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Overview of Invited Talks and Sessions

Invited Talks

BP 1.3	Mon	9:40–10:10	BPa	**Cyclic Strain Steers Animal Cells** — •Rudolf Merkel
BP 2.1	Mon	9:00– 9:30	BPb	**The tortoise and hare: how moving slower allows groups of bacteria to spread across surfaces** — Oliver Meacock, Amin Doostmohammadi, Kevin Foster, Julia Yeomans, •William Durham
BP 7.3	Mon	14:40–15:10	BPa	**Towards the mechanical characterization of neuronal network formation** — Paulina Wysmolek, Florian Huhnke, Katja Salbaum, Joachim Spatz, •Friedhelm Serwane
BP 9.1	Mon	14:00–14:30	BPc	**From individual to collective intermittent motion: from bacteria to sheep** — •Fernando Peruani
BP 12.1	Tue	9:00– 9:30	BPa	**Molecular simulation meets cryo electron tomography** — •Gerhard Hummer
BP 13.3	Tue	9:40–10:10	BPb	**Active behaviors of cellular monolayers.** — •Benoit Ladoux
BP 21.1	Tue	14:00–14:30	BPa	**Predicting Protein and RNA Structures: from statistical physics to machine learning** — •Alexander Schug
BP 23.4	Tue	15:00–15:30	BPc	**Synthetic cells: De novo assembly with microfluidics and DNA nanotechnology** — •Kerstin Göpfrich

Sessions

BP 1.1–1.4	Mon	9:00–11:00	BPa	**Cell Mechanics I**
BP 2.1–2.4	Mon	9:00–11:00	BPb	**Active Biological Matter I (joint session BP/DY/CPP)**
BP 3.1–3.4	Mon	9:00–11:00	BPc	**Focus Physics of Stem Cells**
BP 4.1–4.6	Mon	11:00–13:30	BPa	**Cell Mechanics II**
BP 5.1–5.6	Mon	11:00–13:30	BPb	**Active Biological Matter II (joint session BP/CPP/DY)**
BP 6.1–6.6	Mon	11:00–13:30	BPc	**Systems Biology I**
BP 7.1–7.5	Mon	14:00–16:30	BPa	**Cell Mechanics III**
BP 8.1–8.6	Mon	14:00–16:30	BPb	**Bioimaging and Biospectroscopy**
BP 9.1–9.5	Mon	14:00–16:30	BPc	**Systems Biology II**
BP 10.1–10.22	Mon	14:00–16:30	DYp	**Posters DY - Fluid Physics, Active Matter, Complex Fluids, Soft Matter and Glasses (joint session DY/BP)**
BP 11.1–11.41	Mon	16:30–19:00	BPp	**Poster A: Single Molecule, Multicellular, Bioimaging, Focus Sessions, etc.**
BP 12.1–12.4	Tue	9:00–11:00	BPa	**Single Molecule Biophysics I**
BP 13.1–13.4	Tue	9:00–11:00	BPb	**Multicellular Systems I**
BP 14.1–14.4	Tue	9:00–11:00	BPc	**Focus Phase Separation in Biological Systems I (joint session BP/CPP)**
BP 15.1–15.3	Tue	9:30–10:30	DYa	**Active Matter 1 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP/CPP)**
BP 16.1–16.6	Tue	11:00–13:30	BPa	**Single Molecule Biophysics II**
BP 17.1–17.6	Tue	11:00–13:30	BPb	**Multicellular Systems II**
BP 18.1–18.3	Tue	11:00–12:00	BPc	**Cell Mechanics IV**

BP 19.1–19.6	Tue	11:00–13:00	DYa	**Active Matter 2 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP/CPP)**
BP 20.1–20.3	Tue	12:00–13:30	BPc	**Focus Biological Cells in Microfluidics I**
BP 21.1–21.4	Tue	14:00–16:00	BPa	**Systems Biology III**
BP 22.1–22.4	Tue	14:00–16:00	BPb	**Focus Phase Separation in Biological Systems II (joint session BP/CPP)**
BP 23.1–23.4	Tue	14:00–16:00	BPc	**Focus Biological Cells in Microfluidics II**
BP 24.1–24.50	Tue	16:00–18:30	BPp	**Poster B: Active Biological Matter, Cell Mechanics, Systems Biology, Computational Biophysics, etc.**
BP 25	Tue	17:45–18:30	BPb	**Nationale Forschungsdateninfrastruktur (NDFI) (joint session BP/CPP/DY/SOE)**
BP 26	Tue	18:30–19:00	BPa	**Annual General Meeting**
BP 27.1–27.5	Wed	9:00–10:40	DYb	**Active Matter 3 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP)**
BP 28.1–28.6	Wed	11:00–13:00	DYb	**Active Matter 4 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP)**
BP 29.1–29.4	Wed	14:30–15:50	DYb	**Active Matter 5 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP)**

Annual General Meeting of the Biological Physics Division

Tue 18:30–19:00 BPa

BP 1: Cell Mechanics I

Time: Monday 9:00–11:00 Location: BPa

BP 1.1 Mon 9:00 BPa

Pulling, failing and adaptation of macrophage filopodia — •Alexander Rohrbach and Rebecca Michiels — Bio- und Nano-Photonik, Universität Freiburg

Macrophages are cells of the immune system, which use filopodia to connect to pathogens and withdraw them towards the cell body for phagocytosis. The withdrawal of living targets requires to overcome counteracting forces, which the cell generates after a mechanical stimulus is transmitted to the filopodium. Adaptation to mechanical cues is an essential biological function of cells, but it is unclear whether optimization strategies are essential for filopodia pulling. We use optically trapped beads as artificial targets and interferometric particle tracking to investigate factors contributing to filopodia performance. We find that bead retractions are interrupted by sudden failure events caused by mechanical rupture of the actin-membrane connection. Filopodia resume pulling only milliseconds after ruptures by reconnecting to the actin backbone. Remarkably, we see a gradual increase of filopodia force after failures, which points towards a previously unknown adaptation mechanism. Fluorescence microscopy reveals that particles are transported in a stop-and-go behavior with the actin retrograde flow via a force-dependent linker at the filopodium tip. Additionally, we see that the strength of the attachment between bead and filopodium increases under load, a characteristic of catch bond adhesion proteins. Our findings show how mechanical adaptation enable macrophage cells to optimize their performance under load.

BP 1.2 Mon 9:20 BPa

The dynamics of burst-like collective migration in 3D cancer spheroids — •Swetha Raghuraman[1], Raphael Wittkowski[2], and Timo Betz[1] — [1]Institute of Cell Biology, ZMBE, Münster, Germany — [2]Center for Soft Nanoscience

Collective migration of cells is a striking behavior observed during morphogenesis, wound healing and cancer cell invasion. Spherical aggregates of cells are known to migrate in 3D matrices like collagen, matrigel or fibronectin *in-vitro*. Although biochemical signaling is a main research focus, the biophysical properties of the spheroid leading to an invasion is less explored. We observe a striking phenotypical difference when HeLa cervical cancer spheroids were embedded in different concentrations of collagen I matrices. HeLa spheroids in lower collagen concentration (LCC) 0.5 mg/ml, displayed an explosion invasion-like behavior within 6 hours, while those in higher collagen concentration (HCC) 2.5 mg/ml were consistently growing over 48 hours, without any invasion like behavior. The migration dynamics of cells in HCC were more fluid-like with lower velocity as compared to the burst-like phenotype in LCC, which showed higher velocity and super diffusive characteristics. We hypothesize that in LCC, spheroids generate an increased pressure due to a volume increase when they fail to engage rigid ECM contacts because of the soft environment. The volume increase then pushed the cells into the soft regions of the ECM, which tends to be inhomogeneous at the LCC. We believe that such mechanical interplay can pave the way to understand migration behavior of cancer cells with respect to their biophysical properties.

Invited Talk BP 1.3 Mon 9:40 BPa

Cyclic Strain Steers Animal Cells — •Rudolf Merkel — Forschungszentrum Jülich, IBI-2 Mechanobiology, 52428 Jülich, Germany

Throughout the organism, all tissue cells experience mechanical strain, e.g. due to the pulsating blood flow. Cells recognize, process, and act upon this signal. To study this mechanoresponse we applied well-defined mechanical strain cyclically to cultivated cells [1]. Cellular mechanoresponses were quantified via reorientation of cytoskeletal fibers. In cultivated endothelial cells we compared responses of actin, microtubules, and vimentin using a correlation-based algorithm and observed distinctly different ordering dynamics and amplitudes [2].

Even though the rigid skull protects the brain, it experiences intense mechanical deformations. Therefore we studied mechanoresponses of primary neurons from cortices of rat embryos. We observed a pronounced reorientation of neuronal dendrites upon cyclic strain and found a surprising mechanical resilience of these cells that survived even several days of uniaxial, cyclic stretching at an amplitude of 28% and a frequency of 300 mHz [3]. Moreover, results on neuronal activity and on the mechanobiology of further cell types of the brain will be shown.

[1] U. Faust et al., PLOS ONE 6, e28963 (2011).
[2] R. Springer et al., PLOS ONE 14, e0210570 (2019)
[3] J.-A. Abraham et al., Langmuir 35, 7423 (2019)

BP 1.4 Mon 10:10 BPa

Elucidating cell mechanics regulators from mechano-transcriptomic data using discriminative network analysis — •Marta Urbanska[1,2], Yan Ge[1], Maria Winzi[1], Shada Abuhattum[1,2], Maik Herbig[1,2], Martin Kräter[1,2], Nicole Töpfner[1], Anna Taubenberger[1], Carlo V. Cannistraci[1], and Jochen Guck[1,2] — [1]BIOTEC, TU Dresden, Dresden, Germany — [2]Max Planck Institute for the Science of Light, Erlangen, Germany

Mechanical properties of cells determine their capability to perform many physiological functions, such as migration, differentiation or circulation through vasculature. Identifying molecular factors that govern the mechanical phenotype is therefore a subject of great interest. Here we present an approach that enables establishing links between mechanical phenotype changes and the genes responsible for driving them. In particular, we employ a discriminative network analysis method termed PC-corr to associate cell mechanical states, measured by real-time deformability cytometry, with large-scale transcriptomic datasets across different biological systems. We obtain a conserved module of five target genes and validate their capacity to discriminate between soft and stiff cell states in silico, obtaining AUC-ROC values of 72-94%. We then show experimentally that the top scoring gene, CAV1, changes the mechanical phenotype of cells when silenced or overexpressed. The data-driven approach presented here has the power of de novo identification of genes involved in cell mechanics, thereby extending the toolbox for tuning the mechanical properties of cells on demand to enable biological function or prevent pathologies.

30 min. Meet the Speaker & coffee break

BP 2: Active Biological Matter I (joint session BP/DY/CPP)

Time: Monday 9:00–11:00 Location: BPb

Invited Talk BP 2.1 Mon 9:00 BPb

The tortoise and hare: how moving slower allows groups of bacteria to spread across surfaces — Oliver Meacock[1,2], Amin Doostmohammadi[3], Kevin Foster[1], Julia Yeomans[1], and •William Durham[1,2] — [1]University of Oxford, United Kingdom — [2]University of Sheffield, United Kingdom — [3]University of Copenhagen, Denmark

Bacteria use tiny grappling hook like appendages called pili to pull themselves across solid surfaces. While pili-based motility has been widely studied in solitary Pseudomonas aeruginosa cells, this species also uses pili to collectively migrate across surfaces when they are densely packed together in a colony. Interestingly, we find genotypes that individually move slower can collectively migrate faster as a group. Using theory developed to study liquid crystals, we demonstrate that this effect is mediated by the physics of topological defects, points where cells with different orientations meet one another. Our analyses reveal that when defects with a topological charge of $+1/2$ collide with one another, the fast-moving mutant cells rotate vertically and become trapped. By moving more slowly, wild-type cells avoid this trapping mechanism, allowing them to collectively migrate faster. Our work suggests that the physics of liquid crystals has played a pivotal role in the evolution of collective bacterial motility by exerting a strong selection for cells that exercise restraint in their movement.

Full paper in Nature Physics available free of charge at: https://rdcu.be/cbcgc

BP 2.2 Mon 9:30 BPb

Light-regulated cell aggregation in confinement — •Alexandros Fragkopoulos[1], Jeremy Vachier[1], Johannes Frey[1], Flora-Maud Le Menn[1], Marco Mazza[1,2], Michael Wilczek[1], David Zwicker[1], and Oliver Bäumchen[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), D-37077 Göttingen, Germany — [2]Department of Mathematical Sciences, Loughborough University, Loughborough, Leicestershire LE11 3TU, United Kingdom — [3]Experimental Physics V, University of Bayreuth, D-95447 Bayreuth, Germany

Photoactive microbes live in complex environments with spatially and temporally fluctuating light conditions. They survive in such habitats by switching their metabolic activity from photosynthesis to aerobic respiration in unfavorable light conditions. We demonstrate that this adaptation in a suspension of soil-dwelling *Chlamydomonas reinhardtii* cells under confinement leads to a spontaneous separation into regions of high and low cell densities. We show that the inhibition of the photosynthetic machinery is necessary but insufficient to generate the observed aggregation. Microfluidic experiments, simulations, and mean-field theory approaches demonstrate that the emergence of microbial aggregations is governed by the oxygen concentration field inside the microhabitat. In fact, in regions where the energy production is completely arrested by both, the photosynthetic and respiratory systems, the cell speed decreases resulting in an aggregation, which thus takes the form of the underline oxygen field.

BP 2.3 Mon 9:50 BPb

Emergent activity of motile phytoplankton in nutrient landscapes — •Jayabrata Dhar, Francesco Danza, Arkajyoti Ghoshal, and Anupam Sengupta — Physics of Living Matter Group, Department of Physics and Materials Science, University of Luxembourg, 162 A, Avenue de la Faencerie, L-1511, Luxembourg City, Luxembourg

Despite their minuscule size, microbes mediate a range of processes in ecology, medicine, and industrial settings that span orders of nutrient concentrations. Yet, to date, we lack a biophysical framework that could link nutrient availability to phytoplankton behavior and predict the impact of dynamic nutrient conditions on motility. Using a combination of micro-scale imaging, microbiology and fluid dynamic models, we quantify how nutrient availability regulates motility, at both individual and population scales [1]. We extract the time-scales over which phytoplankton actively regulate swimming and morphological characteristics, thus shedding light on the finely tuned biophysical mechanisms that equip cells to tackle spatial and temporal heterogeneity of nutrient landscapes. Our results propose local nutrient levels as a handle to control the activity of motile phytoplankton species, promising an exciting model of tunable motile active matter.

[1] Danza, Dhar, Ghoshal and Sengupta (in prep.)

BP 2.4 Mon 10:10 BPb

Chemotaxis strategies of bacteria with multiple run-modes — Zahra Alirezaeizanjani[1,2], •Robert Grossmann[1], Veronika Pfeifer[1], Marius Hintsche[1], and Carsten Beta[1] — [1]Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]Max Planck Institute of Colloids and Interfaces, 14476 Potsdam, Germany

Bacterial chemotaxis – a fundamental example of directional navigation in the living world – is key to many biological processes, including the spreading of bacterial infections. Many bacterial species were recently reported to exhibit several distinct swimming modes – the flagella may, for example, push the cell body or wrap around it. How do the different run modes shape the chemotaxis strategy of a multimode swimmer? Here, we investigate chemotactic motion of the soil bacterium *Pseudomonas putida* as a model organism. By simultaneously tracking the position of the cell body and the configuration of its flagella, we demonstrate that individual run modes show different chemotactic responses in nutrition gradients and thus constitute distinct behavioral states. Based on an active particle model, we demonstrate that switching between multiple run states that differ in their speed and responsiveness provide the basis for robust and efficient chemotaxis in complex natural habitats.

30 min. Meet the Speaker

BP 3: Focus Physics of Stem Cells

Time: Monday 9:00–11:00 Location: BPc

BP 3.1 Mon 9:00 BPc

How Tissue Microenvironment Impacts Pluripotent Cell Differentiation — •Allyson Quinn Ryan[1,2], Diana Alves-Afonso[1], Jacqueline M. Tabler[1], and Carl D. Modes[1,2] — [1]Max Planck Institute for Molecular Cell Biology and Genetics — [2]Center for Systems Biology Dresden

The importance of stem cell population maintenance throughout both development and adulthood has been evident for several decades. Classically, how these populations are regulated is investigated through genetic and cell biological studies. However, work in recent years has shown forces exerted by and through tissue microenvironments to be of equal importance as molecular and transcriptional profiles to cell potency and identity. Here we show that collagen organization and tissue stiffness of the midline suture, a stem cell like niche in the cranial mesenchyme, is distinct from that of adjacent tissues. Surprisingly, Lamin A/C nuclear envelope expression is higher in suture than bone, despite the soft nature of the tissue. When collagen crosslinking is perturbed, Lamin A/C localization patterns, nuclear morphology and neighbor relationships within the suture are significantly altered. These results point towards a framework of noncellular tissue entities and collective organization influencing the maintenance of potency in developmental tissues.

BP 3.2 Mon 9:20 BPc

Robustness and timing of cellular differentiation through population based symmetry-breaking — Angel Stanoev[1], Dhruv Raina[1], Christian Schröter[1], and •Aneta Koseska[2] — [1]Department of Systemic Cell Biology, Max Planck Institute of Molecular Physiology, Dortmund — [2]Cellular computations and learning, caesar, Bonn

During mammalian development, cell types expressing mutually exclusive genetic markers are iteratively differentiated from a multilineage primed state. The current dynamical framework of differentiation, single-cell multistability, however requires that initial conditions in the multilineage primed state are appropriately controlled to result in robust proportions of differentiated fates.

We propose a fundamentally different dynamical treatment in which cellular identities emerge and are maintained on population level, as a novel unique solution of the coupled system. We show that the subcritical organization of such a coupled system close to the bifurcation point enables symmetry-breaking to be triggered by cell number increase in a timed, self-organized manner. Robust cell type proportions are thereby an inherent feature of the resulting inhomogeneous solution. In accordance with this theory, we demonstrate experimentally that a population-based mechanism governs cell differentiation in an embryonic stem cell model for an early lineage decision of mammalian embryogenesis. Our results therefore suggest that robustness and accuracy can emerge from the cooperative behavior of growing cell populations during development.

BP 3.3 Mon 9:40 BPc

Inference of emergent spatio-temporal processes from single-cell sequencing reveals feedback between de novo DNA methylation and chromatin condensates — •Fabrizio Olmeda[1], Tim Lohoff[2], Stephen Clark[2], Laura Benson[2], Felix Krueger[2], Wolf Reik[2,3], and Steffen Rulands[1,4] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]The Babraham Institute, Cambridge, UK — [3]University of Cambridge, Cambridge, UK — [4]Center for Systems Biology Dresden, Dresden, Germany

Recent breakthroughs in single-cell genomics allow probing molecular states of cells with unprecedented detail along the sequence of

the DNA. Biological function relies, however, on emergent processes in the three-dimensional space of the nucleus, such as droplet formation through phase separation. Here, we use single-cell multi-omics sequencing to develop a theoretical framework to rigorously map epigenome profiling along the DNA sequence onto a description of the emergent spatial dynamics in the nucleus. We show how DNA methylation patterns of the embryonic genome are established through the interplay between spatially correlated DNA methylation and topological changes to the DNA. This feedback leads to the predicted formation of condensates of methylated DNA. Our work provides a general framework of how mechanistic insights into emergent processes underlying cell fate decisions can be gained by the combination of single-cell multi-omics and methods from theoretical physics.

BP 3.4 Mon 10:00 BPc

Competition for stem cell fate determinants as a mechanism for tissue homeostasis — •David J. Jörg[1,2], Yu Kitadate[3,4], Shosei Yoshida[3,4], and Benjamin D. Simons[1,2,5] — [1]Cavendish Laboratory, University of Cambridge, Cambridge CB3 0HE, UK — [2]Gurdon Institute, University of Cambridge, Cambridge CB2 1QN, UK — [3]Division of Germ Cell Biology, National Institute for Basic Biology, National Institutes of Natural Sciences, Okazaki, Japan — [4]Department of Basic Biology, School of Life Science, Graduate University for Advanced Studies (Sokendai), Okazaki, Japan — [5]Department of Applied Mathematics and Theoretical Physics, Centre for Mathematical Sciences, University of Cambridge, Wilberforce Road, Cambridge CB3 0WA, UK

Stem cells maintain tissues by generating differentiated cell types while simultaneously self-renewing their own population. The mechanisms that allow stem cell populations to control their density, maintain robust homeostasis and recover from injury remain elusive. Motivated by recent experimental advances, here we develop a robust mechanism of stem cell self-renewal based on competition for diffusible fate determinants. We show that the mechanism is characterized by signature dynamic and statistical properties, from stem cell density fluctuations and transient large-scale oscillation dynamics during recovery, to scaling clonal dynamics and front-like boundary propagation. We suggest that competition for fate determinants provides a generic mechanism by which stem cells can self-organize to achieve density homeostasis in an open niche environment.

30 min. Meet the Speaker

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

BP 5: Active Biological Matter II (joint session BP/CPP/DY)

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

BP 5.1 Mon 11:00 BPb

Chiral stresses in nematic cell monolayers — •Ludwig A. Hoffmann[1], Koen Schakenraad[1,2], Roeland M. H. Merks[2,3], and Luca Giomi[1] — [1]Instituut-Lorentz, Leiden University, The Netherlands — [2]Mathematical Institute, Leiden University, The Netherlands — [3]Institute of Biology, Leiden University, The Netherlands

Recent experiments on monolayers of spindle-like cells have provided a convincing demonstration that certain types of collective phenomena in epithelia are well described by active nematic hydrodynamics. While recovering some of the predictions of this framework, however, these experiments have also revealed unexpected features that could be ascribed to the existence of chirality over length scales larger than the typical size of a cell.

We elaborate on the microscopic origin of chiral stresses in nematic cell monolayers and investigate how chirality affects the motion of topological defects, as well as the collective motion in stripe-shaped domains. We find that chirality introduces a characteristic asymmetry in the collective cellular flow, from which the ratio between chiral and non-chiral active stresses can be measured. Furthermore, we find that chirality changes the nature of the spontaneous flow transition under confinement and that, for specific anchoring conditions, the latter has the structure of an imperfect pitchfork bifurcation.

BP 5.2 Mon 11:20 BPb

Developmentally driven self-assembly of living chiral crystals — •Alexander Mietke[1], Tzer Han Tan[2], Hugh Higinbotham[2], Yuchao Chen[2], Peter Foster[2], Shreyas Gokhale[2], Jörn Dunkel[1], and Nikta Fakhri[2] — [1]Department of Mathematics, Massachusetts Institute of Technology, Cambridge, MA — [2]Department of Physics, Massachusetts Institute of Technology, Cambridge, MA

The emergent dynamics exhibited by self-organizing collections of living organisms often shows signatures of symmetries that are broken at the single-organism level. At the same time, early organism development itself is accompanied by a sequence of symmetry breaking events that eventually establish the body plan. Combining these key aspects of collective phenomena and embryonic development, we describe here the spontaneous formation of hydrodynamically stabilized active crystals made of hundreds of starfish embryos during early development. As development progresses and embryos change morphology, crystals become increasingly disordered and eventually stop forming. We show that these structures exhibit distinct macroscopic chiral features as a direct consequence of the embryo's chiral swimming properties. We introduce a hydrodynamic near-field model that quantitatively describes the formation and rotation of crystals, as well as the emergence of long-lived chiral deformation waves, all of which can be understood as consequences of broken symmetries on the single-embryo level.

BP 5.3 Mon 11:40 BPb

Thin-Film Model of Resting and Moving Active Droplets — •Fenna Stegemerten[1], Sarah Trinscheck[1,2], Karin John[2], and Uwe Thiele[1,3] — [1]Institut für Theoretische Physik, Westfälische Wilhelms-Universität Münster, Münster, Germany — [2]Université Grenoble-Alpes, CNRS Laboratoire Interdisciplinaire de Physique, Grenoble, France — [3]Center for Nonlinear Science (CeNoS), Westfälische Wilhelms-Universität Münster, Münster, Germany

We propose a long-wave model for free-surface drops of polar active liquid on a solid substrate. The coupled evolution equations for the film height and the local polarization profile are written in the form of a gradient dynamics supplemented with active stresses and fluxes. A wetting energy for a partially wetting liquid is incorporated allowing for motion of the liquid-solid-gas contact line. This gives a consistent basis for the description of drops of dense bacterial suspensions or compact aggregates of living cells on solid substrates. As example, we analyze the dynamics of active drops and demonstrate how active forces compete with passive surface forces to shape droplets and drive contact line motion. We perform parameter continuation in the activity parameters discussing both, resting and moving droplets. Additional direct time simulations investigate transitions from non-uniformly to uniformly polarized as well as resting to moving states.

BP 5.4 Mon 12:00 BPb

Sedimentation and Convection of Bottom-Heavy Squirmers — •Felix Rühle, Jan-Timm Kuhr, and Holger Stark — TU Berlin, Institut für Theoretische Physik, Berlin, Germany

Active particles form appealing patterns, in particular, when hydrodynamic interactions are present [1-3]. A fascinating example known from biology is bioconvection of microswimmers under gravity [4]. In order to study such systems, we simulate bottom-heavy squirmers (neutral squirmers, pushers, and pullers) under different gravitational forces and torques [3]. The relevant parameters are the ratio of swimming to bulk sedimentation velocity α and the normalized torque.

In the state diagram of these parameters, for neutral squirmers at low α we observe sedimentation states, where bottom-heaviness leads to the formation of clusters of different sizes. For high α, finite torques lead to inverted sedimentation. In between, we identify plumes of collectively sinking squirmers that feed convective rolls of circling squirmers at the bottom of the simulation cell. At $\alpha \gtrapprox 1$ and large torques squirmers form a spawning cluster above the wall, from which squirmers occasionally escape. For strong pushers and pullers, we find that the dipolar flow fields weaken the formation of plumes and convective rolls.

[1] M. Hennes, *et al.*, PRL **112**, 238104 (2014)
[2] H. Jeckel, *et al.*, PNAS **116**, 1489 (2019).
[3] F. Rühle, and H. Stark, Eur. Phys. J. E **43**, 26 (2020).
[4] T.J. Pedley, and J.O. Kessler, Annu. Rev. Fluid Mech. **24**, 313 (1992).

BP 5.5 Mon 12:20 BPb

Microscopic scattering of pusher particles in complex environments — •Theresa Jakuszeit[1], Samuel Bell[2], and Ottavio A. Croze[1] — [1]Cavendish Laboratory, JJ Thomson Avenue, CB3 0HE, Cambridge, United Kingdom — [2]Laboratoire Physico Chimie Curie, Institut Curie,PSL Research University, CNRS UMR168, 75005 Paris, France

Active propulsion as performed by bacteria and Janus particles, in combination with hydrodynamic interaction at boundaries, can lead to the breaking of time reversibility. One typical example of this is the accumulation of bacteria on a flat wall. However, in microfluidic devices with cylindrical pillars of sufficiently small radius, self-propelled particles can slide along the surface of a pillar without becoming trapped over long times. This non-equilibrium scattering process can result in large diffusivities even at high obstacle density, unlike particles that undergo classical specular reflection, as in the Lorentz gas. We experimentally study the non-equilibrium scattering as well as the long-term diffusive transport of pusher-like particles by tracking wild-type and smooth-swimming mutants of the model bacterium Escherichia coli in microfluidic obstacle lattices. We relate the determined parameters of the scattering process to previously proposed models and discuss their relevance. Finally, we discuss the potential interpretation of the role of tumbles in the scattering process.

BP 5.6 Mon 12:40 BPb

Swimming behavior of squirmer dumbbells and polymers — •Judit Clopés Llahí, Gerhard Gompper, and Roland G. Winkler — Theoretical Soft Matter and Biophysics, Institute for Advanced Simulation and Institute of Complex Systems, Forschungszentrum Jülich, D-52425 Jülich, Germany

Nature provides a plethora of microswimmers, which can be rather elongated, filament- or polymer-like. Examples are bacteria swarmer cells or marine phytoplankton dinoflagellates assembling in a linear fashion. In order to address the relevance of hydrodynamic interactions for the collective behavior of such organisms, we study the swimming properties of linear polymer-like assemblies by mesoscale hydrodynamic simulations, where an active unit (monomer) is described by a spherical squirmer – which can be a pusher, a neutral swimmer, or a puller. We find that the monomer hydrodynamic flow field leads to correlations in the relative orientation of adjacent monomers, and consequently the swimming efficiency differs from that of active Brownian linear assemblies. In particular, puller dumbbells and chains show a pronounced increase in the rotational diffusion coefficient compared to pushers, while for neutral squirmers, the rotational diffusion coefficient is similar to that of active Brownian particles. Hence, the large-scale conformational and dynamical properties depend on the specific propulsion mechanism. Refs.: J. Elgeti, R. G. Winkler, G. Gompper, Rep. Prog. Phys. 78, (2015). R. G. Winkler, J. Elgeti, G. Gompper, J. Phys. Soc. Jpn. 86, (2017). J. Clopés, G. Gompper, R. G. Winkler, Soft Matter 16, 10676 (2020).

30 min. Meet the Speaker

BP 6: Systems Biology I

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

BP 6.1 Mon 11:00 BPc

Ligation Chain Reactions in Non-Equilibrium Convection Compartments with Microscale pH Cycles — •Annalena Salditt, Dieter Braun, Patrick Kudella, and Leonie Karr — Ludwig-Maximilians-Universität

Early replication mechanisms for the origin of life rely on periodic strand separation to start new rounds of replication necessary to stabilize and accumulate information of long nucleic acids. Especially for catalytically active RNAs, high temperatures required for strand separation promote their hydrolysis, leading to a loss of information. Therefore, a geophysical non-equilibrium environment on early Earth would have required means to separate hybridized strands after replication and to localize long, potentially functional molecules against diffusion while protecting them from hydrolysis. We perform ligation extension experiments in moderate temperature gradients across micrometer thick, water-filled chambers with a water-CO2 interface to induce a miniaturized water cycle while maintaining thermophoretic trapping conditions. In addition to more realistic early atmospheric conditions of the Earth, the CO2-water interface causes periodic pH changes, that induce the hybridization of double strands. We expect this to be a promising autonomous setting for ligation chain reactions starting from a random or semi-random oligomer pool.

BP 6.2 Mon 11:20 BPc

The effects of cross-species gene transfer on genome dynamics — •Mona Förster[1], Isabel Rathmann[1], Jeffrey Power[2], Melih Yüksel[1], and Berenike Maier[1] — [1]Universität zu Köln, Deutschland — [2]Universität Tübingen, Deutschland

Phylogenetic studies have provided strong evidence that gene transfer happens frequently and acts across species. However, the rate at which gene transfer occurs and its short-term effect on genome dynamics are poorly understood. To address the effect of intra- and inter-species gene transfer on genome dynamics we developed an evolution experiment and analysis method to detect horizontal gene transfer. To investigate mechanistic contributions to gene transfer probability, we ensured minimal selection by not allowing for population dynamics. We were able to detect a remarkably high gene transfer rate of 0.4 $\%h^{-1}$ across subspecies of *Bacillus subtilis*. This rate was four times lower when gene transfer was probed between *B. subtilis* and *Bacillus vallismortis* and 125 times lower between *B. subtilis* and *Bacillus atrophaeus*. Interestingly, the average sequence divergence of integrated segments is comparable between all three donors with a mean of about 7 %. We observed that the fraction of replaced genome increases linearly throughout 40 h of DNA uptake, which suggests that transfer of genes, is not yet saturated and could be probed further in evolutionary runs. Following up on this, it will be interesting to use the fitness distribution of the minimal selection replicates to design an evolution experiment with strong selection.

BP 6.3 Mon 11:40 BPc

Genetically engineered control of phenotypic structure in microbial colonies — •Philip Bittihn[1,4], Andriy Didovyk[1,5], Lev S. Tsimring[1], and Jeff Hasty[1,2,3] — [1]BioCircuits Institute — [2]Department of Bioengineering — [3]Molecular Biology Section, Division of Biological Sciences, University of California, San Diego, La Jolla, CA, USA — [4]Department of Living Matter Physics, Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [5]Vertex Pharmaceuticals, San Diego, California, USA

Many essential biological behaviors originate from an entanglement of biological (cellular) and physical processes. This is a challenge not only for traditional biology and physics methodology, but also for synthetic biology, where such interactions severely limit the ability to engineer desired behavior with artificial gene regulatory networks. We show how to achieve control of phenotypic structure in bacterial microcolonies by simultaneously exploiting internal gene expression and metabolism, as well as physical coordination through nutrient diffusion and growth, which leads to self-generated nutrient gradients and a heterogeneous population consisting of both dividing and dormant cells. In microfluidic experiments and a mathematical model, we show that gene circuits which sense and control growth can create a spatio-temporal feedback loop via nutrient transport and generate sustained growth oscillations, while a phenotype-specific lysis circuit can selectively eliminate dormant cells. Our results demonstrate how to understand and control multicellular substrates as complex active physical systems.
Reference: *Nature Microbiology* **5**, 697–705 (2020)

BP 6.4 Mon 12:00 BPc

Dynamics, Statistics and Coding in Random Rate and Binary Networks — •Tobias Kühn[1,2,3], Christian Keup[2,3], David Dahmen[2], and Moritz Helias[2,3] — [1]MSC de l'Université de Paris, ENS, CNRS, Paris, France — [2]INM-6, Forschungszentrum Jülich, Ger-

many — [3]Department of Physics, RWTH Aachen, Germany

Cortical neurons communicate with spikes, discrete events in time. Functional network models often employ rate units that are continuously coupled by analog signals. Is there a benefit of discrete signaling? By a unified mean-field theory for large random networks of rate and binary units, we show that both models can be matched to have identical statistics up to second order. Their stimulus processing properties, however, are different: contrary to rate networks, the chaos transition in binary networks strongly depends on network size, and we discover a chaotic submanifold in binary networks that does not exist in rate models. Its dimensionality increases with time after stimulus onset and reaches a fixed point that depends on the synaptic coupling strength. Low-dimensional stimuli are transiently expanded into higher-dimensional representations that live within the manifold. We find that classification performance first increases and then degrades due to variability in the manifold. During this transient, resilience to noise by far exceeds that of rate models with matched statistics, which are always regular. In their respective chaotic regime, however, rate networks show similar a mechanism of transient signal amplification, same for spiking networks [Keup et al. arXiv:2002.11006]. Ack.: Helmholtz assn. (VH-NG-1028); RWTH (ERS seed fund neuroIC002).

BP 6.5 Mon 12:20 BPc

Long-range and rapid signalling gradient formation by cell-to-cell relay — •Johanna Dickmann[1], Jochen Rink[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute for Biophysical Chemistry, Göttingen, Germany

Development, regeneration and tissue renewal are spectacular tissue patterning events. Tissue patterning, the adaptation of the correct cell fate at the correct position, requires information. This information can be provided by spatially graded distributions of signalling molecules, called signalling gradients. While the formation of signalling gradients is thought to result from diffusion and degradation in the context of embryonic development, it remains controversial how such signalling gradients can be generated on long length scales e.g. during regeneration. We introduce a relay mechanism for gradient formation in which the signal is propagated from cell to cell via a positive feedback loop. That is, each cell produces signalling molecules in response to receiving a signal. We show that polarised secretion of signalling molecules produced in response to the received signal results in an effective drift of signalling molecule concentration through the system, markedly accelerating the formation of signalling gradients. This way, the relay mechanism explains gradient formation on millimetre length scales within hours to days for physiological parameter choices.

BP 6.6 Mon 12:40 BPc

Model for inference of cell dynamics from C14 data — •Julian Rode[1], Fabian Rost[2], Paula Heinke[1], Enikö Lazar[3], Lutz Brusch[1], and Olaf Bergmann[1] — [1]Technische Universität Dresden, Dresden, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Karolinska Institutet, Stockholm, Sweden

Carbon dating is an established method to determine the age of ancient artefacts. Traditionally, radioactive decay changes the C14 ratio of the sample which can be used to determine the age. Recently, a second route has become available as the drastic change of atmospheric C14 due to atomic bomb tests in the 60's allows to invert this classic C14 dating method. Now, the C14 decay is negligible, but the atmospheric C14 changes quickly, allowing an accurate age measurement even of human samples. This method allows to estimate the cell turnover in vivo using the C14 carbon ratio of the DNA from many cells. But a simple matching of C14 values is not sufficient because the measured C14 values are the average of cells with different ages. We introduce a C14-structured population model to predict the average C14 content and accounting for cell division, cell inflow from a fast cycling stem cell population and cell death. Additionally, a priori knowledge such as tissue growth has to be considered resulting in constrains for the model solution. We use variations of this model to analyse C14 data from human liver and muscle tissue.

30 min. Meet the Speaker

BP 7: Cell Mechanics III

Time: Monday 14:00–16:30 Location: BPa

BP 7.1 Mon 14:00 BPa

Highly Reproducible Physiological Asymmetric Membrane with Freely Diffusing Embedded Proteins in a 3D Printed Microfluidic Setup — Paul Heo[1], Sathish Ramakrishnan[1,2], Jeff Coleman[2], James E. Rothman[2], •Jean Baptiste Fleury[3], and Frederic Pincet[1] — [1]Laboratoire de Physiqe Statistique ENS, Paris, France — [2]Department of Cell Biology Yale School of Medicine, New Haven, USA — [3]Department of Experimental Physics and Center for Biophysics, Saarland University Saarbruecken, Germany

Experimental setups to produce and to monitor model membranes have been successfully used for decades and brought invaluable insights into many areas of biology. However, they all have limitations that prevent the full in vitro mimicking and monitoring of most biological processes. Here, a suspended physiological bilayer-forming chip is designed from 3D-printing techniques. This chip can be simultaneously integrated to a confocal microscope and a path-clamp amplifier. The bilayer, formed by the zipping of two lipid leaflets, is free-standing, horizontal, stable, fluid, solvent-free, and flat with the 14 types of physiologically relevant lipids, and the bilayer formation process is highly reproducible. Furthermore, different proteins family can be added to the bilayer in controlled orientation and keep their native mobility and activity. These features allow in vitro recapitulation of membrane process close to physiological conditions, as shown in the following references: Small, 2019, 10.1002/smll.201900725 Advanced Materials, 2020, 10.1002/adma.202070389 PNAS, 2021 (in press)

BP 7.2 Mon 14:20 BPa

Tracking Electrostatically Driven Membrane Transfer between Lipid Vesicles and a Supported Lipid Bilayer on a QCM — •Justus Bednár[1,2], Anastasia Svetlova[1,2], Vanessa Maybeck[1], and Andreas Offenhäusser[1] — [1]Forschungszentrum Jülich, Institute of Biological Information Processing: Bioelectronics (IBI-3) — [2]Fakultät für Mathematik, Informatik und Naturwissenschaften RWTH Aachen

Lipid bilayer systems are used widely in medicine and biotechnology. Supported lipid bilayers (SLBs) for example, can be employed as a biomimetic platform for cell cultures or can be studied as a model system of the cell membrane itself. If SLB and lipid vesicles have opposite surface charges, their electrostatic interaction can be used to modify the lipid composition of the SLB. Studying the underlying process, the quartz crystal microbalance (QCM) stands out for its ability to precisely monitor the acoustic response of a macroscopic SLB and coupled objects with a sub-second time resolution. Unfortunately, standard models that relate the QCM signal response to physical properties of the sample do not apply in this case.

Here, a viscoelastic model for an ensemble of lipid vesicles, coupled to an SLB, is presented. Experimental results demonstrate the capability of this model to estimate relative concentrations of extracellular vesicles (EVs) in bulk solution. Furthermore, throughout numerous experiments of electrostatically driven membrane transfer between lipid vesicles and an SLB, a non-trivial time-dependence of vesicle-adsorption is observed.

Invited Talk BP 7.3 Mon 14:40 BPa

Towards the mechanical characterization of neuronal network formation — Paulina Wysmolek[2], Florian Huhnke[2], Katja Salbaum[1], Joachim Spatz[2], and •Friedhelm Serwane[1,2] — [1]LMU, Department of Physics, Munich — [2]Max Planck Institute for Medical Research, Heidelberg

In recent years, researchers have engineered multicellular 3D systems, organoids, which share the same cell types and tissue organization as their in vivo counterparts. Those in vitro models provide an opportunity to glimpse at how biology self-assembles neuronal networks and how nanoscale building blocks, such as cell-cell adhesion molecules, contribute to the formation of tissue shape, structure and function. In this talk I will present the current and future research of our newly

established ERC-group. We will explore, how tissue mechanical properties affect the formation and function of retina organoids. For this, we build on our expertise in mechanics measurements (1,2) and retina organoid technology. Quantifying the mechanics of neuronal systems opens the door to neurodegenerative disease modeling as it will be performed by our group. In addition, it allows developing a biophysical understanding how neuronal networks are initially formed.

(1) Serwane et al., In vivo quantification of spatially-varying mechanical properties in developing tissues. Nature Methods, 2017

(2) Mongera et al., A fluid-to-solid jamming transition underlies vertebrate body axis elongation. Nature, 2018

BP 7.4 Mon 15:10 BPa

Lattice defects induce microtubule self-renewal — Laura Schaedel[1], Sarah Triclin[1], Denis Chrétien[2], Ariane Abrieu[3], Charlotte Aumeier[1], Jérémie Gaillard[1], Laurent Blanchoin[1,4], Manuel Théry[1,4], and •Karin John[5] — [1]Univ. Grenoble-Alpes, CEA, CNRS, INRA, Biosciences & Biotechnology Institute of Grenoble, Laboratoire de Physiologie Cellulaire & Végétale, CytoMorpho Lab, 38054 Grenoble, France — [2]Univ. Rennes, CNRS, IGDR (Institute of Genetics and Development of Rennes) - UMR 6290, F-35000 Rennes, France — [3]CRBM, CNRS, University of Montpellier, Montpellier, France — [4]Univ. Paris Diderot, INSERM, CEA, Hôpital Saint Louis, Institut Universitaire d'Hematologie, UMRS1160, CytoMorpho Lab, 75010 Paris, France — [5]Univ. Grenoble-Alpes, CNRS, Laboratoire Interdisciplinaire de Physique, 38000 Grenoble, France

Microtubules are dynamic polymers, which grow and shrink at their extremities. Within the microtubule shaft, tubulin dimers adopt a highly ordered lattice structure, which is generally not considered to be dynamic. Here we report a new aspect of microtubule dynamics, whereby thermal forces are sufficient to remodel the lattice, despite its apparent stability. Our combined experimental data and numerical simulations on lattice dynamics and structure demonstrate that dimers can spontaneously leave and be incorporated into the lattice at structural defects. We propose a model mechanism, where the lattice dynamics is initiated via a passive breathing mechanism at dislocations, which are frequent in rapidly growing microtubules.

BP 7.5 Mon 15:30 BPa

Multiplication of gliding microtubules for biocomputational applications — •Cordula Reuther[1], Paula Santos Otte[1], Rahul Grover[1], Till Korten[1], Günther Woehlke[3], and Stefan Diez[1,2] — [1]B CUBE, TU Dresden, Dresden, Germany — [2]Cluster of Excellence Physics of Life, TU Dresden, 01062 Dresden, Germany — [3]Department of Physics, TU München, Garching, Germany

Recently, an approach to solve combinatorial problems was demonstrated by kinesin-1 driven microtubules exploring, as autonomous agents, physical networks of nanometer-sized channels [Nicolau et al., PNAS, 113(10), 2016]. The possibility to multiply the agents exponentially while traversing such networks is crucial for the scalability of these systems. We developed a method for the multiplication of microtubules gliding on surface-immobilized kinesin-1 and kinesin-14 molecules, respectively. Specifically, our method comprises two simultaneously proceeding processes: (1) elongation of microtubules by self-assembly of tubulin dimers and (2) cutting of microtubules by the severing enzyme spastin. The main challenge in doing so is to optimize both processes such that the average length of the filaments stays roughly constant over time while the number of filaments increases exponentially. Additionally, nucleation of new filaments ought to be avoided in order to prevent errors in the calculations performed by the microtubules. Thus, we first studied each of the two processes separately under various conditions before combining the optimized protocols to actually multiply microtubules. Finally, we aim to multiply microtubules in a physical network with channel structures.

40 min. Meet the Speaker

BP 8: Bioimaging and Biospectroscopy

Time: Monday 14:00–16:30 Location: BPb

BP 8.1 Mon 14:00 BPb

Near Infrared Fluorescence Imaging with Carbon nanotubes and Nanosheets — •Sebastian Kruss — Ruhr-Universität Bochum, Germany

We are interested in 1D and 2D materials that provide novel photophysical properties such as near Infrared (NIR) fluorescence. The NIR range (800-1700 nm) of the spectrum is beneficial for many optical applications because it falls into the tissue transparency window. One example of such a material is semiconducting single-walled carbon nanotubes (SWCNTs). SWCNTs fluoresce in the NIR and their optoelectronic properties are very sensitive to changes in the chemical environment and they are therefore versatile building blocks for fluorescent labels and sensors. In my talk I will show fundamental insights into SWCNT photophysics/surface chemistry and how selectivity of SWCNT-based fluorescent sensors can be enhanced. These sensors can be used for multiscale imaging to resolve single molecules such as kinesin motors in vivo, efflux of neurotransmitters (dopamine, serotonin) from cells, identification of pathogens or stress in whole plants. Furthermore, I introduce a novel class of ultrabright 2D NIR fluorescent silicate nanosheets and demonstrate in vivo particle tracking as well as standoff detection in living plants.

BP 8.2 Mon 14:20 BPb

Motion-based segmentation for particle tracking: A fully-convolutional neuronal network that analyses movement — •Till Korten[1], Walter de Back[2], Christoph Robert Meinecke[3], Danny Reuter[3,4], and Stefan Diez[1] — [1]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, Dresden, Germany — [2]Institute for Medical Informatics and Biometry (IMB), Carl Gustav Carus Faculty of Medicine, Technische Universität Dresden, Dresden, Germany — [3]Center for Microtechnologies, TU-Chemnitz, Chemnitz, Germany — [4]Fraunhofer Institute for Electronic Nanosystems (ENAS), Chemnitz, Germany

For single-particle tracking it is often necessary to separate particles of interest from background particles based on their movement pattern. Here we introduce a deep neuronal network that employed convolutional long-short-term-memory layers in order to be able to perform image segmentation based on the motion pattern of particles. Training was performed with ≈ 500 manually annotated 128x128 pixel frames. The segmentation result was used as input for a conventional single particle tracking algorithm. With this workflow 100% of all tracks belonged to microtubules that were propelled by kinesin-1 motor proteins along guiding channels and no tracks belonged to microtubules diffusing in the background. Furthermore, microtubules moving in a different orientation than the guiding channels during training, did not show up during inference. In conclusion, the deep-learning-based tracking resulted in almost twice as many (2800 vs. 1500) usable tracks that were 35 % longer compared to filtering after tracking.

BP 8.3 Mon 14:40 BPb

Molecule counts in complex oligomers with single-molecule localization microscopy — Tim Niklas Baldering[1], •Jakob Tómas Bullerjahn[2], Gerhard Hummer[2], Mike Heilemann[1], and Sebastian Malkusch[1] — [1]Institute of Physical and Theoretical Chemistry, Goethe-University Frankfurt, Frankfurt am Main, Germany — [2]Department of Theoretical Biophysics, Max Planck Institute of Biophysics, Frankfurt am Main, Germany

Single-molecule localization microscopy resolves nano-scale protein clusters in cells, and in addition can extract protein copy numbers from within these clusters. A powerful approach for such molecular counting is the analysis of fluorophore blinking using stochastic model functions. Here, we develop a theoretical model for quantitative analysis of photoactivated localization microscopy (PALM) data that accounts for the detection efficiency. By this, we are able to extract populations of different oligomers reliably and in complex mixtures. We demonstrate this approach analyzing simulated PALM data of a photoactivatable fluorescent protein. We generate simulations of blinking data of oligomers and of mixtures of oligomers, and show robust oligomer identification. In addition, we demonstrate this approach for experimental PALM data. https://doi.org/10.1088/1361-6463/ab3b65

BP 8.4 Mon 15:00 BPb

Dissection of Plasmodium falciparum developmental stages with multiple imaging methods — •Katharina Preissinger[1,2], Beáta Vértessy[1,2], István Készmárki[3,4], and Miklós Kellermayer[5] — [1]Department of Applied Biotechnology and Food Sciences, BME, Budapest, Hungary — [2]Institute of Enzymology, Research Center for Natural Sciences, Budapest, Hungary — [3]Department of Physics, BME, Budapest, Hungary — [4]Department of Experimental Physics V, University of Augsburg, Germany — [5]Department of Biophysics and Radiation Biology, Semmelweis University, Budapest, Hungary

Efficient malaria treatment is a global challenge, requiring in-depth insight into the maturation of malaria parasites during the intraerythrocytic cycle. Exploring structural and functional variations of the parasites and their impact on red blood cells (RBCs) is a cornerstone of antimalarial drug development. In order to trace such changes in fine steps of parasite development, we performed an imaging study of RBCs infected by Plasmodium falciparum, using atomic force microscopy (AFM) and total internal reflection fluorescence microscopy (TIRF), further supplemented with bright field microscopy for the direct assignment of the stages. This multifaceted imaging approach allows to reveal correlations of the parasite maturation with morphological and fluorescence properties of the stages. We established identification patterns characteristic to the different parasite stages based on the height profile of infected RBCs which show close correlation with typical fluorescence (TIRF) maps of RBCs.

BP 8.5 Mon 15:20 BPb

Self-organization of endoplasmic reticulum exit sites — •Konstantin Speckner, Lorenz Stadler, and Matthias Weiss — Experimentalphysik 1, Universität Bayreuth

The endoplasmic reticulum (ER) is a highly dynamic organelle that pervades the entire cell and hosts a variety of vital processes. For example, the exchange of proteins with the secretory pathway occurs at specialized and long-lived membrane domains, called ER exit sites (ERES). In mammalian cells, ERES form protein assemblies that emerge as a lattice-like arrangement of dispersed droplets on the ER membrane. Although ERES were seen to diffuse on short timescales, they appear stationary on longer periods. Notably, their dynamics is different from the cytoskeleton-dependent, shivering motion of ER tubules. To gain insights into the self-organization of ERES patterns, we have studied biochemical perturbations on the morphology of the ER and analyzed the spatial arrangement of ERES by quantitative fluorescence imaging. As a result, we found a significantly changed patterns of ERES components when reducing the amount of curvature-inducing membrane proteins. In contrast, disrupting the ER network into fragments or affecting the cytoskeletons integrity had only mild effects on the ERES patterns. Our findings can be well explained by modelling ER junctions as diffusion barriers for the exchange of ERES protein constituents. Altogether, we provide evidence that the native ERES patterns are the result of a quenched fluctuation-driven two-dimensional demixing process.

BP 8.6 Mon 15:40 BPb

A multisensory interface for exploring nanomechanical tissue properties with human senses — •Robert Magerle, Paul Zech, Martin Dehnert, Alexandra Bendixen, and Andreas Otto — Fakultät für Naturwissenschaften, TU Chemnitz

Tissues display a complex spatial structure and their mechanical properties remain largely unexplored on the nanometer scale. Here we present a multisensory interface that makes nanomechanical tissue properties accessible to human perception and cognition. With a haptic device, we translate the 3D force fields measured with an atomic force microscope (AFM) on the nanometer scale into forces perceivable to humans. This allows human users to explore haptically the specimen's surface shape as well as its local nanomechanical properties while simultaneously employing multiple senses. First tissues studied include native (unfixed), hydrated tendon of sheep, chickens, and mice. AFM imaging in air with controlled humidity preserves the tissue's water content and allows for high-resolution imaging. The force-vs.-distance (FD) data measured with the AFM display a rate-independent hysteresis with return-point memory. A generic hysteresis model that uses FD data collected during one approach-retract cycle predicts the force (output) for an arbitrary indentation trajectory (input). We implemented this hysteresis model with a haptic device which allows human users to perceive a physically plausible tip–sample interaction. They can discriminate the specimen's local hardness, its elastic response, as well as the energy dissipation due to the rate-independent hysteretic process.

30 min. Meet the Speaker

BP 9: Systems Biology II

Time: Monday 14:00–16:30 Location: BPc

Invited Talk BP 9.1 Mon 14:00 BPc

From individual to collective intermittent motion: from bacteria to sheep — •Fernando Peruani — CY Cergy Paris University, Cergy, France

Intermittent behavior is observed in biological systems at all scales, from bacterial systems to sheep herds. First, I will discuss how Escherichia coli explores surfaces by alternating stop and moving phases. Specifically, I will show that a stochastic three behavioral state model is consistent with the empirical data. The model reveals that the stop frequency of bacteria is tuned at the optimal value that maximizes the diffusion coefficient. These results provide a new perspective on how evolution may have reshaped the bacterial motility apparatus. Intermittent motion is also observed in Merino sheep, where again a stochastic three behavioral state model provides a quantitative understanding of the empirical data. However, in sheep, individual transition rates depend on the behavioral state of other individuals and collective behaviors emerge. Specifically, I will show that small sheep herds display highly synchronized intermittent collective motion, with the herd behaving as a self-excitable system. Based on the analysis of these two biological systems (bacteria and sheep), we will discuss the need of three behavioral states to describe intermittent motion in biological systems, providing a unified picture of such behavior across scales.

Refs.: Perez Ipina et al. Nature Physics 15, 610-615 (2019); Gascuel et al. Animal behavior (2021); Gomez Nava et al. (2021)

BP 9.2 Mon 14:30 BPc

Specialisation and plasticity in a primitive social insect — •Adolfo Alsina[1], Solenn Patalano[2], Martin Bachman[3], Irene Gonzalez-Navarrete[4], Stephanie Dreier[5], Shankar Balasubramanian[3], Seirian Sumner[5], Carlos Gregorio-Rodriguez[6], Wolf Reik[2], and Steffen Rulands[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]The Babraham Institute, Cambridge, UK — [3]University of Cambridge, Cambridge , UK — [4]Centre for Genomic Regulation (CRG), Barcelona , Spain — [5]Institute of Zoology, London , UK — [6]Universidad Complutense de Madrid (UCM), Madrid, Spain

Biological systems not only have the remarkable capacity to build and maintain complex spatio-temporal structures in noisy environments, they can also rapidly break up and rebuild such structures. How can such systems can simultaneously achieve both robust specialisation and plasticity is poorly understood. Here we use primitive societies of Polistes wasps as a model system where we experimentally perturb the social structure by removing the queen and follow the relaxation dynamics back to the social steady state over time. We combine a unique experimental strategy correlating measurements across vastly different spatial scales with a theoretical approach. We show that Polistes integrates antagonistic processes on multiple scales to distinguish between extrinsic and intrinsic perturbations and thereby achieve both robust specialisation and rapid plasticity. Such dynamics provide a general principle of how both specialization and plasticity can be achieved in biological systems.

BP 9.3 Mon 14:50 BPc

Plasticity in vertex model of epithelial tissues — •Marko Popović[1,2], Valentin Druelle[1,3], Natalie Dye[4,5], Frank Julicher[2,5], and Matthieu Wyart[1] — [1]Institue of Physics, École Polytechnique Fédérale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland — [2]Max Planck Institute for Physics of Complex Systems,

Nöthnitzer Strasse 38, 01187 Dresden, Germany — [3]Biozentrum, University of Basel, Klingelberstrasse 70, 4056 Basel, Switzerland — [4]Max Planck Institute for Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 10307 Dresden, Germany — [5]Cluster of Excellence Physics of Life, TU Dresden, 01307 Dresden, Germany

Developing tissues are often described as viscoelastic liquids. However, tissues can also be plastic and respond elastically to stresses below the critical value, while flowing plastically at higher stresses. Plasticity is exhibited by a wide class of amorphous solids such as colloidal gels, emulsions, and foams where it corresponds to a yielding transition. Are features of yielding transition, such as dependence on system preparation and non-linear rheology, relevant in developing tissues? Motivated by similarities of disordered tissues and amorphous solids we study the plasticity of the vertex model of epithelial tissues, where the mechanical properties of cells are prescribed and tissue mechanics is obtained from their collective behavior. We describe the mechanics of T1 transitions, which are the elementary plastic events in epithelial tissues. We find that interactions between T1 transitions are analogous to those of particle rearrangements in amorphous solids and our simulations suggest that the vertex model belongs to the same class of universality.

BP 9.4 Mon 15:10 BPc

Selection via phase separation — •Giacomo Bartolucci[1,2], Adriana Serrao[3], Philipp Schwintek[3], Alexandra Kühnlein[3], Yash Rana[4], Dieter Braun[3], Christof Mast[3], and Christoph A. Weber[1,2] — [1]Max Planck for the Physics of Complex Systems, Dresden — [2]Center for Systems Biology Dresden — [3]Ludwig Maximilian University, München — [4]Harvard University, Cambridge, USA

Living cells and pre-biotic systems are complex aqueous mixtures composed of thousands of different heteropolymers. In such multicomponent mixtures, enrichment and selection of a small set of components are important to achieve biological function. However, when the number of components increases, each of them becomes more diluted impeding a significant enrichment of selected components. Here, we propose a selection mechanism relevant for prebiotic mixtures based on cycles of phase separation combined with material exchange of the dense phase with a reservoir. We find a selective enrichment of components up to two orders of magnitude coinciding with a growth of the dense phase up to the system volume. Such enrichment of selective components is robust also in mixtures composed of a large number of components. For a prebiotic soup, our findings indicate that cycles of phase separation and material exchange with a reservoir, e.g. the accumulation DNA gel in rock pores periodically filled with DNA rich aqueous solution, could provide a mechanism for the selection and enrichment of specific heteropolymers sequences in a multi-component mixture at the origin of life.

BP 9.5 Mon 15:30 BPc

Towards an alphabet of random matrix models for large biological networks — •Philipp Fleig[1] and Ilya Nemenman[2] — [1]University of Pennsylvania, Philadelphia, USA — [2]Emory University, Atlanta, USA

Biological interaction networks such as populations of neurons or amino acid sequences in proteins are critical to the functioning of any biological system. The trend of modern high-throughput experiments is to record data from a rapidly increasing number of simultaneously measured network units. Such data recorded from a biological network has characteristics of a large random matrix with hidden structures encoded in it. We present first steps towards the design of an alphabet of random matrix models to describe data of biological networks. Here, we focus on how to detect different random matrix structures in data from simple observable quantities such as pairwise correlations and the eigenvalue spectrum of the correlation matrix. Using random matrix theory we show analytically how properties of the data, such as a hidden dimensionality, are encoded in these observables. Finally, we use a neural network classifier with the observables as input to detect different types of random matrix structures in our alphabet and their hidden dimensionality in noisy data of finite size. Our approach can likely be used to model large and complex data of diverse types of biological networks.

40 min. Meet the Speaker

BP 10: Posters DY - Fluid Physics, Active Matter, Complex Fluids, Soft Matter and Glasses (joint session DY/BP)

Time: Monday 14:00–16:30 Location: DYp

BP 10.1 Mon 14:00 DYp

Jerky active matter: a phase field crystal model with translational and orientational memory* — •Michael te Vrugt, Julian Jeggle, and Raphael Wittkowski — Institut für Theoretische Physik, Center for Soft Nanoscience, Westfälische Wilhelms-Universität Münster, D-48149, Münster, Germany

Most field theories for active matter neglect effects of memory and inertia. However, recent experiments have found inertial delay to be important for the motion of self-propelled particles. A major challenge in the theoretical description of these effects, which makes the application of standard methods very difficult, is the fact that orientable particles have both translational and orientational degrees of freedom which do not necessarily relax on the same time scale. In this work, we combine modern mathematical methods from particle physics and nonlinear dynamics to derive the general mathematical form of a field theory for soft-matter systems with two different time scales. This allows to obtain a phase field crystal model for polar (i.e., nonspherical or active) particles with translational and orientational memory. Notably, this theory is of third order in temporal derivatives and can thus be seen as a spatiotemporal jerky dynamics. An analysis of the model reveals interesting effects of memory on the dynamics of active systems.

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BP 10.2 Mon 14:00 DYp

Dynamic role of coherent structures in two-dimensional Navier-Stokes turbulence — •Jiahan Wang[1], Wolf-Christian Müller[1], and Jörn Sesterhenn[2] — [1]Technische Universität Berlin, Berlin, Germany — [2]Universität Bayreuth, Bayreuth, Germany

Turbulent coherent structures can phenomenologically be described as regions in a flow exhibiting a high level of spatio-temporal correlation. Although these structures are ubiquitously observed in nature, providing a universal and rigorous definition of them is not a straightforward task. Therefore the choice of a suitable structure detection method is generally not unique and problem-dependent. We are interested in structures appearing in statistically isotropic Navier-Stokes turbulence. For this purpose, direct numerical simulations (DNS) of a two-dimensional flow, forced at small spatial scales, are employed to compare different definitions of structural coherence. This setup inherently forms large scale structures due to the inverse cascade of energy. Detection methods such as the identification of Lagrangian coherent structures (LCS), dynamic mode decomposition (DMD) and wavelet denoising are all capable of splitting physical fields into coherent and incoherent contributions. Based on that, the analysis of the scale-to-scale decomposed energy flux yields a physical interpretation for the influence of those structures onto the overall inverse cascade dynamics. As a result, the decomposed fluxes gained from LCS and DMD are related, whereas the wavelet decomposition shows no similarity at all.

BP 10.3 Mon 14:00 DYp

Magnetic helicity inverse transfer in supersonic isothermal MHD turbulence — •Jean-Mathieu Teissier[1,2] and Wolf-Christian Müller[1,2,3] — [1]Technische Universität Berlin, ER3-2, Hardenbergstr. 36a, D-10623 Berlin, Germany — [2]Max-Planck/Princeton Center for Plasma Physics — [3]Berlin International Graduate School in Model and Simulation Based Research

Magnetic helicity is an ideal invariant of the magnetohydrodynamic (MHD) equations which exhibits an inverse transfer in spectral space. Up to the present day, its transport has been studied in direct numerical simulations only in incompressible or in subsonic or transonic flows. Inspired by typical values of the turbulent root mean square (RMS) Mach number in the interstellar medium, this work presents

some aspects of the magnetic helicity inverse transfer in high Mach number isothermal compressible turbulence, with RMS Mach numbers up to the order of ten:

1) a clear Mach-number dependence of the spectral magnetic helicity scaling but an invariant scaling exponent of the co-spectrum of the Alfvén velocity and its curl,

2) the approximate validity of a dynamical balance relation found by incompressible turbulence closure theory,

3) a characteristic structuring of helically-decomposed nonlinear shell-to-shell fluxes that can be disentangled into different spectrally local and non-local transfer processes.

BP 10.4 Mon 14:00 DYp

Molecular dynamics of janus polynorbornenes: glass transitions and nanophase separation — •Mohamed A Kolmangadi, Paulina Szymoniak, Martin Böhning, and Andreas Schönhals — Bundesantalt für Materialforschung und -prüfung (BAM), Berlin, Germany

For the first time, dielectric and calorimetric investigations of a homologous series of Janus polynorbornenes with rigid main backbones and flexible Si(OR)3 side groups of differing length alkyl chains (R = propyl, butyl, hexyl, octyl, and decyl) is reported.Two dielectrically active processes are observed at low temperatures, denoted as β- and α-relaxation. The former can be assigned to localized fluctuations, while the latter is related to the glassy dynamics of the flexible Si(OR)3 side groups, creating a nanophase separation in both the alkyl chain-rich and backbone-rich domains. This is confirmed through temperature-modulated differential scanning calorimetry (TMDSC) measurements and X-ray scattering experiments. The glass transition temperatures of the backbone rich domains, which are beyond or near to their degradation temperatures in terms of conventional DSC, are determined for the first time using fast scanning calorimetry employing both fast heating and cooling rates. This is complemented with scattering experiments that show how the size of the alkyl chain-rich domains increases with the side chain length. Alongside these results, a significant conductivity contribution was observed for all poly(tricyclononenes) with Si(OR)3 side groups, which is interpreted in terms of a percolation model

BP 10.5 Mon 14:00 DYp

Classical Density Functional Theory for Particles with Hard Cores and Soft Square Shoulders — •Markus Hoffmann, Robert F. B. Weigel, and Michael Schmiedeberg — Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

Classical density functional theory is an excellent tool to investigate classical many-body systems from fundamental principles, in particular soft matter systems. We consider particles with hard cores and soft square shoulders in two dimensions. The hard-core is implemented by using a variant of the Fundamental Measure Theory that probably is the best mean field approach to hard particles.

The hard core-square shoulder interaction possesses two independent length scales namely the diameter of the hard core and the diameter of the square shoulders. We observe the expected crystallization transitions into a triangular phase for both very weak shoulders where the hard cores dominate and for strong shoulders effectively leading to a soft sphere system.

However, the most interesting cases are expected when the two length scales of the systems are competing. As a result, not only square patterns are observed but we also want to explore quasicrystals. Note that previous mean field descriptions of quasicrystals (like Phase Field Crystal approaches) usually consider cluster crystals and so far have not been able to explain the formation of quasicrystals for particles with hard cores.

BP 10.6 Mon 14:00 DYp

Organizing bacterial vortex lattices by periodic obstacle arrays — •Henning Reinken[1], Sebastian Heidenreich[2], Markus Bär[2], and Sabine H. L. Klapp[1] — [1]Technische Universität Berlin, Germany — [2]Physikalisch-Technische Bundesanstalt, Berlin, Germany

Recent experimental studies have shown that the turbulent vortex structures emerging in bacterial active fluids can be organized into regular vortex lattices by weak geometrical constraints such as small pillars [1]. Using a continuum-theoretical approach [2,3], we show how these artificial obstacles reorganize self-induced topological defects which guides the flow profile of the active fluid and enables the stabilization of vortex patterns with tunable properties. Beyond the stabilization of square and hexagonal lattices, we also provide a striking example of a chiral, antiferromagnetic lattice induced by arranging the obstacles in a Kagome-like array [3]. In this setup, the interplay of lattice topology, activity and length-scale selection generates a net rotational flow. Further, we explore the connections between the stabilized non-equilibrium vortex patterns and equilibrium phase transitions in classical spin lattice models, e.g., the Ising model.

[1] D. Nishiguchi, I. S. Aranson, A. Snezhko, and A. Sokolov, Nat. Commun. **9**, 4486 (2018)
[2] H. Reinken, S. H. L. Klapp, M. Bär, and S. Heidenreich, Phys. Rev. E **97**, 022613 (2018)
[3] H. Reinken, D. Nishiguchi, S. Heidenreich, A. Sokolov, M. Bär, S. H. L. Klapp, and I. S. Aranson, Commun. Phys. **3**, 76 (2020)

BP 10.7 Mon 14:00 DYp

Active mobile oscillators: Density fluctuations and phase ordering — Astik Haldar[1], •Swarnajit Chatterjee[2], Apurba Sarkar[3], Raja Paul[3], and Abhik Basu[1] — [1]Saha Institute of Nuclear Physics, Kolkata, India — [2]Center for Biophysics & Department for Theoretical Physics, Saarland University, Saarbrücken, Germany — [3]Indian Association for the Cultivation Of Science, Kolkata, India

We consider the collective motion of nearly phase-ordered active oscillators on a substrate. The dynamics include activity-induced couplings between the local phase with the concentration of the mobile oscillators on the interface. We show that such a system can be stable over a wide range of model parameters. When stable, the system can also show a variety of orders. In different regions of the phase space, the system can show phase ordering that is stronger than the conventional quasi long-range order (QLRO) together with hyperuniform number fluctuations, or phase ordering weaker than QLRO together with giant number fluctuations, or even QLRO with uniform density fluctuations. In other parameter regimes, the system becomes unstable with the eventual loss of any phase ordering beyond a finite (small) system size. We have also constructed an appropriate agent-based lattice-gas model. Numerical simulations of this model corroborate the analytical predictions and validate the results on the phase fluctuations.

BP 10.8 Mon 14:00 DYp

Structural and dynamical properties of gel networks — •Matthias Gimperlein and Michael Schmiedeberg — Institut für theoretische Physik 1, FAU Erlangen-Nürnberg

Gelation is connected to a slow-down in dynamics, the onset of percolation and an increasing number of neighboring particles. The slow-down occurs on different time scales depending on the studied length scales.

Using Brownian Dynamics simulation for a system of colloidal particles interacting due to a modified square well and Yukawa potential we investigate the structural properties of gel networks on different time and length scales depending on system parameters as the strength of attraction or repulsion respectively.

The square well potential is modified by introducing an interaction range α to flatten the walls of the square well. The phase diagram was determined by fitting the vapour-liquid binodal. In the square well limit ($\alpha \to 0$) results from the literature are recovered. Structural properties as node distribution or link lengths are extracted from minimal networks which allow an easier analysis of the underlying network structure.

Further research includes distinguishing dynamic regimes or structures on different length and time scales, investigating the history/protocol dependency of the development (i. e. starting from different initial configuration) and finding stable or metastable structures to describe the evolution of gel networks not on the particle level anymore, but on a coarse grained level.

BP 10.9 Mon 14:00 DYp

Simple model for drops on elastic substrates — •Christopher Henkel[1], Uwe Thiele[1], and Jacco Snoeijer[2] — [1]Institut für Theoretische Physik, WWU-Münster, Germany — [2]Fac. of Science and Technologie, University Twente, Netherlands

The investigation of the wetting behavior on viscoelastic or elastic substrates is of great interest. In this talk we present a simple model for steady liquid drops on fully compressible elastic substrates and show that a double transition of contact angles appears under variation of the substrate softness, similar to the one described in [1]. We further discuss whether these angles agree with the Neumann and Young-Laplace conditions in the liquid-liquid and liquid-solid limit respectively and how the transitions depend on drop size. Finally, we employ a gradient dynamics model in the long-wave limit and show

first results of direct time simulations.

[1] Lubbers, L. A., Weijs, J. H., Botto, L., Das, S., Andreotti, B., and Snoeijer, J. H., (2014). Drops on soft solids: free energy and double transition of contact angles. *Journal of fluid mechanics*, 747.

BP 10.10 Mon 14:00 DYp

Flocking and reorientation transition in the q-state active Potts model — •Matthieu Mangeat[1], Swarnajit Chatterjee[1,2], Raja Paul[2], and Heiko Rieger[1] — [1]Saarland University, Saarbrücken, Germany — [2]IACS, Kolkata, India

We study the q-state active Potts model (APM) on a two-dimensional lattice in which active particles have q internal states corresponding to the q directions of motion. A local alignment rule inspired by the ferromagnetic q-state Potts model and self-propulsion via biased diffusion according to the internal particle states leads to a collective motion at high densities and low noise. We formulate a coarse-grained hydrodynamic theory with which we compute the phase diagram of the APM and explore the flocking dynamics in the region, in which the high-density (polar liquid) phase coexists with the low-density (gas) phase and forms a fluctuating band of coherently moving particles. As a function of the particle self-propulsion velocity, a novel reorientation transition of the phase-separated profiles from transversal to longitudinal band motion is found, which is absent in the Vicsek model [1] and the active Ising model [2]. The origin of this reorientation transition is revealed by a stability analysis: for large velocities the transverse diffusion constant approaches zero and then stabilizes longitudinal band motion. Computer simulations corroborate the analytical predictions of the flocking and reorientation transitions and validate the phase diagrams of the APM.

[1] T. Vicsek *et al.*, Phys. Rev. Lett. **75**, 1226 (1995).
[2] A. P. Solon and J. Tailleur, Phys. Rev. Lett. **111**, 078101 (2013).

BP 10.11 Mon 14:00 DYp

Cell fitness in growth driven active matter: decoupling turnover rate and homeostatic pressure predictors — •Yoav G. Pollack[1], Philip Bittihn[1], and Ramin Golestanian[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Goettingen, 37077, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, OX1 3PU, UK

In growth-driven dense cellular active matter, cell dynamics and competition are governed by the intricate relations between growth, proliferation, removal (e.g. death, extrusion) and mechanical interactions. Though the rates at which a cell proliferates or dies have already been established as a significant factor for fitness, homeostatic pressure was recently suggested as an equivalent predictor of fitness and one that can be more easily measured. Here we show that this equivalence in not universal and can be broken. By introducing an additional timescale that governs the duration of the single-cell removal process in a simple growing dumbbell model of cells, the homeostatic pressure is partially decoupled from the turnover rate, leading to a distinct prediction for each. When the two factors are modulated in this way in a simulated competition assay of a mixture of two cell species in a closed 1D channel, we show that while the homeostatic pressure does not predict well which species triumphs, the turnover rate does. A good fitness measure is important in studies of tumor growth, bacterial evolution, etc. and this result is a first step in understanding for which scenarios is the homeostatic pressure a valid predictor.

BP 10.12 Mon 14:00 DYp

Unjamming of Active Rotators — •Linda Ravazzano[1], Silvia Bonfanti[1], Maria C. Lionetti[1], Maria R. Fumagalli[1], Roberto Guerra[1], Oleksandr Chepizhko[2], Caterina A. M. La Porta[1], and Stefano Zapperi[1] — [1]Center for Complexity and Biosystems, University of Milan, Italy — [2]Leopold-Franzens-Universität Innsbruck, Austria

Active particles assemblies are of peculiar interest thanks to the richness of dynamical phases they can undergo varying internal parameters such as density, adhesion strength or self-propulsion. Most theoretical studies of active matter consider self-propelled particles driven by active forces. The observation of the motion of Chlamydomonas reinhardtii algae, in which the active particles have also the ability to self-rotate, suggests, however, that active torques may also play an important role. Inspired by this example, we simulate the dynamics of a system of interacting active 2D disks endowed with active torques and self-propulsive forces. We studied this model system of active rotators in different conditions: at low packing fractions, where adhesion causes the formation of small rotating clusters, at higher densities, where our simulations show a jamming to unjamming transition promoted by active torques and hindered by adhesion, and in presence of both self-propulsion and self-rotation, studying the interplay between those quantities and deriving a phase diagram. Our results yield a comprehensive picture of the dynamics of active rotators, highlighting the importance of the internal degrees of freedom of active particles in determining the collective behavior of the system.

BP 10.13 Mon 14:00 DYp

The thermodynamics and kinetics of protein crystallization probed by isothermal microcalorimetry — Lorena Hentschel, •Jan Hansen, Florian Platten, and Stefan U. Egelhaaf — Condensed Matter Physics Laboratory, Heinrich Heine University, Düsseldorf, Germany

During a first-order phase transition, a thermodynamic system releases or absorbs latent heat. Despite their fundamental importance, the heat or enthalpy change occurring during protein crystallization has been directly measured only in a few cases, and the associated entropy change can only be determined indirectly. Here, the thermodynamics and kinetics of tetragonal lysozyme crystallization are studied for various physicochemical solution parameters. Direct microcalorimetric and indirect van't Hoff enthalpy determinations quantitatively agree, suggesting a two-state crystallization process. Assuming that crystals are electrostatically neutral, the weak dependences of the crystallization enthalphy and entropy on salt concentration and pH value are explained by a Poisson-Boltzmann model. Furthermore, the calorimetric signal is related to the concentration change during nucleation and growth, from which the induction time and the growth rate are inferred. Their dependences on the chemical potential are in line with previous findings and can be modelled by classical nucleation theory and 2D growth models, respectively.

BP 10.14 Mon 14:00 DYp

Real-Time Investigations during Sputter Deposition on Polymer Thin Films — •Matthias Schwartzkopf[1], Marc Gensch[1,2], Thomas Strunskus[3], Franz Faupel[3], Peter Müller-Buschbaum[2] und Stephan V. Roth[1,4] — [1]DESY, Notkestr. 85, D-22607 Hamburg — [2]CAU zu Kiel, Kaiserstr.2, 24143 Kiel — [3]TUM, James-Franck-Str. 1, D-85748 Garching — [4]KTH, Teknikringen 56-58,SE-100 44 Stockholm

The reproducible low-cost fabrication of functional metal-polymer-nanocomposites remains a major issue in applied nanotechnology. In order to obtain full control over the evolution at the nanogranular metal-polymer interface, we employed time-resolved surface sensitive X-ray scattering during sputter deposition of gold on thin polystyrene films [1] and SiOx [2]. We correlate the evolution of the metallic layer morphology with changes in the key scattering features. This enabled us to identify the impact of atomic deposition rate on the growth regimes with their specific thresholds. Our study opens up the opportunity to improve nanofabrication of tailored metal-polymer nanostructures for organic electronics like photovoltaic applications and plasmonic-based technologies. [1] Schwartzkopf et al., ACS Appl. Mater. Interfaces 7, 13547 (2015); [2] Schwartzkopf et al., Nanoscale 5, 5053 (2013).

BP 10.15 Mon 14:00 DYp

Fluid transport by metachronal waves of model cilia — •Albert von Kenne, Thomas Niedermayer, and Markus Bär — Department of Mathematical Modelling and Data Analysis, Physikalisch-Technische Bundesanstalt Berlin, Abbestraße 2-12, Berlin 10587, Germany

Motile cilia are hair-like cell extensions that undergo a cyclic motion with the purpose to transport the extracellular fluid at a low Reynolds number, providing crucial functionality of living matter such as cell locomotion and molecular transport in tissue. A striking feature of populations of cilia is a state of collective motion known as metachronal wave.

To investigate these collective states we generalize a simple phase oscillator model for the elastohydrodynamic coupling in ciliated systems [1], to include the effects due to the confined flow in proximity of a cell substrate. Our model encompasses spontaneous creation of waves as well as directed cycle-average fluid flow, yet it's simple enough to be solved analytically. We obtain analytical results for the linear stability of metachronal waves in presence of long-range hydrodynamic interactions, illustrate their properties by numerical simulations and relate the change in transport efficiency to the specific properties of

metachronal waves.

[1] . Niedermayer, B. Eckhardt, and P. Lenz, Chaos **18**, 037128 (2008)

BP 10.16 Mon 14:00 DYp

Athermal Jamming for particles with exponentially decreasing repulsions — •Nicolas Wohlleben and Michael Schmiedeberg — Institut für Theoretische Physik I, Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Staudtstraße 7, 91058 Erlangen, Germany

We study the jamming of a colloidal system where the particles interact according to a Yukawa potential, i.e., the repulsion decreases exponentially with the distance as expected for screened Coulomb interactions of charged colloids in solution. The decay occurs on a length scale given by the screening length and in addition we consider a cutoff length where the potential is set to zero in a smooth way as often used in simulation.

By determining the athermal jamming transition by trying to remove overlaps we find that the transition packing fraction only depends on the cutoff length but hardly on the screening length. We also explore the radial distribution function and again confirm the importance of the cutoff length.

The picture that emerges is that the influence of a cutoff length on athermal jamming is superior to that of the screening length, although the screening length is expected to control the slowdown of the dynamics (i.e., the dynamical glass transition). As a consequence, athermal jamming (as defined by overlaps) and the glass transition obviously are unrelated in the considered system.

BP 10.17 Mon 14:00 DYp

Detection of defects in soft quasicrystals with neural networks — •Ali Döner and Michael Schmiedeberg — Institut für Theoretische Physik I, Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Staudstr. 7, 91058 Erlangen, Germany

The aim of this work is to construct and employ a neural network for the detection of topological defects in dodecagonal quasicystalline patterns. Even though quasircrystals are aperiodic, they exhibit a longe-range order. Furthermore, in principle any discrete rotational symmetry can occur.

In this work, dodecagonal quasicrystalline patterns in two-dimensions with a built-in dislocation are generated and employed as input images of the neural network. The network then should figure out not only the position but also the type of the Burgers vector of the defect.

Our trained neural network is able to recognize the type of the Burgers vector perfectly. The position of the dislocation is recognized up to a mean deviation from the real position that is much smaller than the small length scale in the quasicrystals. In future, we want to train the network with patterns that contain multiple dislocations as well as phasonic excitations.

BP 10.18 Mon 14:00 DYp

Bistable vortices formed by active particles with retarded interactions - Theory — Xiangzun Wang[1], •Pin-Chuan Chen[2], Viktor Holubec[2,3], Klaus Kroy[2], and Frank Cichos[1] — [1]Molecular Nanophotonics Group, Peter Debye Institute for Soft Matter Physics, University of Leipzig, 04103 Leipzig — [2]Institute for Theoretical Physics, University of Leipzig, 04103 Leipzig, Germany — [3]Department of Macromolecular Physics, Faculty of Mathematics and Physics, Charles University, 18000 Prague, Czech Republic

In a recent experiment (see the companion contribution "Experiment", serial number DY193), thermophoretic microswimmers were observed to self-assemble into a bistable mode of circular collective motion. We explain the underlying mechanism qualitatively by deriving a coarse-grained Langevin model for active Brownian particles with retarded interactions. For a single microswimmer attracted to an immobile attractive sphere, it can be broken down to an effective model for the angular degree of freedom. The reduced one-dimensional overdamped Langevin equation features a virtual potential for the angular velocity, self-generated by the retarded propagation of the interaction. We work out the quantitative analytical predictions for the delay-dependent bifurcation scenario and the Kramers rates and numerical results for spontaneous transitions between the degenerate chiral modes of angular motion, beyond the bifurcation point. Our theoretical predictions are found to agree well with the experimental observations and simulations.

BP 10.19 Mon 14:00 DYp

Bistable vortices formed by active particles with retarded interactions - Experiment — •Xiangzun Wang[1], Pin-Chuan Chen[2], Viktor Holubec[2,3], Klaus Kroy[2], and Frank Cichos[1] — [1]Molecular Nanophotonics Group, Peter Debye Institute for Soft Matter Physics, Universität Leipzig, 04103 Leipzig, Germany — [2]Institute for Theoretical Physics, Universität Leipzig, 04103 Leipzig, Germany — [3]Department of Macromolecular Physics, Faculty of Mathematics and Physics, Charles University, 18000 Prague, Czech Republic

Rotating formations of living species are frequently observed in nature from bacterial systems and insects to larger animals like fish or birds. The ubiquity of this behavior suggests universal underlying principles. One could be related to inevitable delays caused by sensimotoric feedback. We explore experimentally the influence of a delayed interaction between individual self-thermophoretic microswimmers on their collective behaviour. Our microswimmers are gold nanoparticle decorated melamine resin colloids, which are propelled by self-thermophoresis due to a local heating of the gold nanoparticles with a focused laser. Using a feedback algorithm we are able to introduce time-delayed virtual interactions with other particles or targets. We find for a single swimmer attracted to an immobilized particle, a transition from a diffusive to a rotating state with two possible rotation directions. This behavior is captured by a simple theoretical model (see companion contribution). This bifurcation is also observed in ensembles of multiple particles where the rotational phase of the ensemble is synchronized by particle collisions.

BP 10.20 Mon 14:00 DYp

Effect of Alignment Activity on the Collapse Kinetics of a Flexible Polymer — •Subhajit Paul[1], Suman Majumder[1], Subir K Das[2], and Wolfhard Janke[1] — [1]Institut fuer Theoretische Physik, Universitaet Leipzig, Bruederstr. 16, D-04103, Leipzig, Germany — [2]Theoretical Sciences Unit, JNCASR, Bangalore- 560064, India.

Dynamics of various biological filaments can be understood within the framework of active polymer models. Keeping this in mind, we construct a bead-spring flexible polymer chain in which the active interaction among the beads is introduced via an Vicsek-like alignment rule. Following a quench from the high-temperature coil phase to a low-temperature state, we study the non-equilibrium coarsening kinetics of this model via molecular dynamics (MD) simulations. For the passive polymer case the low-temperature equilibrium state is a compact globule. Results from our MD simulations reveal that though the globular state is also expected to be the typical final state in the active case as well, the non-equilibrium pathways change due to the alignment interaction among the beads. We observe that the probability of deviation from the intermediate *pearl-necklace*-like arrangement and the formation of more elongated dumbbell- like structures increases with increasing activity. Also, there exists nonmonotonicity in coarsening with the variation of the strength of activity. In this work, our focus is on such non-equilibrium dynamics results for which we compare with those of the passive case. These are concerning scaling laws related to collapse time and growth of clusters.

BP 10.21 Mon 14:00 DYp

The parameter space of thermohaline stairs — •Axel Rosenthal and Andreas Tilgner — Institut für Geophysik, Georg-August-Universität Göttingen, Deutschland

Convection and diffusion in water can be observed when a gradient in temperature or in salinity takes effect on density in presence of gravity. Both gradients can force or stabilize the process. We conducted experiments where the salt gradient is the driving force and simultaneously the temperature gradient is stabilizing in opposite direction, observed by particle image velocimetry. The question is at which gradients, expressed by Rayleigh numbers, does the transport occure in stable so called "thermohaline stairs"? Thermohaline stairs are a sequence of two flow systems, a finger regime and a large scale circulation.

BP 10.22 Mon 14:00 DYp

Fluctuations of a driven tracer in a viscoelastic bath — •Juliana Caspers — Institut für Theoretische Physik, Göttingen

Recently, viscoelastic fluids have attracted attention as their large structural relaxation times induce a variety of new phenomena such as nontrivial back reactions of the bath on a driven probe particle. Berner *et al* [1] found particle oscillations in the linear response regime, both in theory and experiment. Moreover, Müller *et al* [2] investi-

gated effects of nonlinear baths in equilibrium. They observed interdependencies entering the coefficients in an effective linear generalized Langevin equation. For example, the friction memory kernel depends on properties of the external trap [3] or on the bare tracer friction in the case of an overdamped setting. In [1,2], the simple model of a confined tracer particle interacting via a stochastic Prandtl-Tomlinson model with a bath particle was found to be a good candidate to mimick the properties of a nonlinear viscoelastic bath. This work focuses on the interplay of the external trap that confines the tracer particle and the nonlinearity of the bath. In a nonequilibrium situation we made a first observation of shear thickening, an increase in the microrheological friciton coefficient for a certain regime of driving velocities.

[1] J. Berner, B. Müller, J. R. Gomez-Solano, M. Krüger, and C. Bechinger. *Nat. Commun.*, 9(1):999, 2018
[2] B. Müller, J. Berner, C. Bechinger, and M. Krüger. *New J. Phys.*, 22:023014, 2020
[3] J. O. Daldrop, B. G. Kowalik, and R. R. Netz. *Phys. Rev. X*, 7:041065, 2017

BP 11: Poster A: Single Molecule, Multicellular, Bioimaging, Focus Sessions, etc.

Time: Monday 16:30–19:00 Location: BPp

BP 11.1 Mon 16:30 BPp

How fast do PMCA pumps transport Ca^{2+}? — •Barbara Schmidt[1], Cristina E. Constantin[2], Bernd Fakler[2], and Heiko Rieger[1] — [1]Center for Biophysics and Dep. Theoretical Physics, Saarland University, 66123 Saarbrücken, Germany — [2]Institute of Physiology, University of Freiburg, 79104 Freiburg, Germany

Plasma membrane protein complexes of two PMCA subunits and two Neuroplastin or Basigin proteins are responsible for Ca^{2+} ion transport out of cells. Here we make use of BK-type Ca^{2+}-activated K^+ channels to determine the Ca^{2+} transport activity of PMCA. Due to their large conductance and their particular gating kinetics the BK channels may be used as fast and reliable sensors for intracellular Ca^{2+}-concentration ($[Ca^{2+}]_i$) beneath the plasma membrane. Experimentally we monitor the PMCA-mediated Ca^{2+} clearance (or transport) by the decay of BK-currents following their activation by a short (0.8 ms) period of Ca^{2+}-influx through Cav2.2 channels. To relate the experimentally observed temporal evolution of the K^+ current to the underlying temporal evolution of the Ca^{2+} concentration we implement a theoretical model for the Ca^{2+}-dependence of the BK-current and of the PMCA pump strength. The maximum PMCA pump strength is used to fit the predicted time course of the K^+ current to the experimental data, which turns out to be at least 2 orders of magnitude larger than what has been assumed so far. Implication of this finding for Ca^{2+} signaling in general are discussed.

BP 11.2 Mon 16:30 BPp

Molecular Friction and Adhesion on Porous Membranes — •Kordula Schellnhuber[1,2], Hanna Hübner[2], Johanna Blass[1], Markus Gallei[2], and Roland Bennewitz[1] — [1]INM-Institut für Neue Materialien, Campus D.2.2 Universität des Saarlandes, 66123 Saarbrücken, Germany — [2]Lehrstuhl für Polymerchemie, Naturwissenschaftlich-Technische Fakultät, Universität des Saarlandes, 66123 Saarbrücken, Germany

Understanding and controlling the dynamics of polymer-surface interactions are key to a functional design of nanoscale objects and to reveal mechanisms underlying biological processes. We study friction and adhesion of single polymers at the solid-liquid interface by means of atomic force microscopy (AFM) with focus on entanglement dynamics. As a model system, a single M13mp18 DNA-molecule with a length of 2.5 μm is attached to an AFM probe. Friction measurements are performed by moving the cantilever in parallel to the surface at a height of a few hundred nanometers. Deflection of the cantilever reveals adhesive interactions between the DNA polymer and the membrane. Entanglement of the DNA in the membrane pores is probed by adhesion measurements after varying waiting time at a constant height of few hundred nanometers above the surface.

BP 11.3 Mon 16:30 BPp

The mechanics of single cross-links which mediate cell attachment at a hydrogel surface — Arzu Colak, Bin Li, Johanna Blass, Aranzazu del Campo, and •Roland Bennewitz — INM - Leibniz Institute for New Materials, Saarbrücken, Germany

Cells attach to the surface of a poly(ethylene glycol diacrylate) (PEGDA) hydrogel if linkers are functionalized with the RGD cell adhesive motif. Attachment and spreading of cells on the hydrogel depend on its mechanical properties, for examples when Young*s modulus E of the hydrogel is varied. We were interested in the effective stiffness of those linkers which mediate cell attachment and measured it by means of single-molecule force spectroscopy [1]. For these experiments, the linkers were functionalized with biotin and the tip of an atomic force microscope with streptavidin. A factor of ten in the elastic modulus E of the hydrogel corresponded to a factor of five in the effective spring constant k of single crosslinks, indicating a transition in scaling with the mesh size ζ from the macroscopic $E \propto \zeta^{-3}$ to the molecular $k \propto \zeta^{-2}$. The effective stiffness of single linkers was also measured for a second polymer network based on four-arm star-PEG molecules which interpenetrated the PEGDA hydrogel. The quantification of stiffness and deformation at the molecular length scale contributes to the discussion of mechanisms in force-regulated phenomena in cell biology. [1] A. Colak, B. Li, J. Blass, K. Koynov, A. del Campo, R. Bennewitz, The mechanics of single cross-links which mediate cell attachment at a hydrogel surface, Nanoscale, 11 (2019) 11596-11604.

BP 11.4 Mon 16:30 BPp

Deep reinforcement learning of molecular mechanisms — •Roberto Covino[1], Hendrik Jung[2], Arjun Wadhawan[3], Peter G. Bolhuis[3], and Gerhard Hummer[2,4] — [1]Frankfurt Insitute for Advanced Studies, Frankfurt am Main, Germany — [2]Max Planck Institute of Biophysics, Frankfurt am Main, Germany — [3]Van 't Hoff Institute for Molecular Sciences, University of Amsterdam, Amsterdam, The Netherlands — [4]Institute of Biophysics, Goethe-University Frankfurt, Frankfurt, Germany

We present a deep reinforcement learning artificial intelligence (AI) that learns the molecular mechanism from computer simulations. The AI simulates molecular reorganizations and progressively learns how to predict their outcome. We integrate path theory, transition path sampling (TPS), and deep learning. TPS is a Markov Chain Monte Carlo method to sample the rare trajectories connecting metastable states. Using reinforcement learning, we iteratively train a deep neural network on the outcomes of TPS simulation attempts. In this way, we increase the rare-event sampling efficiency while gradually revealing the underlying mechanism. At convergence, the AI learns the rare events' committor function, encoded in the trained neural network. By using symbolic regression, we distill simplified quantitative models that reveal mechanistic insight in a human-understandable form. Our innovative AI enables the sampling of rare events by autonomously driving many parallel simulations with minimal human intervention and aids their mechanistic interpretation.

BP 11.5 Mon 16:30 BPp

Acidic amino acids do not affect the robustness of protein hydration layers to changes in KCl concentration — •Hosein Geraili[1] and Ana Vila Verde[2] — [1]MPI of Colloids and Interfaces, Dept Theory and Bio-Systems, Potsdam, Germany — [2]U. Duisburg-Essen, Physics, Duisburg, Germany

The proteins of halophilic microorganisms have a higher content in negatively charged amino acids compared to microorganisms living in normal environments. One proposed hypothesis explaining this large content in acidic residues is that they are necessary to maintain the proteins at normal hydration levels in an environment with high salt concentration, i.e., in low water activity. To investigate protein hydration in high salt concentration using Molecular Dynamics, we optimized the interaction potential between potassium ions and the carboxylate side-chain of acidic amino acids; the optimized potential is compatible with the widely-used suite of AMBER force fields and the TIP3P water model. We compared hydration levels of 5 halophilic proteins and 5 non-halophilic ones. Our simulations show that all proteins have almost identical levels of hydration in high and low KCl concentrations: the large fraction of acidic amino acids in halophilic proteins is not necessary to ensure that they remain hydrated. We quantified the translational dynamics of the solvation shell of the halophilic and non-

halophilic proteins, and observe almost no difference between them. The claim that acidic residues cooperatively interacting with the solvated network of ions would markedly decrease the dynamics of the protein solvation shell is not supported by our calculations.

BP 11.6 Mon 16:30 BPp

Optical tweezers and multimodality imaging: a platform for dynamic single-molecule analysis — •Bärbel Lorenz, Ann Mukhortava, and Philipp Rauch — LUMICKS B.V. Amsterdam, Pilotenstraat 51, 1059CH Amsterdam, The Netherlands

The possibility to investigate molecular interactions, structure, and dynamics using single-molecule fluorescence- and force spectroscopy-based methods has led to many new insights over the past decades. Here, we present our efforts in establishing the easy and reliable experimental workflow for further enabling discoveries in the field of biology and biophysics using both the combination of optical tweezers with single-molecule fluorescence microscopy (C-Trap). As a proof of concept, we will discuss an overview of the experimental designs and the workflow for combining FRET with an ultra-stable optical trap for studying binding and colocalization dynamics of histones and a helper protein on DNA and observing protein/DNA hairpin folding dynamics. These experiments show that the technological advances in hybrid single-molecule methods can be turned into an easy-to-use and stable instrument that opens up new venues in many research areas.

BP 11.7 Mon 16:30 BPp

Molecular mechanisms of single alpha helix deformation under tension — Ana Bergues-Pupo[1], Reinhard Lipowsky[2], and •Ana Vila Verde[3] — [1]Max Delbrück Center for Molecular Medicine, Berlin, Germany — [2]MPI of Colloids and Interfaces, Dept Theory and Bio-Systems, Potsdam, Germany — [3]U. Duisburg-Essen, Physics, Duisburg, Germany

Alpha helices (SAHs) that are stable in isolated form have been found in motor proteins, where they connect spatially separated domains. We investigate the force-estension curve and molecular deformation mechanisms of SAHs pulled from the termini, at pull speeds approaching the quasi-static limit, using molecular dynamics simulations with atomistic resolution of the protein and an implicit model for the solvent. SAHs unravel starting from the termini, in a residue-by-residue manner. Contrary to prior simulations of metastable helices, hydrogen bond breaking is not the main event determining the barrier to unfolding of SAHs at all pull speeds we tested. We fit the force-extension curves to the cooperative Sticky Chain model, and extract the distance, $x_E = 0.13$ nm, to the transition state, the natural frequency of bond vibration, $\nu_0 = 0.82\ \mathrm{ns}^{-1}$, and the height, V_0=2.9 kcal/mol, of the free energy barrier associated with the deformation of single residues. The results confirm that the Sticky Chain model could be used to analyze experimental force-extension curves of SAHs and other biopolymers.

BP 11.8 Mon 16:30 BPp

Structural Dynamics Correlation of Peptides derived from Nucleoporins: Time-resolved X-ray Scattering and Computational Modelling — •Naireeta Biswas[1,2], Markus Osterhoff[2], Jakob Soltau[2], Sheung Chun Ng[3], Dirk Görlich[3], and Simone Techert[1,2] — [1]FS-SCS, Deutsches Elektronen-Synchrotron (DESY), Notkestraβe 85, 22607 Hamburg, Germany — [2]University of Göttingen, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [3]Department of Cellular Logistics, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany

FG nucleoporins are intrinsically disordered proteins located in the nuclear pore complexes (NPCs) consist of FG repeating motifs. It has been proposed that repeating motifs play an important role in the formation of hydrogel due to their cohesive interactions and hydrophobic nature. These protein hydrogels show unique features of non-covalent interactions such as hydrogen bonding, Vander Waals interaction or π-π stacking, driving the protein self-assembly, leading to an anisotropic structural growth, thus forming hydrogels with unusual materials properties. Our computational simulations, suggest different conformations and interactions between these FG repeating motifs and that these conformational variety may be the driving forces for the co-existing domains. To understand this molecular rationale of the protein kinetics during their gelation process, we have studied the first steps of self-assembling and structural organization of the protein hydrogels during the formation .

BP 11.9 Mon 16:30 BPp

Heat flows adjust local ion concentrations in favor of prebiotic chemistry — •T. Matreux[1], K. LeVay[2], A. Schmid[1], P. Aikkila[1], L. Belohlavek[3], Z. Caliskanoglu[3], E. Salibi[2], A. Kühnlein[1], C. Springsklee[3], B. Scheu[3], D.B. Dingwell[3], D. Braun[1], H. Mutschler[2], and C.B. Mast[1] — [1]Systems Biophysics, LMU, Amalienstr. 54, 80799 Munich, Germany — [2]MPI für Biochemie, Am Klopferspitz 18, 82152 Martinsried, Germany — [3]Earth and Environmental Sciences, LMU, Theresienstr. 41, 80333 Munich, Germany

Prebiotic reactions often require certain initial concentrations of ions. For example, the activity of RNA enzymes requires a lot of divalent magnesium salt, whereas too much monovalent sodium salt leads to a reduction in enzyme function. However, it is known from leaching experiments that prebiotically relevant geomaterial such as basalt releases mainly a lot of sodium and only little magnesium. A natural solution to this problem is heat fluxes through thin rock fractures, through which magnesium is actively enriched and sodium is depleted by thermogravitational convection and thermophoresis. This process establishes suitable conditions for ribozyme function from a basaltic leach. It can take place in a spatially distributed system of rock cracks and is therefore particularly stable to natural fluctuations and disturbances.

BP 11.10 Mon 16:30 BPp

Structured keratin films as artificial nail plate model — •Kim Thomann, Andreas Späth, and Rainer H. Fink — Lehrstuhl für Physikalische Chemie II, Friedrich-Alexander Universität Erlangen-Nürnberg, Egerlandstr. 3, D-91058, Erlangen, Germany

Human fingernails can be studied ex vivo only in form of clippings which offer limited insight as they do not necessarily reflect the behavior of the whole nail. Keratin films (KFs) can potentially serve as human fingernail substitute which is especially relevant for the medical and beauty sector. In order to model the nail's adhesive characteristics, structured and unstructured films from keratin extracted from human hair and nails were produced.

The fingernail being the reference, the KFs were characterized with a number of methods, including SEM, AFM, contact angle (CA) measurements, XPS, ATR-FTIR and Raman spectroscopy. In terms of composition, KFs show a good resemblance, regardless of keratin origin. The nail's microstructured topography is well matched by the structured KFs. CA measurements revealed that the surface free energy is in the same range for both KF types. However, the unstructured KFs exhibit a much stronger polar component compared to the nail while the structured KFs fit the nail's component composition well. Thus, the structured KFs represent a good approach to achieve a satisfying model in terms of wetting while combining both composition and topography aspects. The research is funded by the BMBF within project 05K19WE2.

BP 11.11 Mon 16:30 BPp

Activity of hydrogel-encapsulated cells monitored by atomic force microscopy — •Mengxiao Li[1,2], Kordula Schellnhuber[1,2], Shardul Bhusari[1,2], Johanna Blass[1], Shrikrishnan Sankaran[1], and Roland Bennewitz[1,2] — [1]INM - Leibniz for New Materials, Campus D22, 66123 Saarbrücken — [2]Saarland University, Naturwissenschaftlich Technische Fakultät, 66123 Saarbrücken

Living materials are an emerging concept in biomaterial research. Living organisms become part of the material and equip it with tailored functions. For example, genetically engineered bacteria are encapsulated in hydrogels to release drugs when triggered by an external stimulus [1]. The aim of this study is to develop a new technique for highly sensitive measurements of mechanical perturbances arising from growth and motion of bacteria trapped in a thin hydrogel film by means of Atomic Force Microscopy (AFM). To probe the activity of E. coli bacteria enclosed in a pluronic diacrylate hydrogel, we contact its surface with a colloidal probe cantilever. Normal and lateral displacements of the contact caused by motion or division of bacteria are recorded for a contact time of 300s at various positions of the hydrogel surface. Over 24 hours, we observe an increase of the mechanical signals with time that we attribute to bacterial colony growth inside the hydrogel film. Characteristic time scales of the processes are determined by means of continuous wavelet transform.

[1] S. Sankaran et al., Small 15 (2019) 1804717.

BP 11.12 Mon 16:30 BPp

Cohesin and condensin extrude DNA loops in a cell cycle-dependent manner — •Stefan Golfier[1,2], Thomas Quail[1,2], and Jan Brugues[1,2] — [1]Max Planck Institute of Molecular Cell Biol-

ogy and Genetics, Dresden, Germany — [2]MPI-PKS, Nöthnitzer Straße 38, Dresden, Germany

How cells spatially organise long DNA polymers inside the confinements of the cell nucleus without creating knots and tangles has been a central question in cell biology. Recent observations have unveiled the physical architecture of the genome as a hierarchy of higher-order structures that deeply impact biological function. Despite their role for gene regulation, DNA repair and genome propagation, the underlying mechanisms shaping the 3D genome remained elusive. The active formation of vast DNA loops by the molecular motors cohesin and condensins has been proposed as a general mechanism to spatially organize the genome across the cell cycle. However, the requirements for genome organisation change dramatically during the cell cycle. To date it remained unclear, if DNA loops shape the drastically different chromatin architectures in inter- and metaphase. Using Xenopus laevis egg extracts, we reconstitute and directly observe DNA loop formation for the first time in a native environment and dependence of the cell cycle. We show that DNA loops are actively formed in both meta- and interphase, but with distinct biophysical properties and responsible factors. Our findings provide fundamental evidence that DNA loops are the physical building blocks of genome architecture, that are molecularly regulated during the cell cycle.

BP 11.13 Mon 16:30 BPp

UV-Induced Selectivity of Short DNA Oligonucleotides in Early Evolution — •Corinna L. Kufner[1], Dominik B. Bucher[2], Wolfgang Zinth[3], Christof B. Mast[3], Gabriella G. Lozano[1], Sukrit Ranjan[4], Zoe R. Todd[5], and Dimitar D. Sasselov[1] — [1]Harvard University, USA — [2]TU München — [3]LMU München — [4]Northwestern University, USA — [5]University of Washington, USA

At early stages of the evolution of life, between 3.5 and 4.2 billion years ago, the ultraviolet (UV) irradiation on the surface of the Earth was much higher than today. In the prebiotic era, particularly in the absence of complex enzymes, UV light both served as an important energy source for photochemical reactions and imposed a strong selection pressure on the building blocks of life. Here, we study the photophysics of short DNA oligonucleotides by irradiation experiments and ultrafast UV pump (266 nm) IR probe (5-7 um) spectroscopy. We find a strong sequence selectivity in the photostability of short oligonucleotides. Charge transfer states can promote sequence selective self-repair of adjacent photolesions via an entirely intrinsic mechanism which resembles the enzymatic repair by photolyases. Particularly charge transfer states which involve Guanine, the strongest electron donor among the canonical nucleobases, play a key role in the photostability of short oligonucleotides. It may be assumed that photophysical mechanisms have strongly influenced the selection of base sequences at early stages of evolution.

BP 11.14 Mon 16:30 BPp

Nanomechanics of DNA self-assemblies and light driven molecular motors — Michael Penth[1,2], Yijun Yijun[1], Arzu Çolak[1], Kordula Schellnhuber[1,2], Mitchell K.L. Han[1], Aránzazu del Campo[1,3], Roland Bennewitz[1,2], and •Johanna Blass[1] — [1]INM - Leibniz for New Materials, Campus D22, 66123 Saarbrücken — [2]Saarland University, Physics Department, 66123 Saarbrücken — [3]Saarland University, Chemistry Department, 66123 Saarbrücken

Single-molecule force spectroscopy has become an essential tool to unravel the structural and nanomechanical properties of biomolecules. In this study, we present Flow Force Microscopy (FlowFM) as a massively parallel approach to study the nanomechanics of hundreds of molecules in parallel. The high-throughput experiments performed in a simple microfluidic channel enable statistically meaningful studies with nanometer scale precision in a time frame of several minutes. A surprisingly high flexibility was observed for a self-assembled DNA construct typically used in DNA origami. The persistence length was determined to be 12.6 nm, a factor of four smaller than for native DNA. The enhanced flexibility is attributed to the discontinuous backbone of DNA self-assemblies. We also quantified the forces actuated by a unique molecular machine that can apply forces at cell-matrix and cell-cell junctions using light as an energy source. Micrometer-sized beads tethered to the surface via entangled rotary motors were retracted against drag forces from 1 pN to 5 pN within the first minute of UV-irradiation.

BP 11.15 Mon 16:30 BPp

In-situ GiSAXS investigations of sprayed drugs on Peptide Hydrogel based matrix — •Naireeta Biswas[1,2], Elisabeth Erbes[1,2], Krishnayan Basuroy[1], Jose Velaquez Garcia[1], Sreevidya Thekku Veedu[1], Matthias Schwartzkopf[1], Calvin Brett[1,4], Stephan Roth[1,3], and Simone Techert[1,2] — [1]Deutsches Elektronen-Synchrotron (DESY), Notkestraβe 85, 22607 Hamburg, Germany — [2]University of Göttingen, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [3]Department of Fibre and Polymer Technology, KTH Royal Institute of Technology, 100 44 Stockholm, Sweden. — [4]Department of Mechanics, KT Royal Institute of Technology, 100 44 Stockholm, Sweden

A controlled and personalized treatment is key to successful medication. We have designed a novel hybrid material- a matrix made of a mixture of hydrophilic carboxymethylated nanocellulose (CMC) hydrogel and disordered hydrophobic peptide hydrogel (P). Our investigations into this material are the first steps towards a novel drug delivery/carrier strategy that allows a controlled dosage of anti-COVID drugs embedded in the system. This gives us the opportunity to vary the local uptake in a hydrophobic or hydrophilic compartment in the matrix. The structural intercalation and the time-resolved process were investigated with in-situ grazing-incidence small-angle X-ray scattering (GISAXS) experiments while spraying the drug on the matrix. In this work, we have focused on the structural analysis of the peptide hydrogel system with the drugs. The structural analysis of the CMC fibers will be presented in the poster of Elisabeth Erbes.

BP 11.16 Mon 16:30 BPp

Cytoplasmic streaming enables inter-nuclear signaling in the giant syncytium *Physarum polycephalum* — •Nico Schramma[1], Siyu Chen[1,2], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Technical University of Munich, Physics Department, Munich, Germany

The slime mold *Physarum polycephalum* is known for its optimized active transport network, which is utilized to spread signals and nutrients over its up to meter-sized cell-body. Intriguingly, this syncytium contains up to billions of nuclei, which are said to divide in a mitotic wave. However, direct experimental evidence of this finding is still missing and the possibility of inter-nuclear signaling remains elusive. Here, by observing fluorescent labeled nuclei with high-speed microscopy, we uncover that individual nuclei not only can be transported in the tubes of the network, but can also get immobilized in the porous, gel-like endoplasm wrapping the tubes. Then, using particle image velocimetry, we resolve the slow flow within the endoplasmic tube-walls. Furthermore, we use a simplified advection-diffusion-reaction model to show that inter-nuclear exchange of large molecules such as mRNA can only happen within physiological time scales between stuck nuclei in the endoplasm, rather than between transported nuclei. Our study provides evidence that immobilised nuclei may play a crucial role in the coordination of mitotic waves or gene-expression patterns in *Physarum* and may pave the way to use *Physarum* as a model syncytium to understand the interplay of fluid-driven transport and signaling of nuclei.

BP 11.17 Mon 16:30 BPp

Resolving Energy Storage in Extra-Embryonic Membranes — •Zoë Lange[1,2], Franziska Krämer[1,3,4], Frederic Strobl[3,4], Ernst Stelzer[3,4], and Franziska Matthäus[1,4] — [1]Frankfurt Institute for Advanced Studies (FIAS) — [2]IfB, FB Physik, Uni Frankfurt/Main — [3]Buchmann Institute for Molecular Life Sciences (BMLS) — [4]IZN, FB Biowissenschaften, Uni Frankfurt/Main

Efficient energy use and storage is crucial in living organisms. In the context of evolution, energy management is continuously optimized to ensure an individual's ability to successfully compete. This is especially true for oviparous species, as all required energy has to be provided at the moment of oviposition in order to give rise to a fully functional organism. Based on our preliminary imaging data in the emerging insect model *Tribolium castaneum*, we formulate the hypothesis that extra-embryonic serosa cells utilize shape change during gastrulation to allocate and store energy that is later on required for their extensive movement during dorsal closure. To investigate this possible functional connection, we want to gain further insights into the multi-scale effects of force propagation from cellular to tissue level. Spatial and temporal dynamics of forces are calculated using non-invasive Force Inference (FI). FI utilizes a biomechanical model, a mathematical inverse method and a Bayesian framework to estimate cell and tissue stress from segmented image data and for the whole system simultaneously. Here we highlight our workflow from obtaining 3D time-lapse light sheet-based fluorescent microscopy images of live *Tribolium* embryos to multi-scale estimation of tensions and pressures acting in the serosa membrane.

BP 11.18 Mon 16:30 BPp

Cell Fate Clusters in Inner Cell Mass Organoids Arise from Cell Fate Heredity — •Tim Liebisch[1,2], Armin Drusko[1,2], Biena Mathew[1,3], Ernst Stelzer[1,3], Sabine Fischer[4], and Franziska Matthäus[1,2] — [1]GU Frankfurt — [2]FIAS — [3]BLMS — [4]JMU Würzburg

Recently, inner cell mass (ICM) organoids have been published as an in vitro model system towards preimplantational development. ICM organoids mimic the second cell fate decision taking place in in vivo mouse embryos. It was shown that cells of the same fate tend to cluster stronger than expected for the currently hypothesised random cell fate distribution. Three major processes contribute to the cell fate arrangements at the 24 h old and 48 h old ICM organoids or mid and late blastocyst, respectively: chemical signalling; cell sorting process; cell proliferation.

An agent-based model was developed, accounting for cellular interactions, cell growth and division. The model was applied to compare current assumptions of how the ICM neighbourhood is formed. The model supports the hypothesis that initial cell fate acquisition is a stochastically driven process. Subsequently, the observed neighbourhood structures can emerge due to cell fate heredity.

Simulations show that the initial cell differentiation process takes place only during a small time window, during ICM organoid composition. Our results leave little room for cellular signalling believed to be important in cell fate decision. Hence, we are discussing an alternative role of chemical signalling in this process.

BP 11.19 Mon 16:30 BPp

Migration of Cytotoxic T Lymphocytes in Collagen Matrices — •Zeinab Sadjadi[1], Heiko Rieger[1], Markus Hoth[2], Bin Qu[2], and Renping Zhao[2] — [1]Department of Theoretical Physics and Center for Biophysics, Saarland University — [2]Department of Biophysics, Center for Integrative Physiology and Molecular Medicine, School of Medicine, Saarland University

Cytotoxic T lymphocytes (CTLs) need to migrate to search for their target cells in complex biological microenvironments, a key component of which is extracellular matrix (ECM). The mechanisms underlying CTL*s navigation are not well understood so far. Here we use a collagen assay as a model for the ECM and analyze the migration trajectories of primary human CTLs in collagen matrices with different concentrations. We observe different migration patterns for individual T cells. Three different motility types can be distinguished: slow, fast and mixed motilities. Slow CTLs remain nearly stationary within the collagen matrix and show slightly anti-persistent motility, while the fast ones move quickly and persistent. We hypothesize that the slow mode describes CTLs creating channels through the collagen matrix by deforming and tearing apart collagen fibers, and that the fast motility mode describes CTLs moving within these channels. The dynamics of the mixed type consists of periods of slow and fast motions. The dynamics can be well described by a two-state persistent random walk model. We extract the parameters of the model by analyzing experimental data.

BP 11.20 Mon 16:30 BPp

Is Cell segregation just like oil and water: A phase field approach — •Florian Franke, Steffen Lange, Hans-Joachim Böhme, Sebastian Aland, and Anja Voss-Böhme — Hochschule für Technik und Wirtschaft Dresden (HTW), Dresden, Germany

Understanding the segregation of cells is crucial to answer questions about tissue formation in embryos or tumor progression. According to Steinberg's differential adhesion hypothesis the separation of cells can be compared to the separation of two liquids, e.g. water and oil. Specifically, it was proposed, that similarly to the demixing of fluids, differences in the strengths of the adhesive forces in homo- and heterotypic cell contact lead to all sorting. This hypothesis has been tested on the basis of cell-based models which simulate motile cells with differential adhesive interaction on the basis of probability cellular automaton models. On the other hand, the segregation of fluids like water and Oil can be well described by phase-field models as the Cahn-Hilliard-Navier-Stokes-equation.

Here we investigate the relation between the two approaches and to what extent parameters can be transformed between the two models. Further, by comparing simulations of either model to in-vitro experiments from the literature, we conclude that cells segregation is best described by the cellular automaton. Only a specific time regime of the segregation resembles the demixing of two liquids. However, experimentally observed cell segregation displays both regimes of logarithmic and power-law segregation with varying exponent. This rich behavior is reproduced by the cellular automaton model.

BP 11.21 Mon 16:30 BPp

Theoretical approaches to mechanics of biofilms — •Hui-Shun Kuan[1], Wolfram Pönisch[2], Leander Self[3], Frank Jülicher[4], Michael Schmiedeberg[3], and Vasily Zaburdaev[1] — [1]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]MRC Laboratory for Molecular Cell Biology, University College London, United Kingdom — [3]Institut für Theoretische Physik 1, Friedrich-Alexander-Universität Erlangen-Nürnberg — [4]Max Planck Institute for the Physics of Complex Systems

Mechanics of biofilms is intrinsically affected by biological processes at different scales: from the activity of molecular motors to motility, and to cell death and division. As a result, the rheological properties of these bacterial colonies are markedly different from those exhibited by systems at thermal equilibrium. In this work, motivated by biofilms of *Neisseria gonorrhoeae* bacteria, we use a continuum theory and agent-based numerical simulations to study dense bacterial colonies shaped by attractive intercellular interactions. We can describe the formation of a colony as a phase separation process while the colony itself behaves as a viscoelastic material. By studying the behaviour of the colonies under oscillatory shear, we can link their mechanical properties to the dynamics of the intercellular forces. Due to the turnover of these active forces, the colonies show a liquid-like behaviour at large times and strong shear-thinning effect under the large amplitude of the oscillatory shear. Our study provides an important insight on how the active intercellular forces define the material properties of living aggregates which can now also be tested experimentally.

BP 11.22 Mon 16:30 BPp

Nanoprobing of osteoblasts adhered to molecular landscapes of dendrimer and protein — Christian Völkner[1], Issam Assi[1], Willi Karberg[1], •Regina Lange[1], Martina Grüning[2], Barbara Nebe[2], Ingo Barke[1], and Sylvia Speller[1] — [1]University of Rostock, Institute of Physics, Physics of Surfaces & Interfaces, 18059 Rostock — [2]Rostock University Medical Center, Dept. of Cell Biology, 18057 Rostock

Molecular surface gradients can constitute electric field landscapes and serve to control local cell adhesion and migration. This may allow the discovery of routes to improve osseointegration of implants. Flat molecule aggregate landscapes of amine-terminated dendrimers (PAMAM, generation 1) or proteins (BSA) were prepared on glass by micro contact printing [1] to provide lateral electric field gradients through their less negative zeta potentials compared to the glass substrate.
The local as well as the mesoscopic responses of adhered osteoblasts (MG-63) were studied by means of Scanning Ion Conductance Microscopy (SICM) [2] and Fluorescence Microscopy, in situ.
A distinct spindle shape oriented parallel to the stripe pattern as well as a preferential adhesion of the cells on the glass site have been observed when the width of the stripes and the spacing is 6 or 20 μm. To explain this effect, we suggest a retraction mechanism according to cathodic taxis, a subtype of galvanotaxis [3].
[1] Whitesides et al., Chem. Rev. 105, 1171 (2005)
[2] Korchev et al., Biophys. J. 73, 653 (1997)
[3] Djamgoz et al., J.of Cell Science 117, 1631 (2004)

BP 11.23 Mon 16:30 BPp

Kinetics of light-switchable surface association of *C. reinhardtii* populations — •Rodrigo Catalan[1], Alexandros Fragkopoulos[1], Nicolas von Trott[1], Simon Kelterborn[2], Peter Hegemann[2], and Oliver Bäumchen[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, 37077 Göttingen, Germany — [2]Humboldt University of Berlin, Institute of Biology, 10115 Berlin, Germany. — [3]University of Bayreuth, Experimental Physics V, 95440 Bayreuth, Germany

Bacterial and microalgal colonization on surfaces produce favorable and adverse effects in technological and medical settings. Therefore, the fundamental aspects of biofilm formation on solid substrates are actively studied. While bacteria have been the main focus of research to understand microbial surface colonization, analogous studies using archetypes in microalgae are thus far elusive. We exploit light-switchable flagellar adhesion of *C. reinhardtii* [Kreis et al., Nature Physics, 2018] to study the kinetics of adsorption and desorption of cell suspensions on glass using bright field microscopy and image analysis. We observe that both processes exhibit a lag response relative to

the time at which blue- or red-light conditions are set and we model this feature using time-delayed Langmuir kinetics. We find that adsorption occurs significantly faster than desorption, with the delay to be an order of magnitude larger. Adsorption experiments of phototactically blind *C. reinhardtii* mutants show that phototaxis does not affect the kinetics of either process. Hence, our method can be used as an assay for characterizing surface colonization.

BP 11.24 Mon 16:30 BPp

Unravelling the biomolecular origin of light-switchable adhesion of *Chlamydomonas* to surfaces — •Antoine Girot[1], Rodrigo Catalán[1], Alexandros Fragkopoulos[1], Marzieh Karimi[1], Simon Kelterborn[2], Peter Hegemann[2], Michael Hippler[3], and Oliver Bäumchen[1,4] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — [2]Institute of Biology, Humboldt University of Berlin, 10099 Berlin, Germany — [3]Institute of Plant Biotechnology and Biology, University of Münster, 48143 Münster, Germany — [4]Experimental Physics V, University of Bayreuth, 95440 Bayreuth, Germany

In this work, we focus on the adhesion of the biflagellated microalga *Chlamydomonas reinhardtii*. We discovered that this alga exhibits light-switchable adhesion, i.e. the flagella of the cells stick to surfaces under blue but not under red light. In order to unravel the biomolecular origin of this specific light-regulated behaviour, two different experimental approaches are carried out. First, we record the kinetics of the adsorption and desorption of a cell suspension to a surface in response to a light switch. Second, we employ *in vivo* micropipette force spectroscopy to measure the adhesion force of single cells. By applying these methods for different wild-type strains, we aim at identifying characteristic gene sequences associated to cells adhesion. To unravel the blue-light sensitive photoreceptor responsible for adhesion, these experiments are performed with specific photoreceptor-deleted mutants. Finally, we investigate how the glycosylation of the flagellar membrane proteins affects the adhesion of *Chlamydomonas*.

BP 11.25 Mon 16:30 BPp

Determination of the effective adhesion parameter for the sorting behavior of a cell system with several cell types using statistical learning methods — •Philipp Rossbach, Steffen Lange, Hans-Joachim Böhme, and Anja Voss-Böhme — Hochschule für Technik und Wirtschaft Dresden

The process of cell sorting plays an essential role in development and maintenance of tissues. To understand this process, mathematical modeling can assist cell biological research by providing means to analyze the consequences of different hypotheses on the underlying mechanisms. In the Differential Adhesion Hypothesis (DAH) by Steinberg (1962) it is assumed that cell sorting is determined by quantitative differences in cell type specific intercellular adhesion strengths. An implementation of the DAH is the Differential Migration Model (DMM) by Voss-Böhme and Deutsch (2010). From this DMM an effective adhesion parameter (EAP) for systems with two cell types can be derived analytically which predicts the asymptotic sorting pattern. However, the existence and form of such an parameter for more than two cell types is unclear.

Here, we investigate numerically the existence of an EAP for systems with more than two cell types. We rely on in-silico time-series data that is produced by a cellular automaton which emulates the DMM and classify the segregation behavior using statistical learning methods such as SVM and Logit Model. We use these tools to demonstrate the existence of an EAP for three cell types which matches our analytical prediction for systems with arbitrary many cell types.

BP 11.26 Mon 16:30 BPp

Optogenetic control of intracellular flows and cell migration: a minimal active gel model — •Oliver M. Drozdowski[1,2], Falko Ziebert[1,2], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, Philosophenweg 19, 69120 Heidelberg, Germany — [2]BioQuant, Heidelberg University, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany

The actin cytoskeleton of cells is in continuous motion due to both polymerization of new filaments and their contraction by myosin II molecular motors. Through adhesion to the substrate, such intracellular flow can be converted into cell migration. Recently, optogenetics has emerged as a new powerful experimental method to control both actin polymerization and myosin II contraction. While optogenetic control of polymerization can initiate cell migration by effecting protrusions, it is less clear if and how optogenetic control of contraction can effect cell migration. Here we analyze the latter situation using a minimal variant of active gel theory into which we include optogenetic activation as a spatiotemporally constrained perturbation. The model can describe the symmetrical flow of the actomyosin system observed in optogenetic experiments but not the long-lasting polarization required for cell migration. Motile solutions become possible if cytoskeletal polymerization is added to the boundary conditions. Optogenetic activation of contraction can then initiate locomotion in a symmetrically spreading cell and strengthen motility in an asymmetrically polymerizing one. If designed appropriately, it can also arrest motility even for protrusive boundaries.

BP 11.27 Mon 16:30 BPp

Reversible elastic phase field approach and application to cell monolayers — •Robert Chojowski, Ulrich S. Schwarz, and Falko Ziebert — Institute for Theoretical Physics and BioQuant, Heidelberg University, Germany

Force generation and motion of individual cells and cell collectives are fundamental constituents for many biological processes, including development, wound healing and cancer metastasis. Wound healing assays are quantitative experiments in which a 2D cell monolayer moves into empty space, often forming finger-like protrusions. Such experiments have revealed that migrating cell monolayers are both dynamic and elastic at the same time. However, such a combination of properties is very challenging to model with conventional approaches. Here we present a new phase field approach enabling us to predict the dynamics of thin elastic sheets under the action of active stresses and localized forces while ensuring reversibility as required by elasticity[1]. The continuum equations of our model can be solved by a combination of spectral and matrix methods and the numerical solutions can be compared to analytical ones. We demonstrate the potential of our modelling approach by studying several biologically relevant situations and geometries for single cells and cell monolayers, including elastic bars, contractile discs and the formation of elastic protrusions in an expanding monolayer scenario.

[1] R. Chojowski, U.S. Schwarz, F. Ziebert, Reversible elastic phase field approach and application to cell monolayers, Eur. Phys. J. E 43, 63 (2020)

BP 11.28 Mon 16:30 BPp

Morphodynamics in the Foraging of *Physarum polycephalum* — •Lisa Schick and Karen Alim — Technische Universit"at M"unchen

Foraging behaviour of animals is generally described as optimized for maximal energy uptake per time spend foraging within optimal foraging theory. Food sources often occur as food patches, so that foraging becomes a balance between time spent for exploration and time spent for patch exploitation leading to the question at which point a patch should be abandoned. Foraging behaviour in a patchy habitat can also be observed in unicellular but spatially extended organisms like *Physarum polycephalum*. However, it is unclear which foraging strategy the large and adaptive network-like morphology allows for. The plasmodial network of *P. polycephalum* adapts its morphology in the process of foraging by mass transport. Recent observations show that on encounter of a food patch, depending on body size, the whole body is relocated for exploitation. We here study the morphological changes as a function of network size and nutritional state by introducing a model for the exploration and exploitation phases in *P. polycephalum*. We estimate the energy uptake from our foraging observations in order to obtain rules for the foraging behaviour.

BP 11.29 Mon 16:30 BPp

A general theoretical framework to describe the influence of electric field on Mesechymal stem cell differentiation — •Jonathan Dawson[1], Ursula van Rienen[1,2,4], Poh Soo Lee[3], and Revathi Appali[1,4] — [1]Institute of General Electrical Engineering, University of Rostock, Germany — [2]Life, Light and Matter, Interdisciplinary Faculty, University of Rostock, Germany — [3]Max Bergmann Center for Biomaterials, Institute for Materials Science, Technical University of Dresden, Dresden, Germany — [4]Ageing of Individuals and Society, Interdisciplinary Faculty, University of Rostock, Germany

Bone regeneration is a highly complex and tightly regulated process which involves concerted and controlled action of human mesenchymal stem cell (hMSC) proliferation and differentiation into osteoblasts. Multiple physiological and environment factors influence the osteogenic differentiation and proliferation of hMSCs. Here we present a quantitative study investigating the influence of external electric field on

stem cell dynamics, specifically proliferation and differentiation. In experiments, hMSCs were exposed to a low-frequency electrical field applied via a transformer-like-coupling (TLC). Osteogenic differentiation was quantified by measuring expression levels of cell alkaline phosphate (ALP) activity over time. Our mean-field theory describes the dynamics of a population of ALP stained hMSCs and takes into account cell division, cell differentiation, and intracellular ALP activity. Our results show that the stem cell differentiation rate is electric field dependent, and the proliferation rate is cell-density dependent.

BP 11.30 Mon 16:30 BPp

Asymmetries & gradients during early C. elegans embryogenesis — •Rebecca Benelli, Philipp Struntz, Dirk Hoffmann, and Matthias Weiss — Universität Bayreuth

To enable differentiation of cells and to facilitate cell organization the establishment of gradients is crucial in early embryogenesis. We have used the model organism C. elegans and a custom built light-sheet microscope to study the formation of protein and organelle gradients in three dimensions over time. Due to the low phototoxicity and reduced bleaching induced by this selective illumination long term observations without developmental perturbations are made possible. The focus of the current study is on evolution until the first cell division, which, next to the different sized daugther cells, is characterized by a lot of accompanying asymmetries. We study the protein concentration of two vital proteins in early development with respect to their axial as well as radial distribution. Also, two organelles with opposing gradients are investigated. Since diffusion plays a vital role in the establishment of gradients a new multiplexed diffusion measurement technique (SPIM-FCS) is used to quantify changes in diffusive behavior of proteins in space and time.

BP 11.31 Mon 16:30 BPp

Characterisation of local membrane height fluctuations on live cells — •Max Ulbrich[1], Christian Völkner[1], Regina Lange[1], Sophie Kussauer[2], Robert David[2], Martina Grüning[3], Barbara Nebe[3], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, Physics of Surfaces & Interfaces, University of Rostock, 18059 Rostock — [2]University Medical Center, Cardial Regeneration, University of Rostock, 18057 Rostock — [3]Rostock University Medical Center, 18057 Rostock

Assessment of cellular membrane fluctuations may aid monitoring of physiologic and pharmacologic effects [1]. Scanning Ion Conductance Microscopy (SICM) is a nanoprobing method to acquire morphology and dynamics on live cells. We operate the nanopipette-probe on fixed lateral locations and record SICM time traces in order to assess membrane fluctuations and cell activities [2]. Membrane fluctuations of live osteoblasts and cardiomyocytes are analysed in the time and frequency domain. Living osteoblasts and paused pacemaker cells, in average, exhibit scaling exponents of -2.8 and -2.5, respectively, however with large variations from cell to cell and site to site. We discuss this behavior in view of reference measurements on fixed cells and in the context of optically obtained results [3].

[1] B Rappaz, et al, Blood Cells Mol. Dis. 42 (2009) 228
[2] S-O Kim, et al, Nano Convergence (2017) 4:5
[3] B Sinha, et al, Biophys. J. (2017) 113

BP 11.32 Mon 16:30 BPp

A single-molecule view of the cytosolic membrane of Trypanosoma brucei — •Paula Büttner, Marie Schwebs, and Susanne Fenz — Julius-Maximilians-Universität Würzburg, Würzburg, Germany

African trypanosomes are the causative agents of sleeping sickness. In the bloodstream of their host, they express a dense coat of GPI-anchored variant surface glycoproteins (VSGs). Fluidity of this coat is fundamental for the evasion of the hosts immune system and thus for the survival of the parasite. However, VSG dynamics is also limited by the lipid matrix. We have recently introduced super-resolution imaging of intrinsically fast-moving flagellates based on cyto-compatible hydrogel embedding and found that the inner membrane leaflet appears to be structured [Glogger et al. JPD 17 & Exp. Parsitol. 17]. We hypothesize that the WCB (whole cell body) protein, that connects the cytoskeleton with the plasma membrane, causes this structure. We present two-color single-molecule measurements of a lipid probe and WCB to address this hypothesis.

BP 11.33 Mon 16:30 BPp

Multi-color fluorescence fluctuation spectroscopy in living cells via spectral detection — •Valentin Dunsing, Annett Petrich, and Salvatore Chiantia — Universität Potsdam, Potsdam, Deutschland

Signaling pathways in biological systems rely on specific interactions between multiple biomolecules. Fluorescence fluctuation spectroscopy is a powerful toolbox to quantify such interactions directly in living cells. Cross-correlation analysis of spectrally separated fluctuations provides information about inter-molecular interactions, but is conventionally limited to two fluorophore species. Here, we present scanning fluorescence spectral correlation spectroscopy (SFSCS), a versatile approach that can be implemented on standard confocal microscopes, allowing the investigation of interactions between multiple protein species at the plasma membrane of cells. We demonstrate that SFSCS enables cross-talk-free cross-correlation, diffusion and oligomerization analysis of up to four protein species labeled with strongly overlapping fluorophores. As an example, we investigate the interactions of influenza A virus (IAV) matrix protein 2 with two cellular host factors simultaneously. We furthermore extend raster spectral image correlation spectroscopy (RSICS) to four species analysis and apply it to determine the stoichiometry of ternary IAV polymerase complexes in the cell nucleus. Based on triple correlation analysis of RSICS data, i.e. detection of coincident fluctuations of fluorescence signals emitted by three fluorophore species, we provide direct evidence for the assembly of ternary protein complexes.

BP 11.34 Mon 16:30 BPp

Conditions for thermodynamic stability and critical points in multicomponent mixtures with structured interactions — •Isabella Graf and Benjamin Machta — Yale University, New Haven, CT, USA

Multicomponent mixtures are ubiquitous in biology, ranging from cellular membranes to liquid-like droplets. There is experimental evidence that their phase behavior plays a functional role for signaling and control of biochemical reactions and is under regulation itself. For instance, it has been demonstrated recently that membranes composed of a large variety of lipids are tuned close to a miscibility critical point. Theoretical work has shed light on the phase behavior of idealized systems with many components and random, mutually independent interactions, but there is little understanding of how these results generalize to systems with more structured interactions. To address this open question, we consider a family of multicomponent models with an interaction matrix of variable rank. The matrix is constructed so that each component is characterized by several scalar "features", each of which conveys an Ising-like interaction between neighboring components and could be interpreted as lipid tail length, headgroup or saturation in the case of membrane lipids. We derive analytical, mean-field conditions for the occurrence of thermodynamic stability and (higher-order) critical points and find that these conditions depend on the cumulants of the principal components of the feature distribution. These results might provide important insights into critical membrane behavior and phase behavior of multicomponent mixtures more generally.

BP 11.35 Mon 16:30 BPp

Modeling RNA Polymerase II clusters by lattice kinetic Monte Carlo simulations — •Tim Klingberg[1,2], Lennart Hilbert[3], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Max-Planck-Zentrum für Physik und Medizin — [3]Karlsruher Institut für Technologie

Eukaryotic genes are mainly transcribed by RNA polymerase II (Pol II). Before active transcription starts, Pol II is recruited to the promoter region of a specific gene and then released from a paused state into transcript elongation. Clusters of paused Pol II of various sizes and morphologies can be observed in zebrafish embryos (Pancholi et al.). Here, we aim to understand the physical mechanisms that are essential for the cluster formation and determine their emerging properties. To this end, we apply two-dimensional lattice kinetic Monte Carlo simulations with single Pol II particles interacting with DNA polymers, whose dynamics are determined by the Verdier-Stockmayer algorithm. The model suggests that formation of Pol II clusters can be rationalized as phase separating phenomenon where polymerases form a liquid phase that wets the chromatin at the promoter region. Cluster properties such as size and morphology can be linked to the size of the promoter region and the respective gene. Despite the simplicity of the model, it is sufficient to qualitatively describe the experimentally observed cluster properties in normal conditions and under drug treatments interfering with the transcription process.

BP 11.36 Mon 16:30 BPp

Euchromatin reorganisation during transcription resembles active microemulsion — •Rakesh Chatterjee[1,2], Hui-Shun Kuan[1,2], and Vasily Zaburdaev[1,2] — [1]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg, 91058 Erlangen, Germany — [2]Max Planck Zentrum für Physik und Medizin, 91058 Erlangen, Germany

During transcription RNA polymerase II (Pol II) attaches and moves along the DNA strand to produce messenger-RNA (mRNA). The selective induction of transcription from DNA into RNA shapes and is being shaped by the chromatin organisation. To investigate this complex interplay, we aim to establish a phenomenological model, which qualitatively mimics the experimental results regarding transcription process in primary cell cultures obtained from zebrafish embryos. Our phenomenological lattice model is based on the framework of microphase separation or microemulsion. DNA, mRNA and Pol II serve as the three basic components similar to the oil-water-surfactant system, which exhibits two and three phase coexistence. Freely diffusing Pol II undergoes chemical transitions reflecting different stages of the transcription process. Similar behaviour can be realised by assuming transient dynamics of the surfactants which switches between active and inactive states. We use lattice model simulations and the correlation function approach to characterises different phases of this three component system. The resulting structures can be understood via the continuum theory that we derive by coarse-graining the lattice model.

BP 11.37 Mon 16:30 BPp

Deformability-based cell sorting by a microfluidic ratchet effect — •Sebastian W. Krauss, Pierre-Yves Gires, Winfried Schmidt, Walter Zimmermann, and Matthias Weiss — University Bayreuth, Bayreuth, Germany

Various physiological states impact on the rigidity of cells, e.g. aging, infection, or cancer. Cellular rigidity can be quantified with a high throughput by monitoring cell deformations during passage through a narrow constriction in a microfluidic device [1]. In contrast to this mere feed-forward approach, we use an asymmetric periodic flow protocol to exploit flow-induced deformations for sorting cells according to their stiffness. In particular, we apply an asymmetrically oscillating flow in a microfluidic channel that leads to a zero net drift of solid polystyrene particles, whereas deformable objects, here taken as red blood cells, experience a nonzero deformation-dependent displacement in each cycle. Preliminary results suggest this approach to be a versatile tool for screening the physiological state of cells.

[1] Otto, O., et al. (2015) Nature Methods 12.3, 199

BP 11.38 Mon 16:30 BPp

Mechanical phenotyping beyond geometrical constraints using virtual fluidic channels — •Muzaffar Panhwar[1], Fabian Czerwinski[1], Venkata A.S. Dabbiru[1], Yesaswini Komaragiri[1], Peter Nestler[1], Bob Fregin[1], Ricardo H. Pires[1], Doreen Biedenweg[2], and Oliver Otto[1] — [1]AG Biomechanic, ZIK-HIKE, Universität Greifswald, Greifswald, Deutschland — [2]Universitätsmedizin Greifswald, Greifswald, Deutschland

Microfluidic techniques have proven to be of key importance for achieving high-throughput cell mechanical measurements. However, their design modifications require sophisticated cleanroom equipment. Here, we introduce virtual fluidic channels as a flexible and robust alternative to Poly-dimethylsiloxane chips. Virtual channels are liquid-bound fluid flows that can be tailored in three dimensions within seconds for rheological studies on a wide size range of biological samples. While cell deformation inside standard hard-wall constrictions is mainly driven by shear stress, virtual channel possess an additional normal stress component originating from the liquid-liquid interface. We demonstrate that this interface acts as a high-frequency liquid cantilever for probing cell rheology on a millisecond timescale. In proof-of principle experiments, cells are treated with cytochalasin D to inhibit actin polymerization. A significant reduction in the Young's modulus is found compared to untreated cells. In addition, we utilize virtual channels to measure the mechanical properties of single cells and spheroids as a tissue model system. Our results indicate that the Young's modulus of single cells exceeds the one of tissue by one order of magnitude.

BP 11.39 Mon 16:30 BPp

Monitor, categorize and manipulate label-free water-in-oil droplets in microfluidic systems — •Tobias Neckernuss[1,3], Chrostoph Frey[2], Jonas Pfeil[1,3], Daniel Geiger[1,3], Ilia Platzman[2], Joachim Spatz[2], and Othmar Marti[1] — [1]Institute for Experimental Physics, Ulm University — [2]Max-Planck-Institute for Medical Research, Heidelberg — [3]Sensific GmbH, Germany

A key point of droplet based microfluidics is the availability of powerful but easy-to-implement methods for high throughput real-time analysis and automated manipulation of the droplets. We developed a novel optical device, consisting of a fast camera with integrated data processing for smart and fast algorithms enabling label-free real-time monitoring and active manipulation of passing droplets. The device continuously analyzes up to 3000 particles per second in real-time with respect to bright-field image parameters like size, brightness, granularity, circumference, speed and many more. According to these parameters and combinations thereof, the passing droplets can be sorted. We measure different droplet production parameters and demonstrate label-free detection of cells encapsulated in droplets. Furthermore, we performed label-free sorting of cell laden droplets from empty droplets. The peripheral sorting electronics are controlled by our device. Decision making is based on predefined parameter ranges that are compared to the measurement results of the droplets right before the sorting gate. Similarly, in another experiment we demonstrate efficient sorting of droplets depending on size.

BP 11.40 Mon 16:30 BPp

Transition of adherent to suspension state: relevance to cell mechanical properties — •Venkata Dabbiru[1], Emmanual Manu[1], Huy Tung Dau[1], Nora Bödecker[1], Doreen Biedenweg[2], Ricardo Pires[1], and Oliver Otto[1] — [1]University of Greifswald, Germany — [2]University Medicine Greifswald, Germany

Adherent cells often detach from their native surface as a result of important physiological changes such as those, for example, found in cancer. While many studies have examined the mechanical properties of cells in their native adherent or suspended state, few studies have addressed the consequences associated with the transition between them. We have approached this question by using atomic force microscopy for adherent and semi-adherent cells as well as real-time deformability cytometry to study the mechanical properties of cells in suspension. As a model system, HEK293T cells have been cultured in the presence and absence of surface-tethering molecules, respectively, to mimic the transition state. Our results show that cell detachment is associated with increased stiffening of cells. Interestingly, surface-tethered transiently suspended cells and fully suspended cells differ in their mechanical properties. Analysing the F-actin distribution by confocal microscopy indicates a passive cell-surface interaction, which is not driven by adhesion molecules.

BP 11.41 Mon 16:30 BPp

Brillouin microscopy studies on phase separated FUS protein droplets — •Timon Beck[1,2], Mark Leaver[2], Raimund Schlüssler[2], and Jochen Guck[1,2] — [1]Max-Planck-Institut für die Physik des Lichts, Erlangen — [2]Biotec TUD, Dresden

The reversible phase separation of protein-RNA condensates plays an important role in intracellular organization and is involved, for example, in metabolic control and DNA repair. These phase-separated compartments can undergo an irreversible solidification, which has been associated with neurodegenerative diseases. This phenomenon has been mostly studied qualitatively and indirectly, and a direct quantitative determination of the bulk material properties during the solidification is still missing. Here, we use Brillouin microscopy to investigate phase-separated FUS protein droplets in vitro. Brillouin microscopy is a non-invasive technique which measures optomechanical properties with optical resolution using (spontaneous) Brillouin scattering. This non-elastic scattering process occurs when light is scattered by (thermally excited) soundwaves. Quantification of the Brillouin frequency shift gives direct access to the longitudinal modulus, refractive index and mass density, while the linewidth is linked to the viscosity. We followed the solidification of FUS protein droplets over time in a controlled environment monitoring the changes in Brillouin shift and linewidth. Our measurements aim to reveal the relevant time-scales and the impact of different buffer conditions on the solidification process. This establishes Brillouin microscopy as a promising quantitative tool for unraveling the mechanisms of this type of phase transition.

BP 12: Single Molecule Biophysics I

Time: Tuesday 9:00–11:00 Location: BPa

Invited Talk BP 12.1 Tue 9:00 BPa

Molecular simulation meets cryo electron tomography — •Gerhard Hummer — Max Planck Institute of Biophysics, Frankfurt am Main, Germany

Cryo electron tomography and molecular dynamics simulations perfectly complement each other. Electron tomograms provide us with a remarkably detailed, three-dimensional view of the molecular architecture of cells and viruses in situ, that is in the natural context; however, this view is essentially static and atomic resolution remains largely out of reach, in particular for dynamic biomolecular machineries. By contrast, molecular dynamics simulations naturally give us an atomistic view that includes dynamics, albeit in an idealized context. The synergistic potential of tomography and simulation can now be realized thanks to an increase in the resolution achievable by cryo electron tomography, a rapid growth in raw computational power, significant improvements in the quality of the potential energy functions entering classical molecular dynamics simulations, and the availability of simulation codes that can handle the complex molecular systems encountered in situ. To illustrate the power of combining molecular simulations with cryo electron tomography, I will present results from studies of the spike protein of the SARS-CoV-2 virus (Turoňová, Sikora, Schürmann et al., Science 2020) and from desmosome cell-cell junctions (Sikora, Ermel, Seybold et al., PNAS 2020).

BP 12.2 Tue 9:30 BPa

Electronic Quantum Coherence in Photosynthetic Protein Complexes — Hong-Guan Duan Duan[1], Ajay Jha[1], Vandana Tiwari[1], Richard J. Cogdell[2], Khuram Ashraf[2], Valentyn I. Prokhorenko[1], •Michael Thorwart[3], and R. J. Dwayne Miller[4] — [1]Max Planck Institute for the Structure and Dynamics of Matter, Hamburg — [2]Institute of Molecular, Cell & Systems Biology, University of Glasgow, UK — [3]I. Institut für Theoretische Physik, Universität Hamburg, Germany — [4]University of Toronto, Canada

The search for quantum effects in biological systems led previous experiments to report long-lived electronic quantum coherence in the primary step of the energy transfer in photosynthetic protein complexes. However, the origin of the coherence became a topic of intense debate. We have revisited this in a joint experimental and theoretical effort studying the quantum dynamics in the Fenna-Matthews-Olson (FMO) complex by two-dimensional electronic spectroscopy at different temperatures. We found that the electronic coherence time is significantly shorter under ambient conditions than previously reported. To capture solid evidence of quantum coherence, lower temperatures are required. We have clearly observed electronic coherence with a time scale of 500 fs at low temperature (20 K). However, the coherence lifetime is rapidly reduced with increasing temperature. At room temperature, electronic coherence is too short (60 fs) to play any functional role in the energy transfer which occurs on a time scale of picoseconds. The long-lived oscillations previously reported in 2D spectra are due to Raman vibrational modes on the electronic ground state.

BP 12.3 Tue 9:50 BPa

Conformational Changes of IDP under Influence of Guanidinium Chloride: Integrative Approach using X-ray/Neutron Scattering and Single Molecule Spectrosopy — •Luman Haris[1,2], Iwo König[4], Martin Dulle[1], Aurel Radulescu[3], Ingo Hoffmann[5], Olaf Holderer[3], Tobias Erich Schrader[3], Ben Schuler[4], and Andreas Maximilian Stadler[1,2] — [1]FZ Jülich, JCNS-1 & IBI-8, Jülich — [2]IPC, RWTH Aachen, Aachen — [3]FZ Jülich, Outstation MLZ, Garching — [4]Biochemisches Institut, Universität Zürich, Zürich — [5]Institut Laue-Langevin, Grenoble

IDPs are identified by the presence of unfolded region due to relatively abundant polar residues content within its amino acid sequence. Together with other residues, IDPs exhibit not only high flexibility but also sensitivity to physico-chemical fluctuation such as pH, temperature, and ions concentration. For this reason, IDPs are involved in cellular processes such as DNA repair scheme and chromatin modification. In this project, we pursue a quantitative description of structure and dynamics of IDPs with different net charges: namely Prothymosin Alpha and Myelin Basic Protein. Here, we employed neutron spin-echo spectroscopy (NSE) and small angle X-ray scattering (SAXS) to gain insight on the emergence of internal friction within the peptide and its conformational change as a function of Guanidinium Chloride (GndCl) concentration respectively. The experimental results obtained from SAXS shows contraction and expansion as measured by FRET. Similarly, from NSE data, we are able to extract the internal friction which is in good agreement with FCS result.

BP 12.4 Tue 10:10 BPa

Do the loops in the N-SH2 binding cleft truly serve as allosteric switch in SHP2 activation? A tale of disorder, crystal contacts, and activation free energies — Massimiliano Anselmi and •Jochen S Hub — Unvierstität des Saarlandes, Saarbrücken, Germany

SHP2 is a multi-domain protein, playing an important role in upregulating cellular processes such as cell survival, proliferation, and programmed cell death. SHP2 mutations cause developmental disorders and were found in many cancer types. In healthy cells, SHP2 mainly takes an autoinhibited, inactive form, and SHP2 is activated upon binding of a phosphopeptide to the N-SH2 domain. For the past two decades, the widening of the binding cleft upon peptide binding has been considered as the key event driving SHP2 activation.

We re-analyzed the manifold amount of crystallographic data of SHP2, and we carried out extensive MD simulations and free energy calculations of SHP2 in solution and in a crystal environment. We found that the "allosteric switch" model is in fact compromised by crystal contacts and flexible, poorly resolved loops, and that the degree of openness of the binding cleft does not even influence the free energy of SHP2 opening. Instead, we detected an alternative allosteric mechanism, namely the unzipping of a central beta sheet of N-SH2, which drives SHP2 activation. Apart from the implications on SHP2 activation and inhibition, the study highlights that MD simulations in crystal and solution environments are a powerful tool to avoid misinterpretation of crystal structures.

30 min. Meet the Speaker

BP 13: Multicellular Systems I

Time: Tuesday 9:00–11:00 Location: BPb

BP 13.1 Tue 9:00 BPb

Elongated Cells Fluidize Malignant Tissues — •Steffen Grosser, Jürgen Lippoldt, Linda Oswald, Frédéric Renner, and Josef A. Käs — Peter Debye Institute for Soft Matter Physics, Universität Leipzig

Tissue morphology changes during tumour progression. In 2D cell cultures, different tissue states, such as fluid, jammed and nematic, are linked to cell shapes. While it is not clear if these results hold true in three dimensions, they suggest to investigate cell shapes and tissue states of matter in 3D. To explain cell motility in tumors, we compare 3D cell spheroids composed of cells from a cancerous and a non-cancerous cell line. Through spheroid fusion experiments and live cell tracking, we show that the epithelial sample behaves solid-like and the malignant sample is fluidized by active cells moving through the tissue. Full 3D-segmentations of the samples show that the fluid-like tissue has elongated cell shapes. This links cell shapes to cell motility and bulk mechanical behaviour. We reveal two active states of matter in 3D tissues: an amorphous glass-like state with characteristics of 3D cell jamming, and a disordered fluid state.

BP 13.2 Tue 9:20 BPb

Relation between tissue homeostasis and mechnosensitivity in model epithelium — •Maxime Hubert[1], Sara Kaliman[1], Carina Wollnik[2], Simone Gehrer[1], Damir Vurnek[1], Diana

Dudziak[3], Florian Rehfeldt[2], and Ana-Suncana Smith[1,4] — [1]PULS Group, Friedrich Alexander University Erlangen-Nurnberg, Erlangen, Germany — [2]Cell & Matrix Mechanics Group, Georg-August-University Gottingen, Gottingen, Germany — [3]Group for the Biology of Dendritic Cells, University Clinic Erlangen-Nurnberg, Erlangen, Germany — [4]Group for Computational Life Sciences, Ruder Boskovic Institute, Zagreb, Croatia

Despite recent efforts to understand homeostasis in epithelial tissues, there are many unknowns surrounding this cooperative steady state. In the context of cell morphology, single cell studies set mechanosensitivity as an important regulatory process. However, mechanoresponse in tissues remains heavily debated. Here we show that changes in matrix stiffness induce a non-equilibrium transition from tubular to squamous tissues. Despite adopting different cell shapes and densities, all homeostatic states display equivalent topologies. This suggests that the latter property is actively targeted in homeostasis. On the contrary, we observe a dramatic change in the self-assembled organization of the colonies on the macroscopic scale. Such behavior is recovered in simulations by introducing stiffness-dependent activity. Our results unequivocally relate the mechanosensitive properties of individual cells to the evolving macroscopic structures, an effect that could be important for understanding the emergent pathology of living tissues.

Invited Talk BP 13.3 Tue 9:40 BPb

Active behaviors of cellular monolayers. — •Benoit Ladoux — Institut Jacques Monod, CNRS & Université de Paris, Paris, France

The actomyosin machinery endows cells with contractility at a single cell level. Within a tissue, cells are not only interacting with their substrate but also with their neighbors. The way forces from adhesion complexes are transmitted leads to various collective behaviors and plays a role in the active nature of cellular monolayers. In the first part, I will show how these active behaviours and stresses govern fundamental biological processes such as cell extrusion. By modelling the epithelium as an active nematic liquid crystal and measuring mechanical parameters such as strain rates and stresses measurements within cellular monolayers, we show that apoptotic cell extrusion is provoked by singularities in cell alignments in the form of comet-shaped topological defects. Cellular monolayers display various active behaviors as exemplified by the contractile nature of fibroblasts and the extensile nature of epithelial cells or neural crest cells. In the second part, I will discuss how these two contradictory modes of force generation can coexist. Through a combination of experiments and in silico modeling, we uncover the mechanism behind this switch in behaviour of cell monolayers from extensile to contractile as the weakening of intercellular contacts. We find that this switch in active behaviour also promotes the buildup of tension at the cell-substrate interface through an increase in actin stress fibers and higher traction forces. Such differences in extensility and contractility act to sort cells, thus determining a general mechanism for mechanobiological pattern formation.

BP 13.4 Tue 10:10 BPb

cell competition in mouse embryo — •Gabriele Lubatti[1], Antonio Scialdone[1], Tristan Tristan[2], Ana Lima[2], and Shankar Srinivas[3] — [1]Institute of Epigenetics and Stem Cells, Helmholtz Zentrum Munich, Munich, Germany — [2]National Heart and Lung Institute, Imperial College London, Hammersmith Hospital Campus, London, UK — [3]Department of Physiology Anatomy & Genetics, University of Oxford, Oxford, UK

Cell competition is a biological process whereby cells eliminate their less fitted neighbours [1] [2]. It has myriad positive roles in the organism: it selects against mutant cells in developing tissues, prevents the propagation of oncogenic cells and eliminates damaged cells during ageing. While it was first characterized in drosophila [3], it is currently unclear what are the transcriptional features of cells eliminated through competition and what are the roles of cell competition during mammalian development. We analysed single-cell transcriptomic data from mouse embryos around the time gastrulation starts (stage E6.5) where apoptosis was inhibited. We show that in these embryos a new population of epiblast cells emerges, expressing markers of cell competition previously characterized [4]. Our analysis also identifies additional features of eliminated cells, including disrupted mitochondrial activity that we validate in vivo. Moreover, by using physical modelling, we show that cell competition might play a role in the regulation of embryo size, which could be particularly important around gastrulation [5].

30 min. Meet the Speaker

BP 14: Focus Phase Separation in Biological Systems I (joint session BP/CPP)

Time: Tuesday 9:00–11:00 Location: BPc

BP 14.1 Tue 9:00 BPc

Intranuclear Phase Separation of a Chromatin Scaffolding Protein — •Davide Michieletto[1], Mattia Marenda[1], David Zwicker[2], and Jan Kirschbaum[2] — [1]University of Edinburgh — [2]Max Planck Institute for Dynamics and Self-Organization

The formation and regulation of phase separated condensates is now widely seen in vitro and cytoplasm, but far more challenging to observe and test in the cell nucleus. In this talk I will present recent work on an abundant nuclear RNA-binding protein called Scaffold Attachment Factor A, or SAF-A, that regulates chromatin decompaction at transcriptionally active loci through its interaction with RNA. Here I show that the intrinsically disordered RNA binding domain of SAFA * known as an RGG domain – undergoes phase separation upon transcriptional inhibition and that the size of the condensates can be controlled by tuning the amount arginine/lysine residues in the RGG domain. By expressing a longer, and closer to native, SAFA domain we observe that the phase separation is suppressed. To explain our findings, we propose an equilibrium model in which a slowly diffusing RNA substrate can sequester RGG fragments; upon transcriptional inhibition the freed up fragments can undergo phase separation via weak self-interactions.

BP 14.2 Tue 9:20 BPc

Quantitative phase microscopy enables precise and efficient determination of biomolecular condensate composition — •Patrick M McCall[1,2], K Kim[3,4], AW Fritsch[1], JM Iglesias-Artola[1], LM Jawerth[1,2], J Wang[1], M Ruer[1], A Poznyakovskiy[1], J Peychl[1], J Guck[3,4], S Alberti[3], AA Hyman[1], and J Brugués[1,2] — [1]MPI-CBG, Dresden — [2]MPI-PKS, Dresden — [3]TU Dresden — [4]MPI Science of Light

Many cellular processes rely on condensed macromolecular phases termed biomolecular condensates. Despite progress in measurements and theoretical descriptions of several condensate properties, an understanding of their most basic feature, composition, remains elusive. Here we combined quantitative phase microscopy and sessile droplet physics to measure the shape and composition of individual model condensates. This technique requires 1000-fold less material than traditional approaches, achieves a precision of better than 2 %, and does not rely on fluorescent tags, which we show can significantly alter phase behavior. The protein concentrations measured in three model condensates span a broad range, from 80 to 500 mg/ml, pointing to a natural diversity in condensate composition specified by protein sequence. We report salt- and temperature-dependent binodals as well as time-resolved measurements revealing that PGL3 condensates undergo a contraction-like process during aging. This leads to doubling of the internal protein concentration coupled to condensate shrinkage. We anticipate that this new approach will enable understanding the physical properties of biomolecular condensates and their function.

BP 14.3 Tue 9:40 BPc

Quantitative Theory for the Diffusive Dynamics of Liquid Condensates — •Lars Hubatsch[1,2], Louise M Jawerth[1,2], Celina Love[2], Jonathan Bauermann[1], Stefano Bo[1], T-Y Dora Tang[2], Anthony A Hyman[2], and Christoph A Weber[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

To unravel the biological functions of membraneless liquid condensates it is crucial to develop a quantitative understanding of the physics underlying their dynamics. Key properties of such condensates are

diffusion and exchange of material with their environment. Experimentally, such diffusive dynamics are typically probed through the direct observation of the individual or collective motion of fluorescently labelled molecules. However, to date we lack a physics-based quantitative framework for the dynamics of labeled condensate components. Here, we derive the corresponding theory, building on the physics of phase separation, and quantitatively validate this framework via experiments. We show that using our theory we can precisely determine diffusion coefficients inside liquid condensates via a spatio-temporal analysis of fluorescence recovery after photobleaching (FRAP) experiments. We showcase the accuracy and precision of our approach by considering space and time resolved data of protein condensates and two different coacervate systems. Strikingly, our theory can be used to determine the diffusion coefficient in the dilute phase and the partition coefficient, purely based on fluorescence measurements in the droplet.

BP 14.4 Tue 10:00 BPc

Interactions of droplets with polymer networks at the mesh and continuum scale — •Thomas J Boeddeker[1], Estefania Vidal[2], Kathryn A Rosowski[1], David Zwicker[2], and Eric R Dufresne[1] — [1]ETH Zurich, Zurich, Switzerland — [2]MPI DS, Göttingen, Germany

Phase-separation of biomolecules in cells takes place in a complex environment crossed by multiple filaments of the cytoskeleton or chromatin. Interactions between the emerging protein droplets and filaments take place over different length scales and may lead to motion and deformation of both network and droplet. In this shared talk, Thomas presents experimental work on the interactions of stress granules, a phase-separated protein-RNA droplet in the cytosol, with the heterogeneous microtubule network at the mesh scale. Inspired by observations in the cell, we then turn to synthetic gels where elastic effects produce ripening in stiffer materials leading to a dissolution front. Estefania presents a theoretical framework for the observed ripening in gradients of network stiffness at the continuum scale. Our combined results present an initial approach to understand the complex interactions throughout phase separation in an elastic network.

30 min. Meet the Speaker

BP 15: Active Matter 1 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP/CPP)

Time: Tuesday 9:30–10:30 Location: DYa

BP 15.1 Tue 9:30 DYa

Swirl formation of active colloids near criticality — •Robert C. Löffler[1], Tobias Bäuerle[1], Mehran Kardar[2], Christian M. Rohwer[3], and Clemens Bechinger[1] — [1]FB Physik, Universität Konstanz, Germany — [2]Dep. Physics, MIT, Cambridge, MA, USA — [3]Dep. Mathematics, University of Cape Town, South Africa

Animal groups like flocks of birds or schools of fish normally show a high degree of order. Yet they are also responsive to external factors in order to optimize nutrition and avoid predation. Various observations of such responsiveness have let to the assumption that those systems represent a state of order close to a critical point.

In our experiments, we use light-responsive active Brownian particles (ABPs) to which we can apply individual torques in a feedback controlled system to study such behavioral rules. Through the variation of a single parameter in our interaction model based on information about a particles local neighbors, we observe a continuous phase transition in the collective motion of the group: The ABPs transition from a disordered swarm to a stable swirl (i.e. milling, vortex-like state). Being able to continuously change our control parameter we observe a critical point with explicit bifurcation dynamics in the rotational order parameter and critical slowing down, as well as hysteresis in the symmetry-breaking regime of the control parameter. Observation of such critical behavior in simple models not only allows for more insight in complex animal behavior but also helps with designing future rules for collective tasks in robotic or other autonomous systems.

Bäuerle *et al.*, Nat. Comm. **11**, 2547 (2020); Löffler *et al.* (in review).

BP 15.2 Tue 9:50 DYa

A particle-field approach bridges phase separation and collective motion in active matter — •Robert Grossmann[1], Igor Aranson[2], and Fernando Peruani[3] — [1]Institute of Physics and Astronomy, University of Potsdam, Potsdam, Germany — [2]Department of Chemistry, Pennsylvania State University, University Park (PA), United States of America — [3]Laboratoire de Physique Théorique et Modélisation, CY Cergy Paris Université, Cergy-Pontoise, France

Linking seemingly disconnected realms of active matter – active phase-separation of repulsive discs and collective motion of self-propelled rods – is a major contemporary challenge. We present a theoretical framework based on the representation of active particles by smoothed continuum fields which brings the simplicity of alignment-based models, enabling an analytical analysis, together with more realistic models for self-propelled objects including their steric, repulsive interactions. We demonstrate on the basis of the collision kinetics how nonequilibrium stresses acting among self-driven, anisotropic objects hinder the emergence of motility-induced phase separation and facilitate orientational ordering. Moreover, we report that impenetrable, anisotropic rods are found to form polar, moving clusters, whereas large-scale nematic structures emerge for soft rods, notably separated by a bistable coexistence regime. Thus, the symmetry of the ordered state is not dictated by the symmetry of the interaction potential but is rather a dynamical, emergent property of active systems. This theoretical framework can represent a variety of active systems: cell tissues, bacterial colonies, cytoskeletal extracts or shaken granular media.

BP 15.3 Tue 10:10 DYa

A Quantitative Kinetic Theory of Flocking in Dry Active Matter Including a Three Particle Closure — •Rüdiger Kürsten and Thomas Ihle — Institut für Physik, Universität Greifswald, Germany

We consider aligning self-propelled point particles in two dimensions. Their motion is given by generalized Langevin equations, however, the qualitative behavior is as for the famous Vicsek model. We develop a kinetic theory of flocking beyond mean field. In particular, we take into account the full pair correlation function. We find excellent quantitative agreement of those pair correlations with direct agent-based simulations within the disordered regime. Furthermore we use a closure relation to incorporate the spatial correlations of three particles. In that way we achieve good quantitative agreement of the onset of flocking with direct simulations. Compared to mean field theory, the flocking transition is shifted significantly towards lower noise because angular correlations favor disorder.

BP 16: Single Molecule Biophysics II

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

BP 16.1 Tue 11:00 BPa

Comparison of continuous and discrete Markov models of biomolecular dynamics — •Benjamin Lickert and Gerhard Stock — Universität Freiburg

Motions of biomolecular systems, recorded by molecular dynamics simulations, are often modeled as Markov processes. A very popular approach is given by Markov state models where the conformational space is divided into different states [1]. To be Markovian, the intrastate dynamics need to be significantly faster than the interstate dynamics. On the other hand, the observed dynamics can be modeled as a continuous

diffusive process, called Langevin dynamics, on some low-dimensional free energy landscapes $F(\vec{x})$. In this case, Markovianity is given if the system, i.e., $\vec{x}(t)$, evolves substantially slower than the neglected degrees of freedom, i.e., the bath surrounding the system. Recently, a data-driven approach was formulated to estimate such a Langevin model from a given trajectory $\vec{x}(t)$. Here, we compare the features of both modeling frameworks. While Markov state models are very appealing due to their clearly structured generation and interpretation, Langevin dynamics have the advantage that they allow for the estimation of continuously defined observables, like free energy and autocorrelations. Using molecular dynamics simulations of systems with varying complexity we have a look at these points in practice [2].

[1]: J.H.Prinz et al., J.Chem.Phys. 134, 174105 (2011)
[2]: B.Lickert and G.Stock, J.Chem.Phys. 153, 244112 (2020)

BP 16.2 Tue 11:20 BPa

Magnetic Tweezers Protein Force Spectroscopy: Applications to Von Willebrand Factor and SARS-CoV-2 Cell Adhesion — •Jan Lipfert[1], Magnus Bauer[1], Steffen Sedlak[1], Achim Löf[1], Tobias Obser[2], Maria Brehm[2], Martin Benoit[1], Adina Hausch[1], and Sophia Gruber[1] — [1]Department of Physics, LMU Munich — [2]Department of Pediatric Hematology and Oncology, University Medical Center Hamburg Eppendorf

The physiological function of proteins is often critically affected by forces acting on them. We have developed a versatile and modular approach for force measurements on proteins in magnetic tweezers [Löf et al. PNAS 2019; Gruber et al. Nanoscale 2020] that enables ultra-stable (>days) and parallel measurements (>50) in a wide force range, in particular at low forces (<1 pN).

We apply our new assay to two systems critical in human pathologies: the blood protein von Willebrand Factor (VWF) and the Spike-mediated adhesion of SARS-CoV-2, the causative agent of the current pandemic. First, we probe regulatory transitions at low forces within VWF. Our results reveal fast (~250 ms) transitions in the dimeric VWF stem around 1 pN, which likely constitute the first steps in its mechano-activation. Second, we use a tethered ligand assay to quantitate how the SARS-CoV-2 spike protein binds to its cellular receptor ACE2. We find that SARS-CoV-2 has a higher force stability and lower off-rate than the previous SARS-CoV-1, which caused the 2002 pandemic, which might contribute to different infection patterns observed for the two viruses.

BP 16.3 Tue 11:40 BPa

Watching an enzyme at work: Time-Resolved Serial Crystallography reveals water mediated allosteric regulation — •Henrike Müller-Werkmeister — Uni Potsdam, Institut für Chemie, Physikalische Chemie, Karl-Liebknecht-Str. 24-25, 14476 Potsdam

We have studied the homodimeric enzyme fluoroacetate dehalogenase by time-resolved serial synchrotron crystallography (TR-SSX). Using a fixed target based sample delivery [1] with an efficient interlacing pattern allowed us to realize "hit-and-return" (HARE) TR-SSX to cover the full timescale from 30 milliseconds to 30 seconds [2]. With a photocaged substrate for reaction initiation, four catalytic turnovers could be resolved [3]. The total of 18 independent structures not only provide unprecedented insight into the reaction mechanism, showing the substrate binding, the Michaelis-Menten-complex and the covalent intermediate, but also reveal the allosteric mechanism leading to half-the-sites reactivity. In fact, a molecular water wire can be observed that together with molecular breathing is clocked to the enzymatic reaction.

[1] I. Martiel, H. M. Müller-Werkmeister, A. E. Cohen, Acta Cryst. D, 2019, D75, 160*177 [2] E. C. Schulz*, P. Mehrabi*, H. M. Müller-Werkmeister*, F. Tellkamp, A. Jha, W. Stuart, E. Persch, R. De Gasparo, F. Diederich, E. F. Pai, R. J. D. Miller, Nature Methods, 2018, 15 (11), 901-904 [3] P. Mehrabi*, E. C. Schulz*, R. Dsouza, H. M. Müller-Werkmeister, F. Tellkamp, R. J. D. Miller, E. F. Pai, Science, 2019, 365 (6458), 1167-1170

BP 16.4 Tue 12:00 BPa

Hybrid Kinetic Monte Carlo / Molecular Dynamics Simulations of Bond Scissions in Proteins — •Benedikt Rennekamp[1,2] and Frauke Gräter[1,2] — [1]Heidelberg Institute for Theoretical Studies, Schloss-Wolfsbrunnenweg 35, 69118 Heidelberg, Germany — [2]Interdisciplinary Center for Scientific Computing, Heidelberg University, INF 205, 69120 Heidelberg, Germany

Proteins are exposed to various mechanical loads that can lead to covalent bond scissions even before macroscopic failure occurs. In regular Molecular Dynamics (MD) simulations covalent bonds are, however, predefined and reactions cannot occur. Furthermore, such events rarely take place on MD time scales.

We have developed a hybrid Kinetic Monte Carlo / Molecular Dynamics (KIMMDY) scheme that overcomes the separation of time scales of these processes and drastically increases the accessible time scales for reactive MD simulations. Here, bond rupture rates are calculated in the spirit of a transition state model based on the interatomic distances in the MD simulation and then serve as an input for a Kinetic Monte Carlo step.

With this new technique we investigated bond ruptures in a multi-million atom system of tensed collagen, a structural protein found in skin, bones and tendons. Our simulations show a clear concentration of homolytic bond scissions near chemical crosslinks in collagen. We suggest that these created mechanoradicals are a yet unknown connection converting mechanical into oxidative stress. This application also demonstrates the scalability of our hybrid computational approach.

BP 16.5 Tue 12:20 BPa

van der Waals Forces in Biomolecular Systems: from Solvation to Long-range Interaction Mechanisms — •Martin Stöhr and Alexandre Tkatchenko — Department of Physics and Materials Science, University of Luxembourg

A decisive characteristic of the biomolecular machinery is the access to a rich set of coordinated processes within a small energy window. Most of these processes involve collective conformational changes and occur in an aqueous environment. Conformational changes of (bio)molecules as well as their interaction with water are thereby largely governed by non-covalent van der Waals (vdW) dispersion interactions. By virtue of their intrinsically collective nature, vdW forces also represent a key influence on collective nuclear behavior. Our understanding of vdW interactions in large-scale (bio)molecular systems, however, is still rather limited. Here, we employ the Many-Body Dispersion framework to investigate the vdW interaction in biomolecular systems and its spatial and spectral aspects. In particular, we show the role of beyond-pairwise vdW forces for protein stability and highlight the delocalized character of the protein-water vdW interaction. We further examine intrinsic electronic behaviors and reveal a coexistence of strong delocalization with spatially-separated, yet correlated, local domains. This, ultimately, forms the basis for a potential, efficient long-range interaction mechanism for coordinated processes in biomolecular systems such as enzymatic action, regulation and allostery.

BP 16.6 Tue 12:40 BPa

Q band mixing in chlorophyll a - spectral decomposition of Qx and Qy absorption bands — •Clark Zahn[1], Till Stensitzki[1], Angelica Zacarias[2], and Karsten Heyne[1] — [1]Institutfür Experimentalphysik, Freie Universität Berlin, Arnimallee 14, 14195 Berlin, Germany — [2]Max Planck Institute of Microstructure Physics, Weinberg 2, D06120 Halle, Germany and ETSF

Chlorophyll a (Chl a) is one of the most abundant pigments on earth. Despite extensive research, the composition of its absorption spectrum is yet not well understood. Here, we apply polarization resolved femtosecond Vis pump - IR probe spectroscopy, providing a detailed insight into Q band mixing of Chl a. The excitation was tuned to various wavelengths covering the Q band absorption. We show, that the dichroic ratio of the keto-C=O stretching vibration at 1698 cm-1 strongly depends on the excitation wavelength. Hence, the angle between the excited electronic transition dipole moment (tdm) and the vibrational keto-C=O tdm changes significantly across the Q band. By tracing this angle Θ for different excitation wavelengths, we are able to determine the Qx contribution along the Q band region. We find that Qx contributes 42-71% to the absorption of the lower energetic peak at 618 nm and to 59-100% to the absorption of the high energy flank at around 580 nm. Complementary measurements on the C=C stretching vibration at 1608 cm-1 provide corroborating evidence for our findings. Our results provide a direct spectral disentanglement of the Q band, without any previous assumptions. Thus, making them a reliable benchmark for quantum chemical calculations.

30 min. Meet the Speaker

BP 17: Multicellular Systems II

Time: Tuesday 11:00–13:30 Location: BPb

BP 17.1 Tue 11:00 BPb

Encoding memory in biological network hierarchy — •Mirna Kramar[1] and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]Physik-Department, Technische Universität München, Garching, Germany

Remembering sources of food and threat is essential for survival. Even very simple organisms are able to encode sensory information that aids them in tackling complex environments. The slime mould *Physarum polycephalum* is a giant unicellular eukaryote whose body consists of a network of tubes which undergoes constant reorganization. The mechanism behind the network reorganization upon food encounter has not been explained previously. Here, we identify the imprint the food stimulus leaves on network morphology as memory and show that the network relies on tube growth and flows to encode stimulus information. We hypothesise an encoding mechanism introducing a local release of a chemical agent that affects the mechanical properties of the tubes and spreading through the network by protoplasmic flows. Using a theoretical model, we test our hypothesis and find the model yields a correct prediction of flow-dependent stimulus response. Finally, we investigate the role of network hierarchy in memory encoding and show that the network directly relies on existing tube diameter hierarchy to encode the stimulus. Our findings [1] demonstrate *P.polycephalum*'s ability to encode and read stored memory and likely open doors to the use of the organism in bioinspired design.

[1] Kramar and Alim, PNAS, in press (2021)

BP 17.2 Tue 11:20 BPb

A lumped-parameter model illustrates information processing and migration in the slime mold *Physarum polycephalum* — •Christina Oettmeier and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

The slime mold *P. polycephalum* exhibits rich spatiotemporal oscillatory behavior. The organism's size spans orders of magnitude, from large meter-sized stationary transport networks down to micrometer-sized amoebae. All morphotypes show actomyosin-based contraction-relaxation cycles resulting in protoplasmic streaming. Furthermore, the giant amoeba shows a very high behavioral plasticity, leading to speculations about the origins of cellular minimal cognition. The underlying functions are not neuron-based, but are emergent phenomena, resulting from mechanochemical processes on the tubular network. In this context, we investigate how the slime mold processes information. At different parts of a migrating amoeba, oscillation frequencies vary. Oscillations in the back cause endoplasm flows through the internal vein system and expand the frontal membrane. We use the electronic-hydraulic analogy, implemented in a lumped-parameter model, to investigate this special case of information processing. A single vein segment can be described as a flexible tube, possessing a fluidic resistance (R) and fluidic capacitance (C) due to wall elasticity. The electronic equivalent is a passive RC low pass filter. Thus, the oscillation frequencies at the back are higher than those at the front due to filtering. The model can also explain the onset of locomotion.

BP 17.3 Tue 11:40 BPb

Morphoelasticity of Large Bending Deformations of Cell Sheets during Development — •Pierre A. Haas[1,2,3] and Raymond E. Goldstein[4] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]Center for Systems Biology, Dresden, Germany — [4]Department of Applied Mathematics and Theoretical Physics, University of Cambridge, United Kingdom

Deformations of cell sheets during morphogenesis are driven by developmental processes such as cell division and cell shape changes. In elastic shell theories of development, these processes appear as variations of the intrinsic geometry of a thin shell. However, morphogenesis often involves large bending deformations that are outside the formal range of validity of classical shell theories.

In this talk, I will therefore discuss a shell theory valid in this new geometric limit of large bending deformations [1]. I will emphasise the geometric material anisotropy that arises in this theory and the elastic role of cell constriction. Finally, taking the invagination of the spherical embryos of the alga *Volvox* as a model, I will compare this shell theory to a classical theory not formally valid for large bending deformations and reveal how the geometry of large bending deformations stabilises invagination [1].

[1] P. A. Haas and R. E. Goldstein, Phys. Rev. E **103** (2021, in press)

BP 17.4 Tue 12:00 BPb

Migration of immune cells in an obstacle park — •Doriane Vesperini[1], Zeinab Sadjadi[2], Heiko Rieger[2], and Franziska Lautenschläger[1] — [1]Experimental Physics, Saarland University, 66123 Saarbrücken, Germany — [2]Theoretical Physics, Saarland University, 66123 Saarbrücken, Germany

Several crucial processes in biological systems can be described as a search problem such as: finding food resources or pathogens. The presence of obstacles like non-targeted cells or extracellular matrix in biological environments induces a perturbation of the initial cell trajectory. For example, the presence of bystander cells has been shown to increase the velocity and the persistence of natural killer cells [1]. Besides obstacles density, their spatial disposition may also influence the search efficiency. It has been demonstrated that the density and geometry of pillar lattices affect migration strategies of cells [2].

We investigate how search efficiency is influenced by spatial arrangement of obstacles. A microfluidic device is designed to track HL60 cells differentiated into neutrophils in confined 2D environments. Our device consists of pillar forests distributed in triangular or square arrangements. We calculate the escape time and diffusion properties of the searcher in different densities and height of pillars and investigate which key parameters influence the search efficiency.

[1] Zhou X., et al. Scientific Reports (2017)
[2] Gorelashvili M., et al. New Journal of Physics (2014)

BP 17.5 Tue 12:20 BPb

Cell-cell adhesion and 3D matrix confinement explain plasticity of breast cancer invasion — •Simon Syga[1], Peter Friedl[2,3,4], and Andreas Deutsch[1] — [1]Center for Information Services and High Performance Computing, Technische Universität Dresden, Germany — [2]Department of Cell Biology, Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, the Netherlands — [3]David H. Koch Center for Applied Genitourinary Cancers, The University of Texas MD Anderson Cancer Center, Houston, TX, USA — [4]Cancer Genomics Centre, Utrecht, the Netherlands

Plasticity of cancer invasion and metastasis depends on the ability of cancer cells to switch between collective invasion modes and single cell dissemination, under the control of cadherin-mediated cell-cell junctions. E-cadherin is considered a tumor suppressor, the downregulation of which causes single-cell scattering in 2D environments. In clinical samples, however, E-cadherin expressing and deficient tumors both invade collectively and metastasize equally, implicating additional mechanisms controlling cell-cell cooperation and dissemination. Using a cellular automaton model we identify physical confinement by the extracellular matrix (ECM) as the dominant physical mechanism that supports collective invasion irrespective of the composition and stability of cell-cell junctions. In particular, we predict that downregulation of E-cadherin results in a transition from coordinated to uncoordinated collective movement along extracellular boundaries, whereas single-cell escape depends on locally free tissue space.

BP 17.6 Tue 12:40 BPb

Learning the dynamics of cell-cell interactions in confined cell migration — •David Brückner[1], Nicolas Arlt[2], Alexandra Fink[1], Pierre Ronceray[3], Joachim Rädler[2], and Chase Broedersz[1,4] — [1]Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität, München — [2]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität, München — [3]Center for the Physics of Biological Function, Princeton University, Princeton, NJ 08544, USA — [4]Department of Physics and Astronomy, Vrije Universiteit Amsterdam, 1081 HV Amsterdam, The Netherlands

Contact-mediated cell-cell interactions play a key role in shaping the stochastic trajectories of migrating cells. But how can we describe the stochastic dynamics of colliding cells in a unifying theoretical frame-

work? To address this question, we monitor stochastic cell trajectories in a micropatterned cell collider in which pairs of cells perform repeated cellular collisions. Capitalizing on this large experimental data set of coupled cell trajectories, we infer an interacting stochastic equation of motion that accurately predicts the observed interaction behaviors. Our approach reveals that interacting non-cancerous MCF10A cells can be described by repulsion and friction interactions. In contrast, cancerous MDA-MB-231 cells exhibit novel and surprising attraction and anti-friction interactions, promoting the predominant relative sliding behavior observed for these cells. Based on the inferred interactions, we show how our framework may generalize to provide a unifying theoretical description of diverse cellular interaction behaviors.

30 min. Meet the Speaker

BP 18: Cell Mechanics IV

Time: Tuesday 11:00–12:00 Location: BPc

BP 18.1 Tue 11:00 BPc

Direct measurements of interactions between intermediate filaments — •Anna V. Schepers[1], Charlotta Lorenz[1], Peter Nietmann[2], Andreas Janshoff[2], Stefan Klumpp[3], and Sarah Köster[1] — [1]Insitute for X-Ray Physics, Georg August University Göttingen — [2]Institute of Physical Chemistry, Georg August University Göttingen — [3]Institute for Dynamics of Complex Systems, Georg August University Göttingen

The cytoskeleton consists of F-actin, microtublues and intermediate filaments (IFs), which form a complex composite network. F-actin and microtubule networks have been studied extensively and a large variety of cross-linkers are known. By contrast, the interactions in reconstituted IF networks are less well understood. It has, however, been shown that multivalent ions cause bundling and network stiffening. While rheological experiments give insight into the slow stiffening and mechanics of vimentin IF networks, it is challenging to distinguish the contributions of filament stiffening and of increased attraction. Combining optical trapping and fluorescence microscopy enables us to bring two single vimentin IFs in contact and directly study the interactions between the filaments. By amplifying electrostatic attraction or diminishing the hydrophobic interactions we are able to study the nature of the interactions between IFs. These results, in combination with studies of the mechanical properties of single IFs, allow us to model the interactions with Monte-Carlo simulations, thereby gaining a deeper understanding of cytoskeletal structures.

BP 18.2 Tue 11:20 BPc

Stiffening of the Ndc80 complex, the main mirotubule-kinetochore linker — •Felix Schwietert and Jan Kierfeld — TU Dortmund University, 44221 Dortmund, Germany

In the mitotic spindle microtubules attach to chromosomes via kinetochores, whose molecular structure and mechanical properties are not completely understood. Over the past years, it became evident that the Ndc80 complex plays a major role for attaching microtubules to the kinetochore and transmitting forces from depolymerizing microtubules to the chromosome. The Ndc80 complex is a rod-like coiled-coil with globular end domains that bind to the kinetochore and the microtubule, respectively. Due to its force transmitting function, its elastic properties are of great interest for modeling and understanding chromosome dynamics in the mitotic spindle. Here, we theoretically explain the recent experimental result that the effective stiffness of a Ndc80 complex increases under tension [1]. Our model is based on the specific architecture of the Ndc80 complex, which has a characteristic flexible kink at approximately one third of its length.

[1] V. A. Volkov, P. J. Huis in 't Veld, M. Dogterom, and A. Musacchio, eLife 7:e36764 (2018)

BP 18.3 Tue 11:40 BPc

Development of microtentacles in suspended cells upon weakening of the actin cortex — •Lucina Kainka, Reza Shaebani, Ludger Santen, and Franziska Lautenschläger — Saarland University, Center for Biophysics, 66123 Saarbrücken

Circulating Tumor Cells (CTCs) pose a significant threat due to their role in metastasis: It has been proposed that CTCs are able to escape the blood stream and reattach to the tissue by the formation of so-called microtentacles (McTNs). McTNs are microtubule based membrane protrusions with a diameter of less than 1 μm and a length of tens of μm.

In CTCs the balance of the outward growing microtubule and the contractive forces of the actin cortex is disrupted enabling microtubules to form these kind of protrusions. Using cytoskeletal drugs which are targeting the actin cortex integrity we induce McTNs even in non-cancerous RPE1 cells. We investigate the presence of microtubules and actin as well as vimentin under those conditions. Furthermore, we established a statistic over the number and lengths of McTNs depending on different drug concentrations applied.

Scanning electron microscopy images of the cytoskeleton beneath the plasma membrane of McTNs give further insight into their cytoskeletal composition.

BP 19: Active Matter 2 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP/CPP)

Time: Tuesday 11:00–13:00 Location: DYa

BP 19.1 Tue 11:00 DYa

Mesoscale turbulence and dynamical clustering in active polar fluids — •Vasco Marius Worlitzer[1], Gil Ariel[2], Avraham Be'er[3], Holger Stark[4], Markus Bär[1], and Sebastian Heidenreich[1] — [1]Department of Mathematical Modelling and Data Analysis, Physikalisch-Technische Bundesanstalt, Abbestrasse 2-12, 10587 Berlin — [2]Department of Mathematics, Bar-Illan University, Ramat Gan 52000, Israel — [3]Zuckerberg Institute for Water Research of the Negev, Sede Boqer Campus 84900 Midreshet Ben-Gurion, Israel — [4]Institute of Theoretical Physics, Technische Universität Berlin, Hardenbergstrasse 36, 10623 Berlin

Bacterial suspensions are fascinating examples for active polar fluids which exhibit large scale collective behavior ranging from polar and disordered states to so-called mesoscale turbulence and vortex lattices. Previous approaches take into account the self-propulsion of bacteria and an effective polar-alignment interaction but assume for simplicity a constant density. Comparison with experiments showed that this modelling approach is successful, to some extent, in a relatively narrow regime corresponding to wild-type swarms in which density is indeed approximately constant and velocity distributions are Gaussian. We seek a unified model that can explain the observed phenomena across the entire phase space of swarming bacteria. To this end, we present a continuum model that allows variations in density. The model predicts new dynamical regimes, such as mixed states with coexisting vortex patterns and dynamical clusters, obeying anomalous statistics, similar to experimental observations.

BP 19.2 Tue 11:20 DYa

Rewarding cargo-carrier interactions: cell-mediated particle transport — •Valentino Lepro[1,2], Robert Grossmann[1], Oliver Nagel[1], Stefan Klumpp[3], Reinhard Lipowsky[2], and Carsten Beta[1] — [1]Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]Max Planck Institute of Colloids and Interfaces, 14476 Potsdam, Germany — [3]Institute for the Dynamics of Complex Systems, University of Göttingen, 37077 Göttingen, Germany

As society paves its way towards devices miniaturization and precision medicine, micro-scale actuation and guided transport become increas-

ingly prominent research fields, with high potential impact in both technological and clinical contexts. To accomplish directed motion of micron-sized cargos towards specific target sites, a promising strategy is the usage of living cells as smart biochemically-powered carriers, developing so-called bio-hybrid systems. In this talk, we discuss eukaryotic active particle transport, using Dictyostelium discoideum as a model organism. We shed light on the underlying mechanics and the emerging dynamics governing such cell-mediated transport. A simple yet powerful model is proposed which reproduces the observed phenomenology and, moreover, elucidates the role of cell-cargo interactions for the long-time mass transport efficiency.

BP 19.3 Tue 11:40 DYa

Predictive local field theories for interacting active Brownian spheres* — Jens Bickmann and •Raphael Wittkowski — Institut für Theoretische Physik, Center for Soft Nanoscience, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany

We present predictive local field theories for the dynamics of interacting spherical active Brownian particles in two and three spatial dimensions. Alongside the general theories, which include configurational order parameters and derivatives up to infinite order, we present reduced models that are easier to apply. We show that our theories contain popular models such as Active Model B + as special cases and that they provide explicit expressions for the coefficients occurring in these models. As further outcomes, the theories yield analytical expressions, e.g., for the density-dependent mean swimming speed and the spinodal corresponding to motility-induced phase separation of the particles. The analytical predictions are found to be in very good agreement with results of Brownian dynamics simulations and results from the literature.

**Funded by the Deutsche Forschungsgemeinschaft (DFG) – WI 4170/3-1*

BP 19.4 Tue 12:00 DYa

Dynamical States in Underdamped Active Matter with Anti-alignment Interaction — •Dominic Arold[1] and Michael Schmiedeberg[2] — [1]TransDeNLab, UKD, Dresden, Germany — [2]Institut für Theoretische Physik 1, FAU, Erlangen, Germany

Many active matter systems, especially on the microscopic scale, are well approximated as overdamped, meaning that any inertial momentum is immediately dissipated by the environment. On the other hand, for macroscopic active systems, the time scale of inertial motion can become large enough to be relevant for the dynamics already on the single-particle level [1]. This raises the question of how collective dynamics and the resulting states in active matter are influenced by inertia. We propose a coarse-grained continuum model for underdamped active matter based on a dynamical density functional theory for passive systems [2]. Further, we apply the model to a system with short-range alignment and distant anti-alignment interaction known from the context of pattern formation. Our simulations of under- and overdamped dynamics both predict a structured laning state. However, activity-induced convective flows only present in the underdamped model destabilize this state when the anti-alignment is weakened, leading to a collective motion state which is not predicted in the overdamped limit. A turbulent transition regime between the two states is distinguished by strong density fluctuations and the absence of global ordering.

[1] Scholz C *et al.* 2018 *Nature communications* **9** 5156
[2] Archer A J 2009 *The Journal of chemical physics* **130** 014509

BP 19.5 Tue 12:20 DYa

Chemokinesis causes trapping and avoidance by dynamic scattering — •Justus Kromer[1] and Benjamin Friedrich[2,3] — [1]Stanford University, Stanford, United States of America — [2]cfaed TU Dresden, Dresden, Germany — [3]PoL TU Dresden, Dresden, Germany

A minimal control strategy for artificial microswimmers with limited information processing capabilities is chemokinesis: the regulation of random directional fluctuations or speed as function of local, non-directional cues. In contrast to chemotaxis, it is not well understood whether chemokinesis is beneficial for the search for hidden targets.

We present a general theory of chemokinetic search agents that regulate directional fluctuations according to distance to a target. We characterize a dynamic scattering effect that reduces the probability to penetrate regions with strong directional fluctuations. If the target is surrounded by such a region, dynamic scattering causes beneficial inward-scattering of agents that had just missed the target, but also disadvantageous outward-scattering of agents approaching the target for the first time. If agents respond instantaneously to positional cues, outward-scattering dominates and chemokinetic agents perform worse than simple ballistic search. Yet, agents with just two internal states can decouple both effects and increase the probability to find the target significantly. We apply our analytical theory to the biological example of sperm chemotaxis of marine invertebrates. Sperm cells need to pass a 'noise zone' surrounding the egg, where chemokinesis masks chemotaxis. Kromer et al., PRL 124, 118101 (2020)

BP 19.6 Tue 12:40 DYa

Magnetic microswimmers exhibit Bose-Einstein-like condensation — Fanlong Meng[1], Daiki Matsunaga[2], •Benoît Mahault[3], and Ramin Golestanian[3] — [1]CAS Key Laboratory for Theoretical Physics, Institute of Theoretical Physics, Chinese Academy of Sciences — [2]Graduate School of Engineering Science, Osaka University — [3]Max Planck Institute for Dynamics and Self-Organization

We study an active matter system comprised of magnetic microswimmers confined in a microfluidic channel and show that it exhibits a new type of self-organized behavior. Combining analytical techniques and Brownian dynamics simulations, we demonstrate how the interplay of non-equilibrium activity, external driving, and magnetic interactions leads to the condensation of swimmers at the center of the channel via a non-equilibrium phase transition that is formally akin to Bose-Einstein condensation. We find that the effective dynamics of the microswimmers can be mapped onto a diffusivity-edge problem, and use the mapping to build a generalized thermodynamic framework, which is verified by a parameter-free comparison with our simulations. Our work reveals how driven active matter has the potential to generate exotic classical non-equilibrium phases of matter with traits that are analogous to those observed in quantum systems.

BP 20: Focus Biological Cells in Microfluidics I

Time: Tuesday 12:00–13:30 Location: BPc

BP 20.1 Tue 12:00 BPc

Numerical Investigation of Cell Deformation during Bioprinting — •Sebastian Johannes Müller and Stephan Gekle — Universität Bayreuth, Bayreuth, Deutschland

In 3D bioprinting, cells suspended in hydrogel are deposited through a fine nozzle, creating three dimensional biological tissues. Due to the high viscosity of the hydrogel, the cells experience hydrodynamic stresses that deform or damage the cells and can ultimately affect the viability and functionality of the cells in the printed construct.

Using numerical methods, we quantify these deformations in dependency of the flow parameters and cell elasticity. We consider shear thinning fluid rheology and validate our Lattice Boltzmann flow calculations with microfluidic flow experiments of typical hydrogel materials. Our hyperelastic cell, modeled as purely elastic continuum with neo-Hookean force calculations, is validated with experimental data for cells obtained via AFM indentation measurements.

By coupling our cell model with the fluid simulations, we investigate the cell deformation in typical flow scenarios, like capillary and shear flow. As essential part of the printing process, we further simulate the cell flowing through the transition from the printer nozzle into the free hydrogel strand, where additional radial flow components stretch the cell at short time scale.

BP 20.2 Tue 12:20 BPc

Microfluidic platforms to study forces on model cells — •Tom Robinson — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Biological cells in their natural environment experience a variety of external forces such as fluidic shear stresses, osmotic pressures, and

mechanical loads. The response of cell membranes to such forces is of great interest and model systems such as giant unilamellar vesicles (GUVs) offer the chance to investigate individual components without interference from cellular complexity (Robinson, Adv Biosyst., 2019). However, being able to handle and apply forces to these delicate objects in a controllable manner is non-trivial. Therefore, we present several microfluidic platforms to create, capture, analyse, and apply forces to GUVs. First, we present platforms for surfactant-free GUV production (Yandrapalli, et al. bioRxiv, 2020) as well as their high-capacity capture and isolation (Yandrapalli & Robinson, Lab Chip, 2019; Yandrapalli, et al. Micromachines, 2020). Lipid rafts are thought to play an important role in the spatial organization of membrane proteins. Therefore, GUVs with membrane domains are used as models to explore their behaviour in response to external forces. We use valve-based systems to apply precise fluidic shear stresses vesicles (Sturzenegger, et al. Soft Matter, 2016) and a device with an integrated micro-stamp to mechanically compress GUVs to study the effects that deformation has on lipid rafts (Robinson & Dittrich, ChemBioChem 2019). Microfluidic valves are also used to apply precise osmotic changes to measure membrane permeability to water (Bhatia et al. Soft Matter, 2020).

BP 20.3 Tue 12:40 BPc

High Throughput Microfluidic Characterization of Erythrocyte Shapes and Mechanical Variability — •Felix Reichel[1,2], Johannes Mauer[3], Ahsan Nawaz[1], Gerhard Gompper[3], Jochen Guck[1], and Dmitry Fedosov[3] — [1]Max Planck Institute for the Science of Light and Max-Planck-Zentrum für Physik und Medizin, Erlangen — [2]Biotechnology Center, Center for Molecular and Cellular Bioengineering, Technische Universität Dresden, Dresden — [3]Theoretical Soft Matter and Biophysics, Institute of Complex Systems and Institute for Advanced Simulation, Forschungszentrum Jülich, Jülich

The circulation of red blood cells (RBCs) in microchannels is important in microvascular blood flow and biomedical applications such as blood analysis in microfluidics. Current understanding of the complexity of RBC shapes and dynamical changes in microchannels is mainly formed by a number of simulation studies, but there are few systematic experimental investigations. Here, we present a first systematical mapping of experimental RBC shapes and dynamics for a wide range of flow rates and channel sizes. Results are compared with simulations and show good agreement. A key difference to simulations is that in experiments there is no single well-defined RBC state for fixed flow conditions, but rather a distribution of states. This result can be attributed to the inherent variability in RBC mechanical properties, which is confirmed by a model that takes the variation in RBC shear elasticity into account. These results make a significant step toward a quantitative connection between RBC behavior in microfluidic devices and their mechanical properties.

30 min. Meet the Speaker

BP 21: Systems Biology III

Time: Tuesday 14:00–16:00 Location: BPa

Invited Talk BP 21.1 Tue 14:00 BPa

Predicting Protein and RNA Structures: from statistical physics to machine learning — •Alexander Schug — John von Neumann Institute for Computing, Jülich Supercomputer Centre, Forschungszentrum Jülich — Faculty of Biology, University of Duisburg-Essen

On the molecular level, life is orchestrated through an interplay of many biomolecules. To gain any detailed understanding of biomolecular function, one needs to know their structure. Yet the structural characterization of many important biomolecules and their complexes - typically preceding any detailed mechanistic exploration of their function- remains experimentally challenging. Tools rooted in statistical physics such as Direct Coupling Analysis (DCA) but also increasingly Machine Learning driven approaches take advantage of the explosive growth of sequence databases and infer residue co-evolution to guide structure prediction methods via spatial constraints. For proteins, systematic large-scale studies of >1000 protein families are already possible. Additional information, such as low-resolution experimental information (e.g. SAXS or FRET) can be used as further constraints in simulations. For RNA there are significantly less data available, which hinders in particular ML based approaches. Still, DCA combined with ML can improve prediction quality.

BP 21.2 Tue 14:30 BPa

Rational optimization of drug-membrane selectivity by computational screening — •Bernadette Mohr and Tristan Bereau — Max Planck Institute for Polymer Research, Mainz, Germany

Success rates of drug discovery are non-satisfactory considering the high cost in time and resources. This leads to an increased demand for development of improved screening methods. In our work, we explore the capabilities of using a coarse-grained (CG) model to efficiently find candidate structures with desired properties. The Martini CG force field is a physics-based model that incorporates both the essential chemical features with a robust treatment of statistical mechanics. Martini simplifies the molecular representation through a small set of bead types that encode a variety of functional groups present in organic chemistry. This offers two advantages: (i) many molecules map to the same CG representation and (ii) screening boils down to systematically varying among the set of CG bead types available. The combination of these two aspects makes Martini a remarkably efficient candidate for high-throughput screening. We apply this approach to the selective binding of drugs between Cardiolipin and phosphoglycerols in mitochondrial membranes. A systematic screening starting from an already-reported compound will be presented. We identify clear design rules for improved selectivity, and rationalize them on a physical basis. As an outlook, we explore prospects of further boosting screening at higher throughput by means of connecting the CG simulations within a deep-learning framework.

BP 21.3 Tue 14:50 BPa

Morphology of spherical epithelial monolayers — •Aboutaleb Amiri[1], Charlie Duclut[2,3], Carl Modes[2,3], and Frank Jülicher[1,3] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]Max Plack Institute for Molecular Cell Biology and Genetics, 01037 Dresden, Germany — [3]Center for Systems Biology Dresden, 01307 Dresden, Germany

We develop a generalised vertex model off the mechanics of epithelial cell monolayers to study morphogenesis in three dimensions. In this approach, a cell is represented by a polyhedron which is characterised by the location of its vertices in 3D space. We take into account apical, basal, and lateral cell surface tension, as well as pressure differences between outside and inside the cells. We consider an epithelium with spherical topology enclosing a lumen and investigate mechanisms that can generate different morphologies. In particular, we are interested in the roles of mechanical feedback on cell behaviours for the morphogenesis of closed epithelial monolayers.

BP 21.4 Tue 15:10 BPa

Load distribution among the main structures of a passively flexed lumbar spine — •Julia M. Riede[1], Falk Mörl[2], Michael Günther[1], Maria Hammer[1], and Syn Schmitt[1] — [1]Computational Biophysics&Biorobotics, IMSB/Simtech, University of Stuttgart, Germany — [2]Biomechanics&Ergonomics, FSA mbH Erfurt, Germany

Mechanical loads may induce degeneration of spinal structures. It is still unknown how the load during spine motion is distributed among the spine's main structures: muscles, vertebrae and facet joints, ligaments, and intervertebral discs. Currently, there are no measurements that capture the load on all spinal structures at once. Therefore, computer simulations are the method of choice to overcome the lack of knowledge about the biophysical properties and processes determining spinal in vivo dynamics.

For predicting the load distribution of spinal structures, we combined experimental and simulation methods. In experiments, we determined the overall stiffness for forward-flexing rotations between the lumbar vertebrae L5 and L4 of subjects lying in sideways position and being bent by a machine, without active muscle resistance. Forward dynamics simulations of this experiment using our detailed musculoskeletal multibody model of the human allowed for a structural resolution of the loads in the L4|5 region. The results indicated that

stiffness values of particularly ligaments and passive muscle tissue put in from literature resources were too high. With now corrected values, our model has gained validity for future investigations on human movement dynamics and modelling applications like e.g. exoskeletons.

30 min. Meet the Speaker

BP 22: Focus Phase Separation in Biological Systems II (joint session BP/CPP)

Time: Tuesday 14:00–16:00 Location: BPb

BP 22.1 Tue 14:00 BPb

Phase separation provides a mechanism to reduce noise in cells — •Florian Oltsch[1,2], Adam Klosin[1], Tyler Harmon[1,3], Alf Honigmann[1,4], Frank Jülicher[2,3,4], Anthony Hyman[1,2,4], and Christoph Zechner[1,2,4] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany — [2]Center for Systems Biology Dresden, 01307 Dresden, Germany — [3]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [4]Cluster of Excellence Physics of Life, TU Dresden, 01062 Dresden, Germany

Noise in gene expression can cause significant variability in protein concentration. How cells buffer variation in protein concentration is an important question in biology. In this talk, I will show that liquid-liquid phase separation provides an effective mechanism to reduce variability in protein concentration. First, I will introduce our theoretical framework that discusses phase separation in the presence of active protein production and turnover. This stochastic non-equilibrium model allows us to study how fluctuations in protein concentration are affected by phase separation. I will then present under which physical conditions noise buffering by phase separation can be effective. Subsequently, I will show experimental data to test our theoretical predictions.

BP 22.2 Tue 14:20 BPb

Parasitic Behavior in Competing Dissipative Reaction Cycles — •Patrick Schwarz[1], Sudarshana Laha[3,4], Jacqueline Janssen[3,4], Tabea Huss[1], Christoph A. Weber[3,4], and Job Boekhoven[1,2] — [1]Department of Chemistry, Technische Universitat München, Lichtenbergstrasse 4, 85748 Garching, Germany — [2]Institute for Advanced Study, Technische Universität München, Lichtenbergstrasse 2a, 85748 Garching, Germany — [3]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden, Germany — [4]Center for Systems Biology Dresden, CSBD, Dresden, Germany

Fuel-driven reaction cycles serve as model systems of the intricate reaction network of life. Rich and dynamic behavior is observed when such reaction cycles regulate phase separation or assembly. However, it remains unclear how the interplay between multiple reaction cycles affects their fate. To tackle this question, we created a library of precursor molecules that compete for a common fuel to transiently activate products. Generally, the competition for fuel means that a competitor decreases the success of the cycle. However, in cases where the transient competitor product can phase separate, this relation can be inverted. The presence of assemblies formed by such a competitor can increase the survival time of one product, analogous to how the presence of a host can increase the survival time of a parasite. Our study of such a parasitic behavior in multiple fuel-driven reaction cycles represents a lifelike trait, paving the way for bottom-up design of synthetic life.

BP 22.3 Tue 14:50 BPb

Surface condensation of a pioneer transcription factor on DNA — •Jose A. Morin[1,2], Sina Wittmann[1], Sandeep Choubey[1,3], Adam Klosin[1], Stefan Golfier[1,3], Anthony A. Hyman[1,5], Frank Julicher[3,4,5], and Stephan W. Grill[1,2,5] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany. — [2]Biotechnologisches Zentrum, Technische Universitat Dresden,Dresden, Germany. — [3]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [4]Center for Systems Biology Dresden, Dresden, Germany. — [5]Cluster of Excellence Physics of Life, Technische Universitat Dresden, Dresden, Germany.

Transcription factors cluster into sub-micrometer sized condensates while initiating transcription of their target genes. How cells achieve liquid-like clusters of constrained size at specific locations on DNA is not known. Here we investigate the role of DNA in the nucleation of condensates, using the pioneer transcription factor KLF-4. We show that KLF-4 forms liquid-like condensates on the DNA surface at physiological concentrations, below the one required for Klf4 phase separation. Through a dialogue between theory and experiments, we demonstrate that condensation occurs via a switch-like transition from a thin adsorbed layer to a thick condensed layer on DNA that is well described as a prewetting transition on a heterogeneous substrate. This phenomenon is thus a form of surface condensation mediated by and limited to the DNA surface.

BP 22.4 Tue 15:10 BPb

Slowing down protein aggregation in liquid compartments — •Wojciech P. Lipiński[1], Brent Visser[1], Mireille Claessens[2], Mohammad A. A. Fakhree[2], Saskia Lindhoud[3], and Evan Spruijt[1] — [1]Institute for Molecules and Materials, Radboud University, Nijmegen, the Netherlands — [2]Nanobiophysics, Faculty of Science and Technology, University of Twente, Enschede, the Netherlands — [3]Molecular Nanofabrication, Faculty of Science and Technology, University of Twente, Enschede, the Netherlands

With increasing life expectancy in modern societies, amyloid-related diseases are becoming alarmingly common. Extensive work has been done to investigate the kinetics of amyloid formation and the structure of aggregates. Recently it has been suggested that protein aggregation can be influenced by the presence of membraneless organelles. Aggregation-prone proteins may be sequestered by liquid compartments, leading to significant changes in concentration and altered aggregation kinetics.

Here, we present a combined computational and experimental study of the fate of aggregation-prone proteins that are sequestered by liquid droplets. We investigated computationally the influence of varying parameters describing aggregation and transport processes and showed that aggregation process can be either accelerated or inhibited by the presence of liquid compartments. Motivated by these findings we have undertaken efforts to develop experimental systems exhibiting diversified influence of the phase-separated environment on the protein aggregation process.

30 min. Meet the Speaker

BP 23: Focus Biological Cells in Microfluidics II

Time: Tuesday 14:00–16:00 Location: BPc

BP 23.1 Tue 14:00 BPc

ROS induces intracellular acidosis associated with increased cell stiffening — •Yesaswini Komaragiri[1,3], Huy T Dau[1], Doreen Biedenweg[2], Ricardo H Pires[1,3], and Oliver Otto[1,3] — [1]Biomechanics, ZIK-HIKE, Universität Greifswald, Greifswald, Germany — [2]Universitätsmedizin Greifswald, Greifswald, Germany — [3]Deutsches Zentrum für Herz-Kreislauf-Forschung e.V., Standort Greifswald, Universitätsmedizin Greifswald, Greifswald, Germany

Reactive oxygen species (ROS) are associated with important alterations in cell physiology. The impact that superoxides and other ROS have on the cytoskeleton has been extensively documented; however, the mechanism by which they may affect cell mechanics remain to be understood. By varying concentrations of hydrogen peroxide, we exposed the human myeloid precursor cell line (HL60) to different levels

of ROS. Using real-time fluorescence and deformability cytometry, we coupled the mechanical characterization of cells with a simultaneous fluorometric assessment of intracellular superoxide levels. Our work reveals a direct correlation between the elastic modulus of cells and levels of superoxide. We did not detect global changes in the F-actin and microtubule network but demonstrate that cell stiffening at elevated ROS levels is driven by intracellular acidosis.

BP 23.2 Tue 14:20 BPc

Lingering dynamics of microvascular blood flow — •Alexander Kihm[1], Stephan Quint[1], Matthias Laschke[2], Michael Menger[2], Lars Kaestner[1], Thomas John[1], and Christian Wagner[1] — [1]Department of Experimental Physics, Saarland University, Saarbruecken, Germany — [2]Institute for Clinical and Experimental Surgery, Saarland University, Homburg, Germany

The microvascular networks in the body of vertebrates consist of the smallest vessels, such as arterioles, venules, and capillaries. The flow of red blood cells (RBCs) through these networks ensures the gas exchange in, as well as the transport of nutrients towards the tissues. Any alterations in this blood flow may have severe implications on the health state. Since the vessels in these networks obey dimensions similar to the diameter of RBCs, dynamic effects on the cellular scale play a key role. The steady progression in numerical modeling of RBCs even in complex networks has led to novel findings in the field of hemodynamics, especially concerning the impact and the dynamics of lingering events. However, these results are yet unmatched by a detailed analysis of the lingering in experiments in vivo. To quantify this lingering effect in in vivo experiments, we analyze branching vessels in the microvasculature of Syrian hamsters via intravital microscopy and the use of an implanted dorsal skinfold chamber. We present a detailed analysis of these lingering effects of cells at the apex of bifurcating vessels, affecting the temporal distribution of cell-free areas in the branches and even causing a partial blockage in severe cases.

BP 23.3 Tue 14:40 BPc

Phenotyping photokinetic and excitable behaviours of single microswimmers in confinement — Samuel Bentley, Vasileios Anagnostidis, Hannah Laeverenz-Schlogelhofer, Fabrice Gielen, and •Kirsty Y. Wan — Living Systems Institute, Exeter, United Kingdom, EX4 4QD

All living organisms are environmentally intelligent. This is the fundamental distinction between life, and other forms of matter. Even unicellular organisms are capable of complex behaviours. Here, we study the detailed motor actions of flagellated algal microswimmers, using motility as a dynamic read-out of whole-organism behaviour. Previous studies have focussed on locomotor transients over short timescales ranging from seconds to minutes. Here we present a novel microfluidic platform which can allow us to monitor single cells over unprecedented timescales. Two representative species of microswimmers were trapped and confined inside circular arenas: a biflagellate which exhibits a form of run-and-tumble, and an octoflagellate which exhibits a distinctive, tripartite behavioural repertoire termed run-stop-shock. Stochastic transitions in swimming gait are projected onto a low-dimensional behavioural state space. Single-cell motility signatures were analysed to reveal species-specific photokinetic and excitable behaviours. Finally, we conduct on-demand pharmacological perturbations within these microenvironments, to shed new light on the physiological basis of excitable flagellar dynamics.

Invited Talk BP 23.4 Tue 15:00 BPc

Synthetic cells: De novo assembly with microfluidics and DNA nanotechnology — •Kerstin Göpfrich — Max Planck Institute for Medical Research, Jahnstr. 29, 69120 Heidelberg, Germany

The future of manufacturing entails the construction of biological systems and synthetic cells from the bottom up. Instead of relying exclusively on biological building blocks, the integration of new tools and new materials may be a shortcut towards the assembly of active and eventually fully functional synthetic cells [Göpfrich *et al., Trends Biotechnol.*, 2018]. This is especially apparent when considering recent advances in DNA nanotechnology and microfluidics. Exemplifying this approach, we use microfluidics for the assembly of synthetic cellular compartments that we equip with natural or synthetic cytoskeletons. Light serves as a non-invasive stimulus to trigger their symmetry-breaking contraction [Jahnke *et al., Adv. Biosys.*, 2020; *Adv. Funct. Mater.*, 2019]. We further demonstrate the division of giant unilamellar lipid vesicles (GUVs) as synthetic cell models based on phase separation and osmosis rather than the biological building blocks of a cell's division machinery. We derive a parameter-free analytical model which makes quantitative predictions that we verify experimentally [Dreher *et al., Angew. Chem.*, 2020]. Remarkably, we show that caged compounds provide full spatio-temporal control to increase the osmolarity locally in an illuminated area, such that a target-GUV undergoes division whereas the surrounding GUVs remain unaffected. All in all, we believe that precision technologies, like microfluidics, can help to accelerate synthetic biology research.

30 min. Meet the Speaker

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], Lu-

cas 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.

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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 cap-

tured 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 scatter-

ing, 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 hydrother-

mal 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 tis-

sue 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

BP 25: Nationale Forschungsdateninfrastruktur (NDFI) (joint session BP/CPP/DY/SOE)

Time: Tuesday 17:45–18:30 Location: BPb

Details will be published in a programme update.

BP 26: Annual General Meeting

Time: Tuesday 18:30–19:00 Location: BPa

Annual General Meeting

BP 27: Active Matter 3 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP)

Time: Wednesday 9:00–10:40 Location: DYb

BP 27.1 Wed 9:00 DYb

Localized States in active Phase-Field-Crystal models — •Max Philipp Holl[1], Lukas Ophaus[1,2], Svetlana Gurevich[1,2], and Uwe Thiele[1,2] — [1]Institut für Theoretische Physik, Münster, Germany — [2]Center for Nonlinear Science, Münster, Germany

The phase-field-crystal (PFC) model represents a gradient dynamics of a single order parameter field related to density and is able to describe crystallisation processes. The model describes a variety of spatially extended periodic and localized steady structures. In an active PFC model, encoding for instance the active motion of self-propelled colloidal particles, the PFC model's gradient dynamics structure is broken by a nonreciprocal coupling of density and an additional polarization field. Then, resting and traveling localized states exist with transitions characterized by parity-breaking drift bifurcations. We briefly review the snaking behavior of localized states in passive and active PFC models before discussing the bifurcation behaviour of localized states in systems of (i) two passive PFC with nonreciprocal coupling and (ii) coupled passive and active PFCs.

BP 27.2 Wed 9:20 DYb

Cooling by Heating in Inertial Active Brownian Particles — •Lukas Hecht and Benno Liebchen — Institut für Physik kondensierter Materie, Technische Universität Darmstadt, Hochschulstraße 8, D-64289 Darmstadt, Germany

The active Brownian particle (ABP) model is commonly used to model active matter consisting of particles which extract energy from their environment to generate directed motion. For both overdamped and inertial ABPs, motility-induced phase separation occurs in a certain parameter regime. Remarkably, inertial ABPs show a coexistence of different effective temperatures of the dilute and the dense phase whereas overdamped ABPs have a uniform effective temperature even in the phase-separated state [1].

The coexistence of different temperatures brings us to the cooling-by-heating idea: Increasing the self-propulsion speed locally could lead to a locally decreased temperature. We investigate the cooling-by-heating idea with numerical simulations of ABPs with translational and rotational inertia. Since a locally increased self-propulsion speed causes a decrease of the local particle density, detailed knowledge about the phase diagram is essential to determine appropriate parameters for which cooling by heating is possible. Therefore, we analyze the phase transition behavior of inertial ABPs and the corresponding phase diagram.

[1] S. Mandal, B. Liebchen, and H. Löwen, "Motility-Induced Temperature Difference in Coexisting Phases", Phys. Rev. Lett. 123, 228001 (2019).

BP 27.3 Wed 9:40 DYb

Active dynamics of microalgae in an anisotropic porous environment — •Florian von Rüling and Alexey Eremin — Otto von Guericke University Magdeburg

Understanding the motion of active colloids in porous media is essential for fundamental physics and a wide range of biological and medical applications. Cell growth and motion is often restricted by complex environments such as the cytoskeleton. Here, we report experimental studies on the motion of the unicellular microalgae Chlamydomonas reinhardtii through a flexible anisotropic lattice of chains formed by magnetic particles. In a thin cell or capillary, the microalgae interact with chain-like aggregates that form in a magnetic field. Shape-anisotropic structures guide the swimmers or initiate tumbling. They affect the persistence time of the microswimmer's motion. As the chains of magnetic particles disintegrate quickly after turning off the magnetic field, the system transforms into an unperturbed state. We investigate the effect of the chains on the orientational velocity correlations in the active dynamics of the algae.

BP 27.4 Wed 10:00 DYb

Effective Langevin equations for a polar tracer in an active bath — •Milos Knezevic and Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstraße 36, D-10623 Berlin, Germany

We study the motion of a polar tracer, having a concave surface, immersed in a two-dimensional suspension of active particles. Using Brownian dynamics simulations, we measure the distributions and auto-correlation functions of force and torque exerted by active particles on the tracer.The tracer experiences a finite average force along its polar axis, while all the correlation functions show exponential decay in time. Using these insights we construct the full coarse-grained Langevin description for tracer position and orientation, where the active particles are subsumed into an effective self-propulsion force and exponentially correlated noise for both translations and rotations. The ensuing mesoscopic dynamics can be described in terms of five dimensionless parameters. We perform a thorough parameter study of the mean squared displacement, which illustrates how the different parameters influence the tracer dynamics, which crosses over from a ballistic to diffusive motion. We also demonstrate that the distribution of tracer displacements evolves from a non-Gaussian shape at early stages to a Gaussian behavior for sufficiently long times. Finally, for a given set of microscopic parameters, we establish a procedure to estimate the matching parameters of our effective model, and show that the resulting dynamics is in a very good quantitative agreement with the one obtained in Brownian dynamics simulations.

BP 27.5 Wed 10:20 DYb

Collective behaviour of self-propelled elliptical particles — •Ashreya Jayaram, Andreas Fischer, and Thomas Speck — Institute of Physics, Johannes Gutenberg University Mainz, Staudingerweg 7-9, 55128 Mainz, Germany

Ensembles of anisotropic self-propelled particles exhibit a rich variety of emergent phases. A combination of short-ranged excluded volume interactions, which induce inter-particle forces and torques, and self-propulsion determines the resulting macroscopic structure. Starting from a point in parameter-space which displays motility-induced phase separation (MIPS) for isotropic particles, we systematically increase the aspect ratio of the constituent ellipses. On doing so, first, MIPS breaks down paving way to a spatially homogeneous state comprising polar domains. Secondly, at sufficiently large aspect ratios, particles aggregate into polar bands. We rationalize these observations from simulations by extracting two effective parameters, *viz.*, the force imbalance coefficient and the coupling to the local polarization, that enter the mean-field description of the system.

BP 28: Active Matter 4 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP)

Time: Wednesday 11:00–13:00 Location: DYb

BP 28.1 Wed 11:00 DYb

Wrinkling instability in 3D active nematics — Tobias Struebing, Amir Khosravanizadeh, Andrej Vilfan, Eberhard Bodenschatz, Ramin Golestanian, and •Isabella Guido — Max Planck Institute for Dynamics and Self-Organization, Goettigen, Germany

Networks of biopolymers and motor proteins are useful model systems for the understanding of emergent behaviour of active matter. An interesting class of such systems comprises active nematics, fluids con-

stituted by self-organising elongated particles that in-vitro assemble in dynamical structures at length scales larger than those of their components by several orders of magnitude. In the last years the active nematic behaviour of biopolymer-motor networks confined on a 2D substrate was reported. Here we present an experimental and theoretical study on 3D active nematics made of microtubules, kinesin-1 motor proteins and a depleting agent. The network is subjected to the force exerted by the motors that crosslinked the filaments and let them slide against each other. In this way the system evolves toward a flattened and contracted 2D sheet that undergoes a wrinkling instability in the third dimension and subsequently transitions into an active turbulent state. We observe that the wrinkle wavelength is independent of the ATP concentration. A theoretical model describes its relation with the appearance time and a numerical simulation confirms the key role of kinesin motors in the contraction and extension of the network. Finally, we show how motor concentration and environmental cues influence the network properties

BP 28.2 Wed 11:20 DYb

A minimal model for dynamical symmetry breaking in active matter — Matthew Davison and •Patrick Pietzonka — Department of Applied Mathematics and Theoretical Physics, University of Cambridge, UK

It is well known that asymmetrically shaped passive particles immersed in active matter move in a persistent direction. Recent work provides a thermodynamic framework and design principles for engines exploiting this mechanism [1]. We build on these results and reveal that symmetric passive particles in contact with active matter perform such a persistent motion as well. Its direction is determined through spontaneous symmetry breaking and remains fixed in time in the limit of a large number of active particles. We present an analytically solvable one-dimensional model for a single passive particle interacting with many active particles, which provides a physical understanding of these effects.

[1] P. Pietzonka *et al.*, Phys Rev. X **9**, 041032 (2019)

BP 28.3 Wed 11:40 DYb

Boundary-interior principle for microbial navigation in complex geometries — •Jan Cammann[1,2], Fabian Jan Schwarzendahl[2,3], Tanya Ostapenko[2], Danylo Lavrentovich[2], Oliver Bäumchen[2,4], and Marco G. Mazza[1,2] — [1]Loughborough University, UK — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [3]Heinrich-Heine-Universität, Düsseldorf, Germany — [4]University of Bayreuth, Germany

Microswimmers have attracted considerable interest due to the biological and ecological implications of understanding the mechanisms governing their dynamics. The motion of a motile cell appears erratic, and yet the combination of nonequilibrium forces and surfaces can produce striking examples of organization in microbial systems. While our current understanding is based on bulk systems or idealized geometries, it remains elusive how self-organization emerges in complex geometries. In this talk I will describe experiments, analytical and numerical calculations [1] to study the motion of motile cells in complex geometries, and demonstrate that a robust topology of probability flux loops organizes active motion even at the level of a single cell in an isolated habitat. Accounting for the interplay of activity and interfacial forces, we find that the boundary's curvature determines the nonequilibrium probability fluxes. We predict a universal relation between fluxes and global geometric properties that is confirmed by experiments.

[1] J. Cammann, et al. "Boundary-interior principle for microbial navigation in geometric confinement." arXiv:2011.02811 (2020).

BP 28.4 Wed 12:00 DYb

The role of inertia in active nematic turbulence — •Colin-Marius Koch and Michael Wilczek — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Suspensions of active agents with nematic interactions can exhibit complex spatio-temporal dynamics such as mesoscale turbulence. Continuum descriptions for such systems are inspired by the hydrodynamic theory of liquid crystals and introduce additional effects of active stresses. The resulting equations feature an advective nonlinearity which represents inertial effects. The typically low Reynolds number of such active flows raises the question of the importance of the inertial effects. To address this question, we investigate mesoscale turbulence in a two-dimensional dense suspension of active nematic liquid crystals. We compare numerical simulations with and without nonlinear advection of the flow field. We find that for sufficiently high activity, the simulations including nonlinear advection exhibit large-scale motion which is not observed when excluding advection. Performing a spectral analysis of the energy budget, we identify an inverse energy transfer to the largest scales highlighting the importance of inertial effects in this model. We additionally show that surface friction, mimicked by a linear friction term, dissipates the transported energy and suppresses the large-scale motion.

BP 28.5 Wed 12:20 DYb

Rheotaxis of active droplets in confinements — •Ranabir Dey[1,2], Carola M. Buness[1,3], Babak Vajdi Hokmabad[1], Chenyu Jin[1,4], and Corinna C. Maass[1,3,5] — [1]Max Planck Institute for Dynamics and Self-Organization, Germany — [2]Indian Institute of Technology Hyderabad, India — [3]Georg August Universitat Goettingen — [4]University of Bayreuth, Germany — [5]University of Twente, the Netherlands

Biological microswimmers commonly navigate confined spaces having liquid flows, e.g. locomotions of spermatozoa through the reproductive tract and bacteria in the gut. The directed motion of the microorganisms in response to the external velocity gradients is classically referred to as 'rheotaxis'. Over the last few years, rigorous efforts have been made to understand the rheotaxis of microorganims, specifically bacteria. In contrast, there is very little quantitative understanding of rheotaxis of artificial microswimmers. It must be noted that artificial microswimmers, e.g. those designed for cargo delivery, are often required to navigate confinements having external flows. Here, we elucidate the swimming dynamics of a common type of artificial microswimmer, i.e. active droplets, in micro-confinements having Poiseuille flow. We experimentally quantify the the swimming characteristics of these droplet microswimmers in response to velocity gradients of varying strength. We also try to understand the observed rheotaxis in confinements by considering the long range hydrodynamic interactions with the confining walls.

BP 28.6 Wed 12:40 DYb

Collective search strategies — •Adam Wysocki and Heiko Rieger — Department of Theoretical Physics and Center for Biophysics, Universität des Saarlandes, Saarbrücken, Germany

How long does it take to find N targets by M searchers? This question arises, for example, if animals search for food or immune cells chase for pathogens (our main motivation). The usual goal is to minimize the time needed to catch all targets. One obvious possibility would be to increase the number of ideal searchers another to search collectively by utilizing communication between the searchers. It is known, that cells of the immune system talk to and influence one another by secreting small proteins that bind to and activate each other. For instance, T cells (a type of lymphocyte) are chemotactic, i.e. they move in response to a chemical stimulus, however, it is unknown if chemotaxis is important in the coordination of the search for pathogens. We use a simulation model of chemotactic active particles together with a self-generated chemorepellent in order to test the possibility and the benefit of collective search strategies in microbiological systems.

BP 29: Active Matter 5 - organized by Carsten Beta (Potsdam), Andreas Menzel (Magdeburg) and Holger Stark (Berlin) (joint session DY/BP)

Time: Wednesday 14:30–15:50 Location: DYb

BP 29.1 Wed 14:30 DYb

Barrier-mediated predator-prey dynamics — •Fabian Jan Schwarzendahl and Hartmut Löwen — Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, 40225 Düsseldorf, Germany

The survival chance of a prey chased by a predator depends not only

on their relative speeds but importantly also on the local environment they have to face. For example, a wolf chasing a deer might no be able to cross a river which can be crossed by the deer. Here, we propose a simple predator-prey model for a situation in which both the escaping prey and the chasing predator have to surmount an energetic barrier. Different barrier-assisted states of catching or final escaping are classified and suitable scaling laws separating these two states are derived. We discuss the effects of diffusion on the catching times and determine states in which catching or escaping is more likely. Including hydrodynamic and chemotactic interactions, we further identify trapping or escaping states which are determined by hydrodynamics and chemotaxis. Our results are of importance for both microbes and self-propelled unanimous microparticles following each other by nonreciprocal interactions in inhomogeneous landscapes.

BP 29.2 Wed 14:50 DYb

Irreversibility of active particles: Fluctuation Theorem and Mutual Information — Lennart Dabelow[1], •Stefano Bo[2], and Ralf Eichhorn[3] — [1]Fakultät für Physik, Universität Bielefeld — [2]Max Planck Institute for the Physics of Complex Systems — [3]Nordita, Royal Institute of Technology and Stockholm University

The defining feature of active particles is that they locally consume energy, which enables them to self-propel and prevents them from equilibrating with their thermal environment. Within the framework of active Ornstein-Uhlenbeck particles we derive the path probability of a particle subject to both, thermal and active noise. By comparing the path probabilities for observing a particle trajectory forward in time versus observing its time-reserved twin trajectory we obtain a generalized "entropy production" for active Brownian motion, which fulfills an integral fluctuation theorem. We show that those parts of this "entropy production", which are different from the usual dissipation of heat in the thermal environment, can be associated with the mutual information between the particle trajectory and the history of the non-equilibrium environment. We then investigate the time-reversal properties of steady-state trajectories of a trapped active particle. We find that steady-state trajectories in a harmonic potential fulfill pathwise time-reversal symmetry exactly despite their active nature, while this symmetry is typically broken in anharmonic potentials.

BP 29.3 Wed 15:10 DYb

Shape-anisotropic Microswimmers: Influence of Hydrodynamics — •Arne W. Zantop and Holger Stark — Institute of Theoretical Physics, Technische Universität Berlin, Hardenbergstraße 36, 10623 Berlin, Germany

Constituents of active matter, e.g. bacteria or active filaments, are often elongated in shape. The shape and the stiffness of the active components clearly influence their individual dynamics and collective pattern formation. On length scales much larger than the size of the constituents, active materials exhibit many fascinating phenomena such as the formation of vortices or turbulent structures [1,2]. To identify how steric and hydrodynamic interactions as well as thermal fluctuations influence collective behavior is subject of current research. In this context, we model shape-anisotropic microswimmers with rod shape by composing them of overlapping spherical squirmers. We simulate their hydrodynamic flow fields using the method of multi-particle collision dynamics. With increasing aspect ratio of the rods, we find that a force quadrupole moment dominates the hydrodynamic flow field, whereas in quasi-2D confinement between two parallel plates (Hele-Shaw geometry) the far field is determined by a two-dimensional source dipole moment [3]. Investigating the collective dynamics of the squirmer rods, we identify with increasing density and aspect ratio of the rods a disordered, a swarming, and a jamming state.

[1] Dunkel *et al.*, Phys. Rev. Lett. **110**, 228102 (2013)
[2] Wensink *et al.*, Proc. Natl. Acad. Sci. **109**, 14308-14313 (2012)
[3] A. W. Zantop and H. Stark, Soft Matter **16**, 6400-6412 (2020)

BP 29.4 Wed 15:30 DYb

Feedback Control of Multiple Active Microswimmers — •Alexander Fischer[1], Giovanni Volpe[2], and Frank Cichos[1] — [1]Peter Debye Institute for Soft Matter Physics, Universität Leipzig — [2]Physics Department, Gothenburg University

Sensing and reacting to signals is a fundamental component of life. The exchange of information is used to organize ensembles of active objects into collective states that appear as flocks, swarms or even tissue. Here we explore the emergent collective behavior as a result of an information exchange between synthetic microswimmers by computer-controlled feedback processes. We have created a setup where multiple active microswimmers can respond to local signals in space or their distance to other microswimmers [1]. Our system consists of symmetric self-thermophoretic swimmers that are propelled by light-to-heat conversion allowing us to implement almost arbitrary control of propulsion speed and direction. Using this system, we study in particular the delayed response of the swimmers to environmental signals, where the swimmers remember previous information on a signaling landscape or infers future signals from experience. We find that this type of delayed response is modifying the collective behavior enhancing local swimmer densities depending on delay time, extrapolation or memory and the rotational diffusion time. Our data suggest the existence of optimal delays for the given landscapes.

[1] U. Khadka, V. Holubec, H. Yang, F. Cichos, Nat. Commun. 9, 3864 (2018)