BP 4: Cell Mechanics II

Time: Monday 11:00–13:30 Location: BPa

BP 4.1 Mon 11:00 BPa

Stochastic bond dynamics induce optimal alignment of malaria parasite — •Anil Kumar Dasanna, Sebastian Hillringhaus, Gerhard Gompper, and Dmitry Fedosov — Theoretical Physics of Living Matter, IBI-5 and IAS-2, Forschungszentrum Jülich, Germany

Merozoites, malaria parasites during the blood-stage of infection, invade healthy red blood cells (RBCs) to escape from the immune system and multiply inside the host. The invasion occurs only when the parasite apex is aligned with RBC membrane, making the parasite alignment a crucial step for the invasion. Recent experiments have also demonstrated that there is a considerable membrane deformation during the alignment process. In this work, using mesoscopic simulations we assess the exact roles of RBC deformations and parasite adhesion during the alignment. Using coarse-grained models of a deformable RBC and a rigid parasite, we show that both RBC deformation and parasite adhesion bond dynamics are important for an optimal alignment. By calibrating the parasite's motion properties against experiments, we show that simulated alignment times match quantitatively the experimental alignment times. We find that the stochastic nature of adhesion bond kinetics is the key for inducing optimal alignment times. We also show that alignment times increase drastically for rigid RBC which signifies that parasite invasion is less probable into already infected RBC and that membrane deformations during the parasite alignment. Finally, we will demonstrate the importance of parasite shape in the alignment process.

BP 4.2 Mon 11:20 BPa

Mechano-chemical interactions in a one-dimensional description of intracellular reaction-diffusion systems — •Alexander Ziepke and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians-Universität München, Germany

The understanding of self-organization processes in biological systems represents a key challenge in the field of theoretical biology. There are various studies on reaction-diffusion (RD) models in a single spatial dimension (1D) that give insights on the fundamental behavior of pattern formation in biological systems [1]. However, effects of a spatial confinement, e.g. the cell geometry, are not captured by most of the 1D models. With our new approach we bridge this gap between biological systems in a spatio-temporally varying confinement and simple 1D-RD equations. On the basis of an asymptotic perturbation analysis, we reduce the dimensionality of the confined system [2]. The resulting description incorporates the effects of mechano-chemical coupling and, therefore, extends significantly the applicability of 1D models beyond free dynamics on straight lines. Studying the derived equation for mass-conserving RD systems with interacting membrane-bound and cytosolic species, we find conditions for geometry induced pattern formation. Moreover, mechano-chemical interactions can lead to a feedback between RD kinetics and a deformation of the cell membrane, giving rise to a variety of interesting phenomena.

[1] J. Halatek and E. Frey, Nat. Phys., 14, 507 (2018)

[2] A. Ziepke, S. Martens, and H. Engel, J. Chem. Phys., 145, 094108 (2016)

BP 4.3 Mon 11:40 BPa

Stochastic model of T Cell repolarization during target elimination — •Ivan Hornak and Heiko Rieger — Saarland University, Dep. Theoretical Physics, Center for Biophysics

Cytotoxic T lymphocytes (T) and natural killer cells are the main cytotoxic killer cells of the human body to eliminate pathogen-infected or tumorigenic cells (target cells). Once a T or NK cell has identified a target cell, they form a tight contact zone, the immunological synapse (IS). One then observes a rotation of the microtubule (MT) cytoskeleton and a movement of the microtubule organizing center (MTOC) to the center of the IS. Since the mechanism of this relocation remains elusive, we devise a theoretical model for the molecular motor driven motion of the MT cytoskeleton. We analyze the cortical sliding and the capture-shrinkage mechanisms currently discussed in the literature and compare quantitative predictions about the spatio-temporal evolution of the MTOC position and spindle morphology with experiments. The model predicts the experimentally observed biphasic nature of the repositioning process. We confirm that the capture-shrinkage mechanism is dominant over the cortical sliding mechanism when MTOC and IS are initially diametrically opposed and inferior to the cortical sliding in other configurations. We find that the two mechanisms act synergistically reducing the resources necessary for repositioning. When two IS are present, the MTOC undergoes irregular transitions between the two IS and we determine the dependency of the dwell times and transition frequency on the dynein density for both mechanisms.

BP 4.4 Mon 12:00 BPa

Virus motility - Ifluenza's spike protein dynamics as a self-organized motor — •Falko Ziebert[1] and Igor Kulic[2,3] — [1]Institute for Theoretical Physics, Heidelberg University, D-69120 Heidelberg, Germany — [2]Institut Charles Sadron UPR22-CNRS, F-67034 Strasbourg, France — [3]Institute Theory of Polymers, Leibniz-Institute of Polymer Research, D-01069 Dresden, Germany

Directed self-sustained motion is a hallmark of life employed by both eukaryotic cells and bacteria. While viruses are commonly believed to be just passive agents, influenza has recently been shown to actively move across glycan-coated surfaces, mimicking those of to be infected host cells. Starting from known properties of influenza's spike proteins, we develop a physical model. It predicts a collectively emerging dynamics of spike proteins and surface bound ligands that combined with the virus' geometry give rise to self-organized rolling propulsion. We show that in contrast to most Brownian ratchets, the rotary spike drive is not fluctuation driven but operates optimally as a macroscopic engine in the deterministic regime. The mechanism also applies to man-made analogues like DNA-monowheels and should give guidelines for their optimization.

BP 4.5 Mon 12:20 BPa

Thermodynamics of caveolae formation and mechanosensing — •Niladri Sarkar[1,2] and Pierre Sens[2] — [1]Instituut-Lorentz, Universiteit Leiden, P.O. Box 9506, 2300 RA Leiden, Netherlands. — [2]Laboratoire Physico Chimie Curie, Institut Curie, CNRS, 75005 Paris, France.

Caveolae are invaginations in cell membranes formed by proteins in the caveolin and cavin family self-aggregating in the membrane to form buds. These buds also have some proteins from the EHD family aggregating at their necks. We have developed a two component equilibrium model for the thermodynamics of these bud formation process using energy considerations, where the caveolin proteins are considered as one component and the neck proteins are taken to be another. We have found that depending on the surface tension of the membrane, the line tension associated with the different proteins and the concentration of the different proteins, invaginations of different shapes and sizes can be obtained, and there can be a transition from a fully budded state to a non-budded state via a partial budded state. Also neck proteins are found to provide extra mechano-protection against disassembly due to surface tension.

BP 4.6 Mon 12:40 BPa

Erythrocyte-erythrocyte aggregation dynamics under shear flow — •Mehdi Abbasi[1], Alexander Farutin[1], Hamid Ez-Zahraouy[2], Abdelilah Benyoussef[3], and Chaouqi Misbah[1] — [1]Univ Grenoble Alpes, CNRS, LIPhy, F-38000 Grenoble, France — [2]LaMCScI, Faculty of Sciences, Mohammed V University of Rabat, Rabat 1014, Morocco — [3]Hassan II Academy of Science and Technology, Rabat 10220, Morocco

In a previous work [Blood cells, molecules, and diseases 25, 339 (1999)], it has been shown that the Red blood cells (RBCs) aggregation process starts by the formation of RBC doublets. In this work we study, by means of numerical simulations, the dynamics of RBCs doublets under shear flow and the impact on rheology. We present a rich phase diagram of RBCs doublets configurations showing features never evoked before. In particular, we show that RBCs doublet may be robust even for very high shear stress compromizing oxygen delivery to organs and tissues. A link to pathological conditions (several common blood diseases) is highlighted.

30 min. Meet the Speaker