BP 24: Poster B: Active Biological Matter, Cell Mechanics, Systems Biology, Computational Biophysics, etc.

Time: Tuesday 16:00–18:30 Location: BPp

BP 24.1 Tue 16:00 BPp

Chirality-induced rheotaxis of bacteria in bulk shear flows — •Guangyin Jing[1,2], Andreas Zöttl[2,3], Eric Clement[2], and Anke Lindner[2] — [1]Northwest University, Xian, China — [2]ESPCI Paris, France — [3]TU Wien, Austria

The interaction of swimming bacteria with shear flows controls their ability to explore complex environments [1], crucial to many societal and environmental challenges and relevant for microfluidic applications such as cell sorting. We combine experimental, numerical, and theoretical analysis, and present a comprehensive study of the transport of motile bacteria in shear flows [2]. Experimentally, we obtain with high accuracy and, for a large range of flow rates, the spatially resolved velocity and orientation distributions of run-and-tumble E. coli bacteria. They are in excellent agreement with the simulations of a kinematic model accounting for stochastic and microhydrodynamic properties and, in particular, the flagella chirality. Theoretical analysis reveals the scaling laws behind the average rheotactic velocity at moderate shear rates using a chirality parameter and explains the reorientation dynamics leading to saturation at large shear rates from the marginal stability of a fixed point. Our findings constitute a full understanding of the physical mechanisms and relevant parameters of bacteria bulk rheotaxis.

[1] A. J. T. M. Mathijssen, N. Figueroa-Morales, G. Junot, E. Clément, A. Lindner, and A. Zöttl, Nat. Comm. 10, 3434 (2019).

[2] G. Jing, A. Zöttl, E. Clement, and A. Lindner, Sci. Adv. 6, eabb2012 (2020).

BP 24.2 Tue 16:00 BPp

Resistive force theory and wave dynamics in swimming flagellar apparatus isolated from C. reinhardtii — Samira Goli Pozveh[1], Albert Bae[2], and •Azam Gholami[1] — [1]MPI for Dynamics and Self-organization, Göttingen, Germany — [2]Department of Biomedical Engineering, University of Rochester, USA

Cilia-driven motility and fluid transport is ubiquitous in nature and essential for many biological processes. The biflagellated micro-swimmer Chlamydomonas reinhardtii is a model organism to study dynamics of flagellar synchronization. Hydrodynamic interactions, intracellular mechanical coupling or cell body rocking are believed to play crucial role in synchronization of flagellar beating in green algae. Here, we use freely swimming intact flagellar apparatus isolated from wall-less strain of Chlamydomonas to investigate wave dynamics. Our analysis in phase coordinates show that, when the frequency difference between the flagella is high (10-41% of the mean), neither mechanical coupling via basal body nor hydrodynamics interactions are strong enough to synchronize two flagella, indicating that beating frequency is perhaps controlled internally by the cell. We also examined the validity of resistive force theory for a flagellar apparatus swimming freely in the vicinity of a substrate and found a quantitative agreement between experimental data and simulations with drag anisotropy of ratio 2. Finally, using a simplified wave form, we show that by controlling phase or frequency differences between two flagella, steering can occur.

BP 24.3 Tue 16:00 BPp

Magnetic stirbars as a tunable stirrer for cell-like systems — •Mithun Thampi, Pierre-Yves Gires, and Matthias Weiss — University of Bayreuth, Bayreuth, Germany

Transport inside living systems or biofluid droplets is governed by diffusion and energy-dependent active transport. Speeding up these processes remains challenging: here we report on an easy way to gently stir biofluid droplets. We produce micrometer long magnetic stirbars (MSBs) by aligning Fe_3O_4 nanoparticles and stabilizing them by a biocompatible silica coating. The successful production of these MSBs is confirmed by scanning electron microscopy[1]. The rotating magnetic field is achieved by using two pairs of Helmholtz-like coils with a custom build controller, which can tune both the frequency and the strength of the magnetic field. Using single-particle tracking of tracer beads, we demonstrate via a broad palette of measures that local stirring of the fluid at different frequencies leads to an enhanced but apparently normal and homogeneous diffusion process. The signature of stirring is visible in the power-spectral density and in the autocorrelation function of the trajectories[2]. We finally look at their stirring effects on the out of equilibrium self-organization of *Xenopus laevis* egg extract[1].

References:

1. P.-Y. Gires, M. Thampi, M. Weiss. "Miniaturized magnetic stirbars for controlled agitation of aqueous microdroplet". Sci. Rep., 10, 10911, (2020).

2. P.-Y. Gires, M. Thampi, M. Weiss. "Quantifying active diffusion in an agitated fluid". Phys. Chem. Chem. Phys., 22, 21678, (2020).

BP 24.4 Tue 16:00 BPp

RNA polymerase II forms clusters in line with liquid-phase wetting of chromatin — Agnieszka Pancholi[1], Tim Klingberg[2], Weichun Zhang[1], Roshan Prizak[1], Irina Mamontova[1], Amra Noa[1], Gerd Ulrich Nienhaus[1], Vasily Zaburdaev[2], and •Lennart Hilbert[1] — [1]Karlsruhe Institute of Technology — [2]Friedrich-Alexander-University Erlangen-Nuremberg

Two major control points for transcription in eukaryotic cells are recruitment of RNA polymerase II (Pol II) into a paused state and subsequent pause release to begin transcript elongation. Pol II associates with macromolecular clusters during recruitment, but it remains unclear how Pol II recruitment and pause release might affect these clusters. Here, we show that clusters exhibit morphologies that are in line with wetting of chromatin by a liquid phase enriched in recruited Pol II. Applying super-resolution microscopy to zebrafish embryos, we find recruited Pol II associated with large clusters, and elongating Pol II with dispersed clusters. A lattice kinetic Monte Carlo model representing recruited Pol II as a liquid phase and chromatin as a condensation surface reproduced the observed cluster morphologies, see Klingberg et al. Considering previous *in vitro* observations of condensate formation by wetting of DNA, our work indicates that similar liquid-phase wetting of chromatin might occur *in vivo*.

BP 24.5 Tue 16:00 BPp

Hydrodynamic interactions between microswimmers and particles in viscosity gradients — •Sebastian Ziegler[1], Maxime Hubert[1], Thomas Scheel[2], Jens Harting[2], and Ana-Sunčana Smith[1,3] — [1]PULS Group, Friedrich-Alexander-University Erlangen-Nürnberg, Germany — [2]Helmholtz Institute Erlangen-Nürnberg for Renewable Energy, Forschungszentrum Jülich, Germany — [3]Division of Physical Chemistry, Ruder Bošković Institute Zagreb, Croatia

A common theoretical approach to model systems of microswimmers is to prescribe the swimming stroke of each individual. If the system consists of more than one device, the problem of hydrodynamic interactions becomes a purely geometric one. This limitation is overcome by prescribing the forcing instead of the stroke, as shown by our novel perturbative approach, applicable to arbitrary geometries. We elaborate the effects of nearby swimmers on the stroke, swimming speed and direction. We find that for two swimmers, a significant fraction of the parameter space results in both swimmers experiencing a boost from one another.

We furthermore study the interaction of spherical particles in fluids with viscosity gradients. Using an analytical approach we show that a particle in a linear viscosity gradient induces a locally distance-independent flow field. Moreover, we characterize the effect of asymmetric particle placement in the finite-size gradient. Finally, we study the interactions between two particles that are at different temperatures than the surrounding fluid, and calculate the first order correction to the mobility matrix in the regime of low Peclet numbers.

BP 24.6 Tue 16:00 BPp

Motion of Magnetic Microswimmers in Complex Environments — •Konrad Marx[1], Vitali Telezki[1], Omar Muñoz[1], Agnese Codutti[2], Damien Faivre[2,3], and Stefan Klumpp[1,2] — [1]Institute for the Dynamics of Complex Systems, University of Göttingen, Göttingen, Germany — [2]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany — [3]Aix Marseille Université, CNRS, CEA, BIAM, Saint Paul lez Durance, France

We study magnetic microswimmers that tend to align their active motion with the direction of a magnetic field. A biological example are magnetotactic bacteria, which use this effect to navigate towards favorable oxygen conditions. Their natural environment is sediment at the bottom of lakes. Motivated by this, we study a computational

model for how magnetic microswimmers attempt to cross a channel of circular obstacles. Our model accounts for diffusion, interaction with the obstacles and the walls, and for a magnetic field acting along the channel. We generate obstacle configurations from experimental data on size distribution of sand grains. We find that obstacles can play a decisive role for the trajectories of the microswimmers and their chance to cross the channel. Specifically, we identify regions that necessitate backwards swimming ("traps") as a dominant factor and investigate which geometrical parameters of the obstacle configurations determine the arrival rates of the swimmers at the end of the channel.

BP 24.7 Tue 16:00 BPp

Capillary Action In Active Brownian Particles — •Shauri Chakraborty, Adam Wysocki, and Heiko Rieger — Department of Theoretical Physics and Center for Biophysics, Saarland University, Saarbruecken 66123, Germany

We study the rise of active Brownian particles against gravity in a thin capillary tube. Capillarity, a well-understood phenomena in classical liquids, is known to originate due to attractive interactions between the liquid molecules and the capillary walls and the inter-molecular attractive forces among the liquid molecules. By contrast, we observe capillary rise in a minimal model of active Brownian particles with purely repulsive interactions. In such a system, an effective force of attraction emerges because of a damping due to the inter-particle collisions and the particle-wall interactions. We also validate in our numerical simulations, whether our findings agree with the results obtained for a similar system, previously studied in an active lattice gas (ALG) setting which can be described by exact hydrodynamic equations on macroscopic scales.

BP 24.8 Tue 16:00 BPp

Light-powered reactivation of flagella and contraction of microtubules network: towards building an artificial cell — Raheel Ahmad, Vahid Nasirimarekhani, Albert Bae, Samira Goli, Yu-Jung Su, Eberhard Bodenschatz, Isabella Guido, and •Azam Gholami — MPI for Dynamics and Self-organization, Göttingen, Germany

The bottom-up assembly of such systems in the context of synthetic biology is still a challenging task. In this paper, we demonstrate biocompatibility and efficiency of an artificial light-driven energy module and a motility functional unit by integration of light-switchable photosynthetic vesicles with demembranated flagella, thereby supplying ATP for dynein molecular motors upon illumination. Flagellar propulsion is coupled to its beating frequency and light- driven dynamic synthesis of ATP allows us to control beating frequency of flagella as a function of illumination. Additionally, we verified the functionality of light-powered synthetic vesicles in in vitro motility assays by encapsulation of microtubules assembled with force-generating kinesin-1 motors and energy module to investigate dynamics of a contractile filamentous network in cell-like compartments by optical stimulation. Integration of this photosynthetic system with different biological building blocks such as cytoskeletal filaments and molecular motors may contribute to the bottom-up synthesis of artificial cells that are able to undergo motor-driven morphological deformations and exhibit directional motion in a light-controllable fashion. *In collaboration with C. Kleineberg, K. Sundmacher, and T. Vidakovich-Koch from MPI-Magdeburg.

BP 24.9 Tue 16:00 BPp

Mechanochemical dynamics of spherical active surfaces subject to load-dependent cross-linkers — •Mirco Bonati[1,2], Lucas Wittwer[3], Elisabeth Fischer-Friedrich[1,2], and Sebastian Aland[4] — [1]Fischer-Friedrich Lab, Biotechnologisches Zentrum, Technische Universitat Dresden, Dresden, Germany. — [2]DFG Excellence Cluster Physics of Life — [3]HTW Dresden, Friedrich-List-Platz 1, 01069 Dresden, Germany — [4]TU Bergakademie Freiberg, Akademiestrasse 6, 09599 Freiberg, Germany

Mechanochemical dynamics of active surfaces, as the thin cellular actin cortex, play a crucial role in several biological processes such as cell shape regulation and morphogenesis. Relying on a hydrodynamic theory of curved active surfaces and elastic thin shell theory, we aim to study both theoretical and numerical aspects of the self-organized pattern formation of the cell cortex. Our goal is to develop a mathematical model that takes into accounts biologically relevant facts, such as load-dependence of molecular unbinding and cortical strain stiffening. In particular, we want to study the influence of catch and slip bond cross-linkers on active gel pattern formation as it has been shown that the mechanical stiffness of the actin cytoskeleton can vary greatly with small changes in cross-linkers concentration. This force-sensing may give rise to new aspects of pattern formation.

BP 24.10 Tue 16:00 BPp

Simulations of Structure Formation by Dipolar Active Particles — •Vitali Telezki and Stefan Klumpp — Institute for the Dynamics of Complex Systems, University of Göttingen, Germany

Dipolar swimmers describe a class of artificial and biological active particles with an internal magnetic moment. Because of the interplay between different physical interactions such as steric, hydrodynamic and magnetic interactions, complex collective behaviour is expected to emerge in dense systems of dipolar swimmers.

We use Brownian dynamics simulations to investigate the collective behaviour of these dipolar swimmers. We focus on the structure formation of dipolar swimmers in small confined systems and analyze what structures can emerge and how they depend on the self-propulsion speed and the magnetic strength of the swimmers. We are particularly interested in the effect of the geometry and the interactions with the confinement on the emerging structures. In addition, we study how external magnetic fields influence the collective behaviour of large systems of dipolar swimmers.

BP 24.11 Tue 16:00 BPp

Minimum Dissipation Theorem for Microswimmers — •Babak Nasouri[1], Andrej Vilfan[1,2], and Ramin Golestanian[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Goettingen, Germany — [2]J. Stefan Institute, Ljubljana, Slovenia — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, United Kingdom

We derive a theorem for the lower bound on the energy dissipation rate by a rigid surface-driven active microswimmer of arbitrary shape in a fluid at a low Reynolds number. We show that, for any swimmer, the minimum dissipation at a given velocity can be expressed in terms of the resistance tensors of two passive bodies of the same shape with a no-slip and perfect-slip boundary. To achieve the absolute minimum dissipation, the optimal swimmer needs a surface velocity profile that corresponds to the flow around the perfect-slip body, and a propulsive force density that corresponds to the no-slip body. Using this theorem, we propose an alternative definition of the energetic efficiency of microswimmers that, unlike the commonly used Lighthill efficiency, can never exceed unity. We validate the theory by calculating the efficiency limits of spheroidal swimmers.

BP 24.12 Tue 16:00 BPp

Vimentin Intermediate Filaments Stabilize Dynamic Microtubules by Direct Interactions — •Charlotta Lorenz[1,4], Laura Schaedel[1,4], Anna V. Schepers[1,3], Stefan Klumpp[2,3], and Sarah Köster[1,3] — [1]Institute for X-Ray Physics, University of Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [3]Max Planck School "Matter to Life" — [4]Equal contribution.

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. Here, we study the interaction between vimentin IFs and MTs in a minimal in vitro system and show that MTs are stabilized against depolymerization by the presence of vimentin IFs. To explore the nature of this interaction and in particular probe for electrostatic and hydrophobic contributions, we directly measure attractive forces occurring between individual MTs and vimentin IFs using optical tweezers in different buffer conditions. Theoretical modeling enables us to determine the corresponding energy landscape. Feeding back the physical parameters describing the interactions into a Monte Carlo simulation that mimicks dynamic MTs confirms that the additional interaction with IFs stabilizes them. We suggest that within cells, the interactions we observe might be a mechanism for cells to fine-tune cytoskeletal crosstalk and MT stability.

doi.org/10.1101/2020.05.20.106179

BP 24.13 Tue 16:00 BPp

Post-Translational Modifications Soften Vimentin Filaments — •Julia Kraxner, Charlotta Lorenz, and Sarah Köster — Institute for X-Ray Physics, University of Göttingen, Germany

The mechanical properties of biological cells greatly influence their function, such as the ability to move, contract and divide and they need

to flexibly adapt, for example during wound healing or cancer metastasis. These mechanical properties are determined by the so-called cytoskeleton, a complex network consisting of three filamentous protein systems, microtubules, actin filaments and intermediate filaments (IFs). A rather slow way to adapt cell mechanics to varying requirements on the cell is differential expression of the cytoskeleton proteins which affects the network architecture and the interaction between the filaments. Here, we focus on the intermediate filament vimentin and introduce post-translational modifications (PTMs), i.e. changes applied to specific amino acids in the protein after expression in the cell. By such PTMs, e.g. the charge pattern along the protein may be altered. Interestingly, PTMs occur comparatively fast and thus provide a mechanism for mechanical modulation on short time scales. We study the impact of one such PTM, phosphorylation, which is the addition of a phosphate group to an amino acid, on filament mechanics by stretching single filaments using optical traps. Whereas full phosphorylation leads to disassembly of IFs, partial phosphorylation results in softening of the filaments. By employing mutants that mimic phosphorylation as well as Monte Carlo simulations, we explain our observation through the additional charges introduced during phosphorylation.

BP 24.14 Tue 16:00 BPp

Growing with vacancies: Eden growth models suggest that flat clathrin lattices assemble with spatial heterogeneity — •Felix Frey[1,2], Delia Bucher[3], Kem A. Sochacki[4], Justin W. Taraska[4], Steeve Boulant[3], and Ulrich S. Schwarz[1] — [1]ITP and BioQuant, Heidelberg University, DE — [2]Department of Bionanoscience, TU Delft, NL — [3]CIID, University Hospital Heidelberg and DKFZ, DE — [4]NHLBI, NIH, Bethesda, US

Biological cells constantly transport material across their plasma membrane and clathrin-mediated endocytosis is one of the main uptake mechanisms. Recently, it has been shown that clathrin lattices first assemble flat before the clathrin-coated membrane starts to invaginate [1]. However, how this flat-to-curved transition proceeds in detail is still unclear, since energetic and topological barriers exist and it is difficult to observe the assembly process in time and space. Here we hypothesize that clathrin lattices grow with lattice vacancies that would facilitate the flat-to-curved transition. We identify the Eden growth model as the most suitable framework for clathrin lattice growth. We then derive four distinct variants of the model that represent the different binding modes of clathrin triskelia based on their geometry. Our computer simulations show that the different model variants lead to distinct lattice shapes and densities. Comparison with experimental electron microscopy and correlative light microscopy data suggests that clathrin lattices grow with a moderate level of lattice vacancies [2]. [1] D. Bucher*, F. Frey*, et al., Nat. Communs. 9, 1109 (2018). [2] F. Frey et al., New J. of Phys. 22, 073043 (2020).

BP 24.15 Tue 16:00 BPp

Dynamic RT-DC: red blood cell viscoelasticity as a label-free biomarker — •Bob Fregin[1,3], Fabian Czerwinski[1], Konstanze Aurich[2], Doreen Biedenweg[2], Stefan Gross[3], Gerald Kerth[4], and Oliver Otto[1,3] — [1]ZIK HIKE, Universität Greifswald, Greifswald, Germany — [2]Universitätsklinikum Greifswald, Greifswald, Germany — [3]DZHK, Universität Greifswald, Greifswald, Germany — [4]Angewandte Zoologie und Naturschutz, Universität Greifswald, Greifswald, Germany

Real-Time Deformability Cytometry (RT-DC) is a label-free technique for single-cell mechanical analysis with high throughput of up to 1,000 cells/s. Initially, RT-DC was limited to steady-state deformation captured at the end of a microfluidic channel yielding Young's modulus.

Dynamic RT-DC (dRT-DC) introduces the possibility to capture full viscoelastic properties at up to 100 cells/s. Single-cell shape-changes along the entire length of the microfluidic channel are tracked in real-time and are subsequently analyzed by a Fourier decomposition discriminating cell responses to interfering stress distributions. We demonstrate that dRT-DC allows for cell mechanical assays at the millisecond time scale fully independent of cell shape. We use this approach for a fundamental comparison of peripheral blood cells based on their Young's modulus as well as viscosity.

In proof-of-principle experiments, we use dRT-DC to approach the question of temperature control in hibernating animals. Initial experiments on bats and humans suggest a role of red blood cell viscoelasticity to maintain blood flow at low temperatures.

BP 24.16 Tue 16:00 BPp

3D direct and inverse traction force microscopy — •Johannes Wolfram Blumberg and Ulrich Sebastian Schwarz — Institute for Theoretical Physics and BioQuant, Heidelberg University

In traction force microscopy (TFM), the mechanical forces of cells adhering to an elastic substrate are estimated from the substrate displacements as measured by the movement of embedded fiducial marker beads. Usually, this estimate is obtained by minimizing the mean squared distance between experimentally observed and predicted displacements (inverse TFM). In direct TFM, in contrast, the stress tensor and the surface tractions are calculated directly and locally from the deformation field using the underlying material law. This procedure makes it easier to estimate not only tangential, but also normal forces, and to deal with non-planar substrates, but it is also more sensitive to noise. In general, it is not clear how well direct TFM performs compared with inverse TFM. We have compared the direct method for TFM to the standard inverse method, which is Fourier transformed traction cytometry (FTTC). In particular, we developed a method to estimating the local inaccuracy based on the divergence-freeness of the stress tensor. We discuss the relative strengths and weakness of the two methods and find that each of them can be preferable for certain settings.

BP 24.17 Tue 16:00 BPp

Time-resolved MIET measurements of blood platelet spreading and adhesion — •Anna Zelená and Sarah Köster — Institute for X-Ray Physics, Georg-August-University Göttingen, Germany

Human blood platelets are non-nucleated fragments of larger cells (*megakaryocytes*) and highly important for blood clotting. The hemostatic function of platelets is directly linked to their mechanics and cytoskeletal morphology. However, the exact mechanism of spreading and contraction remains elusive. In our study, we employ metal-induced energy transfer (MIET) imaging in time-resolved and static modes to investigate, in vitro, single blood platelets with nanometer resolution. Using static MIET, we are able to quantitatively determine three-dimensional height profiles of the basal platelet membrane above a rigid metal substrate. We observe areas, where the basal platelet membrane approaches the rigid metal substrate more closely than the rest of the membrane. This may be related to previously observed "hot spots" of high traction forces. Time-resolved MIET experiments allow us to follow the temporal evolution of the membrane-to-surface distance during adhesion and spreading. Our experiments reveal distinct behaviors between the outermost rim and the central part of the platelets. Overall, the combination of static and time-resolved MIET provides insights into the platelet adhesion system and improves our understanding of blood clot formation. Additionally, our approach demonstrates the potential of MIET as a three-dimensional reconstruction method for thin membrane formations.

BP 24.18 Tue 16:00 BPp

EMT-induced cell-mechanical changes enhance mitotic rounding strength — •Kamran Hosseini[1,2], Anna Taubenberger[2], Carsten Werner[3], and Elisabeth Fischer-Friedrich[1,2] — [1]Cluster of Excellence Physics of Life, TU Dresden, Germany — [2]Biotechnology Center, TU Dresden, Germany — [3]Leibniz Institute of Polymer Research Dresden, Max Bergmann Center, Dresden, Germany

To undergo mitosis successfully, most animal cells need to acquire a round shape to provide space for the mitotic spindle. This mitotic rounding relies on mechanical deformation of surrounding tissue and is driven by forces emanating from actomyosin contractility. Cancer cells are able to maintain successful mitosis in mechanically challenging environments such as the increasingly crowded environment of a growing tumor, thus, suggesting an enhanced ability of mitotic rounding in cancer. Here, it is shown that the epithelial-mesenchymal transition (EMT), a hallmark of cancer progression and metastasis, gives rise to cell-mechanical changes in breast epithelial cells. These changes are opposite in interphase and mitosis and correspond to an enhanced mitotic rounding strength. Furthermore, it is shown that cell-mechanical changes correlate with a strong EMT-induced change in the activity of Rho GTPases RhoA and Rac1. Accordingly, it is found that Rac1 inhibition rescues the EMT-induced cortex-mechanical phenotype. The findings hint at a new role of EMT in successful mitotic rounding and division in mechanically confined environments such as a growing tumor.

BP 24.19 Tue 16:00 BPp

Measurement of the mechanosensitive binding of actin crosslinkers in the cytoskeleton of live cells — •Valentin

Ruffine, Kamran Hosseini, and Elisabeth Fischer-Friedrich — DFG Cluster of Excellence Physics of Life, BIOTEC, Technische Universität Dresden, Germany

In mammalian cells, actin filaments (F-actin) are bundled and crosslinked by multiple actin-binding proteins. The cytoskeletal structures they form are essential for cell motility, division, mechanosensitivity, intracellular transport and the mechanical protection of the cell. They have a highly nonlinear rheological behavior, which is tuned through their microscopic structure and their composition: the length of the microfilaments, the concentration of filaments and crosslinkers, and the nature of the crosslinkers.

Actin-binding proteins mostly form transient bonds with the filaments. This enable both a protective solid-like response on short timescales and large reorganization of the biopolymer network on longer ones. The average lifetime of these bonds typically depends on the mechanical load applied to them, thus on the mechanical stress in the actin network. Interestingly, this lifetime increases with increasing load for some actin crosslinkers. This behavior is termed "catch-bond" and is far less intuitive than the opposite, "slip-bond" behavior. Here, we report experimental results showing a catch-bond behavior for three major human actin crosslinkers: α-actinin 4, filamin A and filamin B. These were obtained in mitotic HeLa cells, using AFM-based cortical tension measurements coupled with FRAP and confocal imaging.

BP 24.20 Tue 16:00 BPp

Simulating Cells Going Through Constrictions - A Cellular Potts Model Approach — •Miriam Schnitzerlein[1,3], Felix Reichel[2,3], Martin Kräter[2,3], Hui-Shun Kuan[1,3], Jochen Guck[2,3], and Vasily Zaburdaev[1,3] — [1]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — [2]Biological Optomechanics, Max-Planck Institute for the Science of Light, Erlangen, Germany — [3]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

In the human body, many cells types regularly have to struggle through confinements. For example in the blood system where not only blood cells but also cancer cells may encounter capillaries with cross-sections below the cell size. One in vitro experiments to mimic and study such processes is using microfluidic techniques, where living cells suspended in an aqueous solution could be forced through a channel with recurring constrictions. By analyzing cell deformation and passage times we can learn about their mechanical properties. Ultimately linking the characteristics of the passage to cell mechanics requires a simple and tractable model. Here we suggest using a well known Cellular Potts Model (CPM), which represents cells as a set of adjacent spins on a lattice with cell dynamics arising from an energy minimization principle. The major challenge is to link phenomenological parameters of the model to experimental space and time scales and also to mechanical properties of living cells. Our first results demonstrate qualitative agreement with experimental observations and thus indicate the CPM as a promising tool to quantify cell passage through constrictions.

BP 24.21 Tue 16:00 BPp

Optimal hematocrit for ATP release by red blood cell in microcirculation — •Zhe Gou and Chaouqi Misbah — Laboratoire Interdisciplinaire de Physique, Grenoble, France

ATP release by red blood cells (RBCs) acts as an important signaling molecule for various physiological functions, such as vasodilation. When flowing in microcirculation, RBCs experience a cascade of branching vessels, from arterioles to capillaries, and finally to venules, which affects not just flow behavior of blood but also ATP release. In a previous study, we have proposed a model of ATP release by RBCs through two pathways of cell membrane: pannexin 1 channel (Px1), sensitive to shear stress, and cystic fibrosis transmembrane conductance regulator (CFTR) which responds to cell deformation. As a continuation, present work further investigates the effect of flow strength, hematocrit, and vascular diameter by numerical simulations. We found a nontrivial spatial RBC organization and ATP patterns due to application of shear stress on the RBC suspension. Conditions for optimal ATP release per cell are identified, which depend on vessel size and hematocrit Ht. Increasing further Ht beyond optimum enhances the total ATP release but should degrade oxygen transport capacity, a compromise between an efficient ATP release and minimal blood dissipation. Moreover, ATP is boosted in capillaries suggesting a vasomotor activity coordination throughout the resistance network. Further studies of vascular network may help to explore the whole signaling cascade of ATP.

BP 24.22 Tue 16:00 BPp

Influence of NaCl on Neuronal Membranes — •Sebastian Jaksch[1], Alexandros Koutsioubas[1], Piotr Zolnierczuk[1], Olaf Holderer[1], Henrich Frielinghaus[1], Stephan Förster[1], and Peter Müller-Buschbaum[2] — [1]Jülich Centre for Neutron Science (JCNS), Garching (Germany), Jülich (Germany) and Oak Ridge TN (USA) — [2]Lehrstuhl für funktionelle Materialien, Physik-Department, Technische Universität München (Germany)

We previously investigated the structure and the dynamic behavior of L-α-phosphatidylcholine (SoyPC) phospholipid membranes, [1,2] by means of GISANS and GINSES and established a multi-lamellar structure as well as a surface mode, attributed to transient waves in the membranes. Extending those measurements to include various NaCl concentrations within the membrane we could identify two main features:[3] (1) The thickening of the membrane layers as reported by SAXS measurements is due to an enriched ion layer close to the head group of the phospholipid membranes, and not, as for hydrophobic molecules an actual swelling of the membrane. (2) The in-plane dynamics of the membranes is enhanced by the addition of NaCl, while retaining the previously reported surface mode. Those features can play an important role in the understanding of membrane functions, such as the formation of ion channels, and thus their biological function on a fundamental level. [1] S. Jaksch, et al, Phys. Rev. E 91(2), 2015, 022716. [2] S. Jaksch, et al, Scientific Reports 7(1), 2017, 4417. [3] S. Jaksch, et al, Influence of NaCl on the structure and dynamics of phospholipid layers, submitted.

BP 24.23 Tue 16:00 BPp

Viscoelastic properties of Pancreatic cancer cells on Soft supports — •Shruti G Kulkarni[1,2], Malgorzata Lekka[2], and Manfred Radmacher[1] — [1]University of Bremen, Bremen, Germany — [2]Institute of Nuclear Physics, Krakow, Poland

Pancreatic ductal adenocarcinoma (PDAC) is one of the leading causes of cancer-related mortality, with less than 5% of patients having a 5-year survival rate. The dense extra-cellular matrix (ECM) prevents drug-delivery and its remarkably high stiffness may play a role in cancer initiation and progression. Invasive potential of pancreatic cancer cells has also been related to cellular stiffness. We tested the effect of substrate stiffness on stiffness of pancreatic cancer cells using atomic force microscopy. Force curves were measured on primary tumor cell lines (PANC1 and PL45) grown on collagen-coated polyacrylamide gels (PAG) of stiffness 2.8 kPa and 16.6 kPa and plastic petri dishes. PANC1 shape changes in gradient from well-spread to round as stiffness of the substrate decreases. Mechanical parameters like Young's (˜1.4 kPa), storage and loss moduli remain the same, indicating that they display a loss of mechanosensitivity when cultured on PAG. PL45 is rounded on PAG but well-spread on plastic. Cells on the 2.8 kPa gel are 3.5 kPa stiff, while those on 16.6 kPa gel are only 2.2 kPa stiff. PL45 cells may have an increased potential to invade through soft ECMs, because their stiffness increases as the substrate's stiffness decreases. Further experimentation to study the connection between metastatic and invasive cell lines, and other biomimetic substrates, as well as the role of specific ECM proteins has been planned.

BP 24.24 Tue 16:00 BPp

Calcium Dynamics Model in Endothelial Cells — •Ananta Kumar Nayak[1], Zhe Gou[1], Sovan Lal Das[2], and Chaouqi Misbah[1] — [1]Univ. Grenoble Alpes, CNRS, LIPhy, Grenoble 38000, France. — [2]Department of Mechanical Engineering, Indian Institute of Technology Palakkad, Palakkad 678557, India.

Calcium is a ubiquitous molecule and a second messenger that regulates many cellular functions ranging from the exocytosis to the proliferation of cell. Endothelial cells (ECs) form a inner lining of blood vessels and play an important role in transduction of extracellular environment information to the cytoplasm. A robust calcium dynamics model is required to understand these cellular functions occurring at (patho) physiological conditions in the ECs. In this work, we have developed a single cell minimal calcium dynamics model by including cytosol and endoplasmic reticulum (ER) calcium, Inp3 (Inositol Trisphosphate) kinetics, and the receptor dynamics. We find that the receptor desensitization due to phosphorylation and recycling of receptor play a vital role in maintaining the calcium homeostasis in the presence of a constant stimulus due to adenosine triphosphate (ATP). Apart from this, our model is able to capture other experimental facts like refilling of calcium in ER, which is dependent on the extracellular calcium concentration. Overall the model is able to account for

the natural physiological recovery towards homeostasis of active components in the calcium generation cascade. Furthermore, in a future work, we plan to extend this model to include blood flow through the blood vessel to gain insights in the development of vascular diseases.

BP 24.25 Tue 16:00 BPp

Computational Modeling of Nuclear Blebs — •Silvia Bonfanti[1], Maria Chiara Lionetti[2], Maria Rita Fumagalli[3], Francesc Font-Clos[1], Stefano Zapperi[1,4], and Caterina A.M. La Porta[2,3] — [1]Center for Complexity and Biosystems Department of Physics, University of Milan, Milano, Italy — [2]Center for Complexity and Biosystems Department of Environmental Science and Policy, University of Milan, Milano, Italy — [3]CNR-Consiglio Nazionale delle Ricerche, Biophysics institute, Genova, Italy — [4]CNR-Consiglio Nazionale delle Ricerche, Istituto di Chimica della Materia Condensata e di Tecnologie per l'Energia, Milano, Italy

The morphology of the nucleus of eukaryotic cells is determined by the complex interactions among the nuclear lamina forming the nuclear scaffold, the internal chromatin filaments and the coupling with the external cytoskeleton. It is known that nuclear morphological alterations such as blebs are often associated with pathological conditions such as Hutchinson-Gilford progeria syndrome. Here, we investigate the role of mechanical factors in nuclear morphological alterations constructing a model of the cell nucleus, consisting of a flexible coarse-grained shell representing nuclear envelope and lamina endowed with stretching and bending rigidity, coupled to a set of coarse-grained polymers representing chromatin and also to a set of oscillating points modeling contractions of the cytoskeleton. We compare the simulations results with experimental results on a cellular model of progeria and shed light on the important role played by chromatin and nuclear tethering in determining nuclear morphology and fluctuations.

BP 24.26 Tue 16:00 BPp

Contractile activity inhibition of Dupuytren fibroblasts: AFM mechanical approach — •Sandra Pérez-Domínguez and Manfred Radmacher — Institute of Biophysics, University of Bremen, Bremen, Germany

Dupuytren's disease is a fibromatosis of the connective tissue of the palm that causes progressive and permanent contracture of the digits. The mechanical properties of healthy, scar and Dupuytren fibroblasts, all from the same patient, were investigated employing the AFM after inhibiting the myosin light chain kinase. For this purpose, ML-7 was used to block the actin-myosin activity, therefore, reducing inhibiting the cell contraction. The stiffness of Dupuytren fibroblasts was around 3 kPa before adding ML-7 and in almost all cases a decrease to 400 Pa was observed after ML-7 addition. 60% of Dupuytren cells did not recover; nevertheless, 30% of them showed a recovery over time. Scar fibroblasts have a Young's modulus of 2.5 kPa before adding ML-7 and showed a decrease to 300 Pa after adding ML-7 similar to what we observed with the Dupuytren fibroblasts. Most scar fibroblasts reacted to the inhibitor; however, some 20% did not show any response. Healthy fibroblasts showed - in preliminary experiments using a different AFM cantilever tip - a smaller response when ML-7 has been added, and some of the cells did not respond to the inhibitor considerably. This is actually conceivable since healthy fibroblasts shall have less cortical tensity, i.e. less myosin activity, and consequently applying a myosin inhibitor will result in less change.

BP 24.27 Tue 16:00 BPp

A matter of size: Understanding size-dependent organelle transport in cells — •Simon Wieland[1,2], David Gitschier[1], Marius M. Kaiser[1], Christina Steininger[1], Wolfgang Gross[1], Adam G. Hendricks[3], and Holger Kress[1] — [1]Biological Physics Group, University of Bayreuth, Bayreuth — [2]Animal Ecology I, University of Bayreuth, Bayreuth — [3]Department of Bioengineering, McGill University, Montreal

Intracellular transport of organelles is essential for numerous cellular processes, including phagocytosis. Earlier findings indicate that the persistence of organelle transport during phagocytosis strongly depends on cargo size. To understand this behavior on a molecular level, we systematically quantified the size-dependence of phagosomal transport forces using magnetic tweezers. We found that transport forces increase with organelle size. With a simple geometrical model taking the distribution of microtubules around the organelles into account, we explain the scaling behavior of the transport forces. Our findings indicate that intracellular organelles displace microtubules from their original positions, leading to an increased microtubule density at the organelles surface, and thus an increased number of binding possibilities for molecular motors. Additionally, we performed immunofluorescence experiments on isolated phagosomes, allowing us to identify and estimate the relative number of molecular motors on the organelles. Quantifying the size-dependence of phagosomal transport can lead to a deeper understanding of intracellular organelle transport and the dynamics of interactions between molecular motors and the cytoskeleton.

BP 24.28 Tue 16:00 BPp

Extracellular matrix mechanical prestress during morphogenesis of Drosophila wing discs — •Yanín Guerra[2], Elisabeth Fischer-Friederich[2], and Christian Dahmann[1] — [1]Institute of Genetics, Technische Universität Dresden, 01062 Dresden, Germany. — [2]Biotechnology Center of the TU Dresden (Biotec), Tatzberg 47/49, 01062 Dresden, Germany

The folding of tissues is the manner in which two dimensional sheets transform into three dimensional structures. There are many mechanisms involved in fold formation such as apical constriction, cell proliferation, collective migration and cell-ECM adhesion. For a long time it has been thought that the most important process is apical constriction, notwithstanding, how this mechanisms organise to construct healthy three dimensional structures remains as an open question.

A recent study on the mechanical processes involved during hinge fold formation of the Drosophila wing imaginal disc found that there is a decrease of basal tension in the central fold (H/H fold), but no apical constriction [1]. Moreover, they report that this fold exhibits a depletion of the extracellular matrix (ECM) suggesting that the dynamics of such structure drive fold formation. So, how does the interaction between the ECM and the actomyosin networks contributes to basal tension in the morphogenesis of the H/H fold in Drosophila wing disc?

The main goal of this research is to elucidate the role of ECM in the formation of H/H fold in Drosophila wing. To achieve this goal I will culture the wing imaginal discs ex vivo in order tomeasure its mechanical properties using atomic force microscopy.

BP 24.29 Tue 16:00 BPp

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.

We analyse the influence of an external force on the polymerisation speed. The stall force for energetically balanced rates is identical to the stall force for F-Actin without profilin.

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

BP 24.30 Tue 16:00 BPp

Tailored ensembles of neural networks optimize sensitivity to stimulus statistics — •Johannes Zierenberg[1,2], Jens Wilting[1], Viola Priesemann[1,2], and Anna Levina[3,4] — [1]Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, 37077 Göttingen, Germany — [2]Bernstein Center for Computational Neuroscience, Am Fassberg 17, 37077 Göttingen, Germany — [3]University of Tübingen, Max Planck Ring 8, 72076 Tübingen, Germany — [4]Max Planck Institute for Biological Cybernetics, Max Planck Ring 8, 72076 Tübingen, Germany

The capability of a living organism to process stimuli with nontrivial intensity distributions cannot be explained by the proficiency of a single neural network. Moreover, it is not sufficient to maximize the dynamic range of the neural response; it is also necessary to tune the response to the intervals of stimulus intensities that should be reliably discriminated. We derive a class of neural networks where these intervals can be tuned to the desired interval. This allows us to tailor ensembles of networks optimized for arbitrary stimulus intensity distributions. We discuss potential applications in machine learning.

BP 24.31 Tue 16:00 BPp

Timing cellular decisions using transient cues —

•Felix Meigel[1], Lina Hellwig[2], Jörg Contzen[2], Philipp Mergenthaler[2], and Steffen Rulands[1,3] — [1]Max Planck Institute for Physics of Complex Systems, Dresden — [2]Neurology Department, Charité University Medicine Berlin — [3]Center for Systems Biology Dresden

The maintenance of intact tissues relies on precise cellular decision-making despite strongly fluctuating extrinsic cues. These decisions involve processes on vastly different scales, from molecules to organelles and cells in tissues. How can cells manipulate the propagation of fluctuations across these scales to perform biological function? Here, we show how the non-equilibrium interplay between microscopic and mesoscopic dynamics leads to a kinetic low-pass filter facilitating precise sensing of fluctuating cellular states. Specifically, we find that the interplay between molecular and organelle dynamics gives rise to a single, collective degree of freedom. We show that this degree of freedom exhibits rich dynamical behaviour showing different kinetics on different temporal scales and thereby leading to the suppression of fast fluctuations. We demonstrate our findings in the context of the metabolic regulation of cell death via the interplay of Bax protein dynamics with rapid mitochondrial fusion and fission and find an order of magnitude effect on the error rate of the cell death decision. Our work shows paradigmatically how biological function relies on the non-equilibrium integration of processes on different spatial scales to control and respond to fluctuations.

BP 24.32 Tue 16:00 BPp

Dynamic analysis of the SinR/SlrR/SinI genetic circuit for biofilm formation in Bacillus subtilis — •Simon Dannenberg, Jonas Penning, and Stefan Klumpp — Institut für Dynamik komplexer Systeme Georg-August-Universität Göttingen Friedrich-Hund-Platz 1 37077 Göttingen, Germany

Switching between different lifestyles in bacteria serves as a survival strategy under changing environmental conditions. It allows genetically identical cells to develop different phenotypic traits and creates diversity in a colony of cells. Such switches either occur stochastically due to fluctuations in gene expression or are the result of a deterministic process. In our work we investigate biofilm formation by mathematical analysis of the SinR/SlrR/SinI genetic circuit in Bacillus subtilis. Via a rate equation approach for the involved proteins, steady state solutions are found in which parameter regions for bistability exists. For those regions we conducted a stochastic analysis using a Gillespie algorithm, which shows that typical fluctuations are not sufficient to induce the transitions between these states. Instead, we propose a deterministic switching mechanism and analyzed its dynamic.

BP 24.33 Tue 16:00 BPp

Intermediate scattering function in multi-channel dynamics: from model systems to particle-tracking data in live cells — •Cai Dieball[1], Adal Sabri[2], Xinran Xu[3], Diego Krapf[3,4], Matthias Weiss[2], and Aljaz Godec[1] — [1]Mathematical bioPhysics Group, Max Planck Institute for Biophysical Chemistry, 37077 Göttingen, Germany — [2]Experimental Physics I, University of Bayreuth, 95440 Bayreuth, Germany — [3]Department of Electrical and Computer Engineering, Colorado State University, Fort Collins, Colorado 80523, USA — [4]School of Biomedical Engineering, Colorado State University, Fort Collins, Colorado 80523, USA

Several experimental techniques probe collective observables related to the intermediate scattering function, i.e. the expectation value of the Fourier-transformed displacement vectors of the system's particles. These techniques include neutron, X-ray and dynamic light scattering, neutron spin echo and Fourier imaging correlation spectroscopy, and differential dynamic microscopy. Intermediate scattering functions provide useful, complementary information even when applied to experiments that are able to track the motion of individual particles. In our work we analyze the intermediate scattering function in systems with "multi-channel" dynamics, i.e. dynamics stochastically switching between different modes of motion. We first inspect scattering fingerprints in simple model systems with two-channel dynamics. We then analyze trajectories from particle-tracking experiments in the cytoplasm of mammalian cells, and confirm that these display characteristics of anomalous, two-channel fractional Brownian motion.

BP 24.34 Tue 16:00 BPp

Nonlinear Allosteric Effect in Elastic Network Models of Proteins — •Maximilian Vossel and Aljaž Godec — Mathematical bioPhysics Group, Max Planck Institute for Biophysical Chemistry, 37077 Göttingen, Germany

Allostery is a ubiquitous phenomenon in proteins, where the binding of a ligand at one site induces perturbations at another, often spatially distant site. The large scale dynamics of biomolecules is often effectively described by coarse-grained elastic network models that encode the collective motion of proteins around their equilibrium structure. However, despite their conceptual simplicity the manner in which these network models respond to local structural perturbations, such as the binding of a ligand molecule, is highly non-trivial and in the context of allostery remains an unsolved problem. We develop a simple and efficient algorithm for determining the full, nonlinear response of such networks to arbitrary structural perturbations that mimic the binding of a ligand molecule in the limit of high stiffness (or low temperature). Applying the algorithm we find that the response often displays pronounced nonlinearities. This suggests that recent attempts to explain allostery in proteins based on linear response theory are not necessarily accurate and may not always be meaningful.

BP 24.35 Tue 16:00 BPp

Comparative analysis of metabolic and transcriptomic features of Nothobranchius furzeri — •Maria Rita Fumagalli[1,2,3], Francesc Font-Clos[1,4], Simone Milan[1], Stefano Zapperi[1,4,5], and Caterina A.M. La Porta[1,2,3] — [1]Center for Complexity and Biosystems, University of Milan — [2]Biophysics Institute, CNR, Genova — [3]Dep. of Environmental Science and Policy, University of Milan — [4]Dep. of Physics, University of Milan — [5]ICMATE, CNR, Milan

Nothobranchius furzeri is a killifish with an extremely rapid growth and short lifespan with respect to other vertebrates. Despite its short life, N. furzeri shows hallmarks typical of aging. We investigated the aging process of N. furzeri in comparison with other two well characterized animal models (Danio rerio and Mus Musculus) with a combination of computational analysis and modeling.

The analysis of gene expression changes during ageing suggests the presence of alterations in regulatory mechanisms happening early during N. furzeri lifetime. Coherently, N. furzeri shows a specific deregulation pattern of genes involved in chromatin remodeling as well as histone acetylation and deacetylation. Enzymes deregulation could affect metabolic reactions, but changes in terms of efficiency in the production/consumption of metabolites are not easy to address. To this end, we implemented a metabolic network model based on flux balance analysis applying it to the fundamental glycolysis pathway.

Overall, our analysis shows that N. furzeri ageing process is associated to very peculiar chromatin and metabolic dynamics.

BP 24.36 Tue 16:00 BPp

Dynamics of tethered polymers in a circular confinement — •Meng Wang[1,2], Tim Klingberg[1,2], Mauro Battipede[1,2], Vasily Zaburdaev[1,2], and Hui-Shun Kuan[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Max-Planck-Zentrum für Physik und Medizin

During meiosis, the paternal and maternal chromosomes find each other to pair and exchange parts of their genetic material in the process of recombination, which is the major mechanism contributing to genetic diversity in sexually reproducing organisms. As the first steppingstone in understanding how physical mechanisms help chromosomes to align, we study the dynamics of chromosomes in the nucleus. In this poster, we consider meiotic DNA as a freely jointed chain confined in a circle with the ends of the chain being tethered and free to move along the circle. We use the kinetic Monte Carlo algorithms to simulate the stochastic motion of the polymer and compare the results to the Rouse model. Although the Rouse model successfully describes the simulation results, especially the transient subdiffusive regimes, the global motion of the polymer is very different due to the constraint of the circle. For small monomer numbers, the polymer can stretch to match the diameter of the circle, and the trajectory of its each end can wind around the circle. However, with fixed polymer length, for large monomer numbers, the chain tends to form a contracted coil, stochastically moving along the circle like a composite particle in the long-time limit.

BP 24.37 Tue 16:00 BPp

Dimensionality of neural circuit manifolds associated with a salt-and-pepper organization of cortical stimulus preferences — •Michael Sternbach[1,2,3] and Fred Wolf[1,2,3,4,5] — [1]Campus Institute for Dynamics of Biological Networks, Göttingen, Germany — [2]Max Planck Institute for Dynamics and Self-Organization — [3]Bernstein Center for Computational Neuroscience

Göttingen — [4]Institute for Dynamics of Complex Systems, Georg-August University Göttinge — [5]Max Planck Institute of Experimental Medicine

Biological neural circuits are expected to converge to one of many stable network configurations. For the form vision core circuit of primate/carnivore V1 prior work indicates that stable network configurations form toroid high-dimensional continua (Wolf 2005, Kaschube et al. 2010). Similar results for network configurations in rodents V1, called salt-and-pepper organizations (SaP), are currently not available. Here we utilize techniques from the study of spin liquid states (Chalker 2015) to construct mathematically tractable models with SaP optimal states. We demonstrate that these models can exhibit ground state manifolds with extensive dimensionality. This result is consistent with the general expectation that there are a very high number of equivalent SaP configurations. These studies expand the toolbox for analyzing the multiplicity of stable cortical circuit configurations. Our first results suggest that the evolutionary transition from a rodent ancestral circuit configurations of V1 to a primate/carnivore V1 architecture was accompanied by a reduction in cortical circuit state dimension.

BP 24.38 Tue 16:00 BPp

Trading bits in the readout from a genetic network — •Marianne Bauer[1], Mariela Petkova[2], Thomas Gregor[1,3], Eric Wieschaus[1], and William Bialek[1,4] — [1]Princeton University, Princeton, USA — [2]Harvard University, Boston, USA — [3]Institut Pasteur, Paris, France — [4]City University of New York, New York, USA

In genetic networks, information of relevance to the organism is represented by the concentrations of transcription factor molecules. In order to extract this information the cell must effectively "measure" these concentrations, but there are physical limits to the precision of these measurements. We explore this trading between bits of precision in measuring concentration and bits of relevant information that can be extracted, using the gap gene network in the early fly embryo as an example. We argue that cells in the embryo can extract all the available information about their position, but only if the concentration measurements approach the physical limits to information capacity. These limits necessitate the observed proliferation of enhancer elements with sensitivities to combinations of transcription factors, but fine tuning of the parameters of these multiple enhancers is not required.

BP 24.39 Tue 16:00 BPp

Coupling of growth, replication and division in E. coli — •Mareike Berger — AMOLF, Amsterdam, The Netherlands

Growth, DNA replication and division are key features of every living organism. The precise temporal control of these processes is essential for survival. We investigate how the model organism E. coli couples its replication to its division cycle under different growth conditions. According to the phenomenological general growth law, E. coli on average initiates replication at a constant volume per origin of replication and divides a constant time later. This simple mechanism allows E. coli to divide faster than it takes to replicate its DNA while maintaining cell size homeostasis. It is a longstanding open question how the general growth law is realized on a molecular level. We present a theoretical model that is based on experimentally observed molecular mechanisms and that can reproduce the phenomenological general growth law. This novel model allows us to make quantitative predictions on the regulation of replication in E. coli.

BP 24.40 Tue 16:00 BPp

DNA accumulates and concentrates in artificial hydrothermal chimneys mimicking prebiotic geophysical conditions — •Maximilian Weingart, Lea Gigou, Ömer Coskun, William Orsi, and Dieter Braun — LMU München, Munich, Germany

The so called concentration problem on early Earth represents one of the greatest challenges for molecular evolution forcing it to proceed from highly diluted prebiotically formed molecules in an extensive ocean. Origin of Life research is therefore inclined to think about potential locations that provide necessary geophysical conditions to overcome this hurdle.

Recently, Barge and Coworkers [1] showed the formation of oxyhydroxide minerals in alkaline hydrothremal vents suggesting that prebiotic chemical reactions could have happened in such a scenario. Additionally, diffusiophoresis driven by the ionic gradient across the mineral membrane could move dissolved DNA molecules towards the chimneys where the charged strands adsorb to the mineral surface. This could locally increase DNA concentration while prohibiting back diffusion into the ocean at the same time.

To test this hypothesis, herein we used an artificial hydrothermal vent mimic [1] by using crimp flasks and injecting hydrothermal fluid (pH 12) into the Fe(II) containing ocean simulant (pH 5.5) with dissolved DNA ladders. Preliminary results showed higher DNA concentration in the mineral sample after selective analysis of remaining ocean and chimney. [1] Barge et al. PNAS (2019) doi.org/10.1073/pnas.1812098116

BP 24.41 Tue 16:00 BPp

Phase separation in membranes due to matter exchange — •Nirvana Caballero[1], Karsten Kruse[2], and Thierry Giamarchi[1] — [1]Department of Quantum Matter Physics, University of Geneva, 24 Quai Ernest-Ansermet, CH-1211 Geneva, Switzerland — [2]Department of Biochemistry, Department of Theoretical Physics and National Center of Competence in Research Chemical Biology, University of Geneva, CH-1211 Geneva, Switzerland

Heterogeneous lipid composition in cell membranes is key to biological function, acting as one of the main mechanisms to exchange information between cells or between a cell an its environment. The underlying mechanisms controlling pattern formation are still under debate. In this work, we consider a theoretical phase-field model to describe the composition of a two-dimensional membrane exchanging matter with a reservoir. The model includes matter absorption and desorption in the membrane with different rates. By only assuming matter conservation in the system membrane-reservoir, we show with extensive numerical simulations that, depending on these rates, a complex patterned composition distribution emerges in the membrane. The pattern emergence is due to spatio-temporal "memory" effects. Our results show that the causes of heterogeneous lipid composition may be justified in simple physical terms.

BP 24.42 Tue 16:00 BPp

DNA Replication:Accuracy and Speed of elongation — •Mamata Sahoo[1], Arsha Nousad[1], Priyaranjan Baral[2], and Stefan Klumpp[3] — [1]Department of Physics, University of Kerala, Kariavattom Campus-6955881, India — [2]Department of Physics, — [3]Institute for the Dynamics of Complex Systems, University of Gottingen, Gottingen, Germany

Being a dual purpose enzyme, the DNA polymerase is responsible for elongation of the newly formed DNA strand as well as cleaving the erroneous growth in case of a misincorporation. Though this is an efficient mechanism, sometimes DNAP with misincorporated nucleotide may escape to the next site as well as a correctly incorporated nucleotide causing a replication error may get cleaved unnecessarily from the exonuclease site. An error in 10^9 correct nucleotides incorporation has been observed experimentally. Here we propose a theory based kinetic model of DNA replication and find out the exact results for the velocity of elongation as well as the accuracy of replication. Surprisingly it is observed that the velocity of elongation with erroneous stepping passes through a crossover showing exact opposite behaviors at above and below the crossover point. Moreover, we ask the question that how the erroneous stepping with other parameters of the model have to be set in order to have a control over the speed of elongation mechanism. Finally we argue that the theoretical analysis of our results provide a simple picture of the design of a more accurate replication system and follows up with the speed-accuracy linear trade-off rule.

BP 24.43 Tue 16:00 BPp

Protein-ligand dynamics on multisecond timescales from sub-μs atomistic simulations — •Steffen Wolf, Benjamin Lickert, Simon Bray, and Gerhard Stock — Biomolecular Dynamics, Institute of Physics, University of Freiburg, Hermann-Herder-Straße 3a, 79104 Freiburg

Coarse-graining of fully atomistic molecular dynamics simulations is a long-standing goal to allow the prediction of processes occurring on biologically relevant timescales. To achieve the necessary enhanced sampling, we first perform dissipation-corrected targeted molecular dynamics simulations which yield free energy and friction profiles of the molecular process of interest. In a second step, we use these fields to perform Langevin equation simulations which account for the desired molecular kinetics. By introducing the concept of temperature boosting of the Langevin equation, this combination of methods allows for the simulation of biomolecular processes occurring on multisecond timescales and beyond. Adopting the dissociation of solvated sodium chloride and several protein-ligand complexes as test problems, we are

able to reproduce rates from atomistic MD simulation and experiments within a factor of 1.5–4 for rates up to the range of millseconds and 2–20 in the range of seconds.

BP 24.44 Tue 16:00 BPp

Structuring of the epithelial tissue — •Jakov Lovrić[1,3], Michael A. Klatt[2], Sara Kaliman[3], Gerd E. Schröder-Turk[4], and Ana-Sunčana Smith[1,3] — [1]Division of Physical Chemistry, Ruder Bošković Institute, Zagreb, Croatia — [2]Department of Physics, Princeton University, Princeton, New Jersey 08544, USA — [3]PULS Group, Institute for Theoretical Physics, Interdisciplinary Center for Nanostructured Films,Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — [4]Murdoch University, College of Science, Health, Engineering and Education, Murdoch, Australia

Structural properties of space tessellations are important to understand various problems in many fields of science and industry. One of the existing questions is how to tessellate space with the maximized centrality of the cells, usually known as the Quantizer problem. Here we study stable solutions of the Quantizer problem by applying Lloyd's algorithm on various disordered random point processes. We find that Lloyd's algorithm converges to a universal amorphous structure with long-range order. Furthermore, we investigate the role of cell centrality in the epithelium tissue. First, we find that the tissue can be represented by the tessellation based on the nuclear shape of constituting cells. In the following, we explore the interplay between finite-size effects and the Lloyd minimization and find that during the epithelial tissue development, centrality as a concept may play a role and is tightly controlled by the activity of the cell.

BP 24.45 Tue 16:00 BPp

Processive motors as active agents of microtubule lattice regulation — William Lecompte and •Karin John — University of Grenoble-Alpes, CNRS, Laboratoire Interdisciplinaire de Physique, 38000 Grenoble, France

Microtubules and molecular motors are ubiquitous in eukaryotic cells and are vital for many key cellular functions (cell division, organelle transport, motion). Recent experiments have shown that molecular motors modify the underlying microtubule lattice, yet a mechanistic model has remained elusive. Here we investigate theoretically how molecular motors could potentially participate in remodelling the shaft lattice. Our key idea is, that the walk of molecular motors locally destabilizes the lattice and may facilitate the exchange of tubulin dimers with the surrounding medium.

To test this assumption, we investigate a microtubule lattice model with lattice-motor interactions using kinetic Monte Carlo simulations. We propose a simple model with two key ingredients. The walk of molecular motors along the microtubule induces locally a conformational change with life time τ_r in the underlying lattice, which is less stable than the unperturbed lattice. Single lattice vacancies are stabilized via a steric hindrance for GTP dimers to integrate a GDP-lattice environment. As preliminary results we observed that a small flux of molecular motors which weakly destabilizes the lattice is sufficient to decrease the life-time of microtubules in the absence of free tubulin considerably.

BP 24.46 Tue 16:00 BPp

Analysis of cell contact inhibition during growth of epithelial tissue — •Sebastian Rühle, Anja Voss-Böhme, and Steffen Lange — University of applied sciences, Dresden, Germany

Dominating mechanisms in the development of healthy epithelial tissue are still subject to contemporary research, especially for tumour progression. While experiments suggest, that biomechanical cell-cell-interactions are crucial for the development of the tissue, it's usually oversimplified or neglected in theoretical approaches. For instance, the impact of cell migration, competition or contact inhibition on development of the cell colony is barely quantified. Puliafito et al. (2012) did experiments on MDCK-cells and proposed, that the behaviour of the colony during the growth phase can be solely explained by contact inhibition.

To test this hypothesis, we develop a cell-based model and compare the numerical results with the experimental data. using a cellular automaton we emulate single cell behaviour like cell migration, growth, proliferation, and cell-cell interactions like cell adhesion. The parameters are calibrated by experimental single cell tracking measurements. We show that without any mechanism of contact inhibition, this calibrated model reproduces emergent quantities like colony area, density, shape, cell size distribution, and collective cell motion from the experiment only to some extent. The discrepancies are most prominent for the long term cell density and cell size distribution and substantiate the role of contact inhibition in tissue growth.

BP 24.47 Tue 16:00 BPp

Analyzing the replication dynamics of malaria parasites — •Patrick Binder[1,2,3], Severina Klaus[4], Thomas Höfer[3], Nils Becker[3], Ulrich Schwarz[2,3], and Markus Ganter[4] — [1]Institute for Theoretical Physics, Heidelberg University, Germany — [2]BioQuant, Heidelberg University, Germany — [3]German Cancer Research Center (DKFZ), Heidelberg, Germany — [4]Center for Infectious Diseases, Heidelberg University Hospital, Heidelberg, Germany,

At around 200 million cases and half a million of fatalities each year, malaria remains a global health challenge. The predominant malaria-causing pathogen *Plasmodium falciparum* is a eukaryotic parasite with a complex life cycle that includes proliferation within red blood cells. After invasion, the parasite undergoes several rounds of nuclear division, eventually releasing around 24 daughter parasites into the blood. Intriguingly, the nuclei divide asynchronously although they reside in a shared cytoplasm. It is unknown how this process is controlled to yield a well-controlled and well-timed final outcome. We investigate the regulation of DNA replication and nuclear division by confronting simple stochastic branching models with high-resolution time-lapse confocal microscopy. We first found that successive rounds of replication speed up initially and slow down later on. Second, termination of replication is regulated by a counter mechanism and not a timer. Third, DNA replication is less synchronous than in stochastic lineages of mother-daughter correlated nuclei or even independent nuclei. Together, our analysis discovered the unusual mode of replication of a major human pathogen.

BP 24.48 Tue 16:00 BPp

Topology Control and Pruning in Intertwined Biological Flow Networks. — •Felix Kramer[1,2] and Carl Modes[1,2,3] — [1]Max Planck Institute for Molecular Cell Biology and Genetics (MPI-CBG), Dresden 01307, Germany — [2]Center for Systems Biology Dresden (CSBD), Dresden 01307, Germany — [3]Cluster of Excellence Physics of Life (PoL), Dresden 01062, Germany

Any larger organism is dependent on the proper distribution of supplies such as water, oxygen, nutrients etc, through extended and complex vessel systems. Naturally, the morphogenesis of these vessel networks during their earliest developmental stages has been extensively studied, in particular for slime-molds, leaf venation systems and vessel systems in vertebrates. Interestingly enough there is a universal hypothesis for the onset of maturation of any rudimentary network: Mechanic stresses, caused by the fluid flow, drive the development of the system toward a stationary state representing on optimum of dissipation, flow uniformity or metabolite distribution. Nevertheless, the influence of environmental factors on such long-term adaptation dynamics as well as the networks structure and function have not been fully understood. Therefore, interwoven channel systems such as found in the liver, kidney and pancreas, present a novel challenge and key opportunity regarding the field of coupled distribution networks. We here present an advanced version of the discrete Hu-Cai model, coupling two spatial networks in 3D. We show that spatial coupling of two flow-adapting networks can control the onset of topological complexity in concert with short-term flow fluctuations.

BP 24.49 Tue 16:00 BPp

Exploratory analysis and comparison of biomolecular structural ensembles with PENSA — •Martin Vögele[1] and Ron O. Dror[1,2,3,4] — [1]Department of Computer Science, Stanford University — [2]Department of Molecular and Cellular Physiology, Stanford University — [3]Department of Structural Biology, Stanford University — [4]Institute for Computational and Mathematical Engineering, Stanford University

Molecular simulations enable the study of proteins and other biomolecules and their dynamics on an atomistic scale. The large amount of data produced for ever more complex systems often makes it difficult to identify the structural features that are relevant for a particular phenomenon. Whilst most available analysis tools provide methods to analyze one simulation at a time, many common research pursuits necessitate analysis across several conditions - like mutations or different ligands - and finding significant differences between them.

We introduce PENSA, a collection of methods for exploratory analysis and comparison of structural ensembles such as those from molecular dynamics simulations. So far PENSA users can compare

two conditions, e.g., via the relative entropy of their features or a Kolmogorov-Smirnov test, and visualize deviations on a reference structure. PENSA also implements exploratory analysis methods - like principal component analysis and clustering - that are applied across several ensembles. We demonstrate PENSA's usefulness on real-world examples by showing how it helps to determine molecular mechanisms efficiently.

BP 24.50 Tue 16:00 BPp

Morpheus: A user-friendly modeling and simulation framework for multicellular systems — Jörn Starruss, Diego Jahn, Robert Müller, Andreas Deutsch, and •Lutz Brusch — Center for Information Services and High Performance Computing (ZIH), Technische Universität Dresden, Germany

Computational modeling and simulation become increasingly important to analyze tissue morphogenesis. Existing software for multicellular models require scientists to encode their models in an imperative programming language. Morpheus (1,2), on the other hand, is an extensible open-source software framework that is entirely based on declarative modeling. It uses the domain-specific language MorpheusML to define multicellular models through a user-friendly GUI and has since proven applicable by a much broader community, including experimentalists. We here present how MorpheusML enables advanced scientific workflows (3) and cross-software exchange of multicellular models (4). MorpheusML can represent the spatial and mechanical aspects of interacting cells. A numerical simulation is then composed by automatic scheduling of predefined components in the simulator. Moreover, Morpheus supports simulations based on experimental data, e.g. segmented cell configurations, and offers a broad set of analysis tools to extract features right during simulation.

(1) Starruß et al. Bioinformatics 30, 1331, 2014. (2) Morpheus homepage: https://morpheus.gitlab.io (3) Parameter estimation workflow: https://fitmulticell.gitlab.io (4) Model standardization: https://multicellml.org