ensures the coupling. For this mode of motion the assigned viscous drag coefficient is similar to the one for displacing the bundle at the kinociliary bulb, which is mainly due to the external liquid. If the horizontal top connectors are removed, the bundle splays and the related drag coefficient increases by up to thirtytimes for frequencies below a few Hertz.

[1] A.S. Kozlov, J. Baumgart, T. Risler, C.P.C. Versteegh & A.J. Hudspeth, *Nature*, 2011, **474**, 376–379.

BP 32.9 Fri 11:45 H 1028

Temperature-dependent auditory tuning can arise from transduction channel gating — •Björn Nadrowski[1] and Martin Göpfert[2] — [1]Theoretische Physik, Universität des Saarlandes, 66123 Saarbrücken, Germany — [2]Dept. of Cellular Neurobiology, Schwann-Schleiden Research Centre, Julia-Lermontowa-Weg 3, 37077 Göttingen, Germany

Ears achieve their exquisite sensitivity by means of active mechanical feedback. This feedback depends on metabolic energy, which might explain why temperature affects the mechanical tuning of ears. Spontaneous otoacoustic emissions from reptile ears, for example, get faster when the ambient temperature rises, and self-sustained oscillations in mosquito ears likewise speed up when temperature is increased. By analyzing the resulting frequency-shifts in terms of the Arrhenius equation, activation energies of the molecular motors that promote the mechanical feedback have been deduced. Here, we show that apart from motor characteristics the gating of auditory transduction channels can influence auditory mechanics in a temperature-dependent manner, providing an alternative explanation for the temperature-dependent tuning of ears. The link between auditory tuning and channel gating is established using physical models of sensory hair bundles and the Drosophila hearing organ. In both systems, opening or closing all the transduction channels requires larger stimulus forces as temperature rises, decreasing mechanical nonlinearities and causing best-frequency shifts.

BP 32.10 Fri 12:00 H 1028

Rupture dynamics of cytoskeletal networks — •Philip Guthardt Torres[1,2] and Ulrich S. Schwarz[1,2] — [1]Bioquant, University of Heidelberg — [2]ITP, University of Heidelberg

In cell adhesion and migration, mechanical stability of cytoskeletal networks under force has emerged as an important factor. For example, the transition from lamellipodium to lamella at the front edge of migrating tissue cells and the dissociation of the treadmilling actin gel at the back of rapidly migrating keratocytes might both be determined by the mechanical stability of the actin network contracted by myosin II motors. In contrast to traditional fracture mechanics, rupture in cytoskeletal networks is not dominated by stability thresholds, but rather by stochastic rupture events with exponentially distributed waiting times. Moreover, load sharing in such networks is strongly determined by their spatial organization, which can be very variable in the cellular context. We use a simple two-dimensional model for cable networks to study the rupture dynamics of cytoskeletal networks.

BP 32.11 Fri 12:15 H 1028

Measurement of adhesion forces of bacteria on controlled hydroxyapatite surfaces — •Christian Zeitz[1], Peter Loskill[1], Markus Bischoff[2], Mathias Herrmann[2], and Karin Jacobs[1] — [1]Saarland University, Experimental Physics, D-66041 Saarbrücken, Germany — [2]Saarland University Hospital, Microbiology and Hygiene, D-66421 Homburg/Saar, Germany

The aim of the study presented here is to probe the adhesive properties of bacteria on hydroxyapatite (HAP) surfaces. However, "real" surfaces like teeth are very complex due to their natural variation in structure, roughness and chemical composition. Therefore, artificial HAP samples have been prepared, a characterization of which is presented in this work. The sample surface is very smooth (local RMS roughness below 1 nm) and, thus, allows controlled AFM adhesion measurements with bacterial probes. The HAP samples can be fluoridated [1] and the adhesion strength of *Staphylococcus epidermidis*, *Streptococcus oralis* and *Streptococcus mutans* can be probed on both types of surfaces. The results suggest an alternative explanation for the efficiency of fluoridation of teeth for the prevention of cavities.

[1] F.Müller et al., Langmuir, 2010, 26 (24), p 18750

BP 32.12 Fri 12:30 H 1028

Ballistic motion of bacterial membrane proteins — •Holger Kress[1,2], Rostislav Boltyanskiy[2], Alexia A. Belperron[3], Cecile O. Mejean[2], Charles W. Wolgemuth[4], Linda K. Bockenstedt[3], and Eric R. Dufresne[2] — [1]University of Bayreuth — [2]Yale University — [3]Yale University School of Medicine — [4]University of Connecticut Health Center

The mechanical behavior of proteins in bacterial membranes is not well understood. We investigated this behavior in *B. burgdorferi* bacteria with functionalized microparticles and optical tweezers. We attached particles to membrane proteins and tracked the subsequent particle motion. Although *B. burgdorferi* have a symmetric morphology, the particles were transported ballistically with a well defined speed and stall force to a preferred end of the bacteria. Mutant *B. burgdorferi* which lack flagella did not show directed protein transport, but only diffusive motion. We hypothesize that the transport is enabled by the bacterial motility machinery and that it indicates a defense mechanism against immune cells [HK and RB contributed equally].

BP 32.13 Fri 12:45 H 1028

Energy switching of helical bacteria trapped in a light tube — Matthias Koch and •Alexander Rohrbach — University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

A bacterium can undergo continuous transitions between ground states and excited states of mechanical energy. In the case of the wall-less - and therefore flexible - helical bacterium spiroplasma melliferum (SM), the deformations encode a state of mechanical energy storage, which can express a health state of the bacterium. SM has an extreme struc-

tural simplicity and is among the smallest cells in size (~500 genes, ~200nm thin, 3-5μm long). It infects various plants and insects and thereby has done tremendous harm to agriculture industry. Their motility, defined by helicity changes, kinking and propelling is very complex, and enables propagation in complex environments. However, it is unclear which molecular mechanisms work at which forces on which time scales?

We address these questions by optically caging the whole bacterium in an object adapted optical trap, which consists of a high speed scanning line optical trap: the light tube. Tiny phase changes from scattered laser light are recorded at several Kilohertz and allow imaging the whole bacterium at about 1000 Hz with 3D super-resolution. The measured dynamics is analysed and modelled with Fourier-techniques. We show experimental and simulation results, including energies and forces involved in its motility, as well as first models describing the switching of mechanical energy of the bacterium.