Biological Physics Division
Fachverband Biologische Physik (BP)

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Overview of Invited Talks and Sessions

(Lecture halls H13, H15, and H16; Poster P1 and P4)

Invited Talks

BP 2.4	Mon	10:15–10:45	H13	**Integrative modeling of dynamic biomolecular structures** — •Holger Gohlke
BP 4.1	Mon	10:30–11:00	H16	**Computer simulations of self-motile active droplets and colloid-active gels composites** — •Davide Davide Marenduzzo
BP 5.1	Mon	15:00–15:30	H15	**The functional nano-architecture of axonal actin** — •Christophe Leterrier
BP 6.5	Mon	16:15–16:45	H16	**From active bacterial microcolonies to biofilms as model tissues** — •Vasily Zaburdaev
BP 8.1	Tue	9:30–10:00	H15	**Phase separation in cells: gene localization and noise buffering** — •Samuel Safran
BP 13.1	Wed	9:30–10:00	H15	**Cortex mechanics - how subtle modifications matter** — •Andreas Janshoff
BP 15.4	Wed	11:00–11:30	H13	**The importance of water in membrane receptor function** — •Anthony Watts
BP 18.1	Wed	15:00–15:30	H15	**Bottom-up molecular control of biomimetic hydrogels** — •Kerstin G. Blank
BP 22.1	Thu	9:30–10:00	H15	**Cell and tissue mechano-plasticity in development** — •Verena Ruprecht
BP 24.1	Thu	10:30–11:00	H16	**Actin waves as building blocks of cellular function** — •Carsten Beta
BP 26.1	Thu	15:00–15:30	H15	**Molecular robots working cooperatively in swarm** — •Akira Kakugo

Invited Talks of the joint Symposium SKM Dissertation Prize 2022 (SYSD)

See SYSD for the full program of the symposium.

SYSD 1.1	Mon	10:15–10:45	H2	**Charge localisation in halide perovskites from bulk to nano for efficient optoelectronic applications** — •Sascha Feldmann
SYSD 1.2	Mon	10:45–11:15	H2	**Nonequilibrium Transport and Dynamics in Conventional and Topological Superconducting Junctions** — •Raffael L. Klees
SYSD 1.3	Mon	11:15–11:45	H2	**Probing magnetostatic and magnetotransport properties of the antiferromagnetic iron oxide hematite** — •Andrew Ross
SYSD 1.4	Mon	11:45–12:15	H2	**Quantum dot optomechanics with surface acoustic waves** — •Matthias Weiss

Invited Talks of the joint Symposium United Kingdom as Guest of Honor (SYUK)

See SYUK for the full program of the symposium.

SYUK 1.1	Wed	9:30–10:00	H2	**Structure and Dynamics of Interfacial Water** — •Angelos Michaelides
SYUK 1.2	Wed	10:00–10:30	H2	**A molecular view of the water interface** — •Mischa Bonn
SYUK 1.3	Wed	10:30–11:00	H2	**Motile cilia waves: creating and responding to flow** — •Pietro Cicuta

SYUK 1.4	Wed	11:00–11:30	H2	**Cilia and flagella: Building blocks of life and a physicist's playground** — •Oliver Bäumchen
SYUK 1.5	Wed	11:45–12:15	H2	**Computational modelling of the physics of rare earth - transition metal permanent magnets from $SmCo_5$ to $Nd_2Fe_{14}B$** — •Julie Staunton
SYUK 2.1	Wed	15:00–15:30	H2	**Hysteresis Design of Magnetic Materials for Efficient Energy Conversion** — •Oliver Gutfleisch
SYUK 2.2	Wed	15:30–16:00	H2	**Non-equilibrium dynamics of many-body quantum systems versus quantum technologies** — •Irene D'Amico
SYUK 2.3	Wed	16:00–16:30	H2	**Quantum computing with trapped ions** — •Ferdinand Schmidt-Kaler
SYUK 2.4	Wed	16:45–17:15	H2	**Breaking the millikelvin barrier in cooling nanoelectronic devices** — •Richard Haley
SYUK 2.5	Wed	17:15–17:45	H2	**Superconducting Quantum Interference Devices for applications at mK temperatures** — •Sebastian Kempf

Invited Talks of the joint Symposium Interplay of Substrate Adaptivity and Wetting Dynamics from Soft Matter to Biology (SYSM)

See SYSM for the full program of the symposium.

SYSM 1.1	Wed	15:00–15:30	H1	**Statics and Dynamics of Soft Wetting** — •Bruno Andreotti
SYSM 1.2	Wed	15:30–16:00	H1	**Droplets on elastic substrates and membranes - Numerical simulation of soft wetting** — •Sebastian Aland
SYSM 1.3	Wed	16:00–16:30	H1	**Wetting of Polymer Brushes in Air** — Lars Veldscholte, Guido Ritsema van Eck, Liz Mensink, Jacco Snoeijer, •Sissi de Beer
SYSM 1.4	Wed	16:45–17:15	H1	**Elastocapillary phenomena in cells** — •Roland L. Knorr
SYSM 1.5	Wed	17:15–17:45	H1	**Active contact line depinning by micro-organisms spreading on hydrogels** — Marc Hennes, Julien Tailleur, Gaëlle Charron, •Adrian Daerr

Invited Talks of the joint Symposium Collective Social Dynamics from Animals to Humans (SYSO)

See SYSO for the full program of the symposium.

SYSO 1.1	Thu	9:30–10:00	H1	**Capturing group interactions: The next frontier of modeling social and biological systems** — •Frank Schweitzer
SYSO 1.2	Thu	10:00–10:30	H1	**Modelling Individual Mobility Behavior** — •Laura Maria Alessandretti
SYSO 1.3	Thu	10:30–11:00	H1	**Validating argument-based opinion dynamics with survey experiments** — •Sven Banisch
SYSO 1.4	Thu	11:15–11:45	H1	**Self-organization, Criticality and Collective Information Processing in Animal Groups** — •Pawel Romanczuk
SYSO 1.5	Thu	11:45–12:15	H1	**Collective dynamics and physiological interactions in bird colonies** — •Hanja Brandl

Sessions

BP 1.1–1.3	Sun	16:00–18:30	H4	**Tutorial: Stochastic Processes from Financial Risk to Genetics (joint session SOE/TUT/BP/DY)**
BP 2.1–2.9	Mon	9:30–12:15	H13	**Computational Biophysics and Neuroscience**
BP 3.1–3.10	Mon	9:30–12:30	H15	**Cell Mechanics 1**
BP 4.1–4.7	Mon	10:30–12:45	H16	**Active Matter 1 (joint session BP/CPP/DY)**
BP 5.1–5.7	Mon	15:00–17:30	H15	**Focus Session: Super Resolution Microscopy and Dynamics of Supramolecular Complexes**
BP 6.1–6.7	Mon	15:00–17:15	H16	**Statistical Physics of Biological Systems 1 (joint session BP/DY)**
BP 7.1–7.46	Mon	18:00–20:00	P1	**Poster 1**
BP 8.1–8.12	Tue	9:30–13:00	H15	**Focus Session: Phase Separation in Biochemical Systems**
BP 9.1–9.11	Tue	9:30–13:00	H16	**Bioimaging**
BP 10.1–10.9	Tue	10:00–12:30	H13	**Cell Adhesion and Multicellular Systems**
BP 11.1–11.11	Tue	10:00–13:00	H18	**Active Matter 2 (joint session DY/BP/CPP)**
BP 12.1–12.66	Tue	17:30–19:30	P4	**Poster 2**
BP 13.1–13.11	Wed	9:30–12:45	H15	**Cytoskeleton**

BP 14.1–14.10	Wed	9:30–12:30	H16	**Active Matter 3 (joint session BP/CPP/DY)**
BP 15.1–15.7	Wed	10:00–12:15	H13	**Protein Structure and Single Molecules**
BP 16.1–16.6	Wed	10:15–12:45	H11	**Networks: From Topology to Dynamics (joint session SOE/BP/DY)**
BP 17.1–17.7	Wed	15:00–17:00	H13	**Membranes and Vesicles**
BP 18.1–18.8	Wed	15:00–17:30	H15	**Biomaterials (joint session BP/CPP)**
BP 19.1–19.8	Wed	15:00–17:15	H16	**Cell Mechanics 2**
BP 20.1–20.9	Wed	15:00–17:30	H18	**Active Matter 4 (joint session DY/BP/CPP)**
BP 21	Wed	18:00–19:00	H15	**Members' Assembly**
BP 22.1–22.9	Thu	9:30–12:15	H15	**Migration and Multicellular Systems**
BP 23.1–23.3	Thu	10:00–10:45	H13	**Evolution**
BP 24.1–24.6	Thu	10:30–12:30	H16	**Systems Biology, Gene Expression, Signalling**
BP 25.1–25.4	Thu	11:00–12:00	H13	**Bioinspired Systems**
BP 26.1–26.8	Thu	15:00–17:30	H15	**Focus Session: Bioinspired Systems**
BP 27.1–27.6	Thu	15:00–16:30	H16	**Statistical Physics of Biological Systems 2 (joint session BP/DY)**
BP 28.1–28.6	Fri	9:30–11:15	H39	**Biopolymers, Biomaterials and Bioinspired Functional Materials (joint session CPP/BP)**
BP 29.1–29.11	Fri	10:00–12:45	H18	**Active Matter 5 (joint session DY/BP/CPP)**

Members' Assembly of the Biological Physics Division

Wednesday 18:00–19:00 H15

- Report
- Election
- Miscellaneous

BP 1: Tutorial: Stochastic Processes from Financial Risk to Genetics (joint session SOE/TUT/BP/DY)

Macroscopic and microscopic models from Economy to Biology must account for stochasticity on various levels. While classical physics strives for deterministic descriptions through differential equations from fundamental level to thermodynamics, many physics-based models on higher level explicitely include stochasticity from various sources. Discrete and continuous stochastic processes then become the mathematical foundation of these models. This tutorial highlights classical as well as current methods and approaches of probabilistic models and stochastic processes in physics, biology as well as socio-economic systems, thereby bridging the risk to extinction in genetics with its economic counterpart. (Session organized by Jens Christian Claussen.)

Time: Sunday 16:00–18:30 Location: H4

Tutorial BP 1.1 Sun 16:00 H4

Diffusion approximations for particles in turbulence — •Bernhard Mehlig — University of Gothenburg, Gothenburg, Sweden

The subject of this tutorial is the dynamics of particles in turbulence, such as micron-sized water droplets in the turbulent air of a cumulus cloud. The particles respond in intricate ways to the turbulent fluctuations. Non-interacting particles may cluster together to form spatial patterns – even though the turbulent fluid is incompressible [1]. In this tutorial I explain how to understand spatial clustering using diffusion approximations, highlighting an analogy with Kramers' escape problem [2]. I introduce/review the necessary elements of diffusion theory. My goal is to give a pedagogical introduction to diffusion approximations in non-equilibrium statistical physics, using particles in turbulence as an example.

[1] K. Gustavsson and B. Mehlig, Statistical models for spatial patterns of heavy particles in turbulence, Adv. Phys. 65 (2016) 57 (read Sections 1, 3.1, and 6.1).

[2] H. A. Kramers, Brownian motion in a field of force and the diffusion model of chemical reactions, Physica 7 (1940) 284 (read up to eq. (17)).

Tutorial BP 1.2 Sun 16:50 H4

Probabilities in physics, paradoxes and populations — •Tobias Galla — Instituto de Física Interdisciplinary Sistemas Complejos, IFISC (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain

It is notoriously hard for humans to develop a good intuition for probabilities and stochastic processes. Our brains are not able to do this naturally, and there are numerous mistakes which are easy to make. These mistakes are in fact made regularly in the press (sometimes perhaps deliberately). More worrisome, decision makers such as judges, doctors or politicians are also prone to mishandling probabilities. In this tutorial I will outline a few of these traps, and how to avoid them. I will also discuss the nature of probabilistic models of physical processes – is there genuine randomness in the world around us? I will then present a number of instances in which physics approaches combined with stochastic modelling can make a difference. As one example, I will outline experimental and theoretical results which highlight the importance of stochastic processes in population dynamics. Other examples will include stochastic processes in genetics, the evolution of cancer and in game theory.

Tutorial BP 1.3 Sun 17:40 H4

Risk Revealed: Cautionary Tales, Understanding and Communication — •Paul Embrechts — Department of Mathematics, ETH Zürich

The title of the tutorial refers to a forthcoming book, to be published by Cambridge University Press, co-authored with Valérie Chavez-Demoulin (Lausanne) and Marius Hofert (Waterloo). Extreme Value Theory (EVT) offers a mathematical tool for the modeling of so-called What-If events, or stress scenarios. I will present several examples of risk-based decision-making and show how EVT can be used as part of the solution. The current pandemic has clearly shown that the communication of scientific evidence has a difficult stand in the ubiquitous environment of social media. I will discuss some examples of this struggle.

BP 2: Computational Biophysics and Neuroscience

Time: Monday 9:30–12:15 Location: H13

BP 2.1 Mon 9:30 H13

Non-ideality in lipid mixtures, a molecular dynamics study — •Lisa Berezovska[1], Fabrice Thalmann[1], and Raisa Kociurzynski[2] — [1]Institut Charles Sadron, CNRS and University of Strasbourg, 23 rue du Loess, F-67034 Strasbourg, France — [2]Faculty of Biology, Albert-Ludwigs-University Freiburg, Schänzlestraße 1, 79104 Freiburg, Germany

Biological membranes are complex environments characterized by multicomponent lipid mixtures[1]. We investigate in this work binary lipid bilayers using the SPICA coarse-grained molecular dynamics model.

Adapting the Kirkwood-Buff theory of liquid mixtures [2] to finite wavelegth density fluctuations statistics, we compare various practical approaches for determining the interaction parameters in a theory of regular solution description of these numerical lipid mixtures.

[1] Ole G. Mouritsen, L. A. Bagatolli. Life as a matter of fat, Springer-Verlag GmbH, 2015

[2] A. Ben-Naim, Water and Aqueous Solutions: Introduction to a Molecular Theory, Plenum Press, 1974

[3] Lisa Berezovska, Raisa Kociurzynski, Fabrice Thalmann, in preparation

BP 2.2 Mon 9:45 H13

Membrane-mediated interactions between non-spherical elastic particles — •Jiarul Midya, Thorsten Auth, and Gerhard Gompper — Theoretical Physics of Living Matter (IBI-5/IAS-2), Forschungszentrum Jülich, D-52425 Jülich,Germany

Transport of particles across lipid-bilayer membranes is important for biological cells to exchange information and material with the environment. Large particles often get wrapped by membranes [1]. However, many particles in vivo and in vitro are deformable, e.g., vesicles, filamentous viruses, macromolecular condensates, polymer-grafted nanoparticles, and microgels. Vesicles may serve as a generic model system for deformable particles [2]. Using the Helfrich Hamiltonian, triangulated membranes, and energy minimization, we predict the interplay of vesicle shapes and wrapping states. Increasing particle softness enhances the stability of shallow-wrapped and deep-wrapped states over non-wrapped and complete-wrapped states. The free membrane mediates an interaction between partial-wrapped vesicles. For the deep-wrapped vesicles, we predict a purely repulsive interaction. For shallow-wrapped states, interaction potential depends on the mutual orientation of the vesicles. Our predictions may guide the design and fabrication of deformable particles for efficient use in medical applications, such as targeted drug delivery.

[1] S. Dasgupta et al., J. Phys.: Condens. Matter **29**, 373003 (2017); [2] X. Yi et al., Phys. Rev. Lett. **107**, 098101 (2011).

BP 2.3 Mon 10:00 H13

RNA structure prediction via Machine Learning — •Alexander Schug[1,2], Oskar Taubert[4], Christian Faber[1], Mehari Zerihun[1], Fabrizio Pucci[1], Fabrice von der Lehr[3], Philipp Knechtges[3], Marie Weiel[4,5], Charlotte Debus[4,5], Daniel Coquelin[4,5], Stefan Kesselheim[1,5], Achim Basermann[3], Achim Streit[4], and Markus Götz[4,5] — [1]Jülich Supercomputing Centre, FZ Jülich, Jülich — [2]Faculty of Biology, University of Duisburg/Essen — [3]Institute for Software Technology, German Aerospace Centre (DLR) — [4]Steinbuch Centre for Computing, Karlsruhe Institute of Technology — [5]Helmholtz AI

Knowledge of biomolecular structure is necessary to gain any detailed understanding of their function For proteins, tools rooted in statistical physics such as Direct Coupling Analysis (DCA) or Machine Learning driven approaches (ML) such as Alpha Fold 2 exploit massive sequence databases to trace evolutionary patterns for structure predictions. We demonstrate how additional information, such as low-resolution experimental information (e.g. SAXS or FRET) can integrated. For RNA there are significantly less data available than for proteins, which makes ML more challenging. Still, we demonstrate how contact prediction for RNA can be vastly improved both via simple convolutional neural networks but also by unsupervised deep-learning approaches by combining multiple self-supervised learning tasks. In an empirical evaluation for RNA, we find a strong increase of prediction quality.

Invited Talk BP 2.4 Mon 10:15 H13

Integrative modeling of dynamic biomolecular structures — •Holger Gohlke — Institute for Pharmaceutical and Medicinal Chemistry, Heinrich Heine University Düsseldorf, 40225 Düsseldorf, Germany — John von Neumann Institute for Computing (NIC), Jülich Supercomputing Centre (JSC), Institute of Biological Information Processing (IBI-7: Structural Biochemistry), and Institute of Bio- and Geosciences (IBG-4: Bioinformatics), Forschungszentrum Jülich GmbH, 52425 Jülich, Germany

Structures of biomacromolecules and their complexes are essential to understand the underlying molecular mechanisms of the biological processes. If biomolecular systems are complex, information from multiple experimental and computational methods is combined by integrative modeling (IM) for generating integrative structure models. We will describe how molecular modeling and simulations contributed to a high-resolution NMR characterization of all apparent states of the prototypic 10*23 DNAzyme and to rationally selecting a single-atom replacement, with which the performance of the DNAzyme could be considerably enhanced. Furthermore, we will address how to overcome the sparsity of FRET experiments to provide state-specific structural information of complex dynamic biomolecular assemblies and probe the robustness of Maximum Entropy Method reconstructions for a flexible system with ordered parts using FRET data as experimental information.

15 min. break

BP 2.5 Mon 11:00 H13

Mechanical stimulation in stem cell-derived 3D neuronal networks — •Elijah Shelton[1], Katja Salbaum[1,2], Filippo Kiessler[1], Paulina Wysmolek[3], Selina Sonntag[1], and Friedhelm Serwane[1,2,4] — [1]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität, Munich, Germany — [2]Graduate School of Systemic Neuroscience (GSN), Munich, Germany — [3]Max Planck Institute for Medical Research, Heidelberg, Germany — [4]Munich Cluster for Systems Neurology (SyNergy), Germany

Neurons sense and respond to mechanical factors in their local microenvironment. For example, firing activity is modulated in response to amplitude and location of a mechanical stimulation as single cell in vitro experiments have shown. However, it is unclear (i) how these observations translate to the scale of neuronal tissues and (ii) how mechanical stimulation informs the formation and function of neurons in 3D networks. To tackle this problem, we combine stem cell-derived neuronal organoids, magnetic droplets as mechanical actuators, and calcium imaging as tool for neuronal characterization. Using 30-50 micron diameter magnetic droplets, we produce controlled and precise mechanical stimulations inside these 3D tissues. We visualize electrophysiological activity within these networks using genetically encoded calcium sensors and confocal fluorescence microscopy. Here, I present recent mechanical and electrophysiological measurements within these neuronal organoids. Such kinds of recordings might provide insights into how mechanical forces can influence both form and function of neuronal networks.

BP 2.6 Mon 11:15 H13

Characterizing spreading dynamics of subsampled systems with nonstationary external input — Jorge de Heuvel[1], Jens Wilting[2], Moritz Becker[3], Viola Priesemann[2], and •Johannes Zierenberg[2] — [1]University of Bonn, Bonn, Germany — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen Germany — [3]University Medical Center Göttingen, Göttingen Germany

Many systems with propagation dynamics, such as spike propagation in neural networks and spreading of infectious diseases, can be approximated by autoregressive models. The estimation of model parameters can be complicated by the experimental limitation that one observes only a fraction of the system (subsampling) and potentially time-dependent parameters, leading to incorrect estimates. We show analytically how to overcome the subsampling bias when estimating the propagation rate for systems with certain nonstationary external input. This approach is readily applicable to trial-based experimental setups and seasonal fluctuations as demonstrated on spike recordings from monkey prefrontal cortex and spreading of norovirus and measles.

BP 2.7 Mon 11:30 H13

Mesoscopic description of metastability and hippocampal replay in neural networks with short-term plasticity — Bastian Pietras[1], Valentin Schmutz[2], and •Tilo Schwalger[3] — [1]Universitat Pompeu Fabra, Barcelona, Spain — [2]Brain Mind Institute, School of CÉcole Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland — [3]Technische Universität Berlin

Sequences of metastable states in neuronal population activities have been linked to various sensory and cognitive functions. Two prominent mechanisms of metastable dynamics are noise-induced transitions among attractors and deterministic transitions induced by slow fatigue processes. The dependence of these mechansisms on neural circuit parameters at the microscopic scale are largely unclear. Starting with a network of linear-nonlinear Poisson spiking neurons with synaptic short-term plasticity, we use a bottom-up approach and derive a stochastic neural-mass model at the mesocopic scale that links to the microscopic circuit parameters. We apply the mesoscopic model to investigate hippocampal "replay" events, i.e. spontaneous sequences of metastable activations of place cells. We study a spiking-neural-network for depression-induced metastability of place-cell activity. The corresponding mesoscopic model precisely reproduces the statistics of metastastable events in the microscopic network model. This enables us to efficiently explore the full range of neuron numbers including the thermodynamic limit. We find a novel dynamical regime in finite-size networks where metastable replay events are fluctuation-driven and exhibit biologically plausible irregularity.

BP 2.8 Mon 11:45 H13

Decision-making and dynamics in a small neural network — •Monika Scholz — Max Planck Institute for Neurobiology of Behavior - caesar

The nematode C. elegans feeds on small microbes which it ingests using a pumping action of the pharynx. Its pharyngeal nervous system, which controls feeding, comprises only 20 neurons. We aim to understand how the animal adapts its feeding rate to environmental conditions and metabolic needs, using a combination of theoretical modelling, voltage imaging and behavioral observations. When imaging the animals feeding behavior we identify two modes of regulating food intake: First, we find burst-pause dynamics which we link to a decision-making process where the animal attempts to measure the external food concentration. We also find a second mode of action, in which the pumping frequency is smoothly adapted to reflect the quality of the available food. Using a conductance model of the pharyngeal muscle and its key regulatory circuit, we ask which of these modes of regulation are in the muscular excitability and which are driven by phasic inputs by the nervous system. We will discuss the utility of this small nervous system in understanding computational principles connecting neural activity to behavior.

BP 2.9 Mon 12:00 H13

Available processing time regulates optimal balance between sensitivity and precision — Sahel Azizpour[1], •Johannes Zierenberg[2], Viola Priesemann[2], and Anna Levina[3] — [1]Donders Institute for Brain, Cognition and Behavior, Nijmegen, Netherlands — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen

Germany — [3]Eberhard Karls University of Tübingen, Tübingen, Germany

Solving everyday tasks naturally leads to a trade-off between the time spent on processing some input and the accuracy of the outcome. In particular, fast decisions have to rely on uncertain information about inputs. However, standard estimates of information processing capabilities, such as the dynamic range, are defined based on infinite-time averages that do not incorporate noise effects from finite processing times. Here, we develop estimates of processing capability that explicitly account for noisy outputs. We use these measures to show that limiting the processing time in recurrent neural networks can drastically affect the sensitivity and precision of outcomes. This way, optimal dynamical states shift away from the conventionally expected critical point toward subcritical states for finite processing times. Our results thus highlight the necessity to explicitly account for processing times in future estimates of information processing capabilities.

BP 3: Cell Mechanics 1

Time: Monday 9:30–12:30 Location: H15

Prize Talk BP 3.1 Mon 9:30 H15

Basal tension in the wing disc epithelium - what's collagen got to do with it — Karla Yanin Guerra Santiallan[1,3], Christian Dahmann[2], and •Elisabeth Fischer-Friedrich[1,3,4,5] — [1]Cluster of Excellence Physics of Life, Technische Universität Dresden, Dresden, Germany — [2]Institute of Genetics, Technische Universität Dresdenn, Dresden, Germany — [3]Biotechnology Center, Technische Universität Dresden, Dresden, Germany — [4]Faculty of Physics, Technische Universität Dresden, Dresden, Germany — [5]Laureate of the Hertha-Sponer-Prize 2022

Healthy tissue morphogenesis is an important prerequisite for organ function. During development, epithelial folding is a major element of tissue morphogenesis. It has been shown that epithelial folding can be driven through a reduction of basal cell tension. However, a comprehensive analysis of the regulating factors of basal tension is still lacking. In this study, we use indentation with the cantilever of an atomic force microscope to estimate mechanical tension at the basal cell boundary in the wing disc epithelium of the 3rd instar larva of *Drosophila melanogaster*. We find that basal tension is not only affected by contractility of the actin cytoskeleton but is strongly influenced by the presence of the basement membrane as well as osmotic pressure. Our data suggest that elastic stresses in the basement membrane induced by basement membrane stretch, e.g. via osmotic swelling, may be a key factor in the adjustment of basal tension.

BP 3.2 Mon 10:00 H15

Viscoelasticity of spherical cellular aggregates — •Antoine Girot[1,2], Marcin Makowski[1], Marco Rivetti[1], Christian Kreis[1,3], Alexandros Fragkopoulos[1,2], and Oliver Bäumchen[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — [2]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [3]Department of Physical and Environmental Sciences, University of Toronto, ON Toronto, Canada

Understanding the complexity of many biophysical processes such as the dynamics of biological tissues requires a proper mechanical characterization of multicellular aggregates. Current experimental techniques, however, are typically limited to systems that are not larger than an individual cell. We employ *in vivo* micropipette force measurements combined with optical detection to precisely measure the force response and the deformation of living organisms simultaneously. In this presentation, we use this approach to investigate the mechanical behaviour of *Volvox globator*, a multicellular aggregate composed of thousands bi-flagellated cells forming a spherical monolayer filled with mucilage. *Volvox* is considered a model system, *e.g.* to study the evolution from single cells to multicellular life. We show that a model that couples elastic and viscous components is in excellent agreement with the mechanical response of *Volvox* and therefore can be used to extract the viscoelastic properties. We find that the viscous component is rate-dependent and exhibits a shear-thinning behaviour, while the elasticity of the cellular monolayer depends on the size of the colony.

BP 3.3 Mon 10:15 H15

Phase field model for the mechanics and migration of nucleated cells — •Robert Chojowski, Ulrich S. Schwarz, and Falko Ziebert — Institute for Theoretical Physics and BioQuant, Heidelberg University, Germany

Eukaryotic cells are built from many different constituents of varying sizes and properties. Of these organelles, the nucleus is by far the largest one. During recent years, it has become clear that many cellular functions are modulated by the nucleus, including mechanosensing of the environment and cell migration in complex environments. Its stiffness has been determined by AFM and micropipette experiments to be up to 10-fold higher than the stiffness of the surrounding cytoplasm. Despite its physical and biological importance, the nucleus is often neglected in models for cell mechanics and migration. Here we extend our reversible elastic phase field method [1] by a compartment with nuclear elasticity. We validate our numerical implementation by comparing to the analytical solution of a homogeneously adhered disk-like cell. We then simulate the effect of the nucleus for several interesting experimental setups, in particular for cell migration through a narrow channel.

[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 3.4 Mon 10:30 H15

Mechanical Properties of the Premature Lung — •Jonas Naumann[1], Nicklas Koppe[1], Ulrich Herbert Thome[2], Mandy Laube[2], and Mareike Zink[1] — [1]Research Group Biotechnology and Biomedicine, Peter-Debye-Institute for Soft Matter Physics, Leipzig University, 04103 Leipzig, Germany — [2]Center for Pediatric Research Leipzig, Department of Pediatrics, Division of Neonatology, Leipzig University, 04103 Leipzig, Germany

Even though mechanical ventilation is a life-saving therapy for premature infants suffering from respiratory distress syndrome, prolonged ventilation and related mechanical load may cause subsequent pulmonary diseases such as bronchopulmonary dysplasia. To study the effect of mechanical stress on the immature lung, premature rat lungs were subjected to rheology experiments in compression and tension at different velocities. Here, fetal lungs behaved significantly stiffer with increasing deformation velocities as also used during high-frequency ventilation. A higher Young's modulus of fetal rat lungs compared to adult controls clearly pointed towards altered tissue characteristics. Furthermore, influences of hydrostatic pressure differences on the electrophysiology of lung epithelial cells were studied with a pressure-adjustable Ussing chamber. We observed a strong impact of hydrostatic pressure on vectorial sodium transport, important for alveolar fluid clearance. These pressure-dependent cellular alterations might explain clinical observations of ventilation-induced side effects.

15 min. break

BP 3.5 Mon 11:00 H15

Novel Optofluidic Particle Trap Enables FemtoNewton Force Sensing — •Iliya Stoev[1,2], Benjamin Seelbinder[1,2], Elena Erben[1,2], Nicola Maghelli[1,2], and Moritz Kreysing[1,2,3] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, 01307, Dresden, Germany — [2]Centre for Systems Biology, Pfotenhauerstraße 108, 01307, Dresden, Germany — [3]Cluster of Excellence Physics of Life, TU Dresden, Arnoldstraße 18, 01307, Dresden, Germany

Here we show how thermoviscous expansion phenomena can be used to generate a new contactless particle trap that is characterised by a linear force-extension relationship and can therefore be employed in non-invasively measuring femtoNewton forces with thermally limited sensitivity. Our new method combines optics with microfluidics, lifting prerequisites related to the probe material and resulting in only moderate heating at the position of the micromanipulated object. This offers an appealing alternative to the use of optical tweezers in highly delicate samples and living systems. As a follow-up work, we aim to explore the opportunity of using these thermoviscous flows in a

novel phase-sensitive microrheology approach by building on the formalism established in classic bulk rheology. We anticipate that our new method would be of interest to material scientists and mechanobiologists alike as it provides a route towards measuring the mechanics of highly viscous media, tenuous gels and likely even cellular cytoplasm or embryonic ooplasm. Further refinements of the method aim at removing the need for using fluorescent tags and/or external probes.

BP 3.6 Mon 11:15 H15

Theoretical model reveals significance of microtubules poleward flux in chromosome congression — •Ivan Sigmund, Domagoj Božan, and Nenad Pavin — University of Zagreb, Faculty of Science

At the onset of mitosis, a living cell forms mitotic spindle to ensure proper division of duplicated chromosomes between two daughter cells, whereas malfunctioning spindles can lead to chromosome missegregation. During prometaphase chromosomes are initially randomly distributed and in interaction with microtubules experience forces that congress them in spindle equator. Here we investigate what are the dominant forces that drive chromosome congression. By introducing a theoretical model, we show that length dependent poleward flux generates a net force towards the spindle equator. This poleward flux is generated by motor proteins which accumulate along the region of antiparallel microtubule overlaps. On the other hand, forces exerted by passive crosslinkers, that accumulate within the region of parallel microtubule overlaps, are off-centering, and can impair chromosome congression. Thus, our model reveals the significance of microtubule poleward flux in chromosome congression.

BP 3.7 Mon 11:30 H15

Red blood cell shape transitions and dynamics in time-dependent capillary flow — •Katharina Graessel[1], Steffen M. Recktenwald[2], Felix M. Maurer[2], Thomas John[2], Christian Wagner[2,3], and Stephan Gekle[1] — [1]Biofluid Simulation and Modeling, Theoretische Physik VI, University of Bayreuth — [2]Dynamics of Fluids, Experimental Physics, Saarland University — [3]Physics and Materials Science Research Unit, University of Luxembourg

Red blood cells in small microchannels flow in characteristic shapes, mainly symmetric croissants at the channel center and non-symmetric off-centered slippers. While these shapes have been studied for some time, not much is known about the transition dynamics between different states. Here, we use boundary-integral simulations together with microfluidic experiments in time-dependent flows to observe and understand red blood cell shape transitions. The transition from the croissant to the slipper shape happens much faster than the opposite transition. We find that the center of mass of slipper cells shows lateral oscillations due to the tank-treading movement of the RBC membrane. The oscillation frequency increases with the cell velocity and the viscosity of the surrounding fluid.

BP 3.8 Mon 11:45 H15

Elastic modulus of lipid-loaded platelets investigated with scanning ion conductance microscopy (SICM) — •Hendrik von Eysmondt[1], Johannes Rheinlaender[1], Madhumita Chatterjee[2], and Tilman E. Schäffer[1] — [1]Institute of Applied Physics, Eberhard-Karls-University Tübingen, Germany — [2]Department of Cardiology and Angiology, University Hospital Tübingen, Germany

Platelets are small, anucleate blood cells involved in blood hemostasis, wound healing, and immune response as well as in diseases like atherosclerosis and coronary artery disease. Both low-density lipoprotein (LDL) and its oxidized form (OxLDL) increase the prothrombotic potential of platelets. Recently, it was shown that a chemokine receptor ACKR3/CXCR7 agonist inhibits platelet activation and thrombus formation, offering a new therapeutic choice for hyperlipidemic patients. However, the impacts of LDL, OxLDL, and CXCR7-agonist on platelet morphology and mechanics have not yet been identified.

We therefore investigated the influence of LDL, OxLDL, and CXCR7-agonist on platelet morphology and mechanics using SICM. We showed that CXCR7-agonist pre-treatment reduced the initial spreading rate on collagen, the final spreading area on both collagen and fibrinogen, and the elastic modulus on fibrinogen. We also showed that OxLDL, but not LDL, significantly alters the morphology and elastic modulus of lipid-loaded platelets and that CXCR7-agonist pretreatment can reverse some of the effects of OxLDL.

BP 3.9 Mon 12:00 H15

Measuring the Tension of Droplets and Living Cells with the Scanning Ion Conductance Microscope — •Johannes Rheinlaender and Tilman E. Schäffer — Institute of Applied Physics, University Tübingen, Germany

It is well known that surface tension can dominate the mechanics of micro- and nanoscale systems. However, probing the mechanics of elastic interfaces at the micrometer scale can be difficult because of the complex probe-sample interactions or the unknown underlying geometry. Here, were introduce a method to measure the surface tension of interfaces at the micrometer scale in a contact-free manner using the scanning ion conductance microscope (SICM). The SICM is based on recording the ion current through a nanopipette and was recently extended to also measure the mechanical stiffness of soft samples utilizing a microfluidic flow through the nanopipette opening. By measuring the three-dimensional shape and mechanical stiffness of oil droplets on various surfaces, we show that we can quantitatively measure their surface tension independently of their shape over more than three orders of magnitude. Applying this concept to living cells, we show that we can quantitatively measure their local stiffness and average (cortical) tension in a contact-free way. Living cells exhibit cortical tensions on the order of few mN/m, which we found to strongly vary with cell type and external conditions. For example, we show that normal and cancer cells strongly differ in their cortical tension, which demonstrates that the SICM is a versatile tool to measure the mechanical properties of living cells.

BP 3.10 Mon 12:15 H15

The secret life of sarcomeres: stochastic heterogeneity of sarcomeres in beating stem-cell-derived cardiomyocytes — •Daniel Härtter[1,2], Lara Hauke[1], Wolfram-Hubertus Zimmermann[1], and Christoph F. Schmidt[2] — [1]Institute of Pharmacology and Toxicology, Göttingen University Medical Center, Germany — [2]Department of Physics and Soft Matter Center, Duke University, Durham, NC, USA

Sarcomeres are the basic contractile units of cardiac muscles. We tracked single sarcomere motion in individual hiPSC-derived cardiomyocytes at high resolution, using a novel set of experimental and computational tools. While the emergent cell-level motion is smooth, individual sarcomeres are highly motile and behave heterogeneously during beating cycles. In response to rigid mechanical constraints, sarcomeres are forced into a tug-of-war-like competition. Automated, machine-learning-supported analysis of a large data set (>1200 cells) indicates that sarcomere heterogeneity is not caused by static non-uniformity between sarcomeres (e.g., strong/weak), but can be primarily attributed to the stochastic and non-linear nature of sarcomere dynamics and thus occurs intrinsically during cardiomyocyte beating. We show that a simple dynamic model reproduces crucial experimental findings by assuming a non-monotonic force-velocity relation for single sarcomeres, as previously predicted for ensembles of motor proteins. This led us to a novel, active matter perspective on sarcomere motion, with sarcomeres as interacting, non-linear and stochastic agents, in contrast to the prevailing mechanistic view on muscle contraction.

BP 4: Active Matter 1 (joint session BP/CPP/DY)

Time: Monday 10:30–12:45 Location: H16

Invited Talk BP 4.1 Mon 10:30 H16

Computer simulations of self-motile active droplets and colloid-active gels composites — •Davide Davide Marenduzzo — School of Physics and Astronomy, University of Edinburgh, Edinburgh, UK

In this talk we will show results from computer simulations probing the behaviour of composite materials based on active gels.

In the first part of the talk we will investigate the behavior of active nematic or cholesteric droplets inside an isotropic fluid. In different regions of parameter space, we find regular motility and chaotic behaviour, and discuss the relevance of these results to biophysical systems such as microbial motility.

In the second part of the talk, we will study the dynamics of a dispersion of passive colloidal particles in an active nematic host. We find that activity induces a dynamic clustering of colloids even in the absence of any preferential anchoring of the active nematic director at the particle surface. When such an anchoring is present, active stresses instead compete with elastic forces and re-disperse the aggregates observed in passive colloid-liquid crystal composites.

BP 4.2 Mon 11:00 H16

Chloroplasts in dark-adapted plants show active glassy behavior — •Nico Schramma, Cintia Perugachi Israëls, and Mazi Jalaal — University of Amsterdam, Amsterdam, Netherlands

Photosynthesis in plants is one of the main drivers for the survival of whole ecosystems on earth. To guarantee the efficiency of this process, plants have to actively adapt to ever-changing light conditions. On large time scales plants can grow towards the light. However, this process is too slow to adapt towards transient stimuli. To do this plants can re-arrange the intracellular structure by the active motion of chloroplasts on short timescales. These organelles are confined between the cell membrane and vacuole and can move inside the cytoplasm via actin polymerization forces. Remarkably, the simple - yet elegant - interplay of light-sensing and active forces leads to various modes of collective motion. Here, we show that the chloroplasts under dark conditions are densely packed systems, driven by a-thermal noise and can exhibit active glassy motion. Furthermore, we aim to establish chloroplast motion as a new framework to study the dynamics of light-controlled dense biological systems featuring intriguing dynamic phase transitions.

BP 4.3 Mon 11:15 H16

Activity-induced polar patterns of filaments gliding on a sphere — •Chiao-Peng Hsu, Alfredo Sciortino, Yu Alice de la Trobe, and Andreas Bausch — Center for Protein Assemblies and Lehrstuhl für Zellbiophysik E27, Physics Department, Technische Universität München, Garching, Germany

Active matter systems feature the ability to form collective patterns as observed in a plethora of living systems, from schools of fish to swimming bacteria. While many of these systems move in a wide, three-dimensional environment, several biological systems are confined by a curved topology. The role played by a non-Euclidean geometry on the self-organization of active systems is not yet fully understood, and few experimental systems are available to study it. Here, we introduce an experimental setup in which actin filaments glide on the inner surface of a spherical lipid vesicle, thus embedding them in a curved geometry. We show that filaments self-assemble into polar, elongated structures and that, when these match the size of the spherical geometry, both confinement and topological constraints become relevant for the emergent patterns, leading to the formation of polar vortices and jammed states. These results experimentally demonstrate that activity-induced complex patterns can be shaped by spherical confinement and topology.

15 min. break

BP 4.4 Mon 11:45 H16

The effect of chiral flows on pattern formation on active cell surfaces — Lucas Wittwer[2], Eloy de Kinkelder[1], and •Sebastian Aland[1,2] — [1]TU Freiberg — [2]HTW Dresden

Mechanochemical processes play a crucial role during morphogenesis, the formation of complex shapes and tissues out of a single cell. On the cellular level, the actomyosin cortex governs shape and shape changes. This thin layer of active material underneath the cell surface exerts an active contractile tension, the strength of which being controlled by the concentration of force-generating molecules. Advective transport of such molecules leads to a complex interplay of hydrodynamics and molecule concentration which gives rise to pattern formation and self-organized shape dynamics. In this talk, we present a novel numerical model to simulate an active viscoelastic surface immersed in viscous fluids. The resulting patterning, flows and cell shape dynamics are shown for different parameter configurations. It is further demonstrated that adding a chiral (i.e. counter-rotating) force at the cell surface can promote a ring of high molecule concentration and facilitate cell division.

BP 4.5 Mon 12:00 H16

Premelting controlled active matter in ice — •Jeremy Vachier[1] and John S. Wettlaufer[1,2] — [1]Nordita, KTH Royal Institute of Technology and Stockholm University, Hannes Alfvéns väg 12, SE-106 91 Stockholm, Sweden — [2]Yale University, New Haven, Connecticut 06520-8109, USA

Self-propelled particles can undergo complex dynamics due to a range of bulk and surface interactions. In the case of a foreign particle inside a subfreezing solid, such as a particle in ice, a premelted film can form around it allowing the particle to migrate under the influence of an external temperature gradient, which is a phenomenon called thermal regelation. It has recently been shown that the migration of particles of a biological origin can accelerate melting in a column of ice and thereby migrate faster. We have previously shown that the effect of regelation plays a major role in the migration of inert particles and impurities inside ice, with important environmental implications. In particular, the question of how the activity affects a particle's position over time is essential for paleoclimate dating methods in ice cores. We re-cast this class of regelation phenomena in the stochastic framework of active Ornstein-Uhlenbeck dynamics and make predictions relevant to this and related problems of interest in geophysical and biological problems.

BP 4.6 Mon 12:15 H16

Emergent collective behavior of active Brownian particles with visual perception — •Rajendra Singh Negi, Roland G. Winker, and Gerhard Gompper — Theoretical Physics of Living Matter, Institute of Biological Information Processing (IBI-5), Forschungszentrum Jülich, 52425 Jülich, Germany

Collective behavior of self-propelled agents emerges from the dynamic response of individuals to various input signals [1,2]. One such input signal is visual perception. We explore the behavior of a model of self-steering active Brownian particles with visual perception in two dimensions [3]. Several non-equilibrium structures like motile worms, worm-aggregate coexistence, aggregates, and a dilute-gas phase are obtained, depending on the system parameters. The strength of the response to the visual signal, vision angle, packing fraction,rotational diffusion, and activity (velocity v_0) determine the location and extent of these phases in the phase diagram. The radius-of-gyration tensor is used to distinguish between the worm and the aggregate phase. Our results help to understand the collective behavior of cognitive self-propelled particles, like animal herds and micro-robotic swarms.

[1]. J. Elgeti, R. G. Winkler, and G. Gompper, Rep. Prog. Phys. **78**, 056601 (2015).

[2]. M. R. Shaebani, A. Wysocki, R. G. Winkler, G. Gompper, and H. Rieger, Nat. Rev. Phys. **2**, 181 (2020).

[3]. L. Barberis and F. Peruani, Phys. Rev. Lett. **117**, 248001 (2016).

BP 4.7 Mon 12:30 H16

Diffusiophoretic propulsion of an isotropic active particle near a finite-sized disk — •Abdallah Daddi-Moussa-Ider[1], Andrej Vilfan[1,2], and Ramin Golestanian[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — [2]Jozef Stefan Institute, 1000 Ljubljana, Slovenia — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford OX1 3PU, United Kingdom

We employ a far-field analytical model to quantify the leading-order contribution to the induced phoretic velocity of an isotropic active colloid near a finite-sized disk of circular shape resting on an interface separating two immiscible viscous incompressible Newtonian fluids. To this aim, we formulate the solution of the phoretic problem as a mixed-boundary-value problem which we then transform into a system of dual integral equations on the inner and outer domains. Depending on the ratio of different involved viscosities and solute solubilities, the sign of phoretic mobility and chemical activity, as well as the ratio of particle-interface distance to the radius of the disk, we find the isotropic active particle to be repelled from the interface, be attracted to it, or reach a stable hovering state and remain immobile near the interface. Our results may prove useful in controlling and guiding the motion of self-propelled phoretic active particles near aqueous interfaces.

Reference: A. Daddi-Moussa-Ider, A. Vilfan, and R. Golestanian, *J. Fluid Mech.* **940** A12 (2022)

BP 5: Focus Session: Super Resolution Microscopy and Dynamics of Supramolecular Complexes

organized by Jonas Ries (EMBL Heidelberg) and Ulrich Schwarz (Heidelberg University)

Time: Monday 15:00–17:30 Location: H15

Invited Talk BP 5.1 Mon 15:00 H15

The functional nano-architecture of axonal actin — •Christophe Leterrier — Aix Marseille Université, CNRS, INP UMR7051, NeuroCyto, Marseille, France

The intricate arborization and molecular identity of axons is maintained for decades, but must also continuously adapt to changes in the environment and modulate the activity of neurons. Axons fulfill these paradoxical demands thanks to a unique cytoskeletal organization that ensures the coordinated transport, anchoring and assembly of axonal components. In our lab, we use super-resolution microscopy to delineate and map the nanoscale architecture of actin-based structures within the axon: the periodic actin/spectrin submembrane scaffold, intra-axonal hotspots and trails, and presynaptic actin assemblies. We are exploring their molecular organization and functions by combining versatile labeling approaches, correlative live-cell/super-resolution/electron microscopy and quantitative analysis that allow for high-content, nanoscale interrogation of the axonal architecture.

BP 5.2 Mon 15:30 H15

Photon-stream-based aberration correction for STED microscopy — •Debadrita Ghosh, Claudia Geisler, and Alexander Egner — Institute for Nanophotonics, Goettingen, Germany

Stimulated emission depletion (STED) microscopy is the most prominent super-resolution fluorescence microscopy method and achieves a resolution far beyond the diffraction limit. However, like all these methods, it is adversely affected by sample-induced aberrations, which can degrade the achievable resolution and image quality significantly. These aberrations are caused by wavefront distortions due to refractive index variations, for example within thick biological specimens. This challenge can be addressed by using adaptive optics (AO) in a feedback-controlled manner such that the wavefront distortions are compensated and the image quality is restored. Typically, the feedback loop uses image features which necessitates repeated acquisitions of the same field-of-view. This approach, therefore, is slow and prone to unwanted photo-bleaching. Here, we present an AO correction scheme that does not rely on image features, but exploits the dependence of the fluorescence lifetime on the local STED intensity. In principle, our photon-stream-based metric can be evaluated on a single image pixel, which makes it photon-budget-friendly and allows to correct aberrations rapidly in parallel with image acquisition. We successfully utilized this new metric for automated and continuous aberration correction in biological samples, making imaging fast and easy even for users without expert knowledge.

BP 5.3 Mon 15:45 H15

Cytoskeletal organization of red blood cells during malaria infections investigated with super-resolution microscopy and pair cross-correlation analysis — •Pintu Patra[1], Cecilia P Sanchez[2], Michael Lanzer[2], and Ulrich S Schwarz[1] — [1]Institute for Theoretical Physics & BioQuant, Heidelberg University, Germany — [2]Center of Infectious Diseases, Parasitology, University Hospital Heidelberg, Germany

Measuring the distance between molecules is key to understanding the molecular organization of biological systems. The pair cross-correlation (PCC) function computed from two-color super-resolution microscopy images provides a measure of co-localization between differently labeled molecules. Here, we theoretically compute the PCC-function between two molecules by using 2D Gaussian distribution as the effective point spread function for single molecules. By fitting this function to simulated data based on experimentally measured images, one can estimate both small and large separation distances. We apply this method to malaria-infected red blood cells and demonstrate that the knob-associated histidine-rich protein (KAHRP), which is used by the parasite to remodel the spectrin-actin network from a distance, relocalizes from the ankyrin bridges to the actin-based junctional complexes during the 48 hours course of the infection.

15 min. break

BP 5.4 Mon 16:15 H15

Superresolution microscopy for structural cell biology — •Jonas Ries — EMBL Heidelberg

Superresolution microscopy, such as single-molecule localization microscopy (SMLM), is becoming a key technique for structural cell biology, ideally complementing electron microscopy. I will discuss projects in my group in which we push SMLM towards nanometer resolution in 3D and multicolor with the aim to investigate the structure and dynamics of molecular machines in cells. I will show how these technologies allowed us to gain mechanistic insights into the machinery that drives endocytosis. Endocytosis is an essential cellular function by which cells take up molecules from the environment. We were able to reconstruct the dynamics of this process from thousands of snapshots taken in fixed cells. I will conclude with first results illustrating the potential of MINFLUX to image dynamic structural changes of protein machines in the living cell with nanometer resolution. Specifically, I will show how we resolved the precise stepping motion of the motor protein kinesin in living cells.

BP 5.5 Mon 16:45 H15

Spatiotemporal SARS-CoV-2 binding dynamics investigated with 100 Hz ROCS microscopy and thermal fluctuation analysis — •Dominik Huber and Alexander Rohrbach — Laboratory for Bio- and Nanophotonics, Department of Microsystems Engineering - IMTEK, University of Freiburg, 79110 Freiburg, Germany

The emergence of the new severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) in recent years has caused tremendous interest in investigating the interactions between viruses and cells. Especially the imaging and tracking of viruses are of great importance to see and understand the binding and uptake of viruses into cells and to be able to intervene in these processes. Due to their small size and fast movement imaging virus dynamics is a very challenging task, which has so far been achieved with different fluorescence methods, being limited by photo bleaching and imaging speed.

In our research we apply Rotating Coherent Scattering (ROCS) microscopy in order to visualize the diffusion of SARS-CoV-2 virus like particles (VLPs) close to A549 lung epithelial cells. ROCS microscopy allows for label-free imaging with more than 100 Hz temporal at 150 nm spatial resolution. The high contrast image stacks enable single particle tracking and characterization of the binding process and strength of VLPs with SARS-CoV-2 spike proteins to A549 cells using thermal fluctuation analysis.

BP 5.6 Mon 17:00 H15

Transient Optoplasmonic Detection of Single Proteins on

the Nanosecond Time Scale — •Martin D. Baaske[1,2], Nasrin Asgari[1], Deep Punj[1], and Michel Orrit[1] — [1]Leiden University, Leiden, Netherlands — [2]Johannes Gutenberg-University, Mainz, Germany

Label-free optical detection schemes commonly rely on specific chemical interactions between receptor and target molecule in order to facilitate analyte recognition. Here I present our first steps on a novel pathway to fingerprint proteins via analysis of their motion, i.e., physical properties such as stokes radius and polarizability rather than chemical interactions. We show that via a polarization selective technique and careful optimization of a confocal microscope single gold nanorods, which are commonly used as labels, can be transformed into high-speed nanoscale sensors. We perform photothermal spectroscopy on single gold nanorods and use it as a means to probe their sensitivity to refractive index changes with respect to the experimental parameters * in turn allowing us to optimize the later on a rod-to-rod basis. This enables the detection single protein molecules traversing plasmonic near fields with previously time resolutions on the nanosecond scale.

BP 5.7 Mon 17:15 H15

Modeling the assembly and invagination of clathrin lattices at the cell membrane — •Felix Frey[1,2] and Ulrich S. Schwarz[3] — [1]Department of Bionanoscience, Delft University of Technology, Delft, the Netherlands — [2]Institute of Science and Technology Austria, Klosterneuburg, Austria — [3]Institute for Theoretical Physics and BioQuant-Center, Heidelberg University, Heidelberg, Germany

Biological cells constantly relay material and information across their plasma membranes. For particles with sizes between 50 and 200 nm, clathrin-mediated endocytosis (CME) is the main uptake route. In CME clathrin triskelia assemble at the cell membrane and form a clathrin lattice. After initially growing flat the lattice starts to curve before it reaches its final size [1]. However, how this flat-to-curved transition proceeds in detail is still elusive, because theoretically several pathways can be envisioned [2]. When confronted with conventional imaging data, a microscopic model for the growth of clathrin lattices indeed suggests some level of plasticity as required for bending [3]. Recently we have combined mathematical modeling with 3D superresolution microscopy to determine the dynamics of membrane invagination. We find that membrane curvature is generated cooperatively between the triskelia of the clathrin lattice [4].

[1] D. Bucher, F. Frey et al., Nat. Commun. 9, 1109 (2018). [2] F. Frey and U.S. Schwarz, Soft Matter 16, 10723 (2020). [3] F. Frey et al., New J. of Phys. 22, 073043 (2020). [4] M. Mund et al., bioRxiv, doi:10.1101/2021.10.12.463947 (2022).

BP 6: Statistical Physics of Biological Systems 1 (joint session BP/DY)

Time: Monday 15:00–17:15 Location: H16

BP 6.1 Mon 15:00 H16

Dynamics and Fair Risk Sharing in Groups of Intelligent, Egoistic Individuals — Samuel Monter[1], •Veit-Lorenz Heuthe[1], Emanuele Panizon[2], and Clemens Bechinger[1] — [1]FB Physik, Universität Konstanz, Konstanz, Germany — [2]Department of Quantitative Life Science, ICTP, Trieste, Italy

Many animal species organize in social groups of fascinating complexity. The evolutionary biologist W.D. Hamilton hypothesized that the gregariousness of some animals can be explained solely from the egoistic motivation to decrease the risk of predation [1]. As a quantitative measure of this risk, he considered the Voronoi area around each animal. Many collective behavior studies try to capture this motivation by imposing interaction rules or neglect the driving motive altogether when modeling the dynamics of animals. In this study we train a swarm of individuals in a Multi Agent Reinforcement Learning (MARL) framework according to Hamilton's hypothesis, i.e. to decrease their predation risk. Thus, we gain insights into the dynamics of an ensemble of selfishly motivated individuals unbiased by any a priori assumption about interactions. We find that the individuals learn to cluster into groups which exhibit dynamic steady states resembling the behavior of natural swarms. Additionally, the predation risk is shared evenly within the groups, counterintuitive to the selfish motivation of each individual. Our findings suggest that gregariousness could indeed be driven by selfish motives in accordance with Hamilton's hypothesis.

[1] W. D. Hamilton, Journal of theoretical Biology 1971, 31, 295-311.

BP 6.2 Mon 15:15 H16

Boundary-driven epithelial ordering: from the mouse embryo to topological defects — •Pamela Guruciaga[1], Takafumi Ichikawa[2], Takashi Hiiragi[3], and Anna Erzberger[1] — [1]European Molecular Biology Laboratory, Heidelberg, Germany — [2]Kyoto University, Kyoto, Japan — [3]Hubrecht Institute, Utrecht, The Netherlands

In physical problems boundaries are typically considered to be simple, static and externally fixed. Biological systems however not only interact with their surroundings, but also alter them in ways that feed back on their own dynamics. We address this complex interaction in the context of epithelial development. Motivated by observations of an interplay between apico-basal polarity and boundary geometry in mouse epiblast morphogenesis, we develop a theory for epithelial ordering based on the Landau-de Gennes approach to surface-induced order in liquid crystals. We introduce a vector order parameter to represent the polarity, and model its interaction with the boundaries by a weak anchoring energy. We calculate the alignment fields arising from different boundary curvatures, and compare our predictions with imaging data of the morphogenetic process. Our work highlights the role of extraembryonic tissue in embryogenesis, while identifying interesting physical phenomena, such as boundary-dependent transitions in the structure of topological defects.

BP 6.3 Mon 15:30 H16

A competitive advantage through fast dead matter elimination in confined cellular aggregates — •Yoav G. Pollack[1,2], Philip Bittihn[1], and Ramin Golestanian[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPI-DS), Göttingen, 37077, Germany. — [2]Max Planck Institute for Multidisciplinary Sciences (MPI-NAT), Göttingen, 37077, Germany. — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, OX1 3PU, UK.

Competition of different cell types for limited space is relevant in biological processes such as tissue morphogenesis and tumor growth. Predicting the outcome for non-adversarial competition of such growing active matter is non-trivial, as it depends on how processes like growth, proliferation and the degradation of cellular matter are regulated in confinement; regulation that happens even in the absence of competition to achieve homeostasis. We show that passive by-products of the processes maintaining homeostasis can significantly alter fitness, enabling cell types with lower homeostatic pressure to outcompete those with higher homeostatic pressure. We reveal that interfaces play a critical role for this specific kind of competition: There, growing matter with a higher proportion of active cells can better exploit local growth opportunities that continuously arise as the active processes keep the system out of mechanical equilibrium. Our results show that optimizing the ratio of growing (active) to dead (passive) cells can be as important to survival as growth rates and their sensitivity to mechanical cues.

BP 6.4 Mon 15:45 H16

A biophysical model of DNA methylation ageing — •Aida Hashtroud and Steffen Rulands — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Machine learning models can accurately predict biological age and time of death based on sequencing measurements of DNA methylation marks. The mechanistic basis underlying these methylation clocks is poorly understood. Here, using a combination of tools from statistical physics and sequencing experiments we show that biological age can be predicted as a result of collective processes in the boundaries between genomic regions of different densities of cytosine-guanine pairs (CpGs). Specifically, we define a biophysical model predicting the time evolution of DNA methylation patterns during ageing based on a wave localization mechanism of tilted competition between antagonistic chromatin modifiers. Our work shows that biological age can be predicted from DNA methylation patterns using models with few parameters inspired by statistical physics.

15 min. break

Invited Talk BP 6.5 Mon 16:15 H16

From active bacterial microcolonies to biofilms as model tissues — •Vasily Zaburdaev — Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

Bacterial intrinsic activity is evident on all stages of their life cycle. We will start by following how individual cells deploy forces to attach and move on surfaces. We suggest how these active movements may be harnessed to generate work and, for example, cells can power the rotation of micro-turbines. When let to move and interact, however, bacteria will find each other and form microcolonies that consist of several thousands of cells. Microcolonies are often the functional units of the bacterial existence in natural settings and in the context of disease. We will provide theoretical framework describing the bacterial microcolonies as active viscoelastic materials and discuss how this theory might be useful in eukaryotic systems such as organoids, tumour spheroids or clustering immune cells. Microcolonies may further develop into even more complex bacterial communities known as biofilms - there, bacteria embed themselves in the self-secreted extracellular matrix creating an analogue of multicellular tissues. We will outline some future research avenues deepening this analogy and illustrate it with an intriguing example of wound healing in bacterial biofilms.

BP 6.6 Mon 16:45 H16

Playing it safe: information constrains collective betting strategies — •Philipp Fleig[1,2] and Vijay Balasubramanian[2] — [1]Max Planck Institute for Medical Research, 69120 Heidelberg, Germany — [2]Department of Physics & Astronomy, University of Pennsylvania, Philadelphia, PA 19104, USA

Risk is an inherent part of life and biological functions are partly shaped by the need to reduce risk. Broadly, risk arises from stochastic interactions of an organism with its environment. Every time an organism displays a particular response or behaviour (e.g. expresses a phenotype or exhibits a certain immune response), it is placing a bet with potential impact on its biological fitness. The more precisely the statistics of the environment are known to the organism, the more successfully bets can be placed. However, an organism typically has limited information about the statistics of the environment. This limitation should be accounted for in the adaptation of biological functions to the environment. We develop a theoretical principle where information geometric model complexity guides stochastic biological functions towards less risky betting strategies. In the framework of Bayesian inference, we show that given finite information about the environment, there is an optimally safe adaptation strategy set by the Bayesian prior. Furthermore, in a toy model of stochastic phenotypic switching by bacteria, we demonstrate how the implementation of our principle of "playing it safe" increases the fitness (population growth rate) of the bacterial collective. We suggest that the principle applies broadly to problems of adaptation, learning and evolution.

BP 6.7 Mon 17:00 H16

Quantification of intracellular information flow — •Mirna Kramar[1], Mathieu Coppey[1], Thierry Mora[2], and Aleksandra Walczak[2] — [1]UMR 168, Institut Curie, Paris — [2]Laboratoire de Physique, Ecole Normale Supérieure, Paris

Signalling pathways are cascades of biochemical reactions which transduce signals from the exterior to the interior of the cell. By essence, these pathways convey information about the outside world which cells collect and process to adapt and guide decisions. The cell's ability to govern its functions correctly and precisely while relying on these intricate biochemical networks is surprising given the crowded and noisy cell interior, which indicates that the mechanisms cells use to process information are highly sophisticated. While our understanding of the constituents of the cellular machinery and the processes taking place in the cell is steadily increasing, little is known about the information flow within the cell. Are pathways conveying only on/off signals, or is there more graded information being transduced?

Here, we measure and quantify the information relayed through the MAPK signalling pathway, one of the key signalling pathways in eukaryotic systems. Using a synergy of an optogenetic experimental setup and a data analysis pipeline based on information theory, we quantify the input-output relationships within the MAPK signalling pathway. We show that the capacity of the pathway far exceeds the 1-bit value (on/off), and that collective systems of cell seem to exploit this capacity.

BP 7: Poster 1

Time: Monday 18:00–20:00 Location: P1

BP 7.1 Mon 18:00 P1

Assessing biomolecular interactions across scales using optical tweezers — •Roman Renger, Nicholas Luzzietti Luzzietti, and Philipp Rauch — LUMICKS, Amsterdam, Netherlands

Biological processes involving proteins interacting with nucleic acids, cell membranes or cytoskeletal filaments are key to cell metabolism and hence to life in general. Detailed insights into these processes provide essential information for understanding the molecular basis of physiology and the pathological conditions that develop when such processes go awry. The next scientific breakthrough consists in the direct, real-time observations and measurements of the most fundamental mechanisms involved in biology Single-molecule technologies offer a powerful opportunity to meet these challenges and to study dynamic protein function and activity in real-time and at the single-particle level. Here, we present our efforts for further enabling discoveries in the field of biology and biophysics using the combination of optical tweezers with correlative fluorescence microscopy (widefield, TIRF, confocal and STED) and label-free Interference Reflection Microscopy (IRM). We present several examples in which our technology has enhanced the understanding of basic biological phenomena, ranging from protein structure to intracellular organization. Furthermore, we show that advances in hybrid single-molecule methods can be turned into an easy-to-use and stable instrument that has the ability to open up new avenues in many research areas.

BP 7.2 Mon 18:00 P1

Transport in complex intracellular environments — •Mohammad Amin Eskandari, Bart Vos, Mattias Luber, and Timo Betz — Third Institute of Physics - Biophysics Georg August University Göttingen

Active transport is vital for targeted delivery of organelles, proteins and signaling molecules in eukaryotic cells and defects in active transport are linked to different diseases such as Alzheimer's disease. Kinesin and dynein are two motor proteins which are responsible to carry the cargoes along the microtubule filaments. Since the cytoplasm is a highly crowded environment, the motion of cargoes can be hindered by some sorts of obstacles and this brings us to the question how these motors can generate a processive motion in such an environment to bypass the roadblocks. In this project, we aim to investigate the possible mechanisms that kinesin and dynein can use to overcome the obstacles.

BP 7.3 Mon 18:00 P1

Single Particle Tracking of Molecular Motors under Different Physiological Conditions — •Adrian Lentz, Paulina Blair, Daniel Kuckla, Philipp Hagemann, and Cornelia Monzel — Experimental Medical Physics, Heinrich-Heine University, Düsseldorf, Germany

Single particle tracking (SPT) is a powerful tool to gain insights into the dynamics of molecular motors. These proteins convert the chemical energy of adenosine triphosphate (ATP) into a forward motion to transport vesicles along the microtubule network. In our study we investigate the linear motion of the kinesin variant Kif5C, which is normally found in neuronal cells. A genetically modified Kif5C with fused green fluorescent protein was monitored with millisecond resolution and analysed with an algorithm that links precisely detected particle positions to trajectories. We establish a point density based classification of trajectories into different molecular gaits and determine diffusion, velocity and processivity of the Kif5c motor. We show a systematic analysis of the influence of different acquisition times on the motor motion determination and compare Kif5C transport in the human cell lines HeLa, MCF-7, HEK, NIH/3T3 and COS-7. Of central

interest was then to measure the effect of different physiological conditions, e.g. absence or high concentration of glucose and high amount of ATP, on the Kif5C dynamics.

BP 7.4 Mon 18:00 P1

Towards Advanced Single Particle Tracking of Molecular Motors by Quantum Dot Labeling and Monitoring of the Cytoskeletal Environment — •Paulina Blair, Adrian Lentz, Xiaoyue Shang, Daniel Kuckla, Philipp Hagemann, and Cornelia Monzel — Experimental Medical Physics, Heinrich-Heine Universität, Düsseldorf, Germany

The molecular motor Kif5C plays a central role in the intracellular transport and synaptic transmission of neuronal cells. To understand how Kif5C mediated transport depends on its environment, it is essential to track the motor in the cytoplasmic context. We aim to advance the single molecule tracking of Kif5C by Quantum Dot labeling as well as by characterising the cytoskeletal environment. Quantum Dots are nanoscale semiconductors, which in contrast to genetically encoded fluorophores, offer tracking at enhanced spatio-temporal resolution and over long time scales. In this project we express Kif5C genetically fused to a streptavidin molecule in live cells. Quantum Dots functionalised with biotin are added to the cell sample to bind via streptavidin-biotin interaction to Kif5C. Molecular motors are recorded with millisecond resolution and are analysed using a global Linear Assignment Approach. The microtubule is stained using a silicon rhodamine-based fluorophore. We then derive parameters such as network density or intersections to correlate it with the motor protein dynamics.

Our data will provide insights on the benefit of Quantum Dot labeling, on molecular motor gaits such directed, superdiffusive and subdiffusive motion as well as on effects of the cytoskeletal environment.

BP 7.5 Mon 18:00 P1

Quantification of molecule-spanning protein dynamics with fluorescence correlation spectroscopy — •Veronika Frank[1], Jean-Benoît Claude[2], Jérôme Wenger[2], and Thorsten Hugel[1,3] — [1]Institute of Physical Chemistry, University of Freiburg, Germany — [2]Fresnel Institute, CNRS, Aix Marseille University, France — [3]Signaling research centers BIOSS and CIBSS, University of Freiburg, Germany

Protein conformational kinetics and their regulation occur on many time and length scales. Fluorescence methods have mainly focused on the hundreds of microseconds to minutes time scale and NMR on the picosecond time scale. Here we explore the several nanoseconds to microseconds time scale for the multi-domain molecular chaperone heat shock protein Hsp90, a homodimer with a molecular weight of 90 kDa per monomer. Hsp90 is a therapeutic target for cancer therapy, but its dynamics and its dynamic interactions with other proteins are not yet fully understood.

Here we use fluorescence correlation spectroscopy and zero-mode waveguide nanoapertures to measure and understand fast molecule-spanning dynamics and how they are affected by interactors.

BP 7.6 Mon 18:00 P1

AniMol: A quick interactive web-based molecular trajectory visualiser — James Panayis, James Partington, and •Rudolf A. Römer — Department of Physics, University of Warwick, Coventry, CV4 7AL, UK

We present software developed to interactively visualise dynamic molecular trajectories in web browsers. This tool allows for quick and efficient interaction with large flexing/moving molecular structures and helps to more easily understand results of in-silico modeling processes, for example protein dynamics simulations. The browser-based software simplifies workflows as no installation is required, and there are very few limitations due to hardware or software compatibilities. We achieve this using a lightweight state-of-the-art graphics engine, and compiling our code to WebAssembly (WASM), a portable compilation target for programming languages supported by all major browsers since 2017. We also present a webserver (animol.warwick.ac.uk) utilising this software offering cloud storage and retrieval of molecular trajectories, to aid collaboration and communication of results.

BP 7.7 Mon 18:00 P1

Correlation-based feature selection to identify functional dynamics in proteins — •Georg Diez, Daniel Nagel, and Gerhard Stock — Physikalisches Institut, Albert-Ludwigs-Universität Freiburg

Molecular dynamic simulations provide an effective tool for a deeper understanding of proteins and their functioning. In order to shed light on the underlying mechanisms of processes, one typically models the dynamics using some key internal coordinates (or features) which capture the most important conformational changes of the protein. However, one often ends up in a high-dimensional feature space which hampers a straightforward interpretation of the typically very complex dynamics. Adopting the Leiden community detection algorithm [1], we present an effective and scalable approach to divide the feature space into subsets which describe collective motion. By applying this approach to the functional dynamics of different protein systems with varying size, we show that it allows to identify and discard uncorrelated motion and noise. Moreover, it provides an effective dimensionality reduction scheme by extracting the key features, and leads to a detailed understanding of the underlying mechanisms.

[1] Traag et al., "From Louvain to Leiden: guaranteeing well-connected communities", Sci. Rep., 2019

BP 7.8 Mon 18:00 P1

Reversible protein immobilization and biosensing on liquid-gated GFETs — •Mykola Fomin[1], Lara Jorde[2], Changjiang You[2], Jacob Piehler[2], and Carola Meyer[1] — [1]Department of Physics, Osnabrück University, Germany — [2]Department of Biology/Chemistry and CellNanOs Center, Osnabrück University, Germany

Apart from the standard requirements such as selectivity, sensitivity, and biological compatibility, effective electronic biosensors are facing the demand for the fabrication of cost-efficient devices. Cost and resource efficiency would benefit from re-useage of the biosensor after detection, which can be achieved by reversible immobilization of the molecules in question. While multiple biosensors have already been demonstrated to generate a response to a specific analyte molecule and its various concentrations, reversible protein monitoring remains a challenging task. Besides, during such measurements on graphene exists a risk of unspecific attachment to the channel with following protein denaturation. This work aims to demonstrate reversible protein immobilization detected by current changes of a liquid-gated GFET. PEG-tris-NTA on a lipid monolayer is used for site-specific immobilization of histidine-tagged proteins. The lipid layer forms a 2,5 nm hydrophilic cover over the channel that prevents unspecific protein attachment and its denaturation, resulting in enhanced biocompatibility [1]. We track the current changes upon attachment of histidine-tagged GFP to the device and their removal upon imidazole wash.

[1] L. Jorde. et al.(2021), doi: 10.1063/5.0035871.

BP 7.9 Mon 18:00 P1

Hierarchical dynamics as result of log-periodic oscillations in proteins — •Emanuel Dorbath, Gerhard Stock, and Steffen Wolf — Albert-Ludwigs-Universität, Freiburg, Germany

Logarithmic oscillations were observed in earthquakes, financial crashes and several biomolecular systems such as proteins. In many protein systems it is generally assumed, that the time scales, ranging from femtoseconds up to microseconds and longer, are in fact not independent but structured hierarchical in the sense that the fast time scales are a prerequisite for the slower ones.

This hierarchy can be well described via the free energy landscape which then gives rise to the logarithmic oscillations and a power-law. From the logarithmic oscillations, multiple relaxation times can be derived extending over several orders of magnitude [Metzler 1999].

Here, an analysis is presented to derive the respective time scales using logarithmic oscillations in non-equilibrium simulations. For this three systems are studied: A 1-dimensional model with an inherent hierarchical energy landscape is used as proof of principle and demonstration of the method. The second one is the simple hierarchical peptide Aib9 with two helical states which has been researched already in the past [Buchenberg 2015]. Finally, the widely studied PDZ2 domain is studied which shows complex conformational folding and restructure mechanisms.

BP 7.10 Mon 18:00 P1

The effect of D_2O on the pressure dependent protein-protein interaction in aqueous lysozyme solutions — •Michelle Dargasz, Jaqueline Savelkouls, and Michael Paulus — Fakultät Physik/DELTA, TU Dortmund, 44221 Dortmund, Germany

In some experimental techniques such as neutron scattering, the substitution of H_2O with D_2O is used to obtain a useful signal. It was assumed that the exchange of the solvent does not have a major influence

on the protein structure and interactions. However, measurements with lysozyme in D_2O revealed a larger attractive component of the protein-protein interaction potential [1]. In this study, the pressure-dependent behavior of high concentrated lysozyme solutions with H_2O and D_2O was considered using SAXS at the beamline BL2 of the synchrotron radiation source DELTA (Dortmund Germany). In previous measurements a non-linear relationship between the interaction potential and the exerted pressure was observed [2]. This was also visible in this study, as a shift in the correlation peak of the scattering curve occurs as a function of pressure. Up to approx. 2 kbar, a shift to larger q-values occurs, which is reversed with further increasing pressure up to 4 kbar. Since this effect occurs equally in H_2O as well as D_2O, it can be assumed that the water structure plays a rather minor role for the nonlinear correlation.

[1] C. Gripon, Journal of Crystal Growth 178, 575-584 (1997)
[2] Martin A. Schroer, Phys. Rev. Lett. 106, 178102 (2011)

BP 7.11 Mon 18:00 P1

Coarsening of biomolecular condensates regulate crossover placement in Meiosis I — •Marcel Ernst and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

During meiosis, genetic information from female and male chromosomes is exchanged in a process called crossover. The dynamics that determine the positioning of these crossovers is largely not understood. Experimental observations consistently reveal two key findings: First, the number of crossovers per chromosome is at least one and is usually small, between one and three. Second, there is crossover interference, which prevents nearby crossovers on a single chromosome. We hypothesize that crossovers are determined by biomolecular condensates, which coarsen by exchanging material along chromosomes. We present theoretical and numerical results suggesting scaling laws analogous to Lifshitz-Slyozov-Wagner theory that predict the final number of crossovers, and their spatial structure as a function of coarsening time, chromosome length, and the initial amount of material. These results are consistent with current experimental findings in *Arabidopsis thaliana* and suggest how cells use a fundamental coarsening process to regulate spatial patterns.

BP 7.12 Mon 18:00 P1

Controlling size, phase transitions, and reactions in microfluidic double-emulsion droplets — •Paula Girones Paya, Sebastian W. Krauss, and Matthias Weiss — Experimental Physics I, University of Bayreuth

Double-emulsion based assays have been widely used in a large number of experiments such as in bio-inspired microreactors or in direct evolution assays. Despite the advanced techniques that have been developed to produce picoliter-sized droplets, a better manipulation of the droplet interior remains a challenge. Here, we demonstrate how hundreds of double emulsion droplets, trapped in a microfluidic sieve, can be grown and shrunk by controlling the salt concentration in the carrier liquid. Alternating the osmotic pressure leads to a rapid and reversible volume change of the aqueous droplet interior, resulting in a reversible phase separation of an enclosed binary fluid. The phase separation is shown to be a versatile tool to control, for example, the dissociation and re-association of double-stranded DNA or to monitor an enzymatic reaction via a pH sensitive fluorescence reporter.

BP 7.13 Mon 18:00 P1

Nucleation of chemically active droplets — •Noah Ziethen and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Liquid-liquid phase separation emerged as a crucial organizing principle inside biological cells giving rise to a plethora of intracellular compartments. Unique to the cellular context, these condensates can consist of only a few hundred molecules and are affected by non-equilibrium processes. In particular, active chemical conversion between condensate material and proteins in the surrounding cytoplasm can control their size. Moreover, the significant concentration fluctuations due to the small molecule numbers imply that spontaneous nucleation and dissolution are likely. Yet, it is unclear how the driven reactions affect these stochastic processes. Here, we investigate the influence of chemical reactions on the nucleation behavior of active droplets using a stochastic field theory. We find a decrease in the nucleation rate with the increased strength of the chemical reactions. Using classical nucleation theory, we can reduce the full dynamics to an analytical expression for the free energy, which only depends on the droplet radius and the strength of the chemical reactions. The chemical reactions increase the energy barrier, which the system needs to overcome to form a droplet. Additionally, the binodal and the spinodal line are moved towards the center of the phase diagram. Cells might use these effects to control the nucleation behavior of intracellular droplets or even suppress their formation completely.

BP 7.14 Mon 18:00 P1

Liquid-liquid phase separation of promoter and gene-body condensates in multi-scale simulations — •Arya Changiarath Sivadasan[1,2] and Lukas stelzl[1,2] — [1]Institute of Physics, JGU Mainz — [2]Faculty of Biology JGU Mainz and institute of Molecular Biology (IMB), Mainz

Liquid-Liquid phase separation plays an important role in the formation of localized nuclear hubs of RNAPII during the transcription process. Our research is focused on understanding the molecular basis of phase separation of CTD, the largest subunit of RNAPII, using molecular dynamics (MD) simulation methods. We investigated how the CTD phase separation is affected by differences in CTD sequences using coarse-grained MD simulations and the results indicate that deviation from the ideal heptapeptide sequence has less tendency to phase separate, which suggests that these deviations from the ideal heptapeptide repeats are important for responsive regulation of transcription. Moreover, we are looking at how phosphorylation of CTD and the presence of other biomolecules that can influence CTD phase behavior. Hyperphosphorylation prevents phase separation as the negatively charged phosphate groups repel each other. We show how hyperphosphorylated CTD might co-phase separate in elongation with HRD of Cylin-T1 in accordance with the experiment. To explore more on this, we studied the phase behavior of CTD and phosphorylated CTD in the presence of HRD and the results show that they co phase separate into a large cluster, but do not mix, which may help to physically distinguish between the initiation and elongation stages of transcription.

BP 7.15 Mon 18:00 P1

Mechanical growth and auxin patterning in plant tissues — •Mathias Höfler[1] and Karen Alim[1,2] — [1]Physics Department and CPA, Technische Universität München — [2]Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen

Individual cell shape and growth underlies a high variance in living organisms. It is puzzling how on a larger scale, the morphogenesis of a tissue can be a reliably stable and efficient process. Theory and experiment show that there is a mechanical and biochemical feedback loop for tissue development and morphogenesis. Mechanical forces in plants have a pronounced effect on the microtubule orientation in cells, thereby changing the cell's mechanical properties, causing an impact on the magnitude and direction, hence anisotropy, of cell growth. Here we study the effect of cell mechanics on the bidirectional, radial growth of tissue in the plant stem. We investigate feedback mechanisms, stress patterns and how these affect tissue and early organ shape and development. For the latter, we furthermore study the role of the growth hormone auxin in the shoot apical meristem (SAM). Here, auxin induces cell wall loosening thus enhancing mechanical growth via biochemical feedback.

BP 7.16 Mon 18:00 P1

Characterizing flexibility and mobility in the natural mutations of the SARS-CoV-2 spikes — James Panayis[1], Dom Bellini[2], and •Rudolf A. Römer[1] — [1]Department of Physics, University of Warwick, Coventry, CV4 7AL, UK — [2]MRC Laboratory of Molecular Biology, Cambridge CB2 0QH, UK

We perform in-silico modelling of the SARS-CoV-2 spike protein and its mutations, using structures from the Protein Data Bank (PDB), to ascertain their dynamics, flexibility and rigidity. Identifying the precise nature of the dynamics for the spike proteins enables, in principle, the use of further in-silico design methods to quickly screen both existing and novel drugs that may hinder these natural dynamics. We use a recent protein flexibility modelling approach, combining methods for deconstructing a protein structure into a network of rigid and flexible units with a method that explores the elastic modes of motion of this network, and a geometric modelling of flexible motion. We also conduct this analysis on synthetic structures of some newer variants (α, β, γ, δ, λ, o) for some of which structure files are not yet available from the PDB. All proteins are thermalised for at least 1ns with NAMD to human body temperature before the flexibility analysis.

BP 7.17 Mon 18:00 P1

Effects of CTCF and Cohesin complexes and nucleosome positions on chromatin loops. — •Aymen Attou, TIlo Zülske, and Gero Wedemann — University of Applied Sciences Stralsund, Institute for Applied Computer Science, 18435 Stralsund, Germany

The spatial organization of the eukaryotic genome plays an important role in regulating transcriptional activity. In the nucleus, chromatin forms loops that assemble into fundamental units called topologically associating domains, which facilitate or inhibit long range contacts. These loops are formed and held together by a ring-shaped protein complex involving cohesin and CTCF. To analyse the effects of cohesin and CTCF, an established coarse-grained computer model of chromatin with a resolution of single nucleosomes was extended by integrating potentials describing CTCF and cohesin. We performed Monte Carlo simulations combined with replica exchange procedure with regular spaced nucleosomes and experimentally determined nucleosome positions in presence of cohesin-CTCF as well as depleted systems as control. The simulations generated a statistical representative ensemble of configurations in thermal equilibrium. We studied differences in the spatial structure and of contacts probabilities of different domains. That allowed us to understand the impact of cohesin and CTCF on the 3D structure of chromatin and how nucleosome positions can impact the conformations of the chromatin loops during the residence time of the loop anchor, with presumed consequences for transcriptional activity.

BP 7.18 Mon 18:00 P1

In Silico Tumor Invasion — •Eric Behle[1], Julian Herold[2], and Alexander Schug[1] — [1]JSC, Jülich Research Centre, Wilhelm-Johnen-Straße, 52428 Jülich, Germany — [2]Karlsruhe Institute of Technology, Kaiserstraße 12, 76131 Karlsruhe, Germany

To this day, cancer remains an insufficiently understood disease plaguing humanity. In particular, the mechanisms driving tumor invasion still require extensive study. Current investigations address collective cellular behavior within tumors, which leads to solid or fluid tissue dynamics. Furthermore, the extracellular matrix (ECM) has come into focus as a driving force facilitating invasion. To complement the experimental studies, computational models are employed, and advances in computational power within HPC systems have enabled the simulation of macroscopic tissue arrangements. In line with this, we hereby present our work using Cells in Silico (CiS), a high performance framework for large-scale tissue simulation developed by us. Combining a cellular potts model and an agent-based layer, CiS is capable of simulating tissues composed of millions of cells, while accurately representing many physical and biological properties. We aim to parameterize CiS via a bottom-up approach, starting with experimental data from small systems. We focused our studies on tumor spheroids, spherical aggregates composed of thousands of individual cells, which are one of the main workhorses of tumor analysis. We investigated the invasion dynamics and their dependence on the ECM density, and further aim to apply our model to the realistic simulation of larger systems.

BP 7.19 Mon 18:00 P1

Time resolved signal propagation in a photoswitched PDZ3 domain — •Ahmed Ali, Adnan Gulzar, Steffen Wolf, and Gerhard Stock — Institute of Physics, University of Freiburg, Germany

Allostery is one of the most important mechanisms for biomolecular regulation. Generally, it involves a perturbation such as a binding event at one side of a macromolecule to affect another distant functional site. However, how such a perturbation propagates through the protein in detail is still not well understood. To establish a minimal allosteric model system, the third PDZ domain (PDZ3) of the postsynaptic density-95 (PSD-95) protein has been considered. The PDZ3 domain binds to the C-terminus of target proteins and regulates the signal propagation in PSD-95. In addition to the common and conserved central β-sheets and two α-helices present in all PDZ variants, PDZ3 contains a third C-terminal α-helix (α_3–helix) that packs against the β-sheet at a considerable distance to the ligand binding pocket.

In this work, we aim for a detailed understanding of the microscopic dynamics of allosteric communication between α_3 and the ligand binding pocket. In addition, we explicitly aim at finding intraprotein changes appearing on the same time scales as found in recent time-resolved IR spectroscopic experiments. Consequently, we perform direct nonequilibrium molecular dynamics (MD) simulations of PDZ3. We characterize the α_3-switched response by a combination of principal component analysis, clustering methods, and machine learning and characterize the microscopic mechanism behind the allosteric communication between α_3 and the ligand binding site.

BP 7.20 Mon 18:00 P1

Enabling computer simulations of chromatin at physiological density with a resolution of individual nucleosomes — •Tilo Zülske, Aymen Attou, and Gero Wedemann — University of Applied Sciences Stralsund, System Engineering and Information Management, 18435 Stralsund, Germany

The spatial structure of chromatin in the nucleus is important for processes such as the regulation of transcription by facilitating contacts over long distances or by hindering spatial accessibility. Despite extensive research, the spatial structure of chromatin remains enigmatic. Coarse-grained computer simulation models of chromatin help to understand the existing variation of experimental data. Nucleosomes were modelled as spherocylinders connected by elastic segments describing linker DNA. Interactions include stretching, bending, torsion, electrostatic and internucleosomal interactions. Nucleosomes were spaced equidistantly and randomly. Configurations were sampled utilizing Metropolis Monte Carlo and replica exchange algorithms. We studied synthetic fibers of 1.1 Mbp utilizing with periodic boundary conditions that mimic density behavior at different concentrations. The systems comprised 6000 nucleosomes which was more than an order of magnitude larger than the systems computed by us so far. Comparison with experimental results deliver crucial insights how nucleosome positions and density affect the spatial structure and contacts.

BP 7.21 Mon 18:00 P1

Numerical study of the driving forces behind the slipper formation for RBC cells in rectangular microchannels. — •Berin Becic — Biofluid Simulation and Modeling ,Theoretische Physik VI, Universität Bayreuth

Red blood cells in rectangular microchannel flows exhibit two types of motions. At low velocities they tend to migrate towards the center and take symmetric croissant like shapes whereas for high velocities they migrate along the axis with the larger dimension and take an asymmetric slipper shape. Based on these results the behavior of the asymmetric off-centered slipper-movement was studied further via the boundary integral method. There it was observed that surprisingly this motion is only weakly dependant on the cell's elastic properties. Additionally it was found that the flow profile perpendicular to the direction of the displacement of the centered position plays a crucial role in stabilizing the slipper state and surpressing the tumbling motion expected from considering the behavior in a pure shear flow.

BP 7.22 Mon 18:00 P1

Brownian dynamics simulations of deformable cells in ordered polymer networks — •Jan Timo Bachmann[1,2] and Andreas Zöttl[2] — [1]TU Darmstadt, Germany — [2]University of Vienna, Austria

Various Cells migrate in different environments and in response to different stimuli. Cell migration may include the navigation and locomotion through complex environments, as in the case of Leukocyte migration where cells have to translocate through small pores in the extracellular matrix (ECM) by squeezing their cell body considerably. To investigate the influence of pores in the ECM on cell velocity and deformation we study a simplified model of an externally driven deformable cell moving through ordered polymer networks by means of Brownian dynamics simulations.

The cell velocity shows oscillatory behaviour with minima before and maxima after each network pore. The speed maxima can exceed the terminal velocity of the respective cell in a network-free fluid, indicating that in the squeezing process elastic interaction energy with the network is utilized to locally enhance the cell speed. The mean velocity through the network as a function of the bending modulus of the cell surface bending potential shows a non-linear unimodal curve. We further show how the interplay of pore size and cell elasticity determines the cell velocity.

BP 7.23 Mon 18:00 P1

Modelling of cell proliferation in epithelial tissue — •Kevin Höllring[1], Sara Kaliman[1], Lovro Nuić[2], Luca Rogić[2], Simone Gehrer[1], Maxime Hubert[1], and Ana-Sunčana Smith[1,2] — [1]PULS Group, FAU Erlangen-Nürnberg, Germany — [2]Group for Computational Life Sciences, Ruđer Bošković Institute, Zagreb, Croatia

The extracellular microenvironment (ECM) of epithelial cells is known to mechanically govern the properties and behavior of cells and tissues like cell differentiation, size and motility. Yet its effect on the division

rate of cells in tissues has not been analyzed in detail to our knowledge. In this work, we use MDCK-II cells grown on glass and 11 kPa PDMS substrates to provide evidence for a local cell density dependent division rate in an ECM stiffness dependent manner but independent of the age of the model- tissue, its internal structure or state.

We provide a theoretical model for microscopic tissue growth in a local microenvironment with well-defined average cell-density in agreement with experimental data and Dissipative Particle Dynamics (DPD) tissue simulations. We also propose an extension to the macroscopic tissue description via the Fisher-Kolmogorov equation (FK) accounting for our new findings that is able to reproduce characteristic edge behavior of tissues that has not been able to be reproduced by the FK formalism alone.

This work therefore sheds a new light on the influence of the ECM stiffness on the maturation of epithelial tissues and the important influences of different time scales for tissue growth and cell division.

BP 7.24 Mon 18:00 P1

Finding protein-ligand unbinding pathways in dcTMD simulations using distance-based clustering — •Victor Tänzel — Institute of Physics, Albert Ludwigs University, Freiburg, Germany

The exploration of protein-ligand dynamics by fully atomic simulations is of immense interest, for example in drug design, yet remains unfeasible in unbiased molecular dynamics (MD). To trigger rare events, we employ dissipation-corrected targeted MD (dcTMD) simulations, in which a moving distance constraint biases a prechosen reaction coordinate x, here the protein-ligand distance. The method combines a Markovian Langevin equation with a second-order cumulant expansion of the Jarzynski equality. From the required constraint forces, a free energy profile $\Delta G(x)$ as well as a friction coefficient $\Gamma(x)$ are extracted.

Transitions often occur along multiple pathways. In order to find these pathways, we study distance-based clustering approaches combining a pairwise ligand RMSD with the Leiden community detection algorithm. Here, we demonstrate the capabilities of this approach with the example of the A2A-ZMA complex and estimate (un-)binding rates.

BP 7.25 Mon 18:00 P1

Protein folding as described by different internal coordinates — •Sofia Sartore — Albert-Ludwigs-Universität Freiburg

Proteins reach their final structure (native state) through a process named folding. A powerful tool to investigate such process are molecular dynamics simulations, that can simulate the folding of a protein, giving as output a folding trajectory up to hundreds of microseconds long. This trajectory however needs to be further interpreted and analyzed in order to obtain an understandable model of the process, consisting of states that correspond to metastable conformation of the protein during the folding. To build such states, identifying the main features that are responsible for the folding of the protein is of utmost importance, as well as choosing appropriate coordinates to describe the dynamics under study. Using internal coordinates such as dihedral angles or interatomic distances proves to be convenient, since they disregard the overall motion of the system. In this poster we analyse what influence the choice of different input coordinates has on the resulting picture of the process: we compare an analysis of the fast folding protein HP35 based on dihedral angles as internal coordinates with one based on contacts, a particular set of interatomic distances that satisfy specific requirements. We find that using different input coordinates highlights different dynamics of the system, resulting in different descriptions of the same physical process.

BP 7.26 Mon 18:00 P1

Machine Learning based parametrization of tumor simulation — •Julian Herold[1], Eric Behle[2], and Alexander Schug[2] — [1]Karlsruhe Institute of Technology (KIT), Kaiserstraße 12, 76131 Karlsruhe, Germany — [2]JSC, Jülich Research Centre, Wilhelm- Johnen-Straße, 52428 Jülich, Germany

Despite decades of substantial research, cancer remains a ubiquitous scourge in the industrialized world. Effective treatments require a thorough understanding of macroscopic cancerous tumor growth out of individual cells in the tissue and microenvironment context.

Here, we aim to introduce the critical scale-bridging link between clinical imaging and quantitative experiments focusing on small clusters of cancerous cells by applying machine learning to drive model building between them. We deploy Cells in Silico (CiS), a high performance framework for large-scale tissue modeling developed by us. Based on both a cellular potts model and an agent-based layer, CiS is capable of accurately representing many physical and biological properties, such as individual cell shapes, cell division, cell motility etc.

The strong representational capacity of our model comes with the need to adjust a large number of parameters according to experimental findings. We present a generalized approach to optimize these parameters which allows the use of different sources of experimental data.

One major hurdle to achieve this goal is finding appropriate objective functions. To overcome this we implemented a variation of the Particle Swarm Optimization algorithm which learns the objective function during the optimization process.

BP 7.27 Mon 18:00 P1

Coarse-Grained Force Fields for Intrinsically Disordered Proteins — •Yannick Witzky, D. Janka Bauer, Arash Nikoubashman, and Friederike Schmid — Inst. für Physik, Universität Mainz, Germany

Simulations of systems containing many long proteins that perform liquid-liquid phase separation (LLPS) are usually computed with coarse-grained united residue force fields that allow for feasible runtime. One of these commonly used force fields was developed by Dignon et al.[1], where the proteins are modeled as bead-spring chains in an implicit solvent. As a reference we also used the bottom up coarse-grained UNRES force field [2] that resolves many more protein characteristics and is originally used for folding predictions. The results of simulations of four variants of an intrinsically disordered protein from both force fields are discussed in prospect of their polymer characteristics and the implications for simulations of LLPS-systems.

[1] Dignon et al.(2018) PLoS Comput Biol 14(1): e1005941
[2] Sieradzan et al.(2019) J. Phys. Chem. B, 123, 27, 5721-572

BP 7.28 Mon 18:00 P1

Nano-tribological investigation of the influence of specific synovial fluid components on lubrication of artificial joint materials — •Alex Kreis[1], Lukas Böttcher[1], Regina Lange[1], Paul Henke[2], Rainer Bader[2], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, University of Rostock — [2]Biomechanics and Implant Technology Research Laboratory, University Medical Center Rostock

The human synovial fluid in native and endoprosthetic joints enables outstanding lubrication and low wear. The question is how this fluid or its specific components, such as hyaluronic acid and albumin, participate in this performance on a nanoscopic scale. In this work we aim to determine the frictional forces between the force microscope (AFM) tip (Si3N4) and typical materials for articulating components of endoprosthetic implants, such as ceramics, ultra-high molecular weight polyethylene (UHWMPE) and cobalt-chromium (CoCr) based alloy by means of lateral force microscopy (LFM). As reference we use force loops acquired on borosilicate glass surfaces in water. Further we plan to investigate and discuss the influence of the chain length of hyaluronic acid on tribological properties of each of these materials.

BP 7.29 Mon 18:00 P1

Microscale resonators for microfluidic based Nuclear Magnetic Resonance spectroscopy — •Alaleh Mirhajivarzaneh[1], Piotr Lepucki[1], Adam P. Dioguardi[1], Aleksandr I. Egunov[1], Marco Rosenkranz[1], Renato Huber[1], Daniil Karnaushenko[1], Dmitry D. Karnaushenko[1], Oliver G. Schmidt[3,4], Bernd Büchner[1,2], and Hans-Joachim Grafe[1] — [1]Leibniz Institute for Solid State and Materials Research (IFW) Dresden — [2]Dresden University of Technology, Faculty of Physics — [3]Research Center for Materials, Architectures and Integration of Nanomembranes (MAIN), Chemnitz — [4]Chemnitz University of Technology, Material Systems for Nanoelectronics

Over the past few decades efforts to miniaturize Nuclear Magnetic Resonance (NMR) spectroscopy have resulted in the down-scaling of the core of an NMR system to microscale detectors. This achievement has unfolded a new era of NMR spectroscopy, with applications particularly in biological studies, where the sample size can scale down to micro- or nanoliters (nL), typical of microorganism and cell cultures. Our novel microcoil is a 3D microscale resonator with an integrated microfluidic system that offers high sensitivity and resolution (8ppb) for analyte volumes as small as 1.5nL, one of the smallest reported detection volumes in the field of NMR spectroscopy. Additionally, the integrated microfluidic system optimizes the filling factor of the device to reach almost 100%. The rolled-up microcoil can potentially be employed for high-resolution micro-NMR analysis of biological samples.

BP 7.30 Mon 18:00 P1

Altered local chromatin dynamics in stressed cells — •Rebecca Benelli and Matthias Weiss — Experimental Physics I, University of Bayreuth, Germany

The dynamic re-organization of chromatin is of crucial importance for cell viability and replication. During interphase, chromatin is mostly decondensed to allow for the transcription of genes, i.e. individual chromatin elements can be supposed to move like monomers of a polymer. Yet, recent reports have suggested chromatin to behave like a solid body on mesoscopic scales, questioning any free motion of chromatin elements. To explore the motion of integral chromatin markers, we have performed extensive single-particle tracking on telomeres under varying conditions. In agreement with previous findings, we observed a strongly subdiffusive and anti-persistent motion of telomeres in untreated culture cells, akin to the motion of monomers in a Rouse polymer. Reducing the ambient temperature or challenging cells by hyper- or hypo-osmotic stress resulted in a significant reduction of telomere mobility. In addition, significant jumps of telomeres between dynamically caged loci, observed in untreated cells, subsided or even vanished in response to these challenges. Altogether, our data indicate that local chromatin dynamics with long-range jumps between different loci are possible in untreated cells whereas a more compact/solid configuration of chromatin might explain the strongly reduced mobility of telomeres in stressed cells.

BP 7.31 Mon 18:00 P1

Image segmentation of irradiated tumour spheroids by Fully Convolutional Networks — •Matthias Streller[1], Sona Michlikova[2], Leoni A. Kunz-Schughart[2], Steffen Lange[1], and Anja Voss-Boehme[1] — [1]University of Applied Sciences Dresden — [2]OncoRay, National Center for Radiation Research in Oncology

Multicellular tumour spheroids are an established in-vitro model to quantify the effectiveness of cancer therapies. Spheroids are treated with radiotherapy and their therapeutic response over time is most frequently monitored via microscopic imaging. For analysis, it is necessary to segment the spheroids in these images, to extract their characteristics like the average diameter or circularity. While several image analysis algorithms have been developed for the automatic segmentation of spheroid images, they focus on more or less compact and circular spheroids with clearly distinguishable outer rim throughout growth. In contrast, treated spheroids are usually obscured by debris of dead cells and might be partly detached and destroyed. We train and optimize two Fully Convolutional Networks, in particular UNet and HRNet, to create an automatic segmentation which covers both cases, spheroids with and without therapy. While we successfully demonstrate the automatic segmentation for one spheroid type, we plan to extent the segmentation to other spheroid models.

BP 7.32 Mon 18:00 P1

Investigating Nanoparticle Dynamics in a High-Finesse Optical Microcavity — Larissa Kohler, •Shalom Palkhivala, and David Hunger — Karlsruhe Institute of Technology – Institute of Physics, Karlsruhe, Germany

We explore the dynamics of nanoparticles using a novel fibre-based high-finesse Fabry-Perot microcavity with integrated microfluidic channels. Silica nanospheres with radii down to 25 nm and gold nanorods with lengths of 20 nm have thus been investigated.

The three-dimensional Brownian motion of a single nanosphere in the cavity has been tracked by the simultaneous measurement of the fundamental and higher-order transverse modes. The particle's position was derived with spatial and temporal resolutions of down to 8 nm and 0.3 ms respectively.

To resolve the faster motion of even smaller nanoparticles, a cavity-locking system has been implemented. This achieved an rms stability of 4% of the resonance linewidth in a water-filled cavity having a finesse of 5×10^4. Hence, the dynamics of 20 nm gold nanorods could be detected with high measurement bandwidth. We shall report progress towards a quantitative evaluation of nanorod diffusion, and the measurement of nanoparticle rotation using a cavity-locked polarisation-splitting scheme.

Based on this, we aim to explore the dynamic and optical behaviour of single biomolecules, such as DNA.

BP 7.33 Mon 18:00 P1

Fixed 4-channel detection in 2D polarization fluorescence imaging (2DPOLIM) and compensation of depolarization caused by dichroic mirrors — •Yutong Wang[1,2], Asad Hafeez[1,2], Dijo Moonnukandathil Joseph[1,2], Mohammad Soltaninezhad[1,2], Rainer Heintzmann[1,2], and Daniela Täuber[1,2] — [1]Leibniz Institute of Photonic Technology — [2]Friedrich-Schiller-University Jena, Germany

Polarization resolved fluorescence imaging (POLIM) can reveal macromolecular structure in the range of 2-10 nm via Förster resonance energy transfer between similar fluorophores (homo-FRET, emFRET). 2D POLIM is superior to conventional fluorescence anisotropy methods for studies of anisotropic samples[1,2]. Implementing a variable electrooptic polarization control in the excitation together with a fixed 4-channel detection[3] speeds up the acquisition giving access to polarization resolved snapshots of dynamic samples. A major issue in POLIM setups is depolarization caused by the multilayer coating of dichroic mirrors, which introduces phase shifts between s- and p-polarized components. We implemented two pairs of dichroics with orientations crossed to each other. By this, incident s- and p-polarization is exchanged within each pair. The design proved to be an effective and reliable approach to significantly improve the quality of polarization by compensating the depolarization introduced by a single dichroic. – Funding: DFG-Ta1049/2 – [1] R. Camacho et al. Adv. Mater. 2019, 1805671. [2] R. Camacho et al. Commun. Biol. 2018, 1, 157. [3] F. Zimmermann et al. in Optically Induced Nanostructures, 2015.

BP 7.34 Mon 18:00 P1

Scanning small angle x-ray scattering of hydrated, keratin-rich cells — •Boram Yu[1], Chiara Cassini[1], Sophie-Charlotte August[1], Manfred Burghammer[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, Universität Göttingen, Germany — [2]ESRF, Grenoble, France

Intermediate filaments (IFs), one of the three main components of the cytoskeleton, form a network that contributes to cell mechanic. Thus, collecting structural information about IFs in their physiological setting, i.e., in whole cells, is crucial. We use scanning small angle x-ray scattering(SAXS) to obtain this information, as it offers both real space overview images with moderate resolution and reciprocal space information with high resolution. X-ray imaging of cells in aqueous state is challenging as their electron density contrast is low. Additionally, the aqueous environment contributes to extremely rapidly spreading radiation damage. For this reason, a fast-scanning mode is employed by moving the sample continuously through the beam rather than step by step, resulting in a significant reduction in exposure time, thus diminishing the radiation damage. As a benchmark for ordered intracellular structures, we investigate mammalian cells expressing the IF protein keratin. A purpose-built chamber maintains the cells hydrated while minimizing the volume of the liquid in the optical path. Despite weak contrast and short exposure times, we are able to retrieve the local main orientation of subcellular structures, thus demonstrating how scanning SAXS offers valuable information from hydrated cells.

BP 7.35 Mon 18:00 P1

Microfluidics-based analysis of the mobility and migration pattern of Trypanosoma brucei — •Hannes Wunderlich[1], Lucas Brehm[2], Jana Jentzsch[2], Sebastian Krauss[1], Klaus Ersfeld[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth, Germany — [2]Molecular Parasitology, University of Bayreuth, Germany

Trypanosoma brucei is a unicellular parasite that causes the African sleeping sickness after entering the human bloodstream. An active movement of trypanosomes, mediated by the beating of a microtubule-powered flagellum that spirals along the elastic cell body, is crucial for escaping the host's immune response. A highly ordered, subpellicular array of aligned microtubules beneath the cell membrane determines the effective elasticity of parasite and hence its propulsion during flagellar beating. Using soft lithography to create well-definded two-dimensional chambers, we have studied the mobility and migration pattern of trypanosomes without and with genetically induced changes of posttranslational microtubule modifications. Using a set of informative measures that have been developed for (persistent) random walks, we have analyzed trypanosome trajectories that exhibit clear run-and-tumble patterns. Our data reveal that posttranslational modifications of microtubules significantly alter trypanosome mobility and migration.

BP 7.36 Mon 18:00 P1

Topological artifacts in mid-IR photo-induced force microscopy (PiF-IR) — •Sajib Barua[1,2], Hardik Gadher[1,3], Uwe Hübner[1], and Daniela Täuber[1,2] — [1]Leibniz Institute of Photonic

Technology, Jena — [2]Institute of Physical Chemistry & Abbe Center of Photonics, Friedrich-Schiller-University Jena, Germany — [3]Leibniz University Hannover, Germany

The use of tapping mode atomic force microscopy (AFM) for detecting mid IR absorption can provide nanoscale chemical information. Several studies report on successful applications for qualitative characterization of biomaterials [1]. Implementing such methods for quantitative evaluation of chemical sample compositions requires further understanding of underlying physical processes [2]. In general, the surface of biological cells and tissue is rough on a sub-micron scale. This may cause artifacts in signal detection due to non-planar interactions with the AFM tip. We use structured polymer layers to investigate implications of sample topography on the signal intensity in mid-IR photo-induced force microscopy (PiF-IR). – [1] Wang et al. Super-Resolution Mid-Infrared Spectro-Microscopy of Biological Applications through Tapping Mode and Peak Force Tapping Mode Atomic Force Microscope. Adv. Drug Deliv. Rev. 2022, 180. [2] Täuber et al. Interference Effects in Nanoscale Infrared Spectroscopy Methods, submitted.

BP 7.37 Mon 18:00 P1

Investigation of biofilm formation on metal surfaces — •Bernhard Kaltschmidt[1], Annika Kiel[2], Ehsan Asghari[2], Julian Cremer[3], Dario Anselmetti[3], Barbara Kaltschmidt[2], Christian Kaltschmidt[2], and Andreas Hütten[1] — [1]Thin Films & Physics of Nanostructures, University of Bielefeld — [2]Department of Cell Biology, University of Bielefeld — [3]Biophysics & Nanosciences - "Physics of Life", University of Bielefeld

Biofilms can cause major problems in many different areas, such as corrosion and contamination of medical products. The aim of this work was to investigate biofilm formation on stainless steels and on sputtered transition metals. Steel disks of the chromium steels 1.4016, 1.4301 and 1.4510 were inoculated with bacteria in LB medium for 7 and 14 days. As bacteria we used Pseudomonas aeruginosa, which we use as our in vitro model for strong biofilm formation. After 14 days the first signs of bio-corrosion were detected by scanning electron microscopy (SEM) and atomic force microscopy. In another series of investigations, glass slides were coated with the transition metals Gold, Ruthenium and Tantal by magnetron sputtering and incubated with Pseudomonas aeruginosa for 24 hours. An uncoated glass surface served as a reference. Comparative studies of biofilm growth on the reference and on the different transition metals were carried out using SEM, confocal laser scanning microscopy and the colony forming unit assay. The analysis revealed that biofilm growth on transition metals is severely hindered compared to our non coated glass slide reference.

BP 7.38 Mon 18:00 P1

Observation of two-step aggregation kinetics of amyloid-β42 peptide from fractal analysis — •Soham Mukhopadhyay — Chair of Mathematics in Life Sciences, Friedrich-Alexander Universität Erlangen-Nürnberg, Cauerstr. 11, 91058 Erlangen, Germany — Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

Proteins are responsible for controlling and catalyzing the reactions and processes that make life possible. Proper folding of protein molecules into their native states is critical for them to function correctly; conversely, misfolded proteins often cause damaging effects on the biological processes they are involved in. Misfolded proteins often undergo self-aggregation, a process that has been the subject of intense research due to its importance in biological contexts. Of particular interest is the formation of stable filamentous aggregates termed amyloids — implicated in the pathology of several diseases such as Alzheimer's, Parkinson's, type-II diabetes, etc. Several models propose a two-step aggregation mechanism, with linearly growing fibrils and branch formation through secondary growth.

In this work, we employ tools from fractal geometry to develop an analysis technique for images of protein aggregation obtained from TIRF microscopy. Fractal geometry provides an instinctive framework for analyzing 1- and 2-dimensional growth. We use this framework to study the aggregation of the amyloid-β42 peptide and find the initial aggregation to proceed in a one-dimensional fashion, with later branching events leading to two-dimensional growth. This provides direct evidence for the two-step aggregation model.

BP 7.39 Mon 18:00 P1

Influence of varying pH on individual and collective behavior of filamentous cyanobacteria — •Franziska Papenfuss, Maximilian Kurjahn, Antaran Deka, and Stefan Karpitschka — MPI for Dynamics and Self-Organization, Göttingen, Germany

Photoautotrophic cyanobacteria are responsible for about 10 % of global primary production of reduced carbon and represent a sustainable source of carbon dioxide neutral bio-fuel. Adaptation to environmental changes is a key factor of their evolutionary success, but the emergent phenomena that couple the individual to their collective behavior remain elusive. Here, we investigate three species of filamentous cyanobacteria cultivated in pH-buffered and non-buffered medium over three weeks of cultivation. During cultivation, colony-scale properties like external pH and aggregate morphology were measured as well as properties of individual filaments like gliding velocity and absorption spectra. In the non-buffered cultures, pH varies in dependence on light-driven photosynthesis. Different species seem to adapt colony morphology from compact aggregates to reticulate layers at different pH values in the low alcalic range. Yet, the external pH has no influence on the gliding velocities, but influences the abundance of the dominant photo-pigments Chlorophyll-a, beta-carotene and phycocyanin in some species. Our investigations show that the pH is not only governed by the photosynthetic activity, but also influences the fate of the cyanobacterial colony in a regulating feedback mechanism.

BP 7.40 Mon 18:00 P1

Identifying malignant tissue using Laser Induced Breakdown Spectroscopy (LIBS) and Neural Networks — •Elena Ramela Ciobotea[1], Christoph Burghard Morscher[1], Cristian Sarpe[1], Bastian Zielinski[1], Hendrike Braun[1], Arne Senftleben[1], Josef Rüschoff[2], and Thomas Baumert[1] — [1]Kassel Universität, Kassel, Germany — [2]Institut für Pathologie Nordhessen, Kassel, Germany

The problem of differentiating cancerous tissue from a healthy one is currently solved in the diagnostic process through microscopic imaging of stained biopsy sections by pathologists. During surgical removal of cancerous tissue, oncological safety margins must be established to ensure the complete removal of the tumor without affecting much of the neighboring healthy tissue. For this purpose, on-site pathological analysis is done on freshly frozen, stained cuts, which is time consuming. We investigate a new approach to minimize the time of discrimination between malign and benign tissue by an in situ, non-contact spectroscopic analysis. In a proof of principle experiment, a plasma is generated by focusing an 800 nm femtosecond laser on the pathologic postoperative sample. The spectrum of plasma radiation contains information on the element composition of the ablated tissue. Since the recorded spectra are complex and full of information, neural networks are employed to find differences between malign and benign tissue with a high speed and accuracy. This contribution presents the experimental parameters that allow for the best possible differentiation of some biological tissues through fs-LIBS by minimizing deviations between the measurements.

BP 7.41 Mon 18:00 P1

Deep learning for single particle tracking in noisy data — •Mattias Luber, Mohammad Amin Eskandari, and Timo Betz — University of Goettingen, Goettingen, Germany

The quantitative analysis of particle motion critically depends on the quality of particle trajectory detection. Especially the position detection of particles in fluorescence microscopy images is an important task faced in biophysics. Trajectories are used to study processes like intracellular transport protein diffusion within and through membranes and the reconstruction of force fields driving the particle motion. In such settings, high spatial and temporal resolution are be desired. However, in practice those factors have contradictory measurement requirements. High temporal resolution requires short exposure times, which limit the photon budget and thus lead to low signal to noise ratios. We developed an approach to reconstruct the particle position from noisy images, by applying U-NET based deep learning models to fluorescence microscopy images. Using this we can successfully track particles with shorter exposure times, compared to traditional denoising techniques.

BP 7.42 Mon 18:00 P1

Analyses of the outer membrane of vital mitochondria — •Eric Lieberwirth[1], Christian Völkner[1], Regina Lange[1], Anja Schaeper[2], Magdalena Otte[2], Armin Springer[3], Markus Frank[3], Ingo Barke[1], Simone Baltrusch[2], and Sylvia Speller[1] — [1]University of Rostock, Institute of Physics, 18059 Rostock, Germany — [2]Rostock University Medical Center, Institute for Medical Biochemistry and Molecular Biology, 18057 Rostock, Germany — [3]Rostock University Medical Center, Medical Biology and Electron Microscopy Center, 18057 Rostock, Germany

A network of mitochondria enables a cell to perform oxidative metabolism. These organelles have a double membrane that is subject to constant remodeling during the regular fusion and fission processes. This study aims to gain more knowledge about the outer membrane containing translocase, porin and ion channels. Via Scanning Ion Conductance Microscopy (SICM) is it possible to measure the outer membrane of vital mitochondria at lateral spatial resolution of approx. 50 nm and at height resolution of a few nanometer. We immobilize the organelle in phosphate buffered saline (PBS) on collagen-coated substrates and scan the outer membrane with nanopipettes. Though the nanoprobe was, on each pixel, approached from top, the observed shapes exhibit forward-backward hysteresis and flat plateaus. The corrugation amplitude amounts to a few 10 nm and soft steps are present. Labeling translocase of the outer membrane (TOM) with nanoscopic gold particles may help learning about their spatial distribution and help to identify signatures in SICM and SEM.

BP 7.43 Mon 18:00 P1

Multiple thermophoretic particle trapping at single molecule resolution — •Benjamin Fanselow, Tobias Thalheim, and Frank Cichos — Peter-Debye Institute for Soft Matter Physics, Leipzig University, Germany

Achieving single molecule resolution for microscopy enabled to gain valuable insight into processes, that otherwise would be hidden in the ensemble, such as amyloid fibril fragmentation, volume exclusion of DNA molecules, or localization of proteins within a cell. One technique is the combination of fluorescence microscopy with thermophoretic trapping. It utilizes thermophoresis for confining freely diffusing single molecules within a liquid into a region of interest and allows observing these molecules without surface immobilization, over a time period of several minutes. The required temperature fields are generated via optical heating using a focused laser beam steered on a thin chromium layer. So far, only one trap at a time could be used, entailing multiple time-consuming measurements to achieve a reasonable statistics. We present the realization and characterization of up to four thermophoretic traps, which can be controlled simultaneously while preserving the single molecule resolution. This mode is characterized by a model system of 200-nm polystyrene particles in water, trapped with a feedback assisted mode. Analyzing the molecule displacement framewise, the trap stiffness and temperature induced velocities can be calculated. While it could be shown, that the stiffness is scalable with the laser power and the number of used traps, it also revealed an upper limit caused by the feedback loop frequency.

BP 7.44 Mon 18:00 P1

adaptive interferometric light-sheets for resolution enhanced imaging — •meelad lalenejad and alexander rohrbach — Laboratory for Bio- and Nano-Photonics, Department of Microsystems Engineering (IMTEK), University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

The success of light-sheet microscopy bases on the idea that only the parts of the object being are illuminated with laser beams from the side, which are in focus of the objective lens. This concept leads to increased image contrast and reduces photo-bleaching / -toxicity. In addition, larger volumes are scanned plane-wise or line-wise, such that LSM is significantly faster than point-wise scanning methods. However, compromises in spatial resolution have had to be made because of objective lenses with limited numerical aperture and aberrations from light scattering. On the detection side, such phase aberrations could often be corrected with adaptive optics. However, spatial light modulation and phase adaptation of the illumination side still leave plenty of room for improvements. In our research we want to combine the principles of holographically shaped illumination beams with interferometric arrangements of the illumination beams. Since the modulation contrast can be deteriorated by refractive index inhomogeneities of the sample, future phase adaptation for each of the counter propagating beams shall be used as an effective aberration compensation. Using the principles of structured illumination microscopy, we show 3D images in scattering media such as cancer cell clusters obtained from two laterally scanned, counter-propagating Bessel beams.

BP 7.45 Mon 18:00 P1

Absorption-based specificity in ROCS microscopy — •Victor Chuman and Alexander Rohrbach — University of Freiburg, Department of Microsystems Engineering - IMTEK, Laboratory for Bio- and Nano-Photonics, Georges-Köhler-Allee 102, 79110 Freiburg, Germany

Fluorescence techniques dominate the field of live-cell microscopy, but bleaching and motion blur from too long integration times limit dynamic investigations of small objects. High contrast, label-free life-cell imaging of thousands of acquisitions at 150nm and 200 Hz is possible by Rotating Coherent Scattering (ROCS) microscopy, where intensity speckle patterns from all azimuthal illumination directions are added up within a few milliseconds. However, ROCS lacks the important imaging feature of specificity. We address this deficiency by using different absorption markers, characterized by their different complex valued refractive indices to achieve a difference in image contrast in the observed structures. We demonstrate how different gray values in the image are obtained from interferences between scattered and unscattered light, resulting from material dependent phase shifts of the scattered light. Absorption-based specificity in ROCS imaging may open new fields of applications, adding on top of its high spatio-temporal resolution.

BP 7.46 Mon 18:00 P1

Novel concepts in scanned light-sheet microscopy to improve speed, contrast and resolution — •Yatish Yatish[1,2,3] and Alexander Rohrbach[1,2] — [1]Laboratory for Bio- and Nano-Photonics, Department of Microsystems Engineering-IMTEK, University of Freiburg, 79110 Freiburg, Germany — [2]CIBSS - Centre for Integrative Biological Signalling Studies, Freiburg, Germany — [3]Spemann Graduate School of Biology and Medicine (SGBM), University of Freiburg, Freiburg, Germany

Light-sheet microscopy (LSM) enables fast 3D, high contrast imaging offering effective sectioning and low photo-toxicity. LSM allows to investigate the issue of light scattering in both the illumination and detections, and to better understand the complex image formation. Switchable computer holograms can generate special Bessel beams that are scanned through the object offering increased penetration depths due to their self-reconstruction capability. These beams generate images with better contrast and resolution, when combined with confocal line detection. A future challenge will be to automatically adapt the illumination beam dimensions to the specific structure of object to enhance the 3D image quality. We have investigated the propagation of different beams through classes of spheres. All experiments were performed in combination with advanced computer simulations to better understand the effects of scattering. This includes the loss in quality of bead images along the optical illumination and detection axes through bead clusters, but also the position dependent scattering and absorbing of illumination and fluorescence light in cancer cell clusters.

BP 8: Focus Session: Phase Separation in Biochemical Systems

organized by Christoph Weber (University of Augsburg) and David Zwicker (MPIDS Göttingen)

Time: Tuesday 9:30–13:00 Location: H15

Invited Talk BP 8.1 Tue 9:30 H15

Phase separation in cells: gene localization and noise buffering — •Samuel Safran — Weizmann Institute of Science, Rehovot, Israel

Biomolecular condensates formed by phase separation allow the cell to organize itself in space and can promote or inhibit biochemical reactions. I will focus upon recent observations of phase separation of chromatin (chains of DNA and proteins) in the nucleus that suggests a new paradigm in which the genetic material is separated into domains, which in some cases, have a complex, marshland, mesoscale structure. How this mesoscale structure affects gene expression noise is a topic of current research. While many of the equilibrium properties of biomolecular condensates can be understood by extensions of statistical physics, biological molecules often do not maintain constant overall compositions, in contrast to equilibrium phase separation; over time, the cell stochastically produces and degrades many proteins, resulting in a noise-induced concentration distribution. Our theory shows how in the limit of slow production/degradation relative to molecular diffusion, one can incorporate the effects of such noise into the equilibrium phase diagram to predict the extent of noise reduction (buffering) by the phase separation in multicomponent systems.

BP 8.2 Tue 10:00 H15

RNA polymerase II clusters form in line with surface condensation on regulatory chromatin — •Tim Klingberg[1,2], Agnieszka Pancholi[3], Weichun Zhang[3], Roshan Prizak[3], Irina Mamontova[3], Marcel Sobucki[3], Andrei Yu Kobitski[3], Gerd Ulrich Nienhaus[3], Vasily Zaburdaev[1,2], and Lennart Hilbert[3] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Max-Planck-Zentrum für Physik und Medizin — [3]Karlsruhe Institute of Technology

Transcription of eukaryotic genes by the RNA polymerase II (Pol II) has two major control points: recruitment to the regulatory region of a specific gene, and subsequent release into the elongation of RNA transcripts. We find that recruited Pol II forms macromolecular clusters with a large variety of shapes in the embryos of zebrafish, which we investigated by live and super-resolution microscopy. To delineate the essential physical mechanisms underlying Pol II cluster formation, we use coarse-grained lattice kinetic Monte Carlo simulations containing monomeric particles (recruited Pol II) that can interact with polymer chains (regulatory regions). We propose that the regulatory chromatin regions act as surfaces for the condensation of recruited Pol II into a liquid-phase. The numerical simulations of our model qualitatively reproduce the different forms of RNA Pol II clusters that we detected with microscopy. Taken together, our results suggest that recruited Pol II contributes to the surface-associated condensates, whereas elongating Pol II is excluded from these condensates and thereby drives unfolding of the condensates.

BP 8.3 Tue 10:15 H15

Lattice based model and continuum theory of active microemulsion — •Rakesh Chatterjee[1,2], Hui-Shun Kuan[1,2], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander University, Erlangen-Nuremberg, Erlangen, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

During transcription, RNA polymerase II (Pol II) attaches and moves along the DNA strand to produce messenger-RNA (mRNA) transcript. It has been recently shown that in the nucleus, DNA and RNA are spatially organised in agreement with a microphase separation process [1], where the full phase separation of the RNA-rich phase from DNA is prevented by the transcribing Pol II playing the role of an amphiphile. To gain the comprehensive understanding of physical mechanisms behind this process we propose a phenomenological lattice model where DNA, mRNA and Pol II serve as the three basic components similar to the equilibrium oil-water-amphiphile system, which exhibits two and three phase coexistence. Here however, Pol II undergoes chemical transitions reflecting different stages of the transcription process. In the model, it is realised by assuming transient dynamics of the amphiphiles which switches between active and inactive states. Numerical simulations of the lattice model show that amphiphile activity significantly modifies phase behaviour of the system compared to the equilibrium scenario. Furthermore, by rigorous coarse-graining of the lattice model we could derive the continuum theory and predict the relaxation dynamics of the dynamic structure factor of active microemulsion.

[1] Hilbert et.al, Nature Comm. 12, (1) 2021.

BP 8.4 Tue 10:30 H15

Molecular assembly lines regulate the size of active droplets — •Tyler Harmon — Leibniz Institute for Polymer Research, Dresden, Germany

Large protein complexes are assembled from protein subunits to form a specific structure. In our previous work, we used theory to propose that assembly into the correct structure could be reliably achieved through an assembly line with a specific sequence of assembly steps. We illustrated that the assembly line can be self-organized through utilizing existing membraneless organelles. In this way, the droplet directly regulates the formation of the assembly line.

In this work we explore how the assembly line can directly regulate the droplet. It has been observed that the core element can act as an important structural factor for the droplet formation. By introducing this feature into the model, we see that the assembly line also regulates the size of the droplet in a productive way.

BP 8.5 Tue 10:45 H15

Droplet differentiation induced by chemical reactions — •Xi Chen[1], Frank Jülicher[2], Jens-Uwe Sommer[1], and Tyler Harmon[1] — [1]Leibniz-Institut für Polymerforschung Dresden, Institut Theory der Polymere, 01069 Dresden — [2]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden

Membraneless compartments are formed in cells by liquid-liquid phase separation. The compartments enrich many components including enzymes which resemble chemically active droplets. A major paradigm for studying these droplets is to consider two types of species, scaffolds, which thermodynamically hold the droplets together, and clients, such as enzymes which utilize the droplets that are formed. We investigate through theory a model system where two competing enzymes which can modify the scaffold, for example a kinase and a phosphatase, are clients to the droplets. Interestingly, by introducing a preferential affinity between enzymes and their product scaffold, the system becomes unstable and differentiates into two types of droplets concentrated in either modified scaffold. Additionally, these features can lead to unexpected behaviors such as droplets which repel each other. This may correspond to an unexplored mechanism of the spatial control of biochemical reactions in biological cells.

15 min. break

BP 8.6 Tue 11:15 H15

Non-specific adhesive forces reorganize the cytoskeleton around membraneless organelles — •Thomas J. Böddeker, Kathryn A. Rosowski, Robert W. Style, and Eric R. Dufresne — Department of Materials, ETH Zurich, Switzerland

Phase-separation of biomolecules in cells takes place in a complex environment crossed by multiple filaments of the cytoskeleton or chromatin. To understand the potential coupling between emerging droplets and the surrounding network, we study the interactions of stress granules, a phase-separated protein-RNA droplet in the cytosol, with the microtubule network. Statistical tools similar to the radial distribution function enable us to quantify long-ranged enhancement in microtubule density in the vicinity of stress granules. When microtubules are depolymerized, the molecular subunits partition to the surface of the droplet. We interpret the data using a thermodynamic model, revealing a weak non-specific affinity of the subunits to the surface of about 0.1 k_bT. As filaments polymerize, the affinity is amplified leading to significant adhesion of filaments to the granule surface. This adhesion leads to reorganization of filaments around the granule and makes microtubule rich regions of the cell energetically favorable for stress granules. We find that the liquid nature of membraneless organelles leads to non-specific adhesion of larger particles to their surface due to the surface tension of these protein droplets, reminiscent

of Pickering emulsions.

T.J. Böddeker, et. al. Nature Physics 18, 571 2022

BP 8.7 Tue 11:30 H15

Catalysis-Induced Phase Separation and Autoregulation of Enzymatic Activity — Matthew W. Cotton[1,2], Ramin Golestanian[2,3], and •Jaime Agudo-Canalejo[2,4] — [1]Mathematical Institute, University of Oxford, Oxford, United Kingdom — [2]Department of Living Matter Physics, Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford, United Kingdom — [4]Institute for Theoretical Physics, University of Heidelberg, Heidelberg, Germany

Studying the effect of non-equilibrium activity on intracellular phase separation is a very active research area, but all previous studies have still relied on equilibrium interactions as the driver for phase separation. Here, we present a thermodynamically consistent model describing the dynamics of a multi-component mixture where one enzyme component catalyzes a reaction between other components. We find that the catalytic activity alone can induce phase separation for sufficiently active systems and large enzymes, without any equilibrium interactions between components [1]. In the limit of fast reaction rates, binodal lines can be calculated using a mapping to an effective free energy. We also explain how this catalysis-induced phase separation (CIPS) can act to autoregulate the enzymatic activity, which points at the biological relevance of this phenomenon.

[1] M. W. Cotton, R. Golestanian, and J. Agudo-Canalejo, arXiv:2205.12306 (2022).

BP 8.8 Tue 11:45 H15

Structure and dynamics of water molecules in FUS protein molecular condensates — •Daniel Chavez Rojas, Martin Girard, and Joseph Rudzinski — Max Planck Institute for Polymer Research, Mainz, Germany

There is evidence that molecular condensates of the FUS protein play a role in the development of some neurodegenerative diseases like ALS. For this reason, understanding the molecular mechanism by which these condensates form at an atomistic level is of therapeutic interest. The molecular structure and water-protein interactions of these condensates is poorly understood. In order to study these interactions, we make use of multi-scale molecular dynamics simulations. Through the analysis of these simulations we report on the water-protein hydrogen bonding interactions of the individual amino acids of FUS proteins in the condensate versus in solution.

BP 8.9 Tue 12:00 H15

Regulation of chromatin microphase separation by adsorbed protein complexes — •Omar Adame-Arana, Gaurav Bajpai, Dana Lorber, Talila Volk, and Samuel A. Safran — Weizmann Institute of Science, Rehovot, Israel

The spatial arrangement of chromatin in the nucleus serves as a template for DNA transcription. Regions of chromatin that are loosely packed (active regions) are accessible to the transcription machinery and can be readily transcribed; in contrast, regions that are tightly packed are usually not transcribed (inactive regions). These two types of chromatin regions separate from the nucleoplasm and further form distinct compartments reminiscent of microphase separation. Chromatin phase separation due to self-attraction has been experimentally described in the past. But what controls the further, observed microphase separation into active and inactive chromatin regions? Here, we present a minimal theory in which the inactive regions experience poor solvent conditions (due to self-attraction,) but where the solvent quality for the active chromatin regions can be regulated by the adsorption of protein complexes. Using the theory of polymer brushes as well as Brownian dynamics simulations, we find that such adsorption leads to swelling of the active regions which in turn, decreases the thickness (in a flat geometry) or radius of curvature (in a spherical geometry) of the inactive chromatin microphase. We compare the theory with experiments to suggest that the solvent quality modulated by adsorption of protein complexes may be a key contributing factor in establishing and regulating the physical organization of the genome.

BP 8.10 Tue 12:15 H15

(De)hydration far away from equilibrium can speed up chemical processes — •Ivar Svalheim Haugerud, Pranay Jaiswal, and Christoph Weber — Institute of Physics, Universität Augsburg, Augsburg, Germany

Under early earth conditions, wet-dry cycles and phase-separated droplets are believed to facilitate chemical processes. Recent experimental studies suggest that chemical reactions can accelerate when subject to non-equilibrium conditions of hydration or dehydration. We develop a theoretical model studying the interplay between wet-dry cycles, phase separation, and chemical processes. We find that both hydration and dehydration can significantly increase chemical reaction rates. Interestingly, we show that the conditions that enhance reaction rates coincide with the conditions necessary for the mixture to phase separate. The findings show under what conditions the physics of wet-dry cycles can play a role similar to enzymes in living cells, speeding up slow reactions in prebiotic soups.

BP 8.11 Tue 12:30 H15

Chemically Active Wetting — •Susanne Liese[1], Xueping Zhao[2], Frank Jülicher[2], and Christoph Weber[1] — [1]University of Augsburg, Germany — [2]MPI Physics of Complex Systems, Dresden, Germany

In living cells, the wetting of condensed phases at membrane surfaces provides a mechanism for positioning biomolecules. Biomolecules can also bind to such membrane surfaces. In living cells, this binding is often chemically active since it is maintained away from equilibrium by supplying energy and matter. Here, we investigate how active binding on membranes affects the wetting of condensates. To this, we derive the non-equilibrium thermodynamic theory of active wetting. We find that active binding significantly alters the wetting behavior leading to non-equilibrium steady states with condensate shapes reminiscent of a fried egg or a mushroom. We further show that such condensate shapes are determined by the strength of active binding in the dense and dilute phases, respectively. Strikingly, such condensate shapes can be explained by an electrostatic analogy where binding sinks and sources correspond to electrostatic dipoles along the triple line. Through this analogy, we can understand how fluxes at the triple line control the three-dimensional shape of condensates.

BP 8.12 Tue 12:45 H15

Interface resistance can govern transport of molecules across phase boundaries — •Lars Hubatsch[1,2], Anatol Fritsch[1,2], Tyler Harmon[3], Frank Jülicher[2,4], Christoph Weber[5], and Anthony Hyman[1,2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics — [2]Center for Systems Biology Dresden — [3]Leibniz Institute for Polymer Research — [4]Max Planck Institute for the Physics of Complex Systems — [5]University of Augsburg

Cells can achieve compartmentalization of biochemical processes via organelles by the selective admission of biomolecules. Organelles are enclosed by a membrane or, in the case of biomolecular condensates, by the condensate-bulk interface. While transport across membranes has been studied for decades, it is less clear how biomolecular condensates regulate transport across their interface. Using a combination of live-imaging and theory, we show that the flux of molecules across the condensate-bulk interface exhibits transients that cannot be explained by local equilibrium between the coexisting phases, a phenomenon also referred to as interface resistance. It is unclear whether this interface resistance stems from molecules adsorbing to the interface or from a kinetic barrier reflecting molecules at the interface. Using single-particle imaging of PGL-3 droplets, we observe no accumulation of molecules at the interface. This observation suggests that molecules are reflected rather than adsorbed at the interface. We quantify the strength of interface resistance by accounting for molecule dynamics outside, inside, and at the droplet interface and thus provide a framework to characterize molecular fluxes across condensate-bulk interfaces.

BP 9: Bioimaging

Time: Tuesday 9:30–13:00 Location: H16

BP 9.1 Tue 9:30 H16

Nano-infrared spectroscopic imaging (NanIRim): Promises and Challenges for Application in Biophotonics — •Daniela Täuber — Leibniz Institute of Photonic Technology, Jena, Germany — Friedrich-Schiller University Jena, Germany

A number of nano IR spectroscopic methods have been developed, which provide chemical information at subcellular and single molecule level. High spatial resolution leads to a reduction of the number of chemical bonds contributing to the signal. Thus, variations have to be identified above a heterogeneous background. Since 2019, I have investigated advantages and limitations of mid IR photo-induced force microscopy (PIF-IR) together with my team and collaborators. We applied PIF-IR to materials ranging from organic monolayers on various substrates, and biopolymer compositions to single bacteria and human retina. Recently, we studied interference effects in layered systems comparing experimental and calculated FTIR spectra of polymer films on different substrates to PIF-IR spectra. PIF-IR enables hyperspectral imaging at a fascinating spatial resolution of ~5 nm. A drawback are the small data sets. We applied PIF-IR to well-known interactions of antibiotics with Bacillus subtilis. To meet the challenge of finding the local interactions in hyperspectral images of single bacteria, we developed an advanced cluster analysis together with colleagues in the Heintzmann Lab. Our findings are very promising for successful applications of PIF-IR to the investigation of local variations in the surface areas of cells and tissues. Such visualization at the single cell level will boost our understanding of interactions in the Life Sciences

BP 9.2 Tue 9:45 H16

Phase reconstruction of low-energy electron holograms of individual proteins — •Hannah Ochner[1], Sven Szilagyi[1], Moritz Edte[1], Stephan Rauschenbach[1,2], Luigi Malavolti[1], and Klaus Kern[1,3] — [1]Max Planck Institute for Solid State Research, Stuttgart — [2]Department of Chemistry, University of Oxford — [3]Institut de Physique, École Polytechnique Fédérale de Lausanne

Low-energy electron holography (LEEH) can image proteins and their conformational variability on the single-molecule level [1,2]. However, the technique does not yield a real-space image, but rather a hologram from which the information about the molecule needs to be recovered via a reconstruction process. While a one-step reconstruction process can reproduce molecular size and shape via amplitude imaging, it cannot directly recover the phase information encoded in the hologram. Here, we apply an iterative phase retrieval algorithm to experimentally acquired low-energy electron holograms of proteins. This allows us to reconstruct the phase shift induced by the protein along with its amplitude distribution. We provide evidence that phase imaging is sensitive to changes in local potential, as indicated by the strong correlation between reconstructed phase shift and the number of scatterers in the electron path, and the strong phase signatures induced by localised charges. LEEH phase imaging thus yields insights into structural features beyond size and shape and could, at high spatial resolution, open up the possibility of chemically sensitive single-molecule imaging.

[1] PNAS,2017;114(7) [2] PNAS,2021;118(51) e2112651118

BP 9.3 Tue 10:00 H16

Investigation of human platelet volume changes with scanning ion conductance microscopy (SICM) — •Konstantin Krutzke, Jan Seifert, Johannes Rheinlaender, and Tilman E. Schäffer — Institute of Applied Physics, Eberhard-Karls-Universität Tübingen, Germany

Human blood platelets (thrombocytes) are anucleate cells that play an important role in wound closure in the case of vessel injury. Changes in morphology and activation of platelets are linked to blood vessel diseases such as atherosclerosis or can cause thrombosis. Water-induced swelling promotes procoagulant activity and possibly initiates thrombosis. Volume changes of platelets can be measured by light transmittance or light scattering techniques. However, these studies have only qualitatively shown that platelets regulate their volume as a response to different osmotic conditions and usually have not been performed on a single-cell level. To elucidate the volume regulatory mechanisms of platelets, we used scanning ion conductance microscopy (SICM) to quantitatively measure dynamic volume changes of single adhered platelets under different osmotic conditions with down to sub-minute time-resolution. SICM is a nanopipette-based, contact-free imaging technique ideally suited for sensitive live cells such as platelets. Our data show that rapid volume regulation of non-activated adherent platelets occurs in direct response to different osmotic conditions. Activated platelets, however, seem not to be able to regulate their volume when the osmolarity changes. We thereby highlight the usability of SICM for high-speed volume measurements.

BP 9.4 Tue 10:15 H16

Pool formation of synaptic vesicles by synapsin investigated by X-ray diffraction and cryo-EM — •Jette Alfken[1], Charlotte Neuhaus[1], Moritz Stammer[1], Marcelo Ganzella[3], Arsen Petrovic[4], Rubén Fernández-Busnadiego[4], Reinhard Jahn[3], Dragomir Milovanovic[2], and Tim Salditt[1] — [1]Georg-August-Universität, Institute for X-ray Physics, 37077 Göttingen — [2]Laboratory of Molecular Neuroscience, German Center for Neurodegenerative Diseases (DZNE), 10117 Berlin — [3]Laboratory of Neurobiology, Max Planck Institute for Multidisciplinary Sciences, 37077 Göttingen, Germany — [4]Institute of Neuropathology, University Medical Center Göttingen, 37099 Göttingen

Synaptic vesicles (SVs) are organized in dense pools close to the synaptic membrane. A key protein for this structural arrangement within the synapse is synapsin, which forms droplets containing SVs, due to liquid-liquid phase separation. To study the structure and interactions underlying pool formation in a controlled in vitro model, we have investigated phases made of SVs purified from rat brain and varied synapsin concentration. We have studied the pools by two complementary techniques: cryo-EM yielding the 3D structural arrangement of the adhering vesicles in pools at resolution of a few nanometers in the vitrified state, and solution SAXS under varied buffer conditions and concentrations. In addition, the pools were studied for comparison in a controlled system consisting of artificially prepared lipid vesicles and synapsin. We report these experiments and preliminary results (data analysis still ongoing).

15 min. break

BP 9.5 Tue 10:45 H16

Understanding calcareous biomineralization on the nanoscale through in-vivo growth imaging by x-ray nanodiffraction — •Tilman Grünewald[1], Jeremie Vidal-Dupiol[2], Julien Duboisset[1], Bruno Petton[3], Jacqueline Legrand[3], Michael Sztucki[4], Manfred Burghammer[4], and Virginie Chamard[1] — [1]Institut Fresnel, Marseille, France — [2]Ifremer, Montpellier, France — [3]Ifremer, Plouzané, France — [4]ESRF, Grenoble, France

Biomineralized tissues combine properties such as low weight with high-strength and are formed from abundant atoms via low-energy processes. However, the nanostructural formation process of biominerals is not well understood, relying on post-mortem investigations of the bivalve growth edge [1]. Insights by in-vivo experiments requires studying a live organism in its environment at the crystalline level with sub-um spatial resolution. The associated problems have been overcome by 4th generation synchrotrons, enabling faster measurements.

Here, an experimental approach we developed and validated is outlined, enabling us to observe the first nanoscale-resolved, temporal follow-up of the shell growth in a living, mineralizing Crassostrea gigas oyster shell by nanofocus x-ray Bragg diffraction.

We show that crystallization occurs without the presence of the animal mantle, over several hours and follows a layer-by-layer deposition scheme with slightly misaligned grains. These results imply a cyclic crystallization, driven by a physico-chemical mechanism. This provides the animal with an efficient way of building its shell.

[1] Duboisset et al. 10.1016/j.actbio.2022.01.024

BP 9.6 Tue 11:00 H16

An open-top scanned oblique lightsheet microscope for neuronal network imaging — •Achim Theo Brinkop[1], Stefan Stöberl[1], Florian Schorre[1], and Friedhelm Serwane[1,2,3] — [1]Faculty of Physics, LMU Munich, Germany — [2]Munich Cluster for Systems Neurology (SyNergy), Germany — [3]Graduate School of Systemic Neuroscience (GSN), Munich, Germany

Understanding signal processing in neuronal networks such as brain

organoids on a single-neuron level has remained a challenge. Imaging network activity requires a millisecond temporal resolution with single-neuron spatial resolution, all in an observation volume containing the 3D network. Advances in lightsheet microscopy have brought this goal closer to experimental reach, but at the cost of complex optical set-ups which (i) impose geometrical constraints to sample mounting or (ii) require multiple imaging objectives with custom optical components.

We report on the development of an open-top single-objective oblique lightsheet microscope which reduces the complexity compared to existing set-ups. We implement the open-top geometry by using only two primary objectives. The lightsheet is digital scanned by a fast galvo mirror to maintain high image quality. Our first prototype with excitation wavelengths of 561 (488, 638) nm is expected to allow for a $1/e^2$-resolution of 1.84 (1.47, 1.95) μm axially and 0.27 (0.23, 0.30) μm laterally. It offers a volumetric temporal resolution of 8 (2) Hz for a volume of $400 \times 90\,(360) \times 100\,\mu m^3$.

With this set-up, we aim to gain insights into large neuronal networks of retina organoids, both in wildtype and disease condition.

BP 9.7 Tue 11:15 H16

Extraction of Calcium Traces from Volumetric Lightsheet Images of 3D Neuron Ensembles — •Filippo Kiessler[1], Paulina Wysmolek[4], Katja Salbaum[1,2], Elijah Shelton[1], Selina Sonntag[1], and Friedhelm Serwane[1,2,3] — [1]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität München, Munich — [2]Graduate School of Systemic Neuroscience (GSN), Munich, Germany — [3]Munich Cluster for Systems Neurology (SyNergy), Germany — [4]Max Planck Institute for Medical Research, Heidelberg, Germany

In vitro systems resembling brain regions, such as brain organoids, are slowly changing the field of neuroscience. However, characterization of their electrical activity has remained a challenge as this requires electrophysiological readout in 3D at single-neuron resolution. We use a custom-built single-photon light-sheet microscope to record calcium activity in 3D neuron ensembles which we grow from mouse embryonic stem cells. To extract calcium intensities from the volumetric lightsheet data, we developed a custom software pipeline that augments the CaImAn software. Our pipeline includes a median filter to remove sample bleaching effects. In addition, typical artifacts arising from the illumination of of our light-sheet microscope are removed with a custom Fourier filter. With this setup we obtained connectivity graphs based on correlation of the extracted calcium traces. We envision this platform as a non-invasive toy-model to understand neuronal information generation and processing.

BP 9.8 Tue 11:30 H16

Thermal fluctuations of the trapped bead as the complementary tool to the microscopy for investigation of a phagocytosis. — •Tetiana Udod and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, Department of Microsystems Engineering (IMTEK), University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

Phagocytosis, the uptake of particle by cells, is typically investigated in vivo by different microscopy technics, such as Brightfield, DIC, or Fluorescence microscopy. But even with highest possible resolution we can*t observe receptor binding or derive binding strengths to the cell membrane during binding and uptake. In addition to continuously recording 3D stacks of J774 macrophages cells by DIC microscopy, we record the thermal fluctuations of beads during the engulfment process. We measure the bead*s position in 3D with nanometer precision at MHz rates with back focal plane interferometry. Running both methods in parallel we can correlate the bead position relative to the cell to record changes in binding parameters like stiffnesses or, viscous drags derived from position fluctuations. Furthermore, remaining measurement ambiguities are resolved by Brownian Dynamic simulations.

To better understand such processes we use a combination of experiments with Photonic Force Microscopy, Brownian Dynamic simulation and analytical theory.

BP 9.9 Tue 11:45 H16

Assessing the cochlear morphology from the whole organ down to cellular resolution with multi-scale phase-contrast x-ray tomography — •Jannis Justus Schaeper[1], Christoph Kampshoff[2], Bettina Wolf[2], Daniel Keppeler[2], Tobias Moser[2], and Tim Salditt[1] — [1]Institut für Röntgenphysik, Georg-August-Universität Göttingen — [2]InnerEarLab, Universitätsmedizin Göttingen

The cochlea is the receptor organ of the inner ear which transduces sound into neuronal activity. Both fundamental aspects of signal transduction and neuro-physiology as well as biomedical research (implant technology, hearing loss and disorders) require 3D imaging techniques capable to quantify the micro-anatomy (1).

We present multi-scale 3D imaging of small-animal cochleae by phase-contrast x-ray tomography (PC-CT) using both synchrotron radiation (SR) and lab μ-CT to assess the morphology of the cochlea, orientation of cochlear implants (CIs), and the number and density of spiral ganglion neurons (SGNs). Due to optimization in sample preparation, image acquisition and phase retrieval we achieve high contrast for unstained soft tissue. Without extensive sample preparation, shape and volume of every SGN in the entire organ can be identified. In the high-resolution PC-CT, and in the parallel beam, we reach cellular resolution in the organ of Corti. Lab μ-CT is suitable to analyze cochlear morphology and to assess the correct positioning of CIs and resulting (non-)optimal signal transduction.

(1) Keppeler et al. (2021), PNAS 118(18), e2014472118

15 min. break

BP 9.10 Tue 12:15 H16

Studying biomolecular dynamics and structure with high-speed atomic force microscopy — •Dimitar Stamov, Andreas Kraus, André Körnig, and Heiko Haschke — JPK BioAFM, Bruker Nano GmbH, Am Studio 2D, 12489 Berlin, Germany

Studying the molecular dynamics and structural conformations is important for understanding the function and biological significance of samples ranging from single membrane proteins to complex macromolecular systems. Recent atomic force microscopy (AFM) developments have led to unprecedented imaging rates in fluid, enabling temporal resolution on the sub-20-milisecond scale.

Annexin V (A5) serves as an important regulator of membrane repair in eukaryotic cells, where it shows a strong Ca2+ binding affinity to phosphatidylserine. We have used high-speed AFM to study the 2D crystal formation in a model system containing supported lipid bilayers and A5 molecules. We demonstrate the lateral dynamics and preferred structural orientations of the mobile A5 trimers.

We previously demonstrated that pUC19 plasmids bind to poly-L-ornithine substrate in supercoiled states that are very high in torsional energy, thereby driving dehybridization of the double-helical DNA strands. Here we have quantified the process kinetics with a temporal resolution of 25 ms per frame and identified stages that include formation of metastable dehybridization bubbles, thermodynamic single strand fluctuations, and ultimately rehybridization to an intact double-stranded state.

Prize Talk BP 9.11 Tue 12:30 H16

Super-resolution STED and MINFLUX Nanoscopes by Abberior Instruments — •Gerald Donnert — Abberior Instruments GmbH, Göttingen, Germany — Laureate of the Technology-Transfer-Prize 2022

Abberior Instruments GmbH was founded 10 years ago from the laboratory of Nobel Laureate Stefan Hell at the Max Planck Institute in Göttingen. In 2022, Abberior Instruments was awarded the Technology Transfer Prize of the German Physical Society (DPG).

Abberior Instruments develops and markets super-resolution light microscopes, namely confocal plus STED microscopes and MINFLUX microscopes. The latter are the latest generation of super-resolution instruments with resolutions down to the molecular level, i.e. 1 nm resolution; unrivaled in resolution today. Understanding life at the molecular level - both in terms of structure and dynamics - is a human dream and is becoming feasible with the latest generation of super-resolution instruments with multicolor capabilities. We expect to soon gain new insights into the dynamic structural changes of e.g. protein machines in living cells.

In this talk, I will present the latest imaging and tracking results with our super-resolution STED and MINFLUX nanoscopes, such as single-particle tracking of lipids in lipid membranes, the structure of nuclear pore complex (NPC) subunits, and the nanoscale assembly of proteins in neuronal synapses.

BP 10: Cell Adhesion and Multicellular Systems

Time: Tuesday 10:00–12:30 Location: H13

BP 10.1 Tue 10:00 H13

Physics of gut motility governs digestion and bacterial growth — •Agnese Codutti[1,2], Jonas Cremer[3], and Karen Alim[1,2] — [1]Physics Department and CPA, Technische Universität München — [2]Max-Planck-Institut für Dyanmik und Selbstorgansiation, Göttingen — [3]Stanford University

Malfunctioning of the small intestine contractility and the ensuing bacterial population therein are linked to a plethora of diseases. We, here, study how the small intestine's variety of contractility patterns impacts nutrient uptake and bacterial population. Our analytical derivations in agreement with simulations identify flow velocity as the key control parameter of the nutrients uptake efficiency and bacterial growth, independently of the specifics of contractility patterns. Self-regulating flow velocity in response to the number of nutrients and bacteria in the gut allows achieving 100% efficiency in nutrient uptake. Instead of the specifics of intestine contractility, our work points to the flow velocity and its variation in time within the intestine to prevent malfunctioning.

BP 10.2 Tue 10:15 H13

Blue-light photoreceptors regulating light-switchable adhesion in *Chlamydomonas reinhardtii* — •Rodrigo Catalan[1,2], Antoine Girot[1,2], Alexandros Fragkopoulos[1,2], Simon Kelterborn[3], Darius Rauch[3], Peter Hegemann[3], and Oliver Bäumchen[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen , Germany — [2]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [3]Humboldt University Berlin, Institute of Biology, 10115 Berlin, Germany

Photoactive organisms have evolved a variety of light-sensitive molecules, called photoreceptors, which regulate phenotypes such as phototaxis, circadian life cycle and sexual reproduction. Recently it was discovered that the unicellular, eukaryotic microalga *Chlamydomonas reinhardtii* exhibits light-switchable flagellar adhesion to surfaces [Kreis *et al.*, Nature Physics, 2018]; a phenotype triggered by a blue-light photoreceptor. Using single-cell micropipette force measurements, we show that the action spectrum of flagellar adhesion forces in wild-type (WT) cells resembles the adsorption spectrum of photoreceptors called cryptochromes. Furthermore, adsorption experiments show that the number of WT cells adsorbing to surfaces under blue light increases after the start of the cells' day-phase, which coincides with the light degradation of plant cryptochrome (pCRY). Adhesion force and adsorption experiments of WT and photoreceptor deletion mutants illuminate the role of photoreceptors in this adhesion phenotype.

BP 10.3 Tue 10:30 H13

Motility and collective behavior of gliding *Chlamydomonas* populations — •Alexandros Fragkopoulos[1,2], Sebastian Till[1], Florian Ebmeier[1], Marco G. Mazza[1,3], and Oliver Bäumchen[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — [2]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [3]Department of Mathematical Sciences, Loughborough University, Loughborough, Leicestershire LE11 3TU, UK

The model microbe *Chlamydomonas reinhardtii*, a unicellular biflagellated microalga, can adhere and colonize almost any surface under particular light conditions. Once the cells attach to a surface, an intraflagellar transport machinery translocates the cell body along the flagella, which are oriented in a 180° configuration. This motion is known as gliding motility. We find that gliding enables surface-associated *Chlamydomonas* cells to cluster and form compact, interconnected microbial communities [1]. We detect and analyze the movement of single cells and characterize the spatio-temporal evolution of the morphology of the colony. The motion of single cells exhibits rapid movements, followed by prolonged immobility. By analyzing the cell clustering, we observe the colony transitioning from local clusters to a single global network with increasing cell density. Simulations based on a purely mechanistic approach cannot capture the non-random cell positions. However, by including flagellar mechanosensing through a cognitive model, we quantitavely reproduce the experimental observations.
[1] Till et al., arXiv:2108.03902v1

BP 10.4 Tue 10:45 H13

Spatiotemporally resolved single-cell growth in bacterial biofilms — •Eric Jelli[1,2,3], Takuya Ohmura[2,4], Niklas Netter[2,3,4], Martin Abt[2,3], Eva Jiménez-Siebert[2,3,4], Konstantin Neuhaus[2,3,4], Daniel Karl-Heinz Rode[2,3,4], and Knut Drescher[2,3,4] — [1]Max Planck Institute for Neurobiology of Behavior - caesar, Bonn, Germany — [2]Max Planck Institute for Terrestrial Microbiology, Marburg, Germany — [3]Department of Physics, Philipps-Universität Marburg, Marburg, Germany — [4]Biozentrum - University of Basel, Basel, Switzerland

Bacterial biofilms are dense multicellular communities that are embedded in a self-produced matrix. The high density of cells gives rise to nutrient, oxygen, and metabolite gradients in space and time. To understand the underlying spatio-temporal growth principles in biofilms, single-cell segmentation algorithms are required. Current Deep Learning algorithms provide the required accuracy for tracking-dependent investigations, yet depend on suitable large training datasets.

We used an iterative training pipeline to densely annotate complete biofilms with thousands of cells in 3D. The pipeline reduced the required manual labeling steps which would otherwise be prohibitive for a dataset of a similar size. The collected data enabled us to compare the single-cell segmentation accuracy of recent Deep Learning algorithms with the results of classical biofilm segmentation approaches. We used the trained algorithms for single-cell tracking in 3D time-lapse confocal microscopy data and identified regions with different division rates inside the microbial communities.

15 min. break

BP 10.5 Tue 11:15 H13

The advantage of network topology in avoidance reaction — •Siyu Chen[1], Jean-Daniel Julien[1], and Karen Alim[1,2] — [1]Max-Planck-Institut für Dyanmik und Selbstorgansiation, Göttingen — [2]Physics Department and CPA, Technische Universität München, München

The unicellular slime mould *Physarum polycephalum* stands out among other unicellular organisms for having a network-shaped body. Which advantage does a network structure provide when facing a challenging environment with adverse conditions? We, here, follow how network topology impacts *P. polycephalum*'s avoidance response to adverse blue light. We stimulate either an elongated amoeboid or a simple Y-shaped networked specimen and quantify the retraction velocity of the light-exposed body part. The result shows that Y-shaped specimen can complete the avoidance retraction without increasing the migration velocity, while an elongated amoeboid requires bursts of higher velocities - an energetically costly expense. Our theoretical predictions suggest that a light-triggered change in cytoplasm viscosity may account for the difference in response, as the more complex topology of a network allows *P. polycephalum* to maintain large flows that enable quick retraction out of the blue light. The difference in the retraction behaviour suggest the complexity of network topology provides a key advantage in dealing with adverse environments. Our findings could lead to the better understanding of the evolutionary transition from unicellular to multicellularity.

BP 10.6 Tue 11:30 H13

Model-Based Prediction of an Effective Adhesion Parameter Guiding Multi-Type Cell Segregation — •Philipp Rossbach, Hans-Joachim Böhme, Steffen Lange, and Anja Voss-Böhme — DataMedAssist, HTW - University of Applied Sciences, 01062 Dresden, Germany

The process of cell-sorting is essential for development and maintenance of tissues. With the Differential Adhesion Hypothesis, Steinberg proposed that cellsorting is determined by quantitative differences in cell-type-specific intercellular adhesion strengths. An implementation of the Differential Adhesion Hypothesis is the Differential Migration Model by Voss-Böhme and Deutsch. There, an effective adhesion parameter was derived analytically for systems with two cell types, which predicts the asymptotic sorting pattern. However, the existence and form of such a parameter for more than two cell types is unclear. Here, we generalize analytically the concept of an effective adhesion parameter to three and more cell types and demonstrate its existence nu-

merically for three cell types based on in silico time-series data that is produced by a cellular-automaton implementation of the Differential Migration Model. Additionally, we classify the segregation behavior using statistical learning methods and show that the estimated effective adhesion parameter for three cell types matches our analytical prediction. Finally, we demonstrate that the effective adhesion parameter can resolve a recent dispute about the impact of interfacial adhesion, cortical tension and heterotypic repulsion on cell segregation.

BP 10.7 Tue 11:45 H13

Is cell segregation like oil and water: asymptotic versus transitory regime — •Florian Franke[1,2], Sebastian Aland[2,3], Hans-Joachim Boehme[1,2], Anja Voss-Boehme[1,2], and Steffen Lange[1,2] — [1]DataMedAssist, HTW Dresden — [2]Faculty of Informatics/Mathematics, HTW Dresden - University of Applied Sciences — [3]Faculty of Mathematics and Computer Science, TU Freiberg

Segregation of different cell types is a crucial process for the pattern formation in tissues. Since the involved cell interactions are complex and difficult to measure individually in experiments, mathematical modelling plays an increasingly important role to unravel the mechanisms governing segregation. The analysis of these theoretical models focuses mainly on the asymptotic behavior at large times, in a steady regime and for large numbers of cells. Most famously, cell-segregation models based on the minimization of the total surface energy, a mechanism also driving the demixing of immiscible fluids, are known to exhibit asymptotically a particular algebraic scaling behavior. However, it is not clear, whether the asymptotic regime of the numerical models is relevant at the spatio-temporal scales of actual biological processes and in-vitro experiments. By developing a mapping between cell-based models and experimental settings, we are able to directly compare previous experimental data to numerical simulations of cell segregation quantitatively. We demonstrate that the experiments are reproduced by the transitory regime of the models rather than the asymptotic one. Our work puts a new perspective on previous model-driven conclusions on cell segregation mechanisms.

BP 10.8 Tue 12:00 H13

Self-Buckling of filamentous cyanobacteria reveals gliding forces — •Maximilian Kurjahn[1], Antaran Deka[1], Antoine Girot[1,2], Leila Abbaspour[3,4], Stefan Klumpp[3,4], Maike Lorenz[5], Oliver Bäumchen[1,2], and Stefan Karpitschka[1] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen — [2]Experimental Physics V, University of Bayreuth — [3]Max Planck School Matter to Life, University of Göttingen — [4]Institute for Dynamics of Complex Systems, University of Göttingen — [5]Department of Experimental Phycology and SAG Culture Collection of Algae, University of Göttingen

Filamentous cyanobacteria are one of the oldest and today still most abundant lifeforms on earth, with manifold implications in ecology and economics. These phototrophic organisms form long and flexible filaments that do not actively swim in bulk liquid but exhibit gliding motility in contact with solid surfaces. The underlying force generating mechanism of their gliding apparatus is not yet understood. We measure their bending modulus with micropipette force sensors, and investigate how filaments buckle after gliding onto an obstacle. Comparing Kirchhoff theory to the experiments, we derive the active forces and the friction coefficients associated with gliding from the observed critical filament length for buckling. Remarkably, we find that these two quantities are strongly coupled, while dependencies on other observables are largely absent. The critical length also aligns with the peak of their natural length distribution, indicating the importance of buckling for their collective.

BP 10.9 Tue 12:15 H13

Structural and mechanical properties of filamentous cyanobacteria — •Mixon Faluweki[1,2] and Lucas Goehring[1] — [1]Nottingham Trent University, Nottingham, UK. — [2]Malawi University of Science and Technology, Limbe, Malawi.

Filamentous cyanobacteria, long strands of connected cells, are one of Earth's earliest forms of life. They are found in multiple environments playing different roles and forming large-scale patterns in structures like biomats and stromatolites. The mechanical properties of these structures contribute to cyanobacteria's success in inhabiting their environments and are useful in applications such as algae-based biofuel production. One of the most important mechanical properties of these active polymers is the bending modulus or flexural rigidity. Here, we quantify the flexural rigidity of three cyanobacteria species, of order *Oscillatoriales*, via bending tests in a microfluidic flow device, where single cyanobacteria filaments are introduced into the microfluidic channel and deflected by fluid flow. Our measurements are confirmed separately by measuring the Young's modulus and cell wall thickness using atomic force microscopy and transmission electron microscopy, respectively. These measurements can be used to model interactions between cyanobacteria, or with their environment, and how their collective behaviour emerges from such interactions.

BP 11: Active Matter 2 (joint session DY/BP/CPP)

Time: Tuesday 10:00–13:00 Location: H18

BP 11.1 Tue 10:00 H18

Density fluctuations in bacterial binary mixtures — •Silvia Espada Burriel, Victor Sourjik, and Remy Colin — Max Planck Institute for Terrestrial Microbiology, Karl-von-Frisch-strasse 10, 35043 Marburg & Center for Synthetic Microbiology (SYNMIKRO), Karl-von-Frisch-strasse 14, 35043 Marburg

In wild environments, bacteria are found as mixtures of motile and sessile species, which interact physically and chemically to give rise to complex community organization. Very little is understood of the role of physical interactions in these processes: Numerical works on dry active matter and experiments on colloidal systems have shown that the activity of the active particles may affect the spatial distribution of passive particles with which they are mixed. However, the physical behavior of binary mixtures of bacteria remains largely unexplored. In our study, we present a novel phenomenon in which non-motile bacteria form large density fluctuations when mixed with motile bacteria, distinct from the aforementioned behaviors. We systematically explored the phase diagram of the mixtures in experiments combining microfluidics, fluorescence (confocal) microscopy, quantitative image analysis and parameter tuning by genetic engineering. Our experimental results show that the emergence of these large density fluctuations of the non-motile cells in presence of motile cells is controlled by hydrodynamic interactions between the motile and non-motile cells and by the sedimentation of the non-motile cells, possibly because it breaks the systems symmetry.

BP 11.2 Tue 10:15 H18

Pulsating Active Matter — •Yiwei Zhang and Etienne Fodor — 0 Av. de la Faiencerie, 1511 Luxembourg

Active matter features the injection of energy at individual level keeping the system out of equilibrium, which leads to novel phenomenologies without any equilibrium equivalents. So far, most active matter models assign a velocity to each particle, whilst we herein consider a system of pulsating soft particles where the activity sustains particles' periodic deformation instead of spatial displacement. At sufficiently high density, we reveal the existence of wave propagation independent of any particle migration, and derive the corresponding phase diagram. We study the character of phase transitions, and investigate the underlying physical mechanisms, using both particle-based simulations and hydrodynamic analysis.

BP 11.3 Tue 10:30 H18

Long-Range Nematic Order in Two-Dimensional Active Matter — •Benoît Mahault[1] and Hugues Chaté[2,3] — [1]MPIDS, 37077 Göttingen, Germany — [2]SPEC, CEA-Saclay, 91191 Gif-sur-Yvette, France — [3]CSRC, Beijing 100193, China

Studies of active matter continue to flourish, exploring more and more complex situations in an increasingly quantitative manner. Evidence has accumulated that shows active matter exhibits properties that are impossible in thermal equilibrium or even in driven systems. In spite of all this progress, important fundamental questions remain open. Such a long-standing issue is whether true long-range nematic order can emerge in two space dimensions. In this talk, we will present theoretical and numerical results obtained from minimal models of

self-propelled polar particles aligning nematically. Our study shows that the orientational order emerging from such systems is quasi-long-ranged beyond the scale associated to induced velocity reversals, which is typically extremely large and often cannot even be measured. On scales where particle motion is ballistic, nematic order appears truly long-range. A hydrodynamic theory for this de facto phase is derived, and we show that its structure and symmetries differ from conventional descriptions of both polar flocks and active nematics. Our analysis of this field theory predicts π-symmetric propagative sound modes and the scaling form of space-time fluctuations. Finally, numerical results confirm the theory and allow us to estimate all scaling exponents.

BP 11.4 Tue 10:45 H18

Collective behavior of repulsive chiral active particles with non-reciprocal couplings — •Kim L. Kreienkamp and Sabine H. L. Klapp — Technische Universität Berlin, Germany

Mixtures of chiral active particles [1] as well as non-reciprocal systems [2] show intriguing collective behavior like pattern formation and traveling waves. The combination of both – non-reciprocal couplings in mixtures of chiral active particles – promises a rich variety of collective dynamics.

Here, we investigate how non-reciprocal couplings and naturally occurring repulsive interactions due to finite particle sizes affect the collective behavior in a mixture of two species of particles. We analyze the effects due to non-reciprocity and finite size individually as well as their interplay based on a field description of the system in terms of the particle concentration and director field, measuring the overall orientation of particles at a certain position.

We derive the field equations under the mean-field assumption by coarse-graining microscopic Langevin equations for individual chiral particles, which are modeled as self-propelling circle swimmers with soft repulsive forces, comprising the finite size effects. Particles of the two species rotate with different intrinsic frequencies and align with near-by particles. Focusing on non-reciprocity, we use a non-mutual alignment between the particles.

[1] D. Levis and B. Liebchen, Phys. Rev. E 100, 012406 (2019)

[2] M. Fruchart, R. Hanai, P. B. Littlewood, and V. Vitelli, Nature 592, 363-369 (2021)

BP 11.5 Tue 11:00 H18

Memory-induced chirality in self-freezing active droplets — •Aritra K. Mukhopadhyay[1], Kai Feng[2], José Carlos Ureña Marcos[1], Ran Niu[2], Qiang Zhao[2], and Benno Liebchen[1] — [1]Technische Universität Darmstadt, 64289 Darmstadt, Germany. — [2]Huazhong University of Science and Technology, 430074 Wuhan, China.

We experimentally realize and numerically model a new type of self-propelled droplet swimmer which exhibits chiral motion due to self-induced memory effects without requiring any explicit symmetry breaking caused by specific droplet geometries or complex environments. The droplets are composed of a binary polymer mixture that solidifies over time, simultaneously emitting certain polymers into their environment. A spontaneous asymmetry of the emitted polymer concentration along the stationary droplet surface induces Marangoni flows which cause the droplet to initially self-propel ballistically. However, the emitted polymers diffuse slowly and form long-lived trails with which the droplet can self-interact in the course of time and this leads to a dynamical transition from ballistic to chiral motion. The droplets persistently exhibit chiral motion with the same handedness until at even later times a second transition occurs when the droplets confine themselves leading to self-trapping over the timescale of our experiments and simulations. Our results exemplify a new route to realizing synthetic active particles whose dynamics can be controlled via the pronounced self-induced memory effects.

15 min. break

BP 11.6 Tue 11:30 H18

Role of advective inertia in active nematic turbulence — •Colin-Marius Koch and Michael Wilczek — Theoretical Physics I, University of Bayreuth, Bayreuth

Suspensions of active agents with nematic interactions can exhibit complex dynamics such as mesoscale turbulence. Continuum descriptions for such systems are inspired by the hydrodynamic theory of liquid crystals and feature an advective nonlinearity which represents inertial effects. The typically low Reynolds number of such active flows raises the question whether and under which conditions the active stresses present in these systems can excite inertial flows. To address this question, we investigate mesoscale turbulence in a two-dimensional model for active nematic liquid crystals. In particular, we compare numerical simulations with and without nonlinear advection and frictional damping of the flow field. Studying the nondimensionalized equations of motion, we find that inertia can trigger large-scale motion even for small microscopic Reynolds numbers if the active forcing is sufficiently large and the Ericksen number is sufficiently low. Performing a spectral analysis of the energy budget, we identify an inverse energy transfer caused by inertial advection, whose impact is small in comparison to active forcing and viscous dissipation but accumulates over time. We additionally show that surface friction, mimicked by a linear friction term, dissipates the transported energy and suppresses the large-scale motion. We conclude that, without an a priori knowledge of model parameters matching experiments, including inertia and friction may be necessary for consistent modeling of active nematic turbulence.

BP 11.7 Tue 11:45 H18

Pumping in active microchannels — •Goncalo Antunes[1,2,3], Paolo Malgaretti[1,2,3], Siegfried Dietrich[2,3], and Jens Harting[1,4] — [1]Helmholtz-Institut Erlangen-Nürnberg für Erneuerbare Energien (IEK–11), Forschungszentrum Jülich, Erlangen, Germany — [2]Max–Planck–Institut für Intelligente Systeme, Stuttgart, Germany — [3]Universität Stuttgart, Stuttgart, Germany — [4]Friedrich-Alexander-Universität Erlangen-Nürnberg, Nürnberg, Germany

Much attention is currently being given to the problem of manipulating fluids at the microscale, with successful applications to fields such as 3D fabrication and biomedical research. Often micropumps are a fundamental component of these microfluidic systems. An intriguing technique to manipulate fluid flows in a channel is diffusioosmosis. Fluid flow is obtained upon imposing an inhomogeneous concentration of some solute, which generates flow in a boundary layer around the channel walls. This inhomogeneity is the result of a spatially inhomogenous production rate of solute inside the channel.

We show that a solute-producing, corrugated, active channel can act as a micropump even when it is fore-aft symmetric. This result is obtained by coupling the Stokes equation with an advection-diffusion equation for the solute concentration, which we solve analytically in the limit of thin, weakly-corrugated channels. Lattice Boltzmann simulations further support the existence of the symmetry-breaking. Our calculations are also valid for left-right asymmetric channels, and provide a tool to optimize the pumping rate of an active microchannel by tuning its shape or its solute production rate.

BP 11.8 Tue 12:00 H18

Active Refrigerators Powered by Inertia — •Lukas Hecht[1], Suvendu Mandal[1], Hartmut Löwen[2], and Benno Liebchen[1] — [1]Institut für Physik kondensierter Materie, Technische Universität Darmstadt, Hochschulstr. 8, D-64289 Darmstadt, Germany — [2]Institut für Theoretische Physik II - Soft Matter, Heinrich-Heine-Universität Düsseldorf, Universitätsstraße 1, D-40225 Düsseldorf, Germany

We present the operational principle for a refrigerator which uses inertial effects in active Brownian particles (ABPs) to locally reduce the (kinetic) temperature by two orders of magnitude below the environmental temperature. This principle requires two ingredients: First, we need the feature of inertial ABPs to undergo motility-induced phase separation into coexisting phases with different (kinetic) temperatures and second, a mechanism which localizes the dense phase in the targeted cooling domain is required.

Here, we exploit the peculiar but so-far unknown shape of the phase diagram of inertial ABPs to initiate motility-induced phase separation in the targeted cooling domain only. Remarkably, active refrigerators operate without requiring isolating walls separating the cooling domain from its environment. This feature opens the route towards using active refrigerators to systematically absorb and trap substances such as toxins or viruses from the environment.

BP 11.9 Tue 12:15 H18

The influence of motility on bacterial accumulation in a microporous channel — •Christoph Lohrmann[1], Miru Lee[2], and Christian Holm[1] — [1]Institute for Computational Physics, University of Stuttgart, Allmandring 3, 70569 Stuttgart, Germany — [2]Institute for Theoretical Physics, Georg-August-Universität Göttingen, 37073 Göttingen, Germany

Swimming microorganisms are often encountered in confined geome-

tries where also an external flow is present, e.g. in filters or inside the human body. To investigate the interplay between microswimmer motility and external flows, we developed a model for swimming bacteria based on point coupling to an underlying lattice Boltzmann fluid. Random reorientation events reproduce the statistics of the run-and-tumble motion of the bacterium E. coli. We present the application of the model to the study of bacterial dynamics in a channel with a single cylindrical obstacle. In accordance with experimental measurements, simulations show asymmetric accumulation behind the obstacle only when the bacteria are active and an external flow is present.

Lee, Miru *et al.*, *Soft Matter* **17**, 893-902 (2021)

BP 11.10 Tue 12:30 H18

Inertial dynamics of an active Brownian particle* — •Jonas Mayer Martins and Raphael Wittkowski — Institut für Theoretische Physik, Center for Soft Nanoscience, Westfälische Wilhelms-Universität Münster, 48149 Münster, Germany

Active Brownian motion commonly assumes spherical overdamped particles. However, self-propelled particles are often neither symmetric nor overdamped yet underlie random fluctuations from their surroundings. Active Brownian motion has already been generalized to include asymmetric particles. Separately, recent findings have shown the importance of inertial effects for particles of macroscopic size or in low-friction environments. We aim to consolidate the previous findings into the general description of a self-propelled asymmetric particle with inertia. We derive the Langevin equation of such a particle as well as the corresponding Fokker-Planck equation. Furthermore, a formula is presented that allows to reconstruct the hydrodynamic resistance matrix of the particle by measuring its trajectory. Numerical solutions of the Langevin equation show that, independent of the particle's shape, the noise-free trajectory at zero temperature starts with an inertial transition phase and converges to a circular helix. We discuss this universal convergence with respect to the helical motion that many microorganisms exhibit.

Funded by the Deutsche Forschungsgemeinschaft (DFG) – Project-ID 433682494 - SFB 1459

BP 11.11 Tue 12:45 H18

Stochastic motion under active driving due to inverted dry (solid) friction — •Andreas M. Menzel — Otto-von-Guericke-Universität Magdeburg, Magdeburg, Germany

It has become common to describe the motion of actively driven or self-propelled objects using a driving force of constant magnitude. We assume that this driving force always acts along the current velocity direction. Moreover, we consider objects featuring a nonpolar axis, along which driving and propagation occur [1].

In that case, spontaneous symmetry breaking decides on the heading of propagation, that is, "forward" or "backward" along the nonpolar axis. Stochastic effects may reverse the velocity and thus the direction of the driving force.

As it turns out, active driving under these circumstances corresponds to inverted dry (solid) friction of the Coulomb type. Corresponding tools of theoretical analysis can thus be adopted, mapping the velocity spectrum to the one of a quantum-mechanical harmonic oscillator subject to a repulsive delta potential. In this way, the diffusion coefficient can be calculated analytically. We evaluate velocity and displacement statistics. Outward propagating displacement maxima emerge under increased active driving. The trajectories feature pronounced cusps when velocity reversals occur.

Our results should apply, for instance, to certain types of vibrated nonpolar rods and swimming bacteria that may reverse their propagation direction.

[1] A. M. Menzel, submitted.

BP 12: Poster 2

Time: Tuesday 17:30–19:30 Location: P4

BP 12.1 Tue 17:30 P4

Holographic vibration spectroscopy: Probe- and contact-free viscoelastic analysis of adherent cells — •Bob Fregin[1,2], Stefanie Spiegler[1,2], and Oliver Otto[1,2] — [1]ZIK HIKE, University of Greifswald, Greifswald, Germany — [2]DZHK, University Medicine Greifswald, Greifswald, Germany

Cell mechanical properties can be used as an inherent biomarker for cell state, fate and function. Several high-throughput methods are available to characterize suspension cells, e.g., peripheral blood cells, without any labeling. However, fast and robust methods are lacking for adherent cells, although the majority of cells, e.g., in our human body, is aggregated into tissues.

Here, we introduce a new probe- and contact-free method for label-free mechanical phenotyping of adherent cells at high spatiotemporal resolution. While cells are excited mechanically by a vibration in the range of 100 kHz, their response is determined optically from cell height oscillations utilizing holographic laser Doppler interferometry. In proof-of-concept experiments on a monolayer of induced pluripotent stem cells (iPSCs), we present a cell amplitude response as a function of varying excitation amplitudes. This amplitude response is proportional to the elastic properties of a cell.

In future work, we plan to perform a spectroscopic evaluation, where experiments are carried out at multiple frequencies. Further, we aim to extend our analysis to a complete viscoelastic description.

BP 12.2 Tue 17:30 P4

Heterogenous cell structures in AFM and shear flow simulations — •Sebastian Wohlrab, Sebastian Müller, and Stephan Gekle — Theoretical Physics VI, University of Bayreuth

In biophysical cell mechanics simulations, the complex inner structure of cells is often simplified as homogeneous material. However, this approach neglects individual properties of the cell's components, e.g., the significantly stiffer nucleus.

By introducing a stiff inhomogeneity inside our hyperelastic cell, we investigate it during AFM compression and inside shear flow in finite-element and Lattice Boltzmann calculations.

We show that a heterogenous cell exhibits almost identical deformation behavior under load and in flow as compared to a homogeneous cell with equal averaged stiffness, supporting the validity of the homogeneity assumed in both mechanical characterization as well as numerical computations.

BP 12.3 Tue 17:30 P4

Cell migration dynamics and nuclear deformation in three-dimensional micro-dumbbells — •Stefan Stöberl[1], Johannes Flommersfeld[2], Maximilian M. Kreft[1], Chase P. Broedersz[2], and Joachim O. Rädler[1] — [1]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-University, Munich, Germany — [2]Department of Physics and Astronomy, Vrije Universiteit Amsterdam, 1081 HV Amsterdam, The Netherlands

Cell migration plays a key role in physiological processes such as wound healing, cancer metastasis and immune response. In previous work we have studied the non-linear dynamics of single cells migrating between two surface-patterned adhesion sites guided by a bridging line.

Here we study the dynamics of MDA-MB-231 cells captured in three-dimensional (3D)-dumbbell-like microcavities. The structures formed by photolithography of PEG-norbonene hydrogels provide a soft and hence deformable frame, while cells attach and migrate on a fibronectin coated bottom. In our experiments we find that the dwell-time of cells before transitioning is retarded when the width of the dumbbell-constriction is narrowed below 8 m. We are hypothesizing that the observed deformation of the nucleus, which is the biggest organelle in the cell, determines the time course of the repeated stochastic transitions. To study the external and internal forces involved we measure the displacement field of beads embedded in the vicinity of the 3D constriction.

BP 12.4 Tue 17:30 P4

The Weakness of Senescent Dermal Fibroblasts — •Lydia Rebehn[1], Samira Khalaji[1], Fenneke KleinJan[1], Anja Kleemann[1], Patrick Paul[1], Constantin Huster[3], Ulla Nolte[1], Karmveer Singh[2], Taner Pula[4], Pamela Fischer-Posovszky[4], Karin Scharffetter-Kochanek[2], and Kay-E Gottschalk[1] — [1]Institute for Experimental Physics, Ulm University, Ulm, Germany — [2]Department of Dermatology and Allergology, Ulm University,

Ulm, Germany — [3]Institut für Theoretische Physik, Universität Leipzig, Leipzig, Germany — [4]Department of Pediatrics and Adolescent Medicine, Ulm University, Ulm, Germany

As human tissues age, there is chronological accumulation of biophysical changes from internal and environmental factors. Skin aging leads to loss of dermal matrix integrity via degradation and decreased elasticity. The mechanical properties of the dermal matrix are maintained by fibroblasts, whose properties change during replicative aging. Here, we compare biophysical properties of young versus proliferatively aged primary fibroblasts via fluorescence and traction force microscopy, single-cell AFM, and microrheology of the cytoskeleton. Results show senescent fibroblasts have decreased cytoskeletal tension and myosin II regulatory light chain phosphorylation, in addition to significant loss of traction force. The alteration of cellular forces is harmful to the process of building and maintaining extracellular matrix, while decreased cytoskeletal tension can amplify epigenetic changes involved in senescence. Exploration of these mechanical phenomena provide possibilities for unexplored pharmaceutical targets against aging.

BP 12.5 Tue 17:30 P4

Unravelling the collective behaviour of protrusions for directed migration — •Lucas Tröger[1] and Karen Alim[1,2] — [1]Physics Department and CPA, Technische Universität München — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen

Living systems are often challenged to coordinate collective behaviour of individual entities across large spatial scales. The morphology of amoeboid cells, for example, arises due to the coordination of randomly forming protrusions that facilitates the cell's directed migration. The slime mold Physarum polycephalum grows as a single giant cell of network-like shape, spanning orders of magnitude in size ranging from 500 micrometers to tens of centimeters. Due to the large extent, chemotaxis and morphogenesis of the entire cell require a mechanism for coordination among competing protrusions. P. polycephalum is renowned for its organism-wide cytoplasmic fluid flows spanning the fluid-filled tubular network in a peristaltic wave. These strong and large-scale flows make this organism an ideal model to investigate the role of fluid flows in coordinating the collective behaviour of competing protrusions during the morphological changes in chemotaxis. We perform experiments of chemotacting P. polycephalum specimen of varying sizes and quantify the dynamics of individual protrusions in addition to the chemotactic performance of the entire specimen. We correlate growing and retracting protrusions over time to identify the mechanism of communication. The project will teach us how fluid flows control the collective behaviour of protrusions during directed migration.

BP 12.6 Tue 17:30 P4

Neutrophil mechanotransduction during durotaxis — •Fatemeh Abbasi[1], Matthias Brandt[2], and Timo Betz[1] — [1]Third Institute of Physics-Biophysics, Georg August University Göttingen — [2]Institute of Cell Biology, ZMBE, University of Münster

In Vivo, cells experience complex tissue environments with various chemical and physical features. 3D confinement is one of the major physical obstacles for cells in their natural environment. Neutrophils are among the most abundant immune cells in our body, which have to cope with various physical constrictions on their way from production to the infection site. In addition to confinement, the stiffness of the microenvironment is another mechanical feature these rapidly moving cells are exposed to. Neutrophils experience various tissue stiffness, from 1 kPa (bone marrow) to 20 MPa (bone). Previous studies have demonstrated that these cells are responsive to their microenvironment stiffness by adjusting their adhesion and spreading. Based on this knowledge we decided to combine confinement and stiffness change and investigate the impact of 3D stiffness gradient on cell behaviour and migration, a fact called durotaxis. We hypothesized that stiffness gradient might be a triggering factor of neutrophil migration toward the infection site. We confine neutrophils in between 2 layers of polyacrylamide hydrogels with 2 different stiffness and keep this distance stable for the desired period of time to investigate cell mechanotransduction during durotaxis from different points of view. Our preliminary results regarding the neutrophil durotaxis show a surprising and transient force peak on the soft substrate during cell shifting.

BP 12.7 Tue 17:30 P4

Cytoskeletal Networks in Cells Under Strain — •Ruth Meyer, Anna V. Schepers, Peter Luley, and Sarah Köster — Institute for X-Ray Physics, University of Göttingen

The cytoskeleton of eukaryotic cells mainly consists of three types of filamentous proteins: F-actin, microtubules and intermediate filaments (IFs). In contrast to microtubules and actin filaments, IFs are expressed in a cell-type specific manner, and keratins are found in epithelial cells. In certain cell types, the IF keratin forms a layer close to the membrane, referred to as an "IF-cortex". It has been observed that this IF-cortex arranges in a "rim-and-spokes" structure in epithelia. Based on this hypothesis, IFs and actin filaments might add complementary mechanical properties to the cellular cortex. When stretching single IFs, it was previously shown that IFs remain undamaged even at high forces. We now ask the question of whether this unique force-extension behavior of single IFs is also relevant in the filament network within a cell. The experiment is conducted by seeding cells on an elastic substrate and then stretching the substrate uniaxially or equibiaxially to high strains. In combination with fluorescence and atomic force microscopy, this setup allows us to study the structure and the mechanical properties of actin and IF networks close to the cell membrane.

BP 12.8 Tue 17:30 P4

Cell mechanics and cytoskeletal structures under unifor, equibiaxial strain — •Anna V. Schepers, Ruth Meyer, Peter Luley, and Sarah Köster — Universität Göttingen

The cytoskeleton, which largely determines the mechanical properties of cells, has to withstand various mechanical stresses throughout the lifetime of a cell. In mechanically stressed cells, structural and mechanical changes often go hand-in-hand. Understanding how cytoskeletal remodelling accompanies the mechanical changes will give insight into the mechanism by which cells adjust to mechanical load and how this reaction might be altered in diseases. Remodelling of the cytoskeleton has been observed under uniaxial and equibiaxial stretching. However, combined structural and force measurements under well-defined mechanical conditions are sparse. We therefore present a uniform, equibiaxial cell stretching device that is compatible with fluorescence microscopy as well as single cell force spectroscopy. The device allows for the study of living single cells or cell monolayers throughout equibiaxial stretching. Changes in the mechanical properties of cells can thus be linked to the remodelling of the cytoskeleton.

BP 12.9 Tue 17:30 P4

Force generation in human blood platelets mediated by actin structures — •Anna Zelena[1], Johannes Blumberg[2], Ulrich S. Schwarz[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]Institute for Theoretical Physics, University Heidelberg, Germany

Blood platelets are known for their importance in blood clotting: Their correct function significantly affects the early steps of wound closing and thus restoration of blood circulation. The hemostatic function of platelets is directly connected to their mechanics and cytoskeletal morphology, however, the exact mechanism and connection between them remain elusive. As was previously investigated, the reorganization of the platelet cytoskeleton upon spreading is a very fast process, which occurs within minutes, and it leads to pronounced stress fiber morphologies. In this study, we investigate single platelets by combining traction force measurements with fluorescence imaging of the actin structures in a time-resolved manner. Thus, we can spatially and temporally correlate the force generation with the emerging acting structures. Interestingly, the spots of highest force remain very stable in time and spatially align very closely with the visualized end points of fibrous actin structures. Additionally, our data show that the force generation is a very robust mechanism independent of changes in the amount of added thrombin in solution or fibrinogen coverage on the substrate, which may be physiologically important so as to ensure reliable blood clotting independent of environmental parameters.

BP 12.10 Tue 17:30 P4

Mechanical fingerprint of the intra-cellular space — •Till M Muenker and Timo Betz — University of Goettingen, Goettingen, Germany

Many important cellular functions such as organelle positioning and internal cargo transport are dependent on the viscoelastic intracellular mechanical properties of cells. A range of different mechanical models has been proposed to describe these properties. Whilst simple models such as Maxwell or Kelvin-Voigt models don't seem sufficient to capture the full complexity of cells, more elaborate models like generalized Kelvin-Voigt models require a huge number of parameters. This hinders the comparison and interpretation of experimental

findings. Further, from a physics perspective, cells are systems out of thermodynamic equilibrium, permanently consuming metabolic energy to carry out mechanical work. The level of "non-equilibrium" can be proposed as an indicator for cell type, cell state or even diseases. To determine both, the viscoelastic properties and the cellular activity, we use optical tweezers based active and passive microrheology in a diverse group of 9 different cell-types. Surprisingly, despite differences in origin and function, the complex moduli of all cell types can be described using a 4 parameter based fractional Kelvin-Voigt model. Additionally, the frequency dependent activity can be described with a simple power law. This approach allows to reduce those complex and frequency dependent properties down to a fingerprint of 6 parameter. Further principal component analysis shows that only 2 of them may be sufficient to characterize the mechanical intracellular state.

BP 12.11 Tue 17:30 P4

Measuring the stiffness of neuronal growth cones with scanning ion conductance microscopy — •Aylin Balmes[1], Hannes Schmidt[2], and Tilman E. Schäffer[1] — [1]Institute of Applied Physics, University Tübingen, Germany — [2]Interfaculty Institute of Biochemistry (IFIB), University Tübingen, Germany

It was recently demonstrated that nanoscale dynamic structural changes in live neurons can be visualized using scanning ion conductance microscopy (SICM). In SICM imaging the sample is scanned with an electrolyte-filled nanopipette to which a voltage and a pressure are applied and the ion current through the nanopipette is measured. The sample topography and stiffness (Young's modulus) can thereby be derived with high spatial and temporal resolution. There is no direct mechanical contact between the probe and the sample during SICM imaging, making it a very suitable technique to study fragile samples such as neurons. In this study we use SICM to investigate the stiffness of growth cones of dorsal root ganglion (DRG) neurons, which have previously been used to study axonal branching, an important process in neuronal development. Studies showed that a signaling cascade involving the second messenger cyclic guanosine monophosphate (cGMP) which is generated upon binding of C-type natriuretic peptide (CNP) to the receptor guanylyl cyclase B regulates the bifurcation of DRG axons. Our measurements show that the presence of cGMP and CNP reduces growth cone stiffness. This alteration in stiffness could be linked to changes in the actin cytoskeleton and might play a role in the regulation of axon bifurcation.

BP 12.12 Tue 17:30 P4

Optimization of patterned polyacrylamide gels for traction force microscopy — •Ina Braun, Mohammad Armin Eskandari, Fatemeh Abassi, and Timo Betz — Third Institute, Biophysics, Georg August Universität, Göttingen, Germany

Combining micropatterned adhesion with soft polyacrylamide gels is widely described in literature, however the practical experience shows a series of possible artifacts. The problems are typically a variation of fluorescent bead localization in response to the ECM proteins applied. In detail we find changes in the bead distribution that we aim to understand and avoid. Micropatterns of various ECM proteins are initially created on glass coverslips using a photomask. Subsequently, they are transferred on the polyacrylamide gels containing fluorescent beads during the polymerization process. In an additional step we compare the classical protocol of pattern tranfer during polymerization with a more specific approach by including NHS-acrylamide in the hydrogel premix. After pattern transfer we quantify the bead localization, homogeneity and potential clustering at the pattern sites with the non-patterned regions. We optimize the bead distribution by systematic variation of pH value and ion composition of the premix. The potential of cell adhesion and traction force microscopy is assed in the final step.

BP 12.13 Tue 17:30 P4

Dystrophin as a tension regulator in human skeletal muscles — •Mariam Ristau[1], Arne Hofemeier[1,2], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics, Georg-August-University Göttingen, Germany — [2]ZMBE - Institute of Cell Biology, University of Münster, Germany

Skeletal muscles are associated with contraction, movement and force generation. They are important for maintaining posture and maintaining bone and joint stability. Muscular dystrophies such as Duchenne muscular dystrophy (DMD) result in progressive weakening of skeletal muscles. DMD is caused by the loss of the protein dystrophin which is thought to stabilize and protect muscle fibers from injury. In the progression of the disease, damaged muscle fibers degrade, muscle mass is lost and greater functional impairments develop. We have studied the contractile potential of myoblasts and reconstituted tissue derived from healthy and DMD patients, and found that they were mechanically different in muscle tension and contractility. DMD derived myoblast exhibited an overall weaker contractility compared to healthy derived myoblast. In contrast, DMD derived myoblast showed an overall higher muscle tension, suggesting that dystrophin may function as a tension regulator in skeletal muscles. In order to rule out the possibility that these findings are due to patient variability we intend to establish a genetic model in which we knockout dystrophin with the CRISPR/Cas9 system in healthy myoblasts and rescue dystrophin in DMD myoblasts by integrating micro-dystrophins (μDys).

BP 12.14 Tue 17:30 P4

Modelling internal cell structure for bioprinting processes — •Richard Kellnberger, Fabian Häusl, Moritz Lehmann, and Stephan Gekle — Universität Bayreuth, Bayreuth, Deutschland

The deformation cells experience during bioprinting processes depends on the structure of the cell and the stresses exerted by the surrounding fluid. We extended a Lattice-Boltzmann solver with a cell model using the immersed boundary method to model the cell membrane as well as discretizing the cell as elastic tetrahedrons in order to model the cytoskeleton. Furthermore, we extended the fluid model to take viscoelastic effects into account. With these extended models we improve our qualitative investigations of the deformation of cells during the printing process.

BP 12.15 Tue 17:30 P4

Neutrophil cell behavior as a response to mechanical confinement and substrate stiffness — •Katharina Rieck[1,2,3], Fatemeh Abbasi[2,3], Matthias Brandt[2], and Timo Betz[2,3] — [1]Department of Physics, University of Münster, Germany — [2]Institute of Cell Biology, ZMBE, University of Münster, Germany — [3]Third Institute of Physics, Biophysics, University of Göttingen, Germany

Neutrophils are among the first immune cells attacking invading microorganisms in our body. To reach the site of infection they must undergo extreme cellular deformations while experiencing high shear stress during their migration through highly confined microenvironments. In order to investigate the mechanisms driving their confined migration and cell shape adjustment, we probe cell behavior and traction force generation in different levels of confinement with variable stiffnesses of the confining boundaries. We seed Neutrophils between two polyacrylamide (PAA) gels of the same stiffness and vary substrate Young*s modulus (3kPa, 15kPa, 30kPa) as well as the distance between the gels. This allows to examine the impact of microenvironment stiffness and confinement level on cell migration and forces. Using the substrate elastic modulus and cell induced gel deformation we are able to measure their traction stress. Our preliminary results demonstrate that cells exert higher traction forces on stiffer substrates. In confinement cells show higher traction forces than on 2D substrates. Furthermore, cells are more motile in confinement and show more motility on gels of higher stiffnesses. However, no significant difference of traction forces in different levels of confinement was observed.

BP 12.16 Tue 17:30 P4

Development of a platform for accessing the membrane tension of cells in microchannels — •Eric Sündermann, Bob Fregin, Doreen Biedenweg, Stefanie Spiegler, and Oliver Otto — ZIK HIKE, University of Greifswald, Greifswald, Germany

Real-time deformability cytometry (RT-DC) is a biomechanical method which is able to characterise the physical properties of cells. To do so, the cells travel through a microfluidic chip assembled on an inverted microscope. Every cell is imaged by a high-speed camera, and its shape is fitted to calculate the deformation. While the acting stress and cell tension can be derived from hydrodynamic simulations we can not disentangle different tension contributors.

Here, we introduce a new method of directly accessing the membrane tension of a cell, passing a microfluidic constriction. Measurements are carried out in a microfluidic channel, and the cells are illuminated with a pulsed laser. The cells were stained with the Flipper-TR probe, which has a fluorescent lifetime depending on the membrane tension. The signal is acquired with a fluorescence lifetime imaging (FLIM) point detector.

In preliminary experiments, we measure the membrane tension and simultaneously image the cells to perform RT-DC leading to the cell mechanical properties. Having access to the ensemble mechanical prop-

erties of a cell as well as its membrane tension, the method allows for studying the interaction between the latter and the derived cortex tension. In future studies, we also want to investigate the tension distribution on the cell membrane.

BP 12.17 Tue 17:30 P4

Nuclear mechanics probed by optical tweezers-based active microrheology — •Bart Vos[1], Ivan Avilov[2], Till Müncker[1], Peter Lenart[2], and Timo Betz[1] — [1]Third Institute of Physics, University of Göttingen, Göttingen, Germany — [2]Max Planck Institute for Biophysical Chemistry, Göttingen, Germany

Mechanics play a crucial role in a wide range of cellular processes, from differentiation to division and metastatic invasion. Consequently, the mechanical properties of the cytoskeleton, providing shape, motility and mechanical stability to the cell, have been extensively studied. However, remarkably little is known about the mechanical environment within the nucleus of a cell, and fundamental questions remain unanswered, such as the role of nuclear actin or the sudden "freezing" of the cell during cellular division that prevents diffusion or active mixing of the nucleus and the cytoplasm.

To address these questions, we perform optical tweezers-based microrheology in the nucleus. Microrheology has proven to be a suitable tool for intracellular mechanical measurements, as it enables local, non-invasive measurements. However, although the cytoskeleton has been extensively studied this way, the cell nucleus has not been investigated, mainly due to difficulties with inserting appropriate probe particles. By using starfish oocytes that have larger dimensions than most other cell types, we are able to perform microinjection of micrometer-sized particles. We observe, similar to the cytoskeleton, viscoelastic behavior of the nucleoplasm. In addition, we mechanically follow the oocyte during its development after fertilization.

BP 12.18 Tue 17:30 P4

Predicting the distribution of mechanical stresses in the *S. aureus* cell wall during the cell cycle — •Sheila Hoshyaripour[1], Marco Mauri[1], Jamie K. Hobbs[2], Simon J. Foster[2], and Rosalind J. Allen[1] — [1]Friedrich-Schiller-Universität Jena, Jena, Germany — [2]University of Sheffield, Sheffield, United Kingdom

Staphylococcus aureus is a Gram-positive bacterium which is clinically important due to its ability to act as an opportunistic pathogen and to generate antibiotic-resistant strains. During the cell cycle, the cell synthesizes a flat septum that divides the spherical cell into two hemispheres. Division then happens in few milliseconds, suggesting an important role for mechanics in the separation process. In this work, we used concepts from mechanical engineering to create an elastic model of the cell wall, in order to predict the spatial distribution of stress in the cell wall, and the induced deformations, during the cell cycle. Our modelling shows that the presence of the growing septum decreases the cell wall stress in its vicinity and leads to an invagination. The amount of this invagination and reduction in stress depends on the mechanical and geometrical properties of the cell wall and the septum. For a smaller cell with thicker wall, the stress is less during the whole cell cycle, and a stiffer septum leads to more invagination. Comparing these predictions with experimental data for various mutants in the presence and absence of cell-wall targeting antibiotics should provide a useful tool for understanding the role of mechanical stress in the *S. aureus* cell cycle.

BP 12.19 Tue 17:30 P4

Optical Stretcher for Adherent Cells — •Alexander Janik, Tobias Neckernuss, and Othmar Marti — Institute of Experimental Physics, Ulm University

We have demonstrated a method to stretch adherent cells with a parallel laser beam, that is capable of distinguishing between stiff and softened cells. Recently, a new method for the detection of the membrane displacement was developed. It relies on off-axis interferometry, which allows for high precision as well as arbitrary positioning of the probed spot and makes the method completely contact-free.

BP 12.20 Tue 17:30 P4

Cell volume changes in confined environments on short timescales — •Felix Graf, Bob Fregin, Doreen Biedenweg, Yesaswini Komaragiri, Stefanie Spiegler, and Oliver Otto — ZIK HIKE, University of Greifswald, Greifswald, Germany

Dynamic real-time deformability cytometry (dRT-DC) is a high-throughput method for extracting the viscoelastic material properties of cells. Cells are dynamically tracked while they translocate through a microfluidic channel and deform in response to the hydrodynamic stress. We extend the time-dependent analysis of dRT-DC towards cellular volume and perform experiments on vesicles and different cell lines in a channel of $30 \times 30 \mu m^2$ cross-section with buffers as well as cell velocities resembling physiological conditions. Our measurements reveal a volume change of $\approx 5 - 10\%$ on a millisecond timescale over the entire length of the microchannel, which is $300 \mu m$. We propose an explanation of our observation by water transport through transmembrane channel proteins. In preliminary experiments, we examined the relationship between the presence and amount of channel proteins, as well as the applied stress and the volume change observed in vesicles and cells. We expect our results to provide insights into the processes involved in physiological volume changes of cells in flow.

BP 12.21 Tue 17:30 P4

New directions in traction force microscopy — •Johannes W. Blumberg[1,2], Timothy J. Herbst[3], Ullrich Koethe[4], and Ulrich Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, Germany — [2]BioQuant, Heidelberg University, Germany — [3]German Cancer Research Center (DKFZ), Heidelberg, Germany — [4]Visual Learning Lab, IWR, Heidelberg University, Germany

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 marker beads. While it is straightforward to calculate the deformation field resulting from a given traction pattern (direct problem), it is challenging to estimate the traction pattern from the deformation field (ill-posed inverse problem). Usually, an estimate is obtained by minimizing the mean squared distance between experimentally observed and predicted displacements (inverse TFM). Here we explore two alternative approaches in TFM. First, we compare inverse TFM to the direct method, in which the stress tensor is calculated directly from the displacement data, thus avoiding the use of a loss function. Second, we explore the potential of machine learning and convolutional neuronal networks. By applying recently developed conditional invertible neuronal networks (cINN), we can address questions regarding the stability and uniqueness of the obtained traction field estimates.

BP 12.22 Tue 17:30 P4

Quantifying the relation between cell membrane and nucleus through Shape-based Voronoi tessellation — •Madhura Ramani[1], Maxime Hubert[1], Sara Kaliman[1], Simone Gehrer[1], Florian Rehfeldt[2], and Ana-Sunčana Smith[1,3] — [1]PULS group, FAU Erlangen-Nürnberg, Erlangen, Germany — [2]Experimental Physics 1, Universität Bayreuth, Bayreuth, Germany — [3]Group for Computational Life Sciences, Ruđer Bošković Institute, Zagreb, Croatia

Numerous disorders caused by genetic alterations empathize the im portance of nuclear shape and position within the cell. It is crucial to understand how the cell and nuclei relate mechanically to each other in various conditions. We investigate this relation using confluent MDCK-II monolayers grown unconstrained on substrates of various elasticities. The synergy between the cell mem brane and nucleus is measured through the quality of the Shape-based Voronoi Tessellation (SVT), which is then compared to the tessella tion of space provided by the cell membranes in the tissue. To address the precision, we compare SVT-extracted morphological information to the corresponding membrane-segmented ones and show that the method outclasses classical Voronoi Tessellation. As the SVT relies on the nuclei position to approximate the cell membrane, we present a systematic measure of the distance between the cell and nucleus center of mass. Our method offers insights regarding the mechanical feedback between the cell membrane shape and nuclei positioning, and is central in the creation of theoretical and numerical models of tissues.

BP 12.23 Tue 17:30 P4

Reactive oxygen species induce cell stiffening through lysosomal disruption and subsequent intracellular acidosis in HL60 cells — •Yesaswini Komaragiri[1,2], Ricardo Hugo Pires[1,2], Stefanie Spiegler[1,2], Huy Tung Dau[1], Doreen Biedenweg[1], Clara Ortegon Salas[3], MD Faruq Hossain[1], Bob Fregin[1,2], Stefan Gross[2,3], Manuela Gellert[3], Uwe Lendeckel[3], Christopher Lillig[3], and Oliver Otto[1,2] — [1]ZIK HIKE, University of Greifswald, Greifswald, Germany — [2]DZHK, University Medicine Greifswald, Greifswald, Germany — [3]University Medicine Greifswald, Greifswald, Germany

Reactive oxygen species (ROS) are important players of redox homeostasis and associated with cellular alterations in both, physiological and pathological conditions. Effects of different ROS on the cytoskeleton have been reported earlier; however, the exact mechanism by which they alter cell mechanics remains to be understood. Here, we used varying concentrations of hydrogen peroxide to induce intracellular ROS in human myeloid precursor cells (HL60). Using real-time fluorescence and deformability cytometry, we combined the mechanical characterization of cells with simultaneous fluorometric assessment of intracellular superoxide levels. Our work reveals a direct correlation of cell stiffening with increasing levels of superoxide. While no global changes of F-actin or microtubule networks could be observed, we show increased elastic properties as a consequence of lysosomal damage followed by intracellular acidification.

BP 12.24 Tue 17:30 P4

Nuclear Volume, Density and Dry Mass are Controled by Chromatin and Nucleocytoplasmic Transport — •Omar Muñoz[1,2], Abin Biswas[1,3,4], Kyoohyun Kim[1,3], Simone Reber[4], Vasily Zaburdaev[1,2], and Jochen Guck[1,3] — [1]Max Planck Zentrum für Physik und Medizin — [2]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg — [3]Max Planck Institute for the Science of Light — [4]IRI Life Sciences, Humboldt-Universität zu Berlin

The cell nucleus is an organelle responsible for hosting essential processes such as DNA replication and transcription. Many important biophysical properties of the nucleus are not well understood, for example, its density is lower than the density of the cytoplasm despite the nucleus hosting the highly compressed genome. Motivated by this observation, we combined optical diffraction tomography and confocal fluorescence microscopy and measured, in real time, the material properties of nuclei reconstituted in *Xenopus* egg extract. We found that nuclear growth has two phases: the first one driven by chromatin decondensation and the second one, by nucleocytoplasmic transport and replication. We also developed a simple theoretical model, where nuclear volume is determined by an entropic polymer pressure exerted by chromatin and an osmotic pressure caused by the protein concentration gradient across the nuclear envelope. The good agreement between the model predictions and experimental results supports a view, where chromatin and nucleocytoplasmic transport are essential contributors to the biophysical properties of the nucleus.

BP 12.25 Tue 17:30 P4

Mechanical Characterization of Pharmaceutical Nanoparticles — •Henrik Siboni[1,2], Leonhard Grill[1], and Andreas Zimmer[2] — [1]Single Molecule Chemistry, Institute of Chemistry, University of Graz — [2]Pharmaceutical Technology & Biopharmacy, Institute of Pharmaceutical Sciences, University of Graz

Nanoscale Drug Delivery Systems are becoming an essential part of modern medicine, but lack of understanding of the underlying physical mechanisms hinders its progress. Focusing on self-assembled nanoparticles called proticles, we employ Atomic Force Microscopy to gain new insights. We find that we are able to characterize particle shape and its dependence on formulation. We further show that proticles can be imaged on biological cells and that the mechanical changes in cells can be measured using nanoindentation experiments. Our methods can be used in the future to accelerate early-stage development of pharmaceutical nanoparticles.

BP 12.26 Tue 17:30 P4

The role of vimentin phosphorylation in mechanotransduction — •Julia Kraxner[1,2] and Holger Gerhardt[1,2] — [1]Max Delbrück Center for Molecular Medicine in the Helmholtz Association (MDC), Berlin — [2]German Centre for Cardiovascular Research (DZHK)

Vascular endothelial cells (VECs) need to be able to constantly sense, withstand and adapt to varying mechanical stresses. One way cells adapt their mechanics to these varying requirements is through differential expression of cytoskeletal proteins. Here, we focus on the intermediate filament vimentin and introduce post-translational modifications (PTMs). Interestingly, PTMs provide a mechanism for mechanical modulation on short time scales. We study the impact of one such PTM, phosphorylation and one effect of phosphorylation is, for example, the disassembly of intermediate filaments. Experiments on VECs under flow reveal an increase of specific phosphorylation sites in vimentin. We investigate the role of these phosphorylation sites on the mechanotransduction. Therefore, we want to combine traction force microscopy under flow with mutations in vimentin which inhibit phosphorylation of specific sites. Additionally, we plan on tuning the substrate stiffness to study the effect of tissue mechanics observed in aging of the vascular system and possible effects on mechanotransduction. These insights have the potential to improve our understanding of the complex mechanism of mechanotransduction in vascular endothelial cells.

BP 12.27 Tue 17:30 P4

Towards observing entry of Particulate Matter into lung cells using Photonic Force Microscopy — •Jeremias Gutekunst and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, Department of Microsystems Engineering (IMTEK), University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany,

The uptake of Particulate Matter (PM) into lung cells increases the risk of stroke and coronary heart disease. Following an in vitro approach, we expose single particulates to lung epithelial cells on a coverslip and examine their fluctuation based binding and entry paths with a photonic force microscope (PFM). The PFM consists of a highly focused laser beam, which is used to optically trap and interferometrically track a PM particle at 1 MHz frequency and with nm precision.

The central part of this work is to investigate the influence of additional scatterers below and above the nano particle of a PFM. The understanding of their optical influence is crucial, as in particle entry experiments the cell scatters light and alters the interference signal used to track the probe. We address the problem by simplifying and controlling the situation: In addition to the particle used as a probe, we introduce a further particles positioned in the same beam path, but trapped with a second laser. By decorrelating the combined scattering signals on different frequencies, we want to recover the precise position of the trapped PM probe on a broad temporal bandwidth to reliably study cell particle interactions.

BP 12.28 Tue 17:30 P4

Motion-correlated particle transport along filopodia and lamellipodia — •Mario Brehm and Alexander Rohrbach — Laboratory for Bio- and Nanophotonics, Department of Microsystems Engineering - IMTEK, Georges-Köhler-Allee 102, 79110 Freiburg, Germany

Macrophages play an important role in cleaning up the body from cell debris, bacteria and viruses. As a prior step to phagocytosis, extracellular particles can attach to cell protrusions like filopodia and be pulled towards the cell body. Our data points to the idea that particles such as bacteria or viruses get mechanically coupled to the actin fibers within the cell, similarly to focal adhesions. The aim of this study is to improve mechanistic models that describe the mechanical coupling of extracellular particles to proteins connected to the retrograde flow of actin fibers. In addition, we investigate whether and how the transport along filopodia and lamellipodia differ from each other.

The high image contrast combined with the high temporal and spatial resolution of ROCS microscopy enables us to observe directed motion and fluctuations along filopodia at 100 Hz and without fluorescence. By recording, tracking and analyzing the nanoparticle's fluctuations it is possible to derive changes of the particle's viscoelastic properties and their relation to molecular bonds during their transport along the cell's protrusions.

BP 12.29 Tue 17:30 P4

Local organization of F-actin studied via Förster resonance energy transfer using 2D polarization fluorescence imaging (2DPOLIM) — •Mohammad Soltaninzehad[1,2], Rainer Heintzmann[1,2], Adrian T. Press[3,4], and Daniela Täuber[1,2] — [1]Leibniz Institute of Photonic Technology, Jena — [2]Institute of Physical Chemistry & Abbe Center of Photonics, Friedrich-Schiller-University Jena, Germany — [3]Department of Anesthesiology and Intensive Care Medicine, Jena University Hospital — [4]Faculty of Medicine, Friedrich Schiller University Jena, Germany

2D polarization fluorescence imaging (2DPOLIM) provides complete in-plane evaluation of the polarization state of the sample[1,2], giving access to macromolecular arrangement in the range of 2-10 nm via Förster resonance energy transfer between similar fluorophores (homo-FRET, emFRET). Phalloidin-dye complexes map the structure of F-Actin, by binding specifically. We applied 2DPOLIM to phalloidin-DY490 stained liver tissue of mice from different treatment groups in the context of polymicrobial sepsis[1,3]. Qualitative analysis showed significant differences in the molecular arrangement of F-actin in agreement with the survival of the animals. Further information will be

obtained from comparing the experimental data to a series of simulations[2]. – Funding by DAAD-GSSP, DFG-Ta1049/2, Interdisziplinäre Zentrum für Klinische Forschung Jena (AMSP-05). – [1] D. Täuber et al. ELMI 2021, https://doi.org/10.22443/RMS.ELMI2021.6. [2] R. Camacho et al. Commun. Biol. 2018, 1, 157. [3] A.T. Press et al. EMBO Mol. Med. 2021, 13 (10), e14436.

BP 12.30 Tue 17:30 P4

Interactions between cytoskeletal filaments — •Magdalena Haaf, Anna Schepers, and Sarah Köster — Institute of X-Ray Physics, Göttingen, Germany

The cytoskeletal filaments –F-actin, microtubules and intermediate filaments (IFs)– constitute an interpenetrating network that performs essential cellular functions. Next to the mechanical properties of the single filaments, the interactions between the filamentous proteins play an important role in cytoskeletal network mechanics. To gain a deeper understanding of the composite network it is useful to quantify such interactions in a controlled setting. Cell experiments have revealed a functional and structural interplay between F-actin and vimentin IFs. However, in reconstituted systems studies of mixed networks come to conflicting conclusions. To clearly solve this conflict, it is crucial to simplify the system even further to the single filament level. We use a quadruple optical trap in combination with microfluidics and confocal microscopy to directly quantify the interaction strength and dynamics between F-actin and vimentin IFs. Our approach allows us to characterize the interactions independent of the network morphology. This setup further enables us to probe the influence of electrostatic and hydrophobic effects on the interactions between single filaments.

BP 12.31 Tue 17:30 P4

Comparative investigation of F-actin using Nano IR spectroscopic and polarization resolved fluorescence microscopy imaging — •Dijo Moonnukandathil Joseph[1,2], Lukas Spantzel[2,3], Katharina Reglinski[1,2], Asad Hafeez[1,2], Yutong Wang[1,2], Mohammad Soltaninezhad[1,2], Christian Eggeling[1,2], Rainer Heintzmann[1,2], Michael Börsch[2,3], and Daniela Täuber[1,2] — [1]Leibniz Institute of Photonic Technology, Jena — [2]Friedrich-Schiller University Jena — [3]University Hospital Jena, Germany

Fibrillar actin is one of the major structural components in cells. Thus, its organization has been studied extensively. Nevertheless there are still open questions, in particular, related to pathogenic infections. We examine the potential contributions of two complementary recently developed imaging methods for increasing our understanding on local F-actin: IR spectroscopic photo-induced force microscopy (PiF-IR) and 2D polarization resolved fluorescence microscopy imaging (2DPOLIM). PiF-IR provides local chemical information at high spatial resolution below 10 nm. 2DPOLIM allows to study the local aggregation of fluorescence labeled F-actin via Förster resonance energy transfer (FRET) in the range of 2-10 nm [1]. – Funding by DAAD-GSSP, DFG-Ta1049/2 – [1] R. Camacho et al. Commun. Biol. 2018, 1, 157.

BP 12.32 Tue 17:30 P4

How do muscles self-assemble? — •Francine Kolley[1], Ian D. Estabrook[1], Clement Rodier[2], Frank Schnorrer[2], and Benjamin M. Friedrich[1,3] — [1]cfaed, TU Dresden — [2]IBDM, Aix Marseille University — [3]Physics of Life, TU Dresden.

For voluntary movements, all animal life relies myofibrils in striated muscle, which are highly organised crystal-like cytoskeletal structures comprising chains of micrometer-sized sarcomeres. The size of sarcomeres is supposedly set by giant proteins such as titin. Titin elastically links myosin molecular motors in the middle of a sarcomere to a structure called Z-disc rich in actin crosslinkers at the sarcomere boundary. To investigate putative mechanisms for the self-assembly of myofibrils, we develop minimal mathematical models. We show that minimal models accounting for non-local interactions between three key proteins is sufficient to account for the spontaneous emergence of periodic sarcomeric patterns. We employ mean-field models, as well as agent-based simulations, which reveal the influence of small-number fluctuations on emergent patterns. Additionally, analysing images of the *Drosophila* flight muscle during early development provided by the Schnorrer lab (IBDM, Marseilles), we were able to identify titin as the first protein forming periodic patterns, with myosin and later actin following subsequently, which constrains possible models.

BP 12.33 Tue 17:30 P4

Simulation and machine-learning-based analysis of active Brownian magnetic microswimmers — •Anas Hussin, Sascha Lambert, and Stefan Klumpp — Institute for the Dynamics of Complex Systems, University of Göttingen, Göttingen

Magnetic microswimmers, whether these are biological organisms or designed nanomachines, show promise in biomedical microrobotics, as they can be steered remotely with a magnetic field. Often, these swimmers encounter complex environments characterized by obstacles and confinement. To understand their navigation in such complex environment, we simulate their swimming as active Brownian particles with an intrinsic magnetic moment and interactions with obstacles and walls that can be of hydrodynamic and/or steric nature. In addition, we use the resulting trajectories to train a neural network with an optimized architecture in order to explore the ability of machine learning algorithms to infer parameters of the motion from trajectories.

BP 12.34 Tue 17:30 P4

Function of Morphodynamics in Foraging *Physarum polycephalum* — •Lisa Schick[1,2] and Karen Alim[1,2] — [1]Physics Department and CPA, Technische Universität München — [2]Max-Planck-Institut für Dyanmik und Selbstorgansiation, Göttingen

Foraging for nutrients and shelter in an heterogeneous environment is key for the survival of living organisms. Foraging behaviour of animals is generally viewed as optimised for maximal energy uptake per search time by balancing time spent for environmental exploration and food exploitation. Yet, it is unclear which foraging behaviour can be adopted by spatially extended organisms like the unicellular slime mould *Physarum polycephalum*. What foraging strategy does the large and adaptive network-like morphology allow for? Here, we follow the plasmodial network of *P. polycephalum* as it adapts its morphology, gradually moving its body mass as it is foraging for food. We evaluate the morphodynamics of the foraging plasmodia by calculating morphology and velocity of the specimen. We identify three different morphological states by network compactness and the density of moving fronts. In order to understand the purpose of the continuous morphological changes, we investigate the energy distribution within the different morphologies. In particular we discuss how the morphological variability allows the organism to adjust its energetic costs during foraging.

BP 12.35 Tue 17:30 P4

Lattice based model to study wound healing in biofilms — •Yusong Ye[1], Mnar Ghrayeb[2], Liraz Chai[2], and Vasily Zaburdaev[1] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU) & Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [2]Institute of Chemistry, The Hebrew University of Jerusalem, Jerusalem, Israel

Biofilms are multicellular heterogeneous bacterial communities excelling in social-like cooperation, division of labor, and resource capture. Bacteria in biofilms are embedded in the self-produced extracellular matrix (ECM). Increasingly more often an analogy between biofilms and higher multicellular organisms is drawn. One illustrative example is the process of wound healing. While it is extensively studied in eukaryotic tissues, the mechanisms of wound healing in biofilms are barely understood. The wound healing in biofilm is a regulated growth by which bacteria alter their physiological state in response to a damage. Motivated by experiments in a model biofilm forming bacteria Bacillus subtilis, we developed a lattice based model of a biofilm growth. It explicitly considers cells and ECM produced by cells, as well as nutrient fluxes and helps to elucidate the role of biofilm components (matrix, cells), aging, and nutrient availability in damage repair. Division of labor (growth vs. ECM production) and nutrient consumption play key roles in heterogeneous wound closure. Even under most general assumptions, the model qualitatively reproduces the wound healing phenotypes observed in our experiments and can be further generalised to include signalling and regulatory mechanisms.

BP 12.36 Tue 17:30 P4

Fluid Flow and Microvascular Remodeling — •Fatemeh Mirzapour-Shafiyi[1] and Karen Alim[1,2] — [1]Physics Department and CPA, Technische Universität München — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen

As a transport network optimised through evolution, vessel morphology is adapted to minimise energetic costs of dissipation and homogenize flow transport in the network. Resource-deprived tissues produce chemotactic agents to induce vessel formation during develop-

ment and in tissue homeostasis. The primitive, mesh-like vascular network formed through neovascularisation is highly ramified. Later, vascular network is normalised into a hemodynamically preferred tree-like structure. The normalisation process, termed vessel remodeling, leads to an organ-specific network architecture which better meets the metabolic needs of its surrounding tissue. As vessel growth and remodeling is found impaired in various disease states, several factors regulating vessel formation and branching morphology were identified over the past decades. However, while some of these factors have been undergoing clinical trials, their effects on transport properties of the altered vessel morphology are not fully elucidated yet. Establishing a perfusable human capillary-on-a-chip (hCOC) model system, here we aim to investigate how vascular morphology correlates with fluid flows. Our hCOC model allows extensive quantitative analyses of network morphology and adaptive remodeling under fluid flow applied by a low-pressure syringe pump. Results of our analyses will contribute to the next generation therapeutics targeting vessel development.

BP 12.37 Tue 17:30 P4

Cancer tissue dynamics as active liquids — •Mahboubeh Farajian[1], Swetha Raghuraman[2], Alejandro Jurado Jimenez[1], Fatemeh Abbasi[1], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics Georg August University Göttingen — [2]Institute for Cell biology ZMBE - University of Münster

Collective cell migration can be found in some key biological processes such as Metastasis, wound healing and tissue rearrangement. While the molecular mechanisms of collective migration already represent a strong research focus, the mechanical processes driving it are currently less studied. Here we propose to answer this question: "Can statistical mechanics explain the local and global characteristics of cell migration in the tumors?" Someone can imagine 3 kinds of phenotypes regarding the collective cell migration: "Sub-diffusive", "Diffusive" and "Super-diffusive" motion. We aim to change the physical parameters of the environment such as Volume (by letting the tumor models grow) and Pressure (by addition of Dextran to the environment), and then look at the statistical mechanics of the cells' collective motion, different phenotypes and the transition between different phenotypes. and we use 3D individual cell tracks for this aim.

BP 12.38 Tue 17:30 P4

Assessing statistical properties of resident tissue macrophages — •Miriam Schnitzerlein[1,2], Anja Wegner[3], Stefan Uderhardt[3], and Vasily Zaburdaev[1,2] — [1]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [3]Department of Internal Medicine 3 - Rheumatology and Immunology, Friedrich-Alexander-Universität Erlangen-Nürnberg und Universitätsklinikum Erlangen, Germany

Resident tissue macrophages (RTMs) are present in essentially all tissues in the human body. While macrophages in general are mostly known as part of the immune response, RTMs are additionally crucial for ensuring tissue homeostasis. This includes removing dead cells, providing growth factors and protecting the tissue from inflammatory damage. To monitor their surroundings, RTMs show continuous sampling behaviour by extensions and retractions of protrusions as well as endocytosis behaviour. Quantifying the growth and shrinkage of protrusions under different conditions is thereby essential to understand the overall dynamics of RTMs together with their approach of ensuring tissue homeostasis. In this project, we have employed a high-resolution intravital imaging protocol to generate movies of RTMs *in vivo*. Subsequently we have built an image processing pipeline to assess cell properties - such as area and perimeter of whole RTMs or the diffusion coefficient and thereby the dynamics of their protrusions. Such measurements will help to build a mathematical model for protrusion dynamics as well as to establish a biophysical model of RTMs.

BP 12.39 Tue 17:30 P4

3D Force Model of early zebrafish development via NeuralODEs — •Leon Lettermann, Sebastian Herzog, Alejandro Jurado, Florentin Wörgötter, and Timo Betz — 3rd Institute of Physics - Biophysics, University of Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen

The astonishing process of embryo development still poses a great variety of unanswered questions today. Motivated by the importance of understanding cell migration and organization patterns, we want to study the movements in the early development of zebrafish embryos on a mesoscopic scale. A coarse-grained tissue flow obtained from light sheet microscopy data is analyzed based on a hydrodynamic model. This model is enhanced by active stresses and forces, redirecting the flow away from a dead liquid's description. Using a Neural Ordinary Differential Equation, the active contributions can be reconstructed from observations, shedding light on the distribution of active forces and stresses in the embryo. This allows for quantifying symmetry breaking due to active effects and early recognition of the forming body axes.

BP 12.40 Tue 17:30 P4

Tissue tension during zebrafish development — •Ming Hong Lui[1,2], Alejandro Jurado[1], Leon Lettermann[1], and Timo Betz[1,2] — [1]3rd Institute of Physics - Biophysics, University of Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen — [2]Max Planck School Matter to Life

Understanding the morphogenesis during development is one of the emerging fields where the interaction between developmental and tissue biology with biophysics has provided a series of deep new insights into natures physical working principles. In particular, during embryonic development of zebrafish, cells in the blastoderm exhibit collective migration towards the yolk in a process known as epiboly, as well as the subsequent gastrulation that involves symmetry breaking. These elegantly robust processes are facilitated by both biochemical and mechanical interactions. To determine how tissue stresses contribute mechanically we use photoablation to create mechanical defects in the tissue and record the subsequent tension relaxation using light sheet microscopy of the whole embryonic volume. We analyze and contrast the nuclei trajectories, density, velocity and force maps with and without the ablative perturbation. From the changes in these quantities, we can infer the adaptive response of the embryo, the source of force generation, and the role played by tissue tension in guiding the coordinated movement.

BP 12.41 Tue 17:30 P4

Single Cell Force Spectroscopy: The Impact of Cell Contact Area — •Sophie Geiger[1], Maria Villiou[1,2,3], and Christine Selhuber-Unkel[1,2,3] — [1]Institute for Molecular Systems Engineering, University of Heidelberg, DE — [2]Max Planck Schools: Matter to Life, University of Heidelberg, DE — [3]Cluster of Excellence 3DMM2O KIT & Heidelberg University, DE

Single cell force spectroscopy is a versatile method for characterising cell-substrate interactions. It has already been applied in several studies to investigate the effect of photomechanical stimulation and the influence of structuring molecules on cell detachment forces.

A critical aspect is the contact area between cell and substrate, as a larger contact area usually leads to higher cell detachment forces. However, the contact area between cell and substrate varies with cell size and with the deformation of the cell pressed onto the surface.

We aim to avoid the distortion that these variations exert on the cell detachment forces by limiting the adhesion area. This is achieved using micropatterned substrates. We use light-induced molecular adsorption of proteins (LIMAP) to generate circular fibronectin micropatterns on an inert background. In a systematic study, we investigate the dependence of cell detachment forces on the cell-substrate interaction surface.

BP 12.42 Tue 17:30 P4

Investigation of the binding behaviour of proteins in various patterns — •Jonas Walther[1] and Ana-Sunčana Smith[1,2] — [1]PULS Group, Department of Physics, Interdisciplinary Center for Nanostructured Films, Friedrich-Alexander-Universität Erlangen-Nürnberg, Cauerstraße 3, 91058 Erlangen, Germany — [2]Group for Computational Life Sciences, Ruđer Bošković Institute, Zagreb, Croatia

The coupling of two or more cellular membranes is an important part of cell interactions and therefore affects many biological mechanisms. Cells may restrict the movement of proteins in certain areas of their membrane creating functionally specialized regions, or membrane domains. Here we analyse whether the arrangement of proteins in different patterns changes the binding kinetics of the proteins. In our investigation we combine kinetic Monte Carlo simulations and explicit calculations of the binding rates of the patterns. Results show that there is indeed a difference in binding of the different patterns. An important factor seems to be the amount of proteins within a pattern due to the correlations between the proteins. The exact difference of the binding rates depends on the mechanical properties of the membrane and the proteins. We furthermore analyse the dynamics of bond

formation and compare the results to experimental data on the activation of natural-killer cells binding to analogous patterns (experiment by the group of Mark Schvartzman at the Ben-Gurion Univeristy of the Negev).

BP 12.43 Tue 17:30 P4

Electrostimulation of osteoblasts on coated planar resistive electrodes — •Franziska Dorn[1], Christian Völkner[1], Meike Genzow[2], Martina Grüning[2], Sven Neuber[3], Regina Lange[1], Ingo Barke[1], Christiane A. Helm[3], Barbara Nebe[2], and Sylvia Speller[1] — [1]Institute of Physics, University of Rostock — [2]University Medical Center Rostock, University of Rostock — [3]Institute of Physics, University of Greifswald

The development of electrically active implants may profit from knowledge and understanding of how osteoblasts respond to electrostimulation. Besides the aim to find routes to accelerate adhesion of osteoblasts, the cellular response in terms of migration and deformation is interesting. For our experiments we use a planar resistive electrode configuration with DC electrostimulation. The glass substrate is covered with a few bilayers of polyelectrolyte (PDADMA/PEI) with carbon nanotubes incorporated to enhance electrical conductivity. In physiologic medium the sheet resistance increases from few kΩ to more than 10 kΩ. Human osteoblast-like cells (MG-63) were seeded on the electrode and, after 24 h cell growth, stimulated by a couple of cycles at voltages between 1V and 2V. The observed cellular shape changes and mobility are only subtle and the dependence on the orientation of the electric field axes is not obvious. Experiments at an earlier phase in the adhesion process i.e., in a shorter time frame of cell adhesion, are considered. [1] C. Voelkner, et al, Beilstein J. Nanotechnol. 12, 242 (2021) [2] M. Gruening, et al, Front. Bioeng. Biotechnol. 8,1016 (2020) [3] H. Rebl, et al, Adv. Engin. Mater. 12, B356 (2010)

BP 12.44 Tue 17:30 P4

The zeta potential as parameter in electric field landscapes for guiding cell adhesion — •Wanda Witte[1], Christian Völkner[1], Regina Lange[1], Susanne Seemann[2], Barbara Nebe[2], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, University of Rostock, Rostock, Germany — [2]Department of Cell Biology, Rostock University Medical Center, Rostock, Germany

In osseointegration of implants, chemical and physical material properties influence inital cell adhesion. The relevant surface potential for cells is the zeta potential at the shear plane or hydrodynamic distance. We investigate how the zeta potential of glass can be modified by an aggregated molecular monolayer, with the aim of using the zeta potential to create electric field landscapes. To achieve the aggregation of a molecule monolayer, amine-terminated dendrimers and albumin were deposited on the glass by micro-contact printing or immersion. An electrokinetic analyzer was used to determine the zeta potential of the coated and uncoated samples. The successful physisorption of molecules was verified by fluorescence microscopy and force microscopy (AFM). It could be shown that the application of albumin or amine-terminated dendrimers increases the zeta potential by approx. 25 eV and 40 eV. The choices and shape responses of osteoblasts (MG-65) in molecule stripe landscapes are discussed.

BP 12.45 Tue 17:30 P4

Quantification of the dynamics of confluent endothelial cells — •Anselm Hohlstamm, Andreas Deussen, and Peter Dieterich — Institut für Physiologie, Medizinische Fakultät, TU Dresden

Cooperative cell dynamics resulting from a complex interplay of single cell migration and cell-to-cell interactions plays a fundamental role in maintaining a confluent cell layer despite continuous changes in cell numbers and environmental conditions. It is the aim of this work to extract the essential components of this dynamics. Therefore, we seeded human umbilical vein endothelial cells and stained their nuclei with a fluorescent dye. Cells were observed within 48 hours (dt = 10 minutes). We obtained up to 50.000 cell trajectories within an area of 6 x 7 millimeters for 10 different experiments. All analyses were performed under nearly confluent conditions. Cells continued to show lively proliferations and a non-stationary behavior indicated by a two-phase decay of the mean squared velocity. This behavior is accompanied by a decay of the velocity correlation. In addition, we found an exponential repulsion between cells that could transiently rise cell velocities due to cell proliferations. We put these observations into a mathematical model coupling cell proliferation and mean squared velocities over time. Bayesian analysis was applied to determine the best model and its parameters. In summary, we are able to perform a characterization of the complex cell dynamics. This approach can be used for simulations and application to different experimental conditions.

BP 12.46 Tue 17:30 P4

Adaptive microfluidics using hydrogels with irreversible response — •Onurcan Bektas[1,2,3,4], Charlott Leu[3], Joachim Rädler[1,3], and Karen Alim[1,2,5] — [1]Max Planck School Matter to Life, Germany — [2]Physics Department and CPA, Technische Universität München — [3]Faculty of Physics and and Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München, München, Germany — [4]Physics Department, University of Göttingen, Göttingen — [5]Max Planck Institute for Dynamics and Self-Organization, Göttingen

Microfluidic devices have triggered technological revolutions in biology and separation technology. Their increased surface-to-volume ratio shortens reaction times, and make reactions more accurate and effective in an automated fashion, thus reducing error rates and allowing for highthroughput assays. However, fabricating multifunctional devices with integrated modules requires complicated control systems and is by far from being trivial. Here we present a novel bio-inspired approach to design adaptable microfluidic devices that can adapt the sizes of its channels using local feedback mechanisms for uniform flow. We fabricate a random porous media using an hydrogel made of Poly(ethylene glycol)-norbornene backbone and MMP-degradable cross-linker. When perfused with MMP-1 enzyme, the boundaries of the channels are cleaved such that the size of the channels and the flow are coupled. We investigate how the feedback mechanism between the flow and the channel size allows the network to optimise the flow rate distribution. Our methodology will lay the foundation for designing microfluidic devices that are adaptive to biological activity.

BP 12.47 Tue 17:30 P4

Adaptive microfluidics using irreversibly responsive hydrogels — •Onurcan Bektas[1,2,3,4], Charlott Leu[3], Joachim Rädler[1,3], and Karen Alim[1,2,5] — [1]Max Planck School Matter to Life, Germany — [2]Physics Department and CPA, Technische Universität München — [3]Faculty of Physics and and Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München, Germany — [4]Physics Department, University of Göttingen, Göttingen — [5]Max Planck Institute for Dynamics and Self-Organization, Göttingen

Microfluidic devices have triggered a technological revolution in the pharmaceutical industry and biotechnology. Integrated modular microfluidic devices allow for high throughput assays while making them more precise by eliminating human-induced errors. The fabrication process, however, introduces inhomogeneities which limit the efficiency and the precision of the produced devices. Here, we present a novel bio-inspired approach to designing adaptable microfluidic devices that can adapt the sizes of their channels using local feedback mechanisms for uniform flow. We test our approach by fabricating a random porous media using Matrix-Metalloproteinase(MMP)-degradable poly(ethylene glycol)-norbornene hydrogel and measure how the flow rate distribution changes by using Particle Image Velocimetry technique. As the device is perfused with an MMP-enzyme, the degradation of the hydrogel is coupled to the flow. We investigate how this coupling could result in a uniform flow. Our method could be used to eliminate inhomogeneities introduced during the fabricating processes to produce spatially homogeneous microfluidic devices.

BP 12.48 Tue 17:30 P4

Self-organization of microtubule filaments in energy dissipativeevaporating droplet — •Vahid Nasirimarekani, Olinka Ramirez-soto, Stefan Karpitschka, and Isabella Guido — Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany

Cytoskeletal assemblies such as microtubule networks and motor proteins of the kinesin family drive vital cellular processes that, together with cargo delivery and cell division, also include providing mechanical stability when cells are exposed to external stresses. How these self-organising structures can orchestrate such response is not yet well understood. In this study, we develop a bioinspired system resembling intracellular cytoskeletal networks and characterise its activity under the influence of external stress. For this purpose, we confine an active network of microtubules and kinesin motors in an evaporating aqueous droplet. This setup serves as a bioreactor that enables to apply forces to the active system. Namely, the flow field generated by the Marangoni and capillary flow couples with the active stress of the microtubule-motor protein network. We observe that this coupling influences the spatio-temporal distribution of the driving forces and the

emergent behaviour of the system, which shows contracting and relaxing behaviour. By analysing such non-equilibrium systems, our study can contribute to understand the response of biological structures to cues from the external environment.

BP 12.49 Tue 17:30 P4

Establishment of a microfluidic UV-Vis analysis of single cell E. coli — •Tim R. Baumann[1], Alexander Grünberger[2], Dario Anselmetti[1], Harald Gröger[3], and Martina Viefhues[1] — [1]Experimental Biophysics & Applied Nanosciences, Department of Physics, Bielefeld University — [2]Multiscale Bioengineering, Department of Technology, Bielefeld University — [3]Industrial organic chemistry and biotechnology, Department of Chemistry, Bielefeld University

Whole-cell biocatalysts like, E. coli DH5-α are widely used in industrial organic chemistry and biotechnology. For efficient production an appropriate cultivation media composition is of high importance. Harmful organic solvents, like ethanol are needed to solve insoluble substrates, those often lead to a permeabilisation of the bacterial membranes. In this study, we established a microfluidic method to analyse the impact of ethanol on leaching of certain intracellular cofactors e.g., NAD(P)H and exploited the contribution of NAD(P)H to the cells autofluorescence. In order to detect the losses in intensity due to leaching, a UV-LiF analysis of single cells was conducted, using a Nd:YAG Laser (λ = 266 nm). We evaluated the impact of incubation in 5 % ethanol for either 5 or 10 minutes on single cells in a PDMS microfluidic chip with a UV transparent fused silica base layer, including a carbon black PDMS spot at the detection point to reduce the PDMS's autofluorescence. The intensity data was assessed and plotted in histograms. Those exhibited a reduction of the FWHM and a displacement of the distribution maxima to smaller intensities depending on the incubation time and proved the cofactor leaching due to ethanol exposition.

BP 12.50 Tue 17:30 P4

Study of the temporal stability of evaporated SLBs for technological applications — •Nancy Gomez-Vierling[1], Marcelo A. Cisternas[2], María José Retamal[1], Nicolás Moraga[1], Marco A. Soto-Arriaza[3], Tomás P. Corrales[4], Felix Kleemann[5], and Ulrich G. Volkmann[1] — [1]Instituto de Física and CIEN-UC, P. Univ. Católica de Chile — [2]Escuela de Ingeniería Industrial, Univ. de Valparaíso, Chile — [3]Facultad de Química y Farmacia and CIEN-UC, P. Univ. Católica de Chile — [4]Departamento de Física, UTFSM, Valparaíso, Chile — [5]Departamento de Física, Technische Universität Clausthal, Clausthal, Germany.

Artificial membranes are models for biological systems. We introduce a dry two-step self-assembly method, first performing a high-vacuum evaporation of phospholipid molecules over silicon, followed by an annealing step in air. Our evaporated membranes show long-term stability and no restructuring after storage in air during at least fifteen months. This extreme stability of the Supported Lipid Bilayer (SLB) structures make this system interesting for technical applications in the field of functional biointerfaces, e.g., for fabrication of biosensors and membrane protein platforms, including cleanroom-compatible fabrication technology. It is expected that SLBs can help to gain insight into the lifetime of viral structures protected by a surrounding phospholipid bilayer adsorbed on static solid surfaces or on inhalable particulate material (PM), which contributes to the spread of the SARS-CoV-2 virus. Acknowledgment: FONDECYT grant numbers 1180939 (UGV), 1171047 (MS-A) and 1211901 (TPC).

BP 12.51 Tue 17:30 P4

Measurements of topologies and Young moduli of DPPC films deposited from the gas phase onto silicon substrates at different temperatures — •Nicolás Moraga[1], Gabriel Alfaro[1], Nancy Gomez-Vierling[1], Daniel Saavedra[1], Marcelo A. Cisternas[2], María José Retamal[1], Marco A. Soto-Arriaza[3], Tomás P. Corrales[4], Felix Kleemann[5], and Ulrich G. Volkmann[1] — [1]Instituto de Física and CIEN-UC, P. Univ. Católica de Chile — [2]Escuela de Ingeniería Industrial, Univ. de Valparaíso, Chile — [3]Facultad de Química y de Farmacia and CIEN-UC, P. Univ. Católica de Chile — [4]Departamento de Física, UTFSM, Valparaíso, Chile — [5]Departamento de Física, Technische Universität Clausthal, Clausthal, Germany.

Supported lipid bilayers (SLBs) are suited to gain insight into the physical behavior of cell membranes. In this work, DPPC deposition by Physical Vapor Deposition (PVD) is performed on silicon (100) substrates at different substrate temperatures and deposition rates. Our goal is finding growth parameters, to optimize coverage and homogeneity of the DPPC SLBs. We observe a modification of topologies and Young moduli and an optimization of the homogeneity for substrate temperatures between 310 and 315 K and deposition rates in the range of 0,78 to 0,93 Å/min. Homogeneous, planar biomimic phospholipid membranes avail protein insertion and an easier detection of ionic channels which will form in case of Gramicidin [Kelkar et. al, BBA 1768 (2007) 2011-25]. Acknowledgment: FONDECYT grant numbers 1180939 (UGV), 1171047 (MS-A) and 1211901 (TPC).

BP 12.52 Tue 17:30 P4

The effect of additives on the lamellar-to-cubic transition dynamics of monoolein at excess water conditions — •Jaqueline Savelkouls, Michelle Dargasz, Göran Surmeier, and Michael Paulus — Fakultät Physik/DELTA, Technische Universität Dortmund, 44221 Dortmund, Germany

Monoolein is an amphiphilic lipid, which is of particular interest in the pharmaceutical industry. Monoolein swells in excess water and forms several lyotropic liquid crystalline structures. In the cubic Pn3m phase, monoolein can release a previously added drug by slow diffusion in the human body [1]. Measurements are performed at the beamline BL2 of the synchrotron radiation source DELTA (Dortmund, Germany) using the small angle X-ray scattering (SAXS) set-up to study the pressure-induced transition from the lamellar crystalline phase to the cubic Pn3m phase. 20 wt% monoolein was mixed in water with salts or drugs. Diffraction patterns are recorded, from which the lattice constants for each phase can be determined. The results show that a much larger lattice constant of the Pn3m phase is formed after the pressure jump compared to the equilibrium state before the pressure increase. Given some time, the system relaxes, causing the lattice constant to approach the equilibrium lattice constant. The rate of relaxation depends on the added additives. In summary, the formation of the liquid crystalline phases of monoolein allows drugs to be released over a long period of time. The speed of diffusion can be optimized by the addition of salts.

[1] Adriana Ganem-Quintanar, "Monoolein: A Review of the Pharmaceutical Applications", p.813 (2000)

BP 12.53 Tue 17:30 P4

Simulation of Double-Walled Vesicles Surrounded by Mixed Membranes — •Paul Louis Sonek and Friederike Schmid — Johannes Gutenberg-Universität, Mainz, Germany

The simulation of membranes from cells and organelles has been a subject of research for quite some time. Some organelles, like the mitochondria, are surrounded by two membranes, where the area of the inner one is much larger than that of the outer one. Such organelles are characterized by numerous invaginations in the inner membrane. The goal of our work is to investigate to which extent simple membrane models can reproduce such structures.

We use the triangulated surface model of Noguchi and Gompper [1] to model double-walled vesicles and combine it with a field model on the model's surface to simulate a membrane with different lipid compositions on different parts of the membrane. Depending on the volume and surface of the inner membrane, we obtain different stable and metastable shapes for the resulting invagination, including flat invaginations, which have a shape similar to the ones observed in mitochondria. Furthermore, configurations with more than one of such folds are found to be metastable.

Our results may shed light on the mechanisms responsible for the peculiar membrane shapes observed in organelles.

[1] H. Noguchi, G. Gompper, Phys. Rev. E 72, 011901 (2005).

BP 12.54 Tue 17:30 P4

Single-particle Diffractive Imaging at the European XFEL: Instrumentation, Data Acquisition and Hit-finding — •Moritz Stammer[1], Charlotte Neuhaus[1], Jette Alfken[1], Markus Osterhoff[1], Richard Bean[2], Johan Bielecki[2], Juncheng E[2], Safi Rafie-Zinedine[2], Raphael de Wijn[2], Romain Letrun[2], Adrian Mancuso[2], Reinhart Jahn[3], and Tim Salditt[1] — [1]Georg-August-Universität, Institute for X-ray Physics, 37077 Göttingen — [2]Scientific Instrument SPB/SFX, European XFEL GmbH, Holzkoppel 4, 22869 Schenefeld Germany — [3]Laboratory of Neurobiology, Max Planck Institute for Multidisciplinary Sciences, 37077 Göttingen, Germany

The European XFEL provides state-of-the-art instrumentation for absolving single-pulse, single-particle coherent diffractive imaging, which we have used to investigate synaptic vesicles, harvested from rat brain, with high spatial resolution. The method involves serial bio-sample de-

livery by aerosol jet such that droplets incorporating single particles are probed by femto-second pulses. In this way two prevalent challenges of SAXS (polydispersity and radiation damage for high brilliance beams) can be met. Stochastic distribution of sample and a nano-focused beam means only a fraction of the recorded data was of interest (1.2 PB in total, roughly $3 \cdot 10^8$ images). We present technical details behind the data acquisition used for this proof-of-concept experiment at the SPB instrument of the European FEL as well as our strategy in "hit-finding". Further, first steps towards electron density reconstruction will be presented as well as comparison to preceding SAXS work.

BP 12.55 Tue 17:30 P4

Live imaging on single cell arrays (LISCA) as platform to study mRNA codon optimization based on ribosome modelling — •Judith Müller[1], Gerlinde Schwake[1], Anita Reiser[1], Daniel Woschée[1], Zahara Alirezaeizanjani[3], Joachim Rädler[1], and Sophia Rudorf[2] — [1]Ludwig-Maximilians-Universität, München — [2]Leibniz Universität, Hannover — [3]Max Planck Institute of Colloids and Interfaces, Potsdam

mRNA based therapies have the potential to evolve as one of the most powerful therapeutic technologies of our future. Massive efforts have been made to deeply study the underlying mechanisms of mRNA delivery and translation. Synonymous re-coding of the mRNA's open reading frame is one approach to investigate and optimize the physics of mRNA translation. In this project, we evaluate the potential of bias in codon usage on influencing the mRNA's translation and degradation kinetics. Live imaging on single cell arrays (LISCA) enables the quantification of translation of hundreds of single cells in parallel on microstructured surfaces. By describing the translation in biochemical rate equations, we analyse mRNA expression and degradation rates with high accuracy. Ribosome movement on the open reading frame (ORF) is simulated to generate mRNA constructs coding for reporter genes with varying ribosome speeds and densities. We observe distinct differences in expression and degradation rates for GFP mRNAs with various optimized ORFs in agreement with simulation. Secondly, we study how specifically provoked ribosome jams on the ORF influence mRNA stability.

BP 12.56 Tue 17:30 P4

The pH dependent phase transition in lipid nanoparticle cores leads to changes of protein expression in single cells — •Julian Philipp[1], Lennart Lindfors[2], and Joachim Rädler[1] — [1]LMU, Munich, Germany — [2]AstraZeneca, Mölndal, Sweden

Lipid nanoparticles developed into the most powerful delivery platform for mRNA based vaccination and therapies. In general LNPs are core/shell particles exhibiting PEG-lipid and DSPC at the surface and ionizable lipid, cholesterol and mRNA in the core. However, the pH dependent changes induced by ionizable lipids in the context of endosomal release are little understood. Here we study the ionizable lipids MC3, KC2, DLin-DMA as model systems as they exhibit different efficacy despite similar pK values. Using synchrotron X-ray scattering we study the structure of bulk phases containing ionizable lipid/cholesterol with and without polyA as mRNA surrogate. The bulk phases exhibit ordered mesophases at low pH and a transition into isotropic swollen phases at higher pH. We find inverse hexagonal H_{II} lipid phases in case of MC3 and KC2 and cubic Pn3m and H_{II} phases in case of DLin. Bulk phases with polyA show coexistence of pure lipid phases and condensed nucleic acid lipid phases. We show that the observed bulk structures are consistent with the SAXS scattering profile of mRNA containing LNPs. The difference in structural features is also consistant with the delayed onset and reduced level of GFP expression observed in single cell time courses after transfection with DLin LNPs compared to MC3 and KC2. We conclude that pH dependent bulk phase transitions trigger endosomal release.

BP 12.57 Tue 17:30 P4

Spatial-Stochastic Model of Cell Fate Decisions in Early Mouse Development — •Michael Alexander Ramirez Sierra[1], Tim Liebisch[1,2], Sabine C. Fischer[3], Franziska Matthäus[1,2], and Thomas R. Sokolowski[1] — [1]Frankfurt Institute for Advanced Studies (FIAS), Frankfurt am Main, Germany — [2]Goethe Universität Frankfurt am Main, Germany — [3]Julius-Maximilians-Universität Würzburg, Germany

The delicate balance necessary for ensuring reliable specification of cell lineages is an intriguing problem in developmental biology. As an important paradigm in tissue development, the early mouse embryo cell fate decisions have been extensively researched, but the underlying mechanisms remain poorly understood. Current approaches to this problem still primarily rely on deterministic modeling techniques, although stochasticity is an inherent feature of this biological process. We are developing a multi-scale event-driven spatial-stochastic simulator for emerging-tissue development. We build up new simulation schemes for incorporating suitable tissue-scale phenomena, and we fix important parameters by using experimental values or numerical optimization to infer biophysically-feasible regimes. We first explore the characteristics of this system in a single-cell setting. We then extend the study to a multi-cellular setting in order to understand how positional information is robustly achieved and preserved. Our latest results indicate a potential signaling mechanism for reliable patterning emergence, despite strong constraints imposed by cell cycles. We are closely exploring how these signals redefine cell fates.

BP 12.58 Tue 17:30 P4

Protein Dynamics in the Complex Physical Environment of the Synapse — •Simon Dannenberg, Sarah Mohammadinejad, and Stefan Klumpp — Institut für Dynamik komplexer Systeme Georg-August-Universität Göttingen, Göttingen, Germany

The synapse is a complex environment that is densely packed with proteins and has an internal geometry structured by membranes. This affects the mobility of proteins involved in signal transmission and hence, their availability at corresponding reaction sides.

In our work we use dynamic Monte Carlo simulations to investigate the individual influences of different physical features of the synapse on protein mobility. The simulations are parameterized by mobility measurements via FRAP experiments. By simulating protein mobility in synapses with different geometric features such as synapse volume and vesicle number, we study the influence of these features on concentration profiles in the synapse and other key aspects of signal transmission.

BP 12.59 Tue 17:30 P4

Single Cell Prime Editing Kinetics — •Nathalie Schäffler[1], Julian Geilenkeuser[2], Dong-Jiunn Jeffery Truong[2], Gil Westmeyer[2], and Joachim Rädler[1] — [1]LMU München, Deutschland — [2]Institute for Synthetic Biomedicine, Helmholtz-Zentrum München, Deutschland

CRISPR-Cas technology opens up new ways of approaching biological computing, taking advantage of the native language of biology and the inherent possibilities of DNA which could enable easier parallelism and higher storage capacities. However, to effectively leverage this technology a solid understanding of the kinetics and efficiency of gene editing is essential.

A key advancement in CRISPR-Cas is Prime Editing (PE), which enables precise "search-and-replace" of specific DNA sections without templates. However, PE requires delivery of both the PE specific Cas-9 protein and a guide RNA (pegRNA) into living cells. Two common strategies of non-viral in vivo delivery are via mRNA or pDNA constructs encoding both PE components. We compare these two methods and study their efficiency and timing using Live Imaging on Single Cell Arrays (LISCA).

Our experiments use a HEK293T cell line with stable expressing blue shifted mGreenLantern (mGL) as reporter system, taking advantage of the fact that only a short DNA sequence edit is needed to reverse the blue shift back to the green mGL. By recording the single cell kinetics and statistics of PE converting bs-mGL into mGL starting from the time point of transfection, we can assess editing times and efficiencies.

BP 12.60 Tue 17:30 P4

Self-generated oxygen gradients control the collective aggregation of photosynthetic microbes — •Alexandros Fragkopoulos[1,2], Jeremy Vachier[1], Johannes Frey[1], Flora-Maud Le Menn[1], Marco G. Mazza[1,3], Michael Wilczek[1,4], David Zwicker[1], and Oliver Bäumchen[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [3]Interdisciplinary Centre for Mathematical Modelling and Department of Mathematical Sciences, Loughborough University, Loughborough, Leicestershire LE11 3TU, UK — [4]University of Bayreuth, Theoretical Physics I, 95447 Bayreuth, Germany

In the absence of light, photosynthetic microbes can still sustain essential metabolic functionalities and motility by switching their energy production from photosynthesis to oxygen respiration. For suspensions of motile *C. reinhardtii* cells above a critical density, we demonstrate that this switch reversibly controls collective microbial aggregation [1].

Aerobic respiration dominates over photosynthesis in conditions of low light, which causes the microbial motility to sensitively depend on the local availability of oxygen. For dense microbial populations in self-generated oxygen gradients, microfluidic experiments and continuum theory based on a reaction-diffusion mechanism show that oxygen-regulated motility enables the collective emergence of highly localized regions of high and low cell densities.
[1] Fragkopoulos et al., J.R. Soc. Interface 18, 20210553 (2021).

BP 12.61 Tue 17:30 P4

Physical heterogeneities in bacterial mixtures under flow — •Giacomo Di Dio, Victor Sourjik, and Remy Colin — Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

Bacteria are often found in heterogeneous communities organized thorough physical interaction with their surrounding environment. Although external physical constraints like shear flow are frequent in natural situations, little is still known about their effect on the distribution of bacteria within complex communities. Under no flow condition, previous experiments have shown the emergence of large density fluctuations of passive bacterial cells driven by the activity of motile bacteria with which they are mixed. Through microfluidic experiments, we investigate how the spatiotemporal organization and the density distribution of a binary mixture of active and passive E. coli bacteria react under different configurations of shear flow. Our initial focus is on the effect of Poiseuille flow (linear shear profile) on the mixture, but we also plan to study the behavior under Couette flow. We notably focus on possible transport effects emerging from the combined action of external shear and active swimming on the non-motile species of the mixture. Our experiments aim at understanding the physical roles of flow and shear in the spatiotemporal organization of multispecies bacterial communities

BP 12.62 Tue 17:30 P4

Fast sorting of microfluidic droplets by content type with combined bright field and fluorescence detection — •Jonas Pfeil, Patricia Schwilling, and Othmar Marti — Universität Ulm, Ulm, Germany

Droplet-based microfluidics in context of fluorescent imaging can be used for a multitude of applications in biophysics, medicine, and lab-on-a-chip. One remaining issue in the encapsulation process of particle-like objects is that the number of encapsulated objects is Poisson or Poission-like distributed. A sorting step immediately after the encapsulation reduces the number of falsely-laden droplets.

Here we present results of sorting of beads with similar diameters and different fluorescent signals. Therefore, we encapsulate similar sized beads with different fluorescent signature and sort them using a time multiplexed imaging approach to simultaneously detect the population for each bead type. Thereby, we show that it is possible to achieve a user-defined, homogeneous configuration of fluorescent and non fluorescent particles in droplets.

BP 12.63 Tue 17:30 P4

Physics of optimal odor detection — •Swati Sen and David Zwicker — Max Planck Institute for Dynamics and Self-organization, Göttingen, Germany

Animals need to detect and discriminate odors for survival. In contrast to other senses, olfaction is shaped by physical processes, including odorant transport by the airflow and adsorption in the nasal mucus layer. These processes crucially affect what the brain can learn about the chemical composition of the environment. We study how the olfactory system relays information by using a simplified theoretical description of the airflow and the adsorption in the mucus. We predict the length scales over which odorants absorb along the olfactory epithelium. This length scale depends significantly on the odorant's solubility but is only weakly affected by odorant diffusivity and adsorption strength of mucus wall. We use these predictions to obtain the optimal arrangement of odorant receptor neurons that maximizes the information relay to the brain. We notice that the receptors sensitive to odorants with shorter adsorption length scale always reside closer to the cavity inlet side and cover the cavity in an increasing fraction of total cavity length with adsorption length scale. Taken together, we study design principles of optimal odor information encoding using a simple fluid dynamical model and information theory. Our approach could help to understand the natural olfaction process and develop artificial noses.

BP 12.64 Tue 17:30 P4

Assembly of plant-pollinator networks with rare and common plants — •Luca Schäfer, Lara Becker, and Barbara Drossel — TU Darmstadt, Darmstadt, Germany

Species interaction networks are subject to natural and anthropogenic disturbances that lead to their disassembly, while natural regeneration or restoration efforts facilitate their reassembly. Since over 90% of all angiosperms are pollinated by animals, understanding the stability and assembly of plant-pollinator networks is crucial for ecosystem conservation.

We introduce and investigate a model for the assembly of plant-pollinator networks from an infinite species pool, based on trait-matching between plants and animals. Population dynamics equations include different intraspecific competition strengths and niche width, to allow for the occurrence of rare (high intraspecific competition and small niche width) and common plants. We show that computer simulations of the model lead to the emergence of plant-pollinator networks where rare plants can persist despite the effect of pollen dilution. Over time, pollinators become more specialized, but this trend is stopped if stochasticity in the form of demographic noise is taken into account.

BP 12.65 Tue 17:30 P4

Statistical modelling of cerebral blood flow and transport in microvascular networks — •Florian Goirand[1], Tanguy Le Borgne[2], and Lorthois Sylvie[3] — [1]Center for Protein Assemblies, Physics Department, Technische Universität München, Garching bei München, Germany — [2]University of Rennes, CNRS, Géosciences Rennes, UMR 6118, Rennes, France — [3]Institut de Mécanique des Fluides de Toulouse, UMR 5502, CNRS, University of Toulouse, Toulouse, France

Despite of the high dependency of brain cells function on the efficiency of blood transport throughout the micro-vasculature, only little is known about the physical processes that drive neural cell supply. Here, based on the statistical analysis of realistic blood flow computations in mouse brain micro-vascular networks, we develop a statistical framework relating the structure of micro-vascular networks to the observed blood flow and transport heterogeneities. In particular, this framework enables to investigate the detrimental consequences of the cerebral blood flow decrease, a key phenomenon at early stage of Alzheimer's disease. We notably predict, in agreement with simulations, that the anomalous nature of the transport induces a non-linear evolution of the size of the regions exhibiting a critical concentration in oxygen or in neuro-toxic metabolic wastes with the decrease of the cerebral blood flow, unraveling an additionnal mechanism contributing to Alzheimer's disease progress.

BP 12.66 Tue 17:30 P4

Investigation of nonlinear effects on polarizable μbeads in AC/DC-Dielectrophoresis — •Tim R. Baumann, Dario Anselmetti, and Martina Viefhues — Experimental Biophysics & Applied Nanosciences, Department of Physics, Bielefeld University

Dielectrophoresis (DEP) is a common selective force used for separation applications in microfluidics. Due to a non-uniform electric field, polarizable particles migrate through a fluid. Depending on the applied electric field, intrinsic parameters like surface charge, polarizability or ion mobility and extrinsic parameters like pH-value objects lead to acceleration, deceleration or trapping in dielectrophoretic potentials. Thus, analysis of the migration in electric fields yields access to characteristic electric parameter of particles. The direction of movement is given by the value of charge and the direction of the electric field. Here a constant direct current (DC) is set in range $0 - 40\,V$ and incrementally raised by $5\,V$ to drive the beads through a microfluidic device. An alternating current (AC) ($f = 1\,kHz$) ranging from $100 - 450\,V$ in amplitude (increment size: $50\,V$) was superimposed to generate dielectrophoretic trapping forces that should decelerate the beads. An increase of migration velocity was observed though, which is assumed to be due to higher order terms of the electric field as recently presented by the group of Perez-Gonzales for DC electric fields [1]. In this work, we investigate if this effect also applies in AC electric fields.
[1]Anal. Chem. 2020, 92, 12871-12879

BP 13: Cytoskeleton

Time: Wednesday 9:30–12:45 Location: H15

Invited Talk BP 13.1 Wed 9:30 H15

Cortex mechanics - how subtle modifications matter — •Andreas Janshoff — Institute of Physical Chemistry, Tammannstr. 6, University of Goettingen, 37077 Goettingen

Cell cortices are responsible for the resilience and morphological dynamics of cells. Measuring their mechanical properties is impeded by contributions from other filament types, organelles, and the crowded cytoplasm. Therefore, we established two routes to examine its essential features using i) a bottom-up approach to create artificial minimal actin cortices (MACs) and b) by extracting cortices from living cells. Apical cell membranes of confluent MDCK II cells as well as MACs were deposited or formed on porous substrates and either locally deformed using an atomic force microscope setup or explored by microrheology techniques. Force cycles could be described with a time-dependent area compressibility modulus obeying the same power law as employed for whole cells. We found that subtle modifications such as the composition of the plasma membrane and origin of actin, i.e., the chosen isoform or its posttranslational modification are important for the dynamics and mechanics of the cortex. We found that the presence of phosphatidylserine in the inner leaflet of the plasma membranes is crucial for cortex contractility and efficient binding of F-actin to the membrane.

BP 13.2 Wed 10:00 H15

Dynamic bridging explains sub-diffusive movement of chromosomal loci — •Srikanth Subramanian and Seán Murray — Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

Chromosomal loci in bacterial cells show a robust sub-diffusive scaling of the mean square displacement (MSD) $\sim \tau^{\alpha}$, with $\alpha < 0.5$ under various growth conditions and antibiotic treatments. Recent experiments have also shown that DNA-bridging Nucleoid Associated Proteins (NAPs) play an important role in chromosome organisation and compaction. Here, using polymer simulations we investigate the role of DNA bridging in determining the dynamics of chromosomal loci. We find that bridging compacts the polymer and reproduces the sub-diffusive dynamics of monomers at timescales shorter than the bridge lifetime. Furthermore, the measured scaling exponent defines a relationship between chromosome compaction and bridge lifetime. Importantly, measuring the MSD of tagged chromosomal loci in WT and NAP mutant (ΔH-NS) we find that the decompacted mutant has a higher scaling exponent as expected. Based on the observed mobility of chromosomal loci and our simulations, we predict a lower bound on the average bridge lifetime of NAPs to be around 5 seconds.

BP 13.3 Wed 10:15 H15

Image analysis and modelling of nascent sarcomeres during myofibrillogenesis — •Ian D. Estabrook[1], Francine Kolley[1], Clément Rodier[2], Frank Schnorrer[2], and Benjamin M. Friedrich[1,3] — [1]cfaed, TU Dresden — [2]IBDM, Aix Marseille University — [3]Physics of Life, TU Dresden.

All animals possess striated muscle, which enable their voluntary movements. Inside muscle cells, actin and myosin molecular motors together with actin crosslinkers and the giant protein titin are arranged in long chains of sarcomeres in so-called myofibrils of almost crystalline regularity. Despite their physiological importance, it remains poorly understood how myofibrils spontaneously self-assemble during myofibrillogenesis. To investigate this molecular pattern formation process, our group combines image analysis and mathematical modelling, in close collaboration with the experimental Schnorrer lab.

We automatically analysed thousands of sarcomeres using a custom Matlab-based feature detection algorithm to analyse three-dimensional multi-channel fluorescence images of the Drosophila flight muscle. This allows us to compute averaged spatial intensity profiles of key proteins at different stages of myofibrillogenesis, providing a pseudo-time course of sarcomere assembly. Additionally, we observe rare abnormal sarcomeres, which reveals a a new mechanism by which a 'mother sarcomere' splits into two 'daughter sarcomeres'. This data drives mathematical modelling: minimal models demonstrate that non-local interactions between spatially extended myosin and titin molecules, as well as actin crosslinkers are sufficient to replicate sarcomeric pattern formation.

BP 13.4 Wed 10:30 H15

Torques within microtubule bundles generate the curved shape of the mitotic spindle — •Arian Ivec[1], Maja Novak[1], Monika Trupinić[2], Ivana Ponjavić[2], Iva Tolić[2], and Nenad Pavin[1] — [1]Department of Physics, Faculty of Science, University of Zagreb, Bijenička cesta 32, 10000 Zagreb, Croatia — [2]Division of Molecular Biology, Ruder Bošković Institute, Bijenička cesta 54, 10000 Zagreb, Croatia

The mitotic spindle is a complex micro-machine made up of microtubules and associated proteins, which are highly ordered in space and time to ensure its proper biological functioning. A functional spindle has a characteristic shape, which includes curved bundles of microtubules that are twisted around the pole-to-pole axis. An understanding of both how the linear and rotational forces define the overall shape of the mitotic spindle and how the twisted shapes arise as a result of interactions between microtubules and motor proteins is still missing. To answer this, we model the entire spindle by using a mean-field approach, in which we describe the forces and torques along microtubule bundles throughout the spindle. We compare our theoretical modeling with experimentally observed shapes of bundles in the mitotic spindle, including both unperturbed spindles and those compressed by an external force. We conclude that the observed shape of the spindle is predominately determined by rotational forces. Additionally, we find that a difference in bending forces explains the disparity in the shapes of inner and outer bundles, and that the chirality of the spindle is the result of a constant twisting moment.

BP 13.5 Wed 10:45 H15

Length-dependent poleward flux of sister kinetochore fibres promotes chromosome alignment — •Domagoj Božan — Department of Physics, Faculty of Science, University of Zagreb, Bijenička cesta 32, 10000 Zagreb, Croatia

Chromosome alignment at the spindle equator promotes proper chromosome segregation and depends on pulling forces exerted at kinetochore fiber tips together with polar ejection forces. However, kinetochore fibers are also subjected to forces exerted by motor proteins that drive their poleward flux. Here we introduce a flux-driven centering model that relies on flux generated by forces within the overlaps of bridging and kinetochore fibers. This centering mechanism works so that the longer kinetochore fiber fluxes faster than the shorter one, moving the kinetochores towards the center. Our collaborators developed speckle microscopy in human spindles and confirmed the key prediction that kinetochore fiber flux is length-dependent. The experiments also confirmed that kinetochores are better centered when overlaps are shorter and the kinetochore fiber flux markedly slower than the bridging fiber flux. Furthermore, we extend the model to describe congression of chromosomes by considering dynamics of microtubule-kinetochore attachments and motor proteins at kinetochores and find that the length-dependent forces exerted by microtubules from farther pole can overcome the forces exerted by the greater number of microtubules from nearer pole. Thus, length-dependent sliding forces exerted by the bridging fiber onto kinetochore fibers promote chromosome congression and alignment.

15 min. break

BP 13.6 Wed 11:15 H15

Mechanical properties of keratin and vimentin intermediate filaments — •Charlotta Lorenz[1], Johanna Forsting[1], Stefan Klumpp[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Göttingen, Germany

Different cell types require different mechanical properties. Prominent examples include cell contracting muscle cells, or migrating versus non-migrating cells. Cells change from a migrating to a non-migrating phenotype during cancer metastasis, wound-healing and embryogenesis (epithelial-to-mesenchymal transition). Interestingly, the expression of different intermediate filament (IF) proteins correlates with this transition: epithelial-like cells express mostly keratin, whereas mesenchymal cells primiarily express vimentin. We compare the mechanical response of keratin and vimentin on the single filament level using optical tweezers. We find that both filament types dissipate a large amount of mechanical input energy, which predestines them to act as a cellular shock

absorbers, yet by very different mechanisms, internal friction of sliding filament subunits, or nonequilibrium unfolding of alpha helices for keratin and vimentin filaments, respectively. We conclude that cells can tune their mechanics by differential expression of keratin versus vimentin.

BP 13.7 Wed 11:30 H15

Influence of vimentin intermediate filaments on microtubules in cells — •Anna Blob[1], Roman David Ventzke[1,2], Carolin Schlein[1], Laura Schaedel[3], Axel Munk[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen — [2]Institute for Mathematical Stochastics, University of Göttingen — [3]Center for Biophysics, Saarland University

The cytoskeleton in eucaryotic cells is an intricate network of three different filamentous proteins: microtubules, actin filaments and intermediate filaments. Together, they are essential for the mechanical properties as well as important functions of the cell, such as intracellular transport and division. Each protein has it own unique properties and there is evidence for important interactions between them. It has been shown that vimentin intermediate filaments stabilize microtubules in vitro and can template the microtubule network in migrating cells. Following up on this idea, we are interested in the influence of vimentin networks on microtubule mechanics. Cellular microtubules show characteristic buckling and bending behavior that is still not fully understood. Investigating the role of vimentin for the bending of microtubules will improve our understanding of the mechanical consequences and importance of the interactions between these filament systems. We compare microtubule networks in vimentin-knockout and wildtype mouse fibroblasts on micropatterns. Microscopy images are processed and analyzed with respect to the curvature of microtubules. We find that the local curvature of microtubules depends on the cellular region and increases with increasing vimentin density.

BP 13.8 Wed 11:45 H15

Microscopic modelling of forces and torques in the mitotic spindles — •Maja Novak[1], Arian Ivec[1], Iva M. Tolić[2], and Nenad Pavin[1] — [1]University of Zagreb, Faculty of Science, Bijenička c. 32, 10 000 Zagreb — [2]Rudjer Bosković Institute, Biophysics of Cell Division, Bijenička c. 54, 10000 Zagreb

The mitotic spindle is a complex micro-machine built from microtubules and associated proteins, with a purpose to properly separate genetic material into two nascent cells. In our previous work we found that microtubule bundles in human spindles follow a left-handed helical path [1], from which we concluded that torques, in addition to forces, exist in the mitotic spindle. However, theoretical description of molecular origin of forces and torques in the mitotic spindle is still missing. Here we show that single-molecule rotational forces regulate the volume of mitotic spindle, where larger twisting moment increases the spindle width. Our model describes microtubules as flexible rods, which are cross-linked by the motor proteins and passive linkers. The model predicts angular distribution of microtubules at the pole, based on experimentally observed shapes of microtubule bundles in the spindle midzone. Finally we found that the bending and twisting moment at the pole change between the inner and outer bundles in a manner qualitatively similar to curvature and twist obtained from the experimental data. In conclusion, our microscopic description opens up the possibility to quantify and understand both function and details of the twisting moment in the mitotic spindle. [1] Novak et al., Nat. Commun.(2018)9:3571

BP 13.9 Wed 12:00 H15

Correlative Super-Resolution Microscopy and Structural Analysis of Cells and Tissues — •Dimitar Stamov, Tanja Neumann, André Körnig, Torsten Müller, and Heiko Haschke — JPK BioAFM, Bruker Nano GmbH, Am Studio 2D, 12489 Berlin, Germany

Active forces in biological systems define the interactions between single molecules, growing cells and developing tissues. Cells adapt their shape and react to the surrounding environment by a dynamic reorganization of the F-actin cytoskeleton. We will demonstrate how cell spreading and migration in living KPG-7 fibroblasts and CHO cells, can be studied with high-speed AFM and associated with spatially resolved cytoskeletal reorganization events. We will further extend this with high-speed mechanical mapping of confluent cell layers, which in combination with optical tiling can be applied to automated analysis of large sample areas. We will show how AFM imaging and super-resolution 2color easy3D STED measurements can be combined and will show results of co-localized imaging and sample manipulation with a precision below the diffraction limit. We will discuss how to calculate the viscoelastic properties, characterized by the dynamic storage and loss modulus distribution in such samples.

BP 13.10 Wed 12:15 H15

Processive molecular motors stimulate microtubule turnover — William Lecompte[1], Sarah Triclin[2], Laurent Blanchoin[2,3], Manuel Théry[2,3], and •Karin John[1] — [1]Univ. Grenoble-Alpes, CNRS, Laboratoire Interdisciplinaire de Physique, 38000 Grenoble, France. — [2]Univ. Grenoble-Alpes, CEA, CNRS, INRA, Institute de Recherche Interdisciplinaire de Grenoble, Laboratoire de Physiologie Cellulaire & Végétale, CytoMorpho Lab, 38054 Grenoble, France — [3]Univ. Paris Diderot, INSERM, CEA, Hôpital Saint Louis, Institut Universitaire d'Hematologie, UMRS1160, CytoMorpho Lab, 75010 Paris, France

Microtubules (MTs) and molecular motors are ubiquitous in eukaryotic cells and are vital for many key cellular functions (eg. chromosome segregation, intracellular protein transport). Recent experiments have shown that processive molecular motors may damage the underlying microtubule lattice yet a mechanistic model has remained elusive. Here we investigate theoretically how molecular motors collectively remodel the shaft lattice, as opposed to a vision, where a single motor damages the microtubule as a rare event. Our leading concept is, that the walk of molecular motors locally and transiently destabilizes the lattice and may facilitate the removal of tubulin dimers. This mechanism (i) accelerates fracture of MTs in the absence of free tubulin and (ii) stimulates localized free tubulin dimer incorporation. The model reveals that a small transient perturbation (a few kT with a lifetime of 0.1 s) induced by the motor's walk is sufficient to modify significantly the lattice dynamics.

BP 13.11 Wed 12:30 H15

investigating cardio-myocyte scar formation on a single cell level using ROCS microscopy — •Arash Felekary[1], Alexander Rohrbach[1], Stephanie Schmid[2], and Eva Rog-Zielinska[2] — [1]IMTEK, Lab for Bio- and Nano-Photonics, Freiburg, Germany — [2]Institute for Experimental Cardiovascular Medicine, Freiburg, Germany

Rotating coherent scattering (ROCS) microscopy is a label-free super-resolution microscopy technique enabling 150 nm spatial and 10 ms temporal resolution, which is highly beneficial for live-cell imaging. We have applied ROCS in total internal reflection (TIR) mode to acquire high-quality images from tunneling nanotubes (TNTs). TNTs or membrane nanotubes, are more than 10 micrometers in length and about 100 nm thin and directly connect distant cells. It seems that after heart injuries, such as myocardial infarction, mechanical and biochemical communication between heart fibroblasts (FB) and cardio myocytes (CM) is established by TNTs, which helped to generate an extracellular matrix (ECM). TNTs could be involved in the exchange of small molecules and ions between neighbor cells, injury-signal recognition, and directed collagen deposition. We measured the interaction between CMs and FBs, i.e. the dynamics of TNT fluctuations by 100 Hz ROCS movies. With a post-processing activity analysis with frequency decomposition, we detected TNT stiffening over minutes. Computer simulations of stimulated TNT motions or thermal particle motions help to confirm or reject the underlying assumptions forming a mechanistic picture.

BP 14: Active Matter 3 (joint session BP/CPP/DY)

Time: Wednesday 9:30–12:30 Location: H16

BP 14.1 Wed 9:30 H16

Collective foraging of microrobots trained by reinforcement learning — •Robert C. Löffler[1], Emanuele Panizon[2], and Clemens Bechinger[1] — [1]Fachbereich Physik, Universität Konstanz, Konstanz, Germany — [2]Department of Quantitative Life Science, International Centre for Theoretical Physics, Trieste, Italy

From bacteria to mammals, collective behavior can be observed on all scales in nature. It is generally driven by the benefit to individuals when cooperating with others. However, the exact motivation of individuals to participate is challenging to investigate, as biological creatures are complex systems theirself. At the same time engineers seek to create collective groups of autonomous systems to perform dedicated tasks by cooperation.

Here we present an experimental model system of feedback-controlled microswimmers which are trained with multi agent reinforcement learning in an actor-critic scheme. A group of active particles is situated in a 2D environment containing a virtual food source which is changing position over time. Despite being rewarded individually for being inside the food source, particles show cohesive collective motion forming flocks and swirls. This is driven by the benefit of social information and collision avoidance, resulting in faster migration to a relocated food source. Understanding those mechanisms behind the emergence of collective behavior is of biological interest as well as to understand human crowd behavior and to design future robotic systems.

BP 14.2 Wed 9:45 H16

Collective response of microrobotic swarms to external threats — •Chun-Jen Chen[1] and Clemens Bechinger[1,2] — [1]Fachbereich Physik, Universität Konstanz, 78464 Konstanz, Germany — [2]Centre for the Advanced Study of Collective Behaviour, Universität Konstanz, 78464 Konstanz, Germany

Many animal species organize within groups to achieve advantages compared to being isolated. Such advantages can be found e.g. in collective responses which are less prone to individual failures or noise and thus provide better group performance. Inspired by social animals, here we demonstrate with a swarm of microrobots made from programmable active colloidal particles (APs) that their escape from a hazardous area can originate from a cooperative group formation. As a consequence, the escape efficiency remains almost unchanged even when half of the APs are not responding to the threat. Our results not only confirm that incomplete or missing individual information in robotic swarms can be compensated by other group members but also suggest strategies to increase the responsiveness and fault-tolerance of robotic swarms when performing tasks in complex environments.

BP 14.3 Wed 10:00 H16

Soft robots powered by magnetically driven active particles — •Hongri Gu and Clemens Bechinger — Fachbereich Physik, University of Konstanz, Germany

Active matter describes systems of a large number of self-driving particles that convert surrounding energy into active motion. Many of the emergent behaviors resemble life-like behaviors in nature. However, it is still unclear how one can utilize such active collective motions for engineering and robotic applications. In this talk, we would like to bridge the research fields of active matter and soft robots by designing soft machines powered by active matter. The main objective is to investigate the general interactions between swarm active particles and soft structures and use this knowledge to design a new type of soft robots that are driven by swarm active particles. To facilitate the investigation, we built a highly customizable fabrication process for magnetic composite soft structures at mesoscales based on two-step micromolding. We also built a modular magnetic actuation system based on rotating permanent magnets. This new experimental platform has an enormous design space for magnetic soft matters with the capability to tune individual system parameters. By carefully designing these parameters, it is possible to precisely tune the local magnetic, elastic, and hydrodynamic interactions between active particles and soft structures. This new type of soft machine can potentially take advantage of the robust dynamic states of the active matter, which can recover their functions from extreme mechanical deformations.

BP 14.4 Wed 10:15 H16

Microswimmers in viscosity gradients — •Sebastian Ziegler[1], Maxime Hubert[1], and Ana-Sunčana Smith[1,2] — [1]PULS Group, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Division of Physical Chemistry, Ruder Bošković Institute Zagreb, Croatia

Regions of variant viscosity are ubiquitous in both inanimate systems as well as in living systems. It is therefore of great interest to understand the effect of viscosity gradients on the mobility of both passive particles as well as on active systems. We firstly study a system of passive spheres and provide a general expression for the asymptotic mobility matrix in small viscosity gradients. We apply this result to linear viscosity gradients, where we unveil the existence of radially constant flows and elaborate on the effect of asymmetry of the particle position within the finite-size gradient, which hitherto has not been considered.

These results are subsequently applied to bead-spring microswimmers as model systems for self-propelling active matter. In contrast to the common approach of prescribing the stroke of the swimmer, we here employ a force-based swimmer model, allowing for an adaption of the swimming stroke to the environment, and reveal the rich viscotactic properties of such a microswimmer. We also construct a simple swimmer inspired by the Chlamydomonas algae and compare the viscotactic behavior of the biological swimmer to ours.

15 min. break

BP 14.5 Wed 10:45 H16

Noisy pursuit of active Brownian particles — •Segun Goh, Roland G. Winker, and Gerhard Gompper — IBI-5, Forschungszentrum Jülich, 52425 Jülich, Germany

Many biological and artificial agents are not only motile, but also capable of adjusting their motion based upon information gathered from their environment. This study considers sensing of a target and as a consequence reorientation of the direction of self-propulsion, which enables active pursuit. Specifically, an active Brownian particle is employed as a model agent to investigate pursuit dynamics in two dimensions, for both stationary as well as moving targets. We discuss how the interplay between intrinsic persistent self-propulsion and active reorientation by sensing gives rise to unexpected complex behaviors. In particular, the noise plays a pivotal role with both positive and negative influences on the success of pursuit. Numerical simulations and analytical calculations reveal that strong motility results in overshooting of the target, while pursuers cannot approach the target effectively at low Péclet numbers. Moreover, we propose a strategy to sort active pursuers according to their motility and reorientation capability by employing particular target trajectories.

BP 14.6 Wed 11:00 H16

Rheotaxis of the ciliate — •Takuya Ohmura[1], Yukinori Nishigami[2], and Masatoshi Ichikawa[3] — [1]Biozentrum, University of Basel, Switzerland — [2]Research Institute for Electronic Science, Hokkaido University, Japan — [3]Department of Physics, Kyoto University, Japan

Rheotaxis, a property of organisms to move against an external flow, has a crucial role to stay in living environment. For instance, freshwater fishes in rivers swim upstream to avoid being swept away to the sea. Interestingly, recent studies reported that not only fish but also swimming cells show rheotaxis. We elucidated the rheotaxis of the ciliate, Tetrahymena, a well-known single-celled freshwater microorganism swimming by cilia [1]. While that microorganism doesn*t have a sensor to detect flow direction and micrometer-sized particles are swept away downstream in a viscous flow, what dynamics underlie the rheotaxis of the ciliate? Our experiments revealed that the ciliate slid upstream along a wall, which indicates that the cells receive rotational torque from shear flow to align swimming orientation. To evaluate the shear torque, we performed a numerical simulation with a hydrodynamic model swimmer adopting cilia dynamics in a shear flow. The result suggests that the ciliate automatically slides upstream by using cilia-stalling mechanics.

[1] T. Ohmura, et al., Science Advances, 7(43), eabi5878 (2021).

BP 14.7 Wed 11:15 H16

Analytical study of active semiflexible ring polymer — •Christian A. Philipps, Gerhard Gompper, and Roland G. Winkler — Forschungszentrum Jülich, Jülich, Germany

Nature provides a variety of active matter systems, with self-propelled agents consuming internal energy or extracting it from their vicinity for locomotion [1]. Examples on the cellular level are self-propelled semiflexible actomyosin ring-like filaments driven by myosin motors in the cytoskeleton. We present a theoretical study of an active ring polymer [2] with tangential propulsion applying the continuous Gaussian semiflexible polymer model [3]. By a normal-mode expansion, the ring polymer conformational and dynamical properties, emerging by the homogeneous active force, and its interplay with rigidity are determined. Remarkably, the ring conformations are unaffected by activity for any rigidity. In contrast to linear filaments, the center-of-mass motion is independent of propulsion. However, activity strongly influences the internal dynamics with an activity enhanced diffusive for the flexible and a ballistic regime for the semiflexible ring polymer. Furthermore, a dominant rotational mode over several orders of magnitude in time emerges for high activities, which implies a rotational motion of the entire ring polymer. [1] R. G. Winkler, G. Gompper, J. Chem. Phys. 153, 040901 (2020); [2] M. Mousavi, R. G. Winkler, G. Gompper, J. Chem. Phys. 150, 064913 (2019); [3] T. Eisenstecken, G. Gompper, R. G. Winkler, Polymers 8, 304 (2016).

BP 14.8 Wed 11:30 H16

Dynamical Renormalization Group approach to the collective behavior of natural swarms — Andrea Cavagna[1], Luca Di Carlo[1], Irene Giardina[1], Tomas Grigera[1,3], •Giulia Pisegna[1,2], and Mattia Scandolo[1] — [1]Sapienza Università di Roma, Roma IT — [2]Max Planck Institute for Dynamics and Self-Organization, Goettingen DE — [3]IFLYSIB, La Plata, Argentina

Recent data on strongly correlated biological systems showed the validity of scaling laws as one of the fundamental traits of collective behaviour. Experiments on natural swarms of insects unveiled traces of critical dynamics, with inertial features and a dynamical critical exponent z=1.2. To rationalize this evidence, we develop an inertial active field theory in which the velocity is coupled to its generator of internal rotations, namely the spin, through a mode-coupling interaction. We study its near-critical regime with a one-loop Renormalization Group approach under the assumption of incompressibility. The presence of friction in the dynamics of the spin rules a paramount crossover between two fixed points: the unstable underdamped fixed point with z=1.3 and the stable overdamped fixed point with z=1.7, where dissipation takes over. We show how finite-size systems with weak dissipation, such as swarms, can actually exhibit the critical dynamics of the unstable fixed point thus providing a theoretical result which is in fair agreement with experimental data.

15 min. break

BP 14.9 Wed 12:00 H16

Dynamics and rheology of active suspensions in viscoelastic media — •Akash Choudhary[1], Sankalp Nambiar[2], and Holger Stark[1] — [1]Institute of Theoretical Physics, Technische Universität Berlin, 10623 Berlin, Germany — [2]Nordita, KTH Royal Institute of Technology and Stockholm University, Stockholm 10691, Sweden

Active suspensions are systems of motile organisms or active motors that are driven out of equilibrium through self-propulsion. This localized energy-work conversion imparts rich phenomenology and anomalous macroscale properties that are in stark contrast to passive suspensions and polymeric fluids. Motivated by the ubiquitous microbial systems in biological fluids, we analyse the impact of non-Newtonian fluids on the rheological response of active suspensions to steady shear flows.

We first study the suspension at an individual scale and show that elongated pushers (representative of *E. coli*) and pullers (*C. reinhardtii*) exhibit diverse orbital dynamics in a viscoelastic fluid. We find that the active stresses not only modify the Jeffery orbits, well-known for viscous fluids, but microswimmers can even resist flow-induced rotation and align themselves at an angle with the flow. To analyze the impact of such behavior on the bulk rheological response, we study an ensemble of a dilute suspension of such swimmers in the presence of stochastic noise from bacterial tumbling and rotary diffusion. In comparison to Newtonian media, the polymeric elastic stresses substantially and non-monotonically amplify the swimmer-induced viscosity, in particular, the superfluid transition of pusher solutions.

BP 14.10 Wed 12:15 H16

Intercellular transport in *Chara corallina* — •Florian von Rüling[1], Anna Alova[2], Alexander Bulychev[2], and Alexey Eremin[1] — [1]Otto von Guericke University Magdeburg, Germany — [2]Moscow, Russia

We explore the kinetics of the intercellular transport between the giant cells of characean algae. The transport involves advection via cytoplasmic streaming and diffusion through the plasmodesmata, pores that penetrate the cell walls. Using fluorescent dye as a tracer, we measure the permeation through the node of tandem cells. The permeability is extracted from the experimental data using an advection-diffusion model. The current work is focused on the roles of cytoplasmic streaming and the nodal cells in the transport mechanism. To separate the diffusive permeation from the advective contribution, cyclosis was temporarily inhibited using action potentials. Streaming cessation results in dye accumulation in the vicinity of the node. The shape of regions with high dye concentration indicates that action potentials may induce closure of the plasmodesmata in central nodal cells.

BP 15: Protein Structure and Single Molecules

Time: Wednesday 10:00–12:15 Location: H13

BP 15.1 Wed 10:00 H13

Using physics to understand and fight viruses — •Jan Lipfert[1], Willem Vanderlinden[1], Pauline Kolbeck[1], Sophia Gruber[2], Magnus Bauer[3], and Hermann Gaub[2] — [1]Utrecht University — [2]LMU Munich — [3]Stanford University

Viruses can cause human disease, with dramatic and global consequences. Here, I will present how we use single-molecule approaches to investigate aspects of the life cycles of SARS-CoV-2 and HIV. First, we have developed a tethered ligand assay to investigate how SARS-CoV-2 attaches to human cells. Using magnetic tweezers and AFM force spectroscopy, we obtain a comprehensive view of the force stability of the critical first interaction of the virus with our cells (Bauer, Gruber, et al. PNAS 2022) and investigate the current variants of concern. We find differences in force stability that help rationalize the epidemiology of the different variants (Gruber et al., unpublished). Second, we use magnetic tweezers and AFM imaging to investigate the interactions of retroviral integrases with DNA. We obtain a comprehensive view of the free energy landscape of retroviral integration for prototype foamy virus (Vanderlinden et al. Nature Comm. 2019) and find that, in addition to it well known catalytic role, HIV integrase can efficiently condense DNA into biomolecular condensates (Kolbeck et al., unpublished).

BP 15.2 Wed 10:15 H13

Angle-dependent strength of a single chemical bond by stereographic force spectroscopy — Wanhao Cai[1], •Jakob Tómas Bullerjahn[2], Max Lallemang[1,3], Klaus Kroy[4], Bizan Balzer[1,3,5], and Thorsten Hugel[1,3] — [1]Institute of Physical Chemistry, University of Freiburg, Germany — [2]Department of Theoretical Biophysics, Max Planck Institute of Biophysics, Frankfurt am Main, Germany — [3]Cluster of Excellence livMatS@FIT - Freiburg Center for Interactive Materials and Bioinspired Technologies, University of Freiburg, Germany — [4]Institute for Theoretical Physics, Leipzig University, Germany — [5]Freiburg Materials Research Center, University of Freiburg, Germany

A wealth of chemical bonds and polymers have been studied with single-molecule force spectroscopy, usually by applying a force perpendicular to the anchoring surface. However, the direction-dependence of the bond strength lacks fundamental understanding. Here we establish stereographic force spectroscopy to study the single-bond strength for various pulling angles. Surprisingly, we find that the apparent bond strength increases with increasing pulling angle relative to the

anchoring surface normal, indicating a sturdy mechanical anisotropy of a chemical bond. This finding can be rationalized by a fixed pathway for the rupture of the bond, resulting in an effective projection of the applied pulling force onto a nearly fixed rupture direction. Our study is fundamental for the molecular understanding of the role of the direction of force application in molecular adhesion and friction.

BP 15.3 Wed 10:30 H13

Rebinding kinetics from single-molecule force spectroscopy experiments close to equilibrium — •Jakob Tómas Bullerjahn[1] and Gerhard Hummer[1,2] — [1]Department of Theoretical Biophysics, Max Planck Institute of Biophysics, 60438 Frankfurt am Main, Germany — [2]Institute of Biophysics, Goethe University Frankfurt, 60438 Frankfurt am Main, Germany

Analysis of bond rupture data from single-molecule force spectroscopy experiments commonly relies on the strong assumption that the bond dissociation process is irreversible. However, with increased spatiotemporal resolution of instruments it is now possible to observe multiple unbinding-rebinding events in a single pulling experiment. Here, we augment the theory of force-induced unbinding by explicitly taking into account rebinding kinetics, and provide approximate analytic solutions of the resulting rate equations. Furthermore, we use a short-time expansion of the exact kinetics to construct numerically efficient maximum likelihood estimators for the parameters of the force-dependent unbinding and rebinding rates, which pair well with and complement established methods, such as the analysis of rate maps. We provide an open-source implementation of the theory, evaluated for Bell-like rates, which we apply to synthetic data generated by a Gillespie stochastic simulation algorithm for time-dependent rates.

15 min. break

Invited Talk BP 15.4 Wed 11:00 H13

The importance of water in membrane receptor function — •Anthony Watts — Biochemistry Department, South Parks Road, Oxford, OX1 3QU, UK

Resolving conformational changes in membrane receptors in response to a stimulus, and capturing their functionally relevant dynamics, is very challenging. Over the years we have addressed this challenge using a range of spectroscopic approaches1,2,3 on functionally competent photoreceptors, often in their natural membranes4 or Lipodisqs*5. We have complemented this work with functional studies, mass spec characterization6 and very high resolution (1.07Å) crystallography7,8, as well as photo-induced x-ray, free electron laser studies (XFELS), without the use of detergents and including natural lipids. This high-resolution information reveals waters and their importance in both receptor activation-desensitization and QM(SCC-DFTB)/MM MD trajectories give information about the activation process. The system studied is achearhodopsin-3 (AR3), a photoreceptor utilized widely in optogenetics despite the lack of structures. The arrangement of internal water networks is responsible for the faster photocycle compared to homologs. These insights have generic implications for other receptors. (1). Higman et al., (2011) Angew. Chemie 50(36):8432 (2). Dijkman et al., (2018) Nature Comms. 9:1710 (3). Dijkman et al., (2020) Science Advances, 6:33 (4). Lavington & Watts (2020) Biophys. Rev. 12:1287 (5). Juarez et al., (2019) Chem. Phys. Lipids 221:167 (6). Hoi et al., (2021) Nano Letters, 21(7):2824 (7). Axford et al., (2022) Acta Cryst D78:52 (8). Juarez et al (2021) Nature Comms. 12:629

BP 15.5 Wed 11:30 H13

Exploring the molecular details of the role of methylation and ATP in chemotaxis signaling — •HIMANSHU JOSHI[1] and MEHER PRAKASH[2] — [1]Jawaharlal Nehru Centre for Advanced Scientific Research (JNCASR), Bengaluru, 560064 — [2]EPFL EssentialTech Center, Switzerland

Chemotaxis is the movement of bacteria in response to the surrounding chemical concentration gradients. Bacteria perform runs and tumbles due to the anti-clockwise and clockwise rotation of their flagella depending on the type and gradient of chemical concentration. The molecular concentration sensed by the binding of nutrients is transmitted across the membrane and over 200 Angstroms for a kinase domain actuation. The question then arises as to what is the molecular basis of this signal propagation? Performing long all atom molecular dynamics (MD) simulations on the CryoEM structures that have become recently available, we study the plausible interactions between the methylation and the ATP hydrolysis. Our study, the MD first one which includes methylation and ATP, finds several correlations with the experimental data such as the matching contacts among the dynamic domains, the intermediate state, higher gamma-phosphate coordination by the methylated protein. The results on this very important signaling mechanism are encouraging, a validation which is non-trivial when performing MD on an extended spatial or time scale or with a new class of proteins (fibrillar in this case), to perform further MD studies on this large protein complex.

BP 15.6 Wed 11:45 H13

Identifying the Functional Dynamics in Proteins - Divide and Conquer the Feature Space — •Daniel Nagel, Georg Diez, and Gerhard Stock — Biomolecular Dynamics, Institute of Physics, Albert-Ludwigs-Universität, 79104 Freiburg, Germany

The function of proteins is closely linked to their conformational changes. To support experiments, molecular dynamics simulations allow high spatiotemporal resolution while generating large amounts of data. To model and interpret them, it is essential to identify suitable features, such as backbone dihedral angles or interresidual distances. However, in this high-dimensional feature space—in addition to the motion of interest—one finds uncorrelated motions described by small subsets of features, which poses a difficult challenge for the subsequent dimensionality reduction and understanding of the underlying biological process.

In the following we present an effective and scalable correlation-based feature selection method (MoSAIC) that identifies functional dynamics in the feature space and separates it from noise in order to facilitate the further analysis. To demonstrate the different application purposes, we adopt the unsupervised method to systems of various complexity.

G. Diez, D. Nagel, and G. Stock, Correlation-based feature selection to identify functional dynamics in proteins, arxiv:2204.02770, 2022

BP 15.7 Wed 12:00 H13

Understanding friction in ligand protein systems — •Miriam Jäger[1], Wanhao Cai[2], Jakob T. Bullerjahn[3], Thorsten Hugel[2], Steffen Wolf[1], and Bizan N. Balzer[2] — [1]Biomolecular Dynamics, Institute of Physics, University of Freiburg, Hermann-Herder-Str. 3, 79104 Freiburg, Germany — [2]Institute of Physical Chemistry, University of Freiburg, Albertstr. 21, 79104 Freiburg, Germany — [3]Department of Theoretical Biophysics, Max Planck Institute of Biophysics, 60438 Frankfurt am Main, Germany

Both experiments and simulations have shown the importance of friction in biomolecular system dynamics. To gain a deeper understanding of the connection between directional forces and friction, we study the streptavidin-biotin complex in a combination of stereographic force spectroscopy experiments and biased molecular dynamics simulations. While experiments show an increasing mean rupture force and rupture force variance with steeper pulling angles, the simulations display similar internal friction, but an anisotropy in the free energy barriers. Based on the simulation results, we propose that this anisotropy in barriers manifests itself in experiments as the increase in friction. This effect can be viewed as anisotropic friction.

BP 16: Networks: From Topology to Dynamics (joint session SOE/BP/DY)

Time: Wednesday 10:15–12:45 Location: H11

BP 16.1 Wed 10:15 H11

Modeling tumor disease and sepsis by networks of adaptively coupled phase oscillators — •Eckehard Schöll[1,2,3], Jakub Sawicki[2], Rico Berner[1,4], and Thomas Löser[5] — [1]Institut für Theoretische Physik, TU Berlin, Germany — [2]Potsdam Institute for Climate Impact Research — [3]Bernstein Center for Computational Neuroscience Berlin — [4]Institut für Physik, HU Berlin — [5]Institut LOESER, Wettiner Straße 6, 04105 Leipzig

In this study, we provide a dynamical systems perspective to the modelling of pathological states induced by tumors or infection. A unified disease model is established using the innate immune system as the reference point. We propose a two-layer network model for carcinogenesis and sepsis based upon the interaction of parenchymal cells (organ tissue) and immune cells via cytokines, and the co-evolutionary dynamics of parenchymal, immune cells, and cytokines [1]. Our aim is to show that the complex cellular cooperation between parenchyma and stroma (immune layer) in the physiological and pathological case can be functionally described by a simple paradigmatic model of phase oscillators. By this, we explain carcinogenesis, tumor progression, and sepsis by destabilization of the healthy state (frequency synchronized), and emergence of a pathological state (multifrequency cluster). The coupled dynamics of parenchymal cells (metabolism) and nonspecific immune cells (reaction of innate immune system) are represented by nodes of a duplex layer. The cytokine interaction is modeled by adaptive coupling weights. [1] Sawicki, J., Berner, R., Löser, T., and Schöll, E., Frontiers Netw. Physiology 1,730385 (2022), arXiv:2106.13325v2.

BP 16.2 Wed 10:45 H11

Analysis of the Football Transfer Market Network — •Tobias Wand — WWU Münster — CeNoS Münster

Football clubs buy and sell players for millions of Euros and until Covid, their combined transfer values were growing steadily at an impressive rate. Instead of analysing their aggregated transfer activities, one can take a look at the topology of the network of player transfers: complex networks have already been used in various sciences [1] including research on sports [2] and provide a novel approach to investigate the football transfer market network and in particular the impact of Covid on football clubs.

[1] G. Caldarelli and A. Vespignani, "Large Scale Structure and Dynamics of Complex Networks". World Scientific Publishing, 2007.

[2] Arriaza-Ardiles et al. "Applying graphs and complex networks to football metric interpretation". Human Movement Science 57, 2018.

BP 16.3 Wed 11:00 H11

Variability in mesoscale structure inference using stochastic blockmodels — •Lena Mangold and Camille Roth — CNRS (Paris) / Centre Marc Bloch (Berlin)

Characterising the mesoscale structure of networks, in terms of patterns variously called communities, blocks, or clusters, has represented both a central issue and a key instrument in the study of complex systems. Clearly, distinct methods designed to detect different types of patterns may provide a variety of answers to the mesoscale structure. Yet, even multiple runs of a given method can sometimes yield diverse and conflicting results, posing challenges of model and partition selection. As an alternative to forcing a global consensus from a distribution of partitions (i.e. choosing one among many by maximising some objective), recent work has emphasised the importance of exploring the variability of partitions. Here we examine how a specific type of mesoscale structure (e.g. assortative communities or core-periphery) may be linked with more or less inconsistency in resulting partitions. We focus on Stochastic blockmodels (SBMs), initially proposed in mathematical sociology and increasingly used to infer mesoscale structure with a relatively general definition of similarity between nodes in the same group, and whose stochastic nature lends itself to the exploration of disagreement within populations of partitions. In particular, we generate families of synthetic networks in which we plant different types of mesoscale structures and explore the transitions between consensus and dissensus in the landscape of partitions over multiple SBM runs.

BP 16.4 Wed 11:15 H11

Extracting signed relations from interaction data — •Georges Andres, Giona Casiraghi, Giacomo Vaccario, and Frank Schweitzer — ETH Zürich, Chair of Systems Design, Switzerland

Social relations influence human interactions and hence, help to explain individual behaviours. Moreover, humans perceive patterns of signed relations, either positive (e.g., friendship) or negative (e.g., enmity), and adapt to them. Data about signed relations are rare, despite their importance for understanding phenomena at the community level. Interaction data is, however, more abundantly available, for example, about proximity or communication events. Interactions and relations change on different time scales; interactions are more volatile and evolve faster than relations. Using this, I will present an ensemble-based approach to infer pair-wise signed relations from interaction data and consequently construct a signed network from them. By studying different datasets on interactions and relations, e.g. between students, I will further evaluate the quality of the inferred networks. Subsequently, I will study the presence of structural balance in the studied communities, describing the cognitive dissonance ensuing from particular triadic constellations of signed relations. Bearing similarities to frustrations in spin systems, structural balance can now be analysed solely from interaction data thanks to the presented method, a task which was previously out of reach.

BP 16.5 Wed 11:45 H11

Disentangling homophily, community structure and triadic closure in networks — •Tiago Peixoto — Central European University, Vienna, Austria

Network homophily, the tendency of similar nodes to be connected, and transitivity, the tendency of two nodes being connected if they share a common neighbor, are conflated properties in network analysis, since one mechanism can drive the other. Here we present a generative model and corresponding inference procedure that is capable of distinguishing between both mechanisms. Our approach is based on a variation of the stochastic block model (SBM) with the addition of a triadic closure dynamics, and its inference can identify the most plausible mechanism responsible for the existence of every edge in the network, in addition to the underlying community structure itself, based only on the final observation of the network. We show how the method can evade the detection of spurious communities caused solely by the formation of triangles in the network, and how it can improve the performance of link prediction when compared to the pure version of the SBM without triadic closure.

[1] Tiago P. Peixoto, Disentangling homophily, community structure and triadic closure in networks, Phys. Rev. X 12, 011004 (2022)

BP 16.6 Wed 12:15 H11

Evolving networks towards complexity: an evolutionary optimization approach — Archan Mukhopadhyay and •Jens Christian Claussen — University of Birmingham, UK

Complexity measures for graphs have been proposed and compared [1,2] widely, but the question how to mathematically define complexity is less clear as for text strings where Lempel-Ziv and Kolmogorov complexity provide clear approaches. In complexity science, the notion of complexity implies distinction from regular structures (lattices) as well as from random structures (here: random graphs). This however has not lead to any constructive definition. Complexity measures therefore typically assess artefacts of complexity (in some cases quite successfully). Here we present a complementary computational approach: we utilize each complexity measure as a fitness function of an evolutionary algorithm, and investigate the properties of the resulting networks. The goal is a better understanding of the existing complexity measures, and to shed some light on (artificial) network evolution: what evolutionary goals lead to complexity?

BP 17: Membranes and Vesicles

Time: Wednesday 15:00–17:00 Location: H13

BP 17.1 Wed 15:00 H13

Lipid domain diffusion in confined geometry — •Claudia Steinem, Nikolas K. Teiwes, and Ole M. Schütte — Georg-August Universität, Göttingen, Germany

Pore-spanning membranes (PSMs) are well-suited to investigate lipid domain diffusion. Recent findings have highlighted the dynamic nature of such lipid domains in the plasma membrane of mammalian cells and the key role of the underlying cytoskeleton network in confining their diffusion. We established PSMs composed of DOPC, sphingomyelin, and cholesterol with co-existing liquid ordered (lo)/liquid disordered (ld) domains on silicon substrates with micrometer-sized pores to investigate the diffusion of lo-domains confined in the freestanding parts of the PSMs. We compared the lo-domains in the artificial PSMs with PSMs derived from spreading giant plasma membrane vesicles (GPMVs) obtained from HEK-293 cells. In both cases, mobile ordered domains are visualized by fluorescence microscopy. From the trajectories of the individual mobile domains, the MSD is determined, which provides the diffusion constants as a function of domain size. The analysis reveals that the domains' diffusion constants are slowed down by orders of magnitude due to the confinement in the PSM, where the drag force is governed by both the friction in the bilayer and the coupling to the aqueous phase compared to the unrestricted case. From the analysis, the membrane surface viscosity can be extracted, which is by a factor of four smaller in case of the naturally derived membranes compared to the artificial ones, which can be explained in terms of the large protein content in the GPMV-derived membranes.

BP 17.2 Wed 15:15 H13

SAXS measurements of photoswitching in azobenzene lipid vesicles — Martina Ober[1], Adrian Müller-Deku[2], Oliver Thorn-Seshold[2], and •Bert Nickel[1] — [1]Faculty of Physics and CeNS, Ludwig-Maximilians-Universiät München, Geschwister-Scholl-Platz 1, Munich 80539, Germany — [2]Department of Pharmacy, Ludwig-Maximilians-Universität München, Butenandtstraße 5-13, Munich 81377, Germany,

We study the switching of photoresponsive lipids that allow for precise and reversible manipulation of membrane shape, permeability, and fluidity. Though these macroscopic responses are clear, it is unclear how large the changes of trans/cis ratio are, and whether they can be improved. Here, we use small-angle X-ray scattering to measure the thickness of photoswitchable lipid membranes, and we correlate lipid bilayer thickness to trans/cis ratios [1]. This reveals an unexpected dependency of photoswitching ratio upon aqueous phase composition. In buffer with ionic strength, we observe thickness variations twice as large as previously observed. Furthermore, soft X-rays can quantitatively isomerise photolipid membranes to the all-trans state; enabling X-ray-based membrane control. High energy X-rays do not influence the state of the photoswitches, presumably because they deposit less dose in the sample.

[1] M. Ober et al, Nanophotonics 2022; 11(10): 2361, DOI https://doi.org/10.1515/nanoph-2022-0053

BP 17.3 Wed 15:30 H13

Buoyant adhered vesicles in finite-range membrane-substrate interactions — •Lucia Wesenberg and Marcus Müller — Georg-August University, Göttingen, Germany

Constructing switchable interlayers between soft, biological objects and hard solids is a major challenge to dynamically regulate interface interactions. Here, we focus on the adhesion of lipid vesicles on bio-inspired polymer substrates. Experiments on the adhesion of liquid droplets or vesicles on switchable surfaces often facilitate contact with the substrate by a density difference. But when compared to theoretical expectations, this key experimental characteristic as well as the finite range of the membrane-substrate interaction have mostly been neglected. Thus, we systematically studied the adhesion of axially symmetric vesicles for finite-range membrane-substrate interaction and buoyancy through simulations. We investigated the adhesion transition of vesicles in the absence of thermal fluctuations. For downward buoyancy, vesicles sediment onto the substrate and there is no mean-field adhesion transition. Whereas for upward buoyancy, adhered vesicles are metastable at best. A proper adhesion transition can only occur at zero buoyancy. Moreover, length scales such as the capillary length, extrapolation length, and curvature-decay scale exhibit a pronounced dependence on interaction range and buoyancy and should not be used uninformed. Whereas these characteristics significantly modified the adhesion diagram, the local transversality condition - relating contact curvature to adhesion strength and vesicle's bending rigidity - remains accurate in the presence of moderate buoyancy.

BP 17.4 Wed 15:45 H13

Seaweed and dendritic domains of erucic acid monolayers — •Florian Gellert, Heiko Ahrens, Harm Wulff, and Christiane A. Helm — Institute of Physics, University of Greifswald, Germany

Nucleation and growth of domains in the liquid expanded/liquid condensed phase transition in monolayers of erucic acid at the air/water interface is studied with a Brewster Angle Microscope. With increase of the compression speed of the monolayer, the growth mode of the domains changes from seaweed to dendritic. Seaweed domains have broad tips, and wide, variable side branch spacing. Dendritic domains have narrower tips, and small, well-defined side branch spacing and a larger fractal dimension. The domains have different growth mechanisms: seaweed domains grow by surface diffusion while dendrite domains grow by diffusion in the subphase (Marangoni effect). The hydrodynamic models of domain growth will be discussed.

15 min. break

BP 17.5 Wed 16:15 H13

Asymmetric membranes, chemical potentials and homeostasis — •Martin Girard — Max-Planck-Institut für Polymerforschung

The properties of membranes in cells are tightly regulated. For instance, Sineski clearly established that E. Coli cells maintain a viscosity of around 2 poise, which is achieved by modulating the chemical composition of the membrane. How cells choose to alter this composition is not obvious, and has been associated with various controversies over the years.

I have recently introduced usage of chemical potential in computer simulations as a proxy for membrane homeostasis in cells. In coarse-grained simulations, this results in surprisingly good agreement between trends measured in cells and simulation results. I have also shown that this model can be used as a proxy for flippase proteins, and thus enables simulations of asymmetric membranes. Using this model, I will show that imposing asymmetries in membranes can result in surprising behavior. For example, that cholesterol concentration can become correlated with the presence of unsaturated lipids, in accord with experimental measurements. I will discuss the biological implications of these results.

BP 17.6 Wed 16:30 H13

Coherent Diffractive Imaging of Synaptic Vesicles by Femtosecond FEL pulses — •Charlotte Neuhaus[1], Jette Alfken[1], Moritz Stammer[1], SPB Team[2], Marcelo Ganzella[3], Reinhard Jahn[3], and Tim Salditt[1] — [1]Georg-August-Universität, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen — [2]European XFEL, Holzkoppel 4, 22869, Schenefeld, Germany — [3]Department of Neurobiology, Max-Planck-Institut for Multidisciplinary Sciences, Am Faßberg 11, 37077, Göttingen, Germany

Synaptic Vesicles (SVs) are secretory organelles which store neurotransmitters in presynaptic nerve endings. Due to the small size of vesicles ($R \approx 20\,nm$), a high spatial resolution is needed to gain more insights into the structure and structural dynamics of SVs, including functional lipid and protein components. To this end, solution SAXS experiments were previously used, yielding information about the average electron density of SVs. However, many of the relevant structural properties and parameters are screened by ensemble averaging, given the substantial polydispersity of SVs and unavoidable contaminations in the preparations. To overcome these limitations, we have carried out serial diffraction experiments on single vesicles (including lipid vesicles, proteoliposomes and SVs) delivered by an aerosol jet into a nano-focused X-ray Free Electron Laser (XFEL) beam. By the *'diffraction before destroy'* principle, the individual vesicles can be probed without radiation damage. Thousands of diffraction patterns can now be analyzed and reconstructed. We report these experiments and preliminary results (data analysis still ongoing).

BP 17.7 Wed 16:45 H13

Dynamics of active vesicles — Priyanka Iyer, Masoud Hoore, Thorsten Auth, Gerhard Gompper, and •Dmitry Fedosov — Institute of Biological Information Processing and Institute for Advanced Simulation, Forschungszentrum Juelich, Juelich 52425, Germany

Biological cells are able to generate intricate structures and respond to external stimuli, sculpting their membrane from inside. Simplified biomimetic systems can aid in understanding the principles which govern these shape changes and elucidate the response of the cell membrane under strong deformations. We employ simulations of vesicles enclosing active self-propelled particles to investigate different non-equilibrium shapes with tether-like protrusions and highly branched, dendritic structures. Furthermore, adhesive interactions between active particles and the membrane result in highly branched tethers at low particle activity, where the system exhibits 'pseudo-equilibrium' shapes. The resulting membrane fluctuations present anomalous behaviour at high adhesive strengths, as they show an initial decrease with increasing activity. The active particles show ordering at the membrane surface which initially increases with activity and then decreases. The obtained state diagram characterizes shapes of active vesicles for various conditions applied.

BP 18: Biomaterials (joint session BP/CPP)

Time: Wednesday 15:00–17:30 Location: H15

Invited Talk BP 18.1 Wed 15:00 H15

Bottom-up molecular control of biomimetic hydrogels — •Kerstin G. Blank — Johannes Kepler University, Institute of Experimental Physics, Altenberger Str. 69, 4040 Linz, Austria

The development of biomimetic hydrogels has greatly facilitated fundamental studies aimed at understanding cellular mechanosensing and mechanotransduction processes. It is now widely accepted that cells sense the elastic and viscoelastic properties of their surroundings and respond to these properties via a range of different mechanisms. It is still unknown, however, how cells determine these material properties. Hydrogels are usually characterized as bulk samples while cells interact with these materials in a highly localized manner via specific receptor-ligand interactions. It is thus essential to adopt the cellular point of view and establish a link between microscopic and macroscopic material properties. Towards this goal, we utilize biomimetic hydrogels consisting of mechanically characterized synthetic polymers and extracellular matrix-inspired peptides that serve as physical crosslinks. Using selected examples, we show how crosslink thermodynamics, kinetics and mechanics as well as network topology affect the linear and non-linear viscoelastic properties of molecularly programmed hydrogels. In particular, we highlight that both individual crosslink properties and network topology affect network stress relaxation and show how molecular bond rupture correlates with bulk material failure. Our modular hydrogel system allows for tuning different parameters independently and thus serves as an excellent platform for disentangling the roles of different material properties on cellular responses.

BP 18.2 Wed 15:30 H15

The role of protein constriction in the fission of membrane tubes — •Russell Spencer and Marcus Müller — Georg-August Universität Göttingen, Institute for Theoretical Physics, 37077 Göttingen, Germany

Membrane remodelling, such as fusion and fission, is involved in a variety of basic, cellular processes. When unaided, the free energy barriers for such remodelling can be prohibitively high, so biological systems employ proteins as catalysts. This work investigates the influence of proteins, such as dynamin, which constrict membrane tubes in order to lower the barrier to fission. We are particularly interested in their role in double-membrane fission as it occurs in mitochondrial division. This work employs self-consistent field theory and utilizes the string method to find the Minimum Free Energy Path (MFEP) in order to determine the most likely pathway for the transition. In addition to lowering the free energy barrier, constriction of the tubes also affects the dominant transition pathway. This work explores the interplay between membrane tension and constriction and the effects that these influences have on fission mechanisms of single and double membrane tubes.

BP 18.3 Wed 15:45 H15

Rate-Independent Hysteretic Energy Dissipation in Collagen Fibrils — Robert Magerle, •Paul Zech, Martin Dehnert, Alexandra Bendixen, and Andreas Otto — Fakultät für Naturwissenschaften, Technische Universität Chemnitz, 09107 Chemnitz, Germany

Nanoindentation data measured with an atomic force microscope on hydrated collagen fibrils above the glass transition, display a rate-independent hysteresis with return point memory. It is caused by the interplay of elastoplastic deformation during tip indentation followed by elastocapillary recovery of the indent during tip retraction. This previously unknown energy dissipation mechanism dominates at slow indentation rates, where viscous friction is negligible. A generic hysteresis model, based on force-distance data measured during one approach-retract cycle, predicts the force (output) for arbitrary indentation trajectories (input). This model describes collagen fibrils' elastic as well as their dissipative nanomechanical properties with high fidelity for a large range of tip velocities and indentation amplitudes.

15 min. break

BP 18.4 Wed 16:15 H15

Partition complex structure arises from sliding and bridging — •Lara Connolley and Sean Murray — Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

Chromosome segregation is vital for cell replication and in many bacteria is controlled by the ParABS system. A key part of this machinery is the association of ParB proteins to the parS-containing centromeric region to form the partition complex. Despite much work, the formation and structure of this nucleoprotein complex has remained unclear. However, it was recently discovered that CTP binding allows ParB dimers to entrap and slide along the DNA, as well as leading to more efficient condensation through ParB-ParB-mediated DNA bridging. Here, we use stiff polymer simulations to show how these properties of sliding and bridging can explain partition complex formation. We find that dynamic ParB bridges condense the DNA through the formation of two structures, hairpins and helices. In separate stochastic simulations, we show that ParB sliding accurately predicts the experimentally measured multi-peaked binding profile of Caulobacter crescentus, indicating that bridging and other potential roadblocks are sufficiently short-lived that they do not hinder ParB spreading. Indeed, upon coupling the two simulation frameworks into a unified sliding and bridging polymer model, we find that short lived ParB bridges do not hinder ParB sliding from the parS sites, and can reproduce the binding profile of ParB as well as the overall condensation of the nucleoprotein complex. Overall, our model clarifies the mechanism of partition complex formation and predicts its fine structure.

BP 18.5 Wed 16:30 H15

Single-chain and condensed-state behavior of hnRNPA1 from molecular simulations — •D. Janka Bauer[1], Lukas Stelzl[1,2], and Arash Nikoubashman[1] — [1]Institute of Physics, Johannes Gutenberg University Mainz, Germany — [2]Biocenter, Institute of Molecular Physiology, Johannes Gutenberg University Mainz, Germany

Intrinsically disordered proteins (IDPs) are essential components for the formation of membraneless organelles, which play key functional and regulatory roles within biological systems. These complex assemblies form and dissolve spontaneously over time via liquid-liquid phase separation of IDPs. Mutations in their amino acid sequence can alter their phase behavior, which has been linked to the emergence of cancer and neurodegenerative diseases. In this work, we study the conformations and phase behavior of a low-complexity domain of heterogeneous nuclear ribonucleoprotein A1 (hnRNPA1), using coarse-grained molecular simulations. We systematically analyze how the single-chain and condensed-state behavior are affected by the number of aromatic residues within the examined sequences. We find a significant compaction of the chains and an increase in the critical temperature with

increasing number of aromatic residues within the IDPs. Both observations strongly support the hypothesis that aromatic residues play a dominant role for driving condensation, which is further corroborated by a detailed analysis of the intermolecular contacts. By establishing quantitative comparisons to the experimental phase behavior, we start to critically assess the reliability of coarse-grained IDP models.

BP 18.6 Wed 16:45 H15

Water flow elastography for minimal invasive surgery — •Paul Kalwa and Tilman Schäffer — University of Tübingen, Germany

Mechanical properties of tissue are of great interest for physicians to differentiate healthy from malign tissue, to determine the status or extent of a disease, and to investigate tissue ageing. The measurement of these properties is therefore a helpful tool for diagnosis. Many elastography techniques have been established and are used in medicine today. However, most of these techniques are not applicable in minimal invasive surgery (MIS), because there the size of probes is limited to a few millimeters and the handling is restricted. We introduce water flow elastography, a novel technique that benefits from a small and inexpensive probe. This technique uses a specialized probe to flow pressurized water against the sample surface, thereby inducing a local indentation. The volume of the indentation, which is measured with a flow meter, is used to quantify the Young's modulus with the help of finite element simulations. We measure the Young's modulus of silicone samples and porcine organs and validate the results with a commercial testing machine, finding agreement within 15 %. We also discuss the suitability of this technique for the determination of viscoelastic tissue properties and for the application in endoscopes for MIS in the future.

BP 18.7 Wed 17:00 H15

Turning the Corner on the Image Method in Linear Elasticity and Low-Reynolds-Number Hydrodynamics — •Tyler Lutz, Lukas Fischer, Sonja Richter, and Andreas Menzel — Institut für Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg

In both linear elasticity and low-Reynolds-number hydrodynamics, extensions of the image method—familiar from elementary electrostatics—have been developed to deduce the displacement (resp. velocity) fields arising from point forces applied in the vicinity of a single, flat, infinitely extended boundary. In this work, we assess the applicability of these methods to domains described by multiple, mutually orthogonal boundaries in 2 and 3 dimensions. Already in the case of a single flat boundary, the necessary image forces depend on the specific boundary conditions considered; the images become progressively more complex as one goes from free-slip to no-slip and stress-free surfaces. By iterating the image method for forces near corners or edges, we explicitly show that this method fails to generate a self-consistent image if any more than one boundary is anything other than a free-slip surface. For the situations in which the image method may be successfully applied, we explicitly construct and survey the qualitative features of the point-force Green's function near corners.

BP 18.8 Wed 17:15 H15

Adsorption of laminin and cellular response of neurons and glial cells on ion implanted titania nanotube scaffolds — •Jan Frenzel[1,2,3], Astrid Kupferer[1,2], Mareike Zink[3], and Stefan G. Mayr[1,2] — [1]Leibniz Institute of Surface Engineering (IOM), Permoserstraße 15, 04318 Leipzig, Germany — [2]Division of Surface Physics, Department of Physics and Earth Sciences, Linnéstraße 5, 04103 Leipzig, Germany — [3]Research Group Biotechnology and Biomedicine, Department of Physics and Earth Sciences, Linnéstraße 5, 04103 Leipzig, Germany

Brain-machine interfaces are used in a wide spectrum of neuroscience, as for time-resolved sensing of neural activities and for tackling neurodegenerative diseases. Currently established cultivation platforms, including cellulose filters, often result in loss of long-term adhesion, rejection reaction and glial scarring or do not allow for electrical contact due to their insulating properties. As we demonstrate, ion implanted titania nanotube scaffolds (TNS) are a promising candidate to overcome these issues, since they combine a high biocompatibility with a sufficient large electrical conductivity. In our experiments, we explain how ion implantation induced changes of surface characteristics affect the adsorption of laminin and the viability and adhesion of neurons and glial cells. We link the hindered laminin adsorption due to implantation to the shrinkage of tube diameter and rise of zeta potential. The stable and high neuron viability on all TNS but suppressed glial cell formation of implanted TNS gives rise for a potential interface material. Funding by SMWK (100331694) is gratefully acknowledged.

BP 19: Cell Mechanics 2

Time: Wednesday 15:00–17:15 Location: H16

BP 19.1 Wed 15:00 H16

Light, proteins, and shape: exploiting protein pattern formation for light-controlled oocyte deformations — Jinghui Liu[2], •Tom Burkart[1], Alexander Ziepke[1], Erwin Frey[1], and Nikta Fakhri[2] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München, Munich, Germany — [2]Department of Physics, Massachusetts Institute of Technology, Cambridge, MA 02139

To coordinate shape deformations, in particular cell division, cells rely on chemical reaction networks that process spatial and temporal cues, such as cell cycle signals, and control the mechanical activity that generates the required deformation. In starfish oocytes, a Rho-GTP protein pattern on the cell membrane regulates actomyosin contractility which induces large-scale cell deformations during meiotic anaphase. By engineering optogenetic activators of Rho-GTP, the native control mechanism can be hijacked to manually trigger the actomyosin contractility and thereby deform the oocyte even before entering meiotic anaphase. We study how such an artificial guiding cue is processed by the mechanochemical machinery in starfish oocytes. We combine simulations of the protein reaction-diffusion dynamics with the dynamic shape deformation of the oocyte to predict spatio-temporal light activation patterns that produce custom cell deformations. Our results contribute to the development of an overarching theoretical framework that allows to study and design minimal artificial cells capable of self-regulated and externally controlled shape changes.

BP 19.2 Wed 15:15 H16

Modeling Cell Shape and Forces on Structured Environments in Three Dimensions — •Rabea Link and Ulrich Sebastian Schwarz — Institute for Theoretical Physics, University Heidelberg, Germany

Micropatterns are a widely used tool to standardize the mechanical environment single cells or cell collectives experience in experiments. In recent years, microstructures manufactured with direct laser writing have tremendously increased the design possibilities of structured environments for cells. We model the shape, spreading dynamics and forces of a single cell with external adhesive cues using a three-dimensional compartmentalized Cellular Potts Model on 2D micropatterns and in 3D structured environments. This allows us to investigate the influence of the nucleus on the cell shape and spreading dynamics. In addition, we compare the cell shapes obtained by the Cellular Potts Model with the minimal energy shape of a surface under tension in the same mechanical environment and with experimental results.

BP 19.3 Wed 15:30 H16

Exploiting nonlinear elasticity for robust mechanosensation in disordered fiber networks — Estelle Berthier[1], •Pierre Ronceray[2], and Chase Broedersz[1,3] — [1]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität München, Germany — [2]Centre Turing and Centre de Physique Théorique, Université Aix-Marseille, France — [3]Department of Physics and Astronomy, Vrije Universiteit Amsterdam, Netherlands

Cell behavior is steered by guiding cues from their surrounding extracellular environment. Cells anchor to the extracellular matrix (ECM) and perform mechanosensation: they probe their surrounding's mechanical response and regulate their behavior according to the stiffness they sense. Yet, the robustness of cellular mechanosensing is physically limited by the ECM intrinsic disorder and complex mechanical

response of both the network and its constituents. Thus, it remains what strategies cells employ to accurately interpret mechanical guiding cues of such a heterogeneous environment.

Using a theoretical framework for disordered fiber networks, we evaluate the mechanical information cell can obtain by performing local measurements. We show that the signal-to-noise ratio of stiffness measurements increases dramatically in the nonlinear regime: the measurements become insensitive to local structural fluctuations of the network. We provide a scaling argument supporting that the local measurement effectively behaves as a sensory device of larger size.

BP 19.4 Wed 15:45 H16

Competition between cell deformation and depletion force: Quantified by 3D image analysis of red blood cell doublets — •Mehrnaz Babaki[1,2], Minne Paul Lettinga[1,2], and Dmitry Fedosov[3] — [1]Biomacromolecular Systems and Processes (IBI-4), Forschungszentrum Jülich GmbH, Jülich, Germany — [2]Laboratory for Soft Matter and Biophysics, KU Leuven, Leuven, Belgium — [3]Theoretical Physics of Living Matter (IBI-5/IAS-2), Forschungszentrum Jülich GmbH, Jülich, Germany

Understanding cell deformation associated with an external force is the key to a full comprehension of the behaviour of cells under mechanical loading. Red Blood Cells (RBCs) are an extreme example of deformable cells. The high deformability of RBCs influences the blood flow and blood circulation in both physiological and pathophysiological conditions as well as RBC aggregation

We investigated the deformation of RBCs using analysis of the 3D reconstructed confocal images of the RBCs in aggregated doublets. Here we use non-absorbing rod-like particles, causing depletion attraction. Our analysis yields the change in the bending energy of RBCs in a doublet, as well as the change in the depletion energy.

We identified a sequence of configurational transitions of RBC doublets upon increasing rod-like particles concentration, thus maximizing the free volume available for the depletants at the cost of deformation energy. We compared the experimental results with simulations, where we explored the different energy contributions to deformation, as well as the stability of RBC doublets at low depletion force.

15 min. break

BP 19.5 Wed 16:15 H16

Butterfly scale morphogenesis: Wrinkling on the micron scale — •Jan Totz[1], Anthony McDougal[2], and Mathias Kolle[2] — [1]Departments of Mathematics and Mechanical Engineering, Massachusetts Institute of Technology, Cambridge MA 02139, USA — [2]Department of Mechanical Engineering, Massachusetts Institute of Technology, Cambridge MA 02139, USA

Micron-scale surface modulations such as wrinkles or folds underly a number of modern engineering applications, such as photonic structures in photovoltaics and flexible metasurfaces. Controlled and precise fabrication of these modulations is a challenge for human manufacturing techniques. In stark contrast, biological systems robustly utilize morphological changes in their developmental program to create multigerm bodies, hairs and scales on spatial scales which would be costly to replicate with human manufacturing. In this talk I will present recent measurements of in-vivo butterfly scale development exhibiting wrinkling. The observations are rationalized with a numerical finite element simulation and a parsimonious continuum mechanics model.

BP 19.6 Wed 16:30 H16

Active morphogenesis of patterned epithelial shells — •Diana Khoromskaia[1] and Guillaume Salbreux[1,2] — [1]The Francis Crick Institute, 1 Midland Road, NW1 1AT, United Kingdom — [2]University of Geneva, Quai Ernest Ansermet 30, 1205 Genève, Switzerland

Shape transformations of epithelial tissues in three dimensions, which are crucial for embryonic development or in vitro organoid growth, can result from active forces generated within the cytoskeleton of the epithelial cells. How the interplay of local differential tensions with tissue geometry and with external forces results in tissue-scale morphogenesis remains an open question. Here, we describe epithelial sheets as active viscoelastic surfaces and study their deformation under patterned internal tensions and bending moments. In addition to isotropic effects, we take into account nematic alignment in the plane of the tissue, which gives rise to shape-dependent, anisotropic active tensions and bending moments. We present phase diagrams of the mechanical equilibrium shapes of pre-patterned closed shells and explore their dynamical deformations. Our results show that a combination of nematic alignment and gradients in internal tensions and bending moments is sufficient to reproduce basic building blocks of epithelial morphogenesis, including fold formation, budding, neck formation, flattening, and tubulation.

BP 19.7 Wed 16:45 H16

Condensed topological defects in compressible active nematics — •Ivan Maryshev[1], Timo Krüger[1], and Erwin Frey[1,2] — [1]LMU, München, Germany — [2]Max Planck School Matter to Life, München, Germany

So far, topological defects with plus/minus 1/2 charges have been considered to be characteristic features of homogeneous active nematics. Phase-separated systems, in turn, have been known for the formation of dense nematic bands. Here, we use the agent-based model for weakly-aligning self-propelled filaments and, for the first time, demonstrate that phase-separated active nematics form -1/2 defects of a new kind. In contrast to the homogeneous case, these new defects correspond to high-density regions and coexist with bending bands. We also observe filamentous arc ejections - formations of lateral arcuate structures that separate from the band's bulk and move in a transverse direction. We show that the key control parameters defining the transition from the topologically charged structures to stable bands are the initial density of particles and their path persistence length. Finally, we develop hydrodynamic theory recapitulating observed phenomena.

BP 19.8 Wed 17:00 H16

Spherical harmonics analysis of in vivo force probes for tissue stress quantification — •Alejandro Jurado[1], Bernhard Wallmeyer[2], Christoph Engwer[2], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics, Friedrich-Hund-Platz 1, University of Göttingen — [2]Institute of Cell Biology, ZMBE, Von-Esmarch-Str. 56, University of Münster

The mechanical analysis of tissue motion offers a new insight in key biological processes such as embryogenesis, cancer cell invasion and wound healing. Force quantification at this scale has been drastically improved with the emergence of in vivo sensors such as oil droplets or hydrogel beads which open up the possibility of non-invasive studies. Many approaches in recent literature rely on numerical processes to iteratively reconstruct the surface of measured beads, which can be computationally expensive and rendering results that are difficult to interpret. In this work we present the analysis of arbitrarily deformed beads based on the expansion in Spherical Harmonics in a Python custom software. We exploit the fast converging algorithms offered by SHTools [1] to reduce the great complexity of three-dimensional radial deformations to an affordable harmonic coefficient table which is directly fed into an analytical solution of the Navier-Cauchy equation. As a first proof-of-concept we show the performance of the software with polyacrylamide beads injected into zebrafish embryo at early developmental stages, in which the stress field could help understanding the processes of epiboly and shield formation. [1] Wieczorek M.A., Meschede M., 2018. Geochem. Geophys. Geosyst. 19(8), 2574-2592

BP 20: Active Matter 4 (joint session DY/BP/CPP)

Time: Wednesday 15:00–17:30 Location: H18

BP 20.1 Wed 15:00 H18

Clusters and fractals in non-reciprocally interacting colloids — •Sebastian Fehlinger and Benno Liebchen — Institut für Physik kondensierter Materie, Technische Universität Darmstadt, Hochschulstraße 8, D-64289 Darmstadt, Germany

Non-reciprocal interactions are widespread in nature. For the specific case of a binary mixture of passive particles, the breaking of the action reaction principle can lead to formation of active colloidal molecules which are capable of self-propulsion. For small systems, such active molecules have already been realized in experiments based on phoretically interacting binary colloidal mixtures [1,2].

The focus of the present work is to understand the many body behaviour of active molecules. Using particle based simulations and continuum theory, we find that non-reciprocal attractions in a binary mixture of non-motile particles can destabilize the uniform disordered phase and lead to clusters which grow in time. Surprisingly, for a wide parameter range, the clusters only grow up to a certain size such that coarsening is arrested. We attribute this to an effective screening effect which hinges on the characteristic spatiotemporal organization of the two species within the clusters. In addition, remarkably, in a different parameter regime, we find porous macroclusters featuring significant holes and a fractal dimension which differs from the one expected for conventional diffusion limited aggregation.

[1]F. Schmidt et al. J. Chem. Phys. 150, 094905 (2019)
[2]J. Grauer et al. Nat. Commun. 12, 6005 (2021).

BP 20.2 Wed 15:15 H18

Analysis of transient dynamics of bioconvection in swimming algae — •Alexander Jarosik, Florian von Rüling, and Alexey Eremin — Otto-von-Guericke Universität, Magdeburg, Germany

Swimming unicellular algae Chlamydomonas reinhardtii exposed to light form intricate hydrodynamic instability patterns called bioconvection. High-density plumes of cells are formed in the top layer, descend to the container's bottom, and rise again to the top. This instability arises from coupling between the gyro- and phototactic behaviour of the cells, their physical properties and the flow. In this work, we analyse the microswimmer's dynamics as a function of the cell density, confinement of the environment and light. The transient behaviour of the plume formation is analysed using the Continuous Wavelet Transformation (CWT). We demonstrate that the plume formation can be controlled by local illumination.

BP 20.3 Wed 15:30 H18

Optimal turbulent transport in microswimmer suspensions — •Henning Reinken[1], Sabine H. L. Klapp[1], and Michael Wilczek[2] — [1]Technische Universität Berlin — [2]Universität Bayreuth

Microwsimmer suspensions, a paradigmatic example of an active fluid, self-organize into complex spatio-temporal flow patterns, including regular vortex lattices and mesoscale turbulence. This work investigates the transport properties of these suspensions by tracking the diffusive motion of passive tracers in the turbulent flow. We apply a continuum model for the effective microswimmer velocity field [1,2], where the dynamics is governed by the competition between relaxation to a regular vortex lattice and destabilization by nonlinear advection. Varying the strength of nonlinear advection, we observe two qualitatively different regimes of flow transport that we distinguish with the help of the dimensionless Kubo number K, which compares different time scales. Right above the transition to turbulence, the flow field evolves very slowly ($K \gg 1$) and the spatial vortex structures lead to dominant trapping effects. In contrast, for large advection strength, much faster dynamics ($K \ll 1$) leads to transport properties completely determined by the temporal correlations of the flow. In between ($K \approx 1$), we observe a regime of optimal transport, where the diffusion coefficient reaches a maximum.

[1] Reinken, Klapp, Bär, Heidenreich, Phys. Rev. E **97**, 022613 (2018)
[2] James, Bos, Wilczek, Phys. Rev. Fluids **3**, 061101(R) (2018).

BP 20.4 Wed 15:45 H18

Interfacial activity dynamics of confined active droplets — •Prashanth Ramesh[1,2], Babak Vajdi Hokmabad[1], Arnold J.T.M. Mathijssen[3], Dmitri O. Pushkin[4], and Corinna C. Maass[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization — [2]University of Twente — [3]University of Pennsylvania — [4]University of York

Active emulsions exhibit a complex hydrodynamic mode spectrum driven by chemical advection-diffusion instabilities. We study such an active emulsion consisting of oil droplets that dynamically solubilize in a supramicellar aqueous surfactant solution. It has been predicted that the interaction with self-generated chemical fields leads to multistable higher-mode flow fields and chemorepulsive phenomena. To investigate such chemodynamic effects, we study cylindrical droplets pinned between the top and bottom surfaces of a microfluidic reservoir, such that they only produce pumping flows, while we simultaneously quantify the chemical concentration field and the hydrodynamic velocity field. With increasing droplet radius we observe: vortical structures generated by the droplet migrating around the interface, bistability between a dipolar and quadrupolar flow mode, and, eventually, a transition to multipolar modes. We further measured flow fields by particle image velocimetry and compared them to a hydrodynamic model based on a Brinkman squirmer. A simultaneous quantification of the flow fields and oil-filled micelle distribution suggests that a local buildup of chemical products leads to a saturation of the surface, which affects the propulsion mechanism and eventually suppresses all activity.

BP 20.5 Wed 16:00 H18

Hydrodynamics and fluctuations in bacterial models — •Subhadip Chakraborti — Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

Motivated by a biological example of the persistent motion of bacteria, we propose two one-dimensional models of active lattice gases with hardcore interactions. Using macroscopic fluctuation theory (MFT), we analytically derive hydrodynamics for those models and calculate two density-dependent transport coefficients – the bulk-diffusion coefficient and the conductivity, and verify the Einstein relation (ER) by comparing the ratio of those transport coefficients with subsystem number fluctuation. The first model consisting of particles with competing mechanisms of short and long-range hopping obeys the Einstein relation, and exhibits, in the limit of infinite range hopping, upon tuning density (or activity), a 'superfluid' transition from a finitely conducting state to an infinitely conducting one. Interestingly, the bulk-diffusion coefficient remains constant throughout. The diverging conductivity induces 'giant' number fluctuations in the system. In the second model, consisting of hardcore run and tumble particles with persistent motion in one direction decided by an associated spin variable until the direction of spin is reversed, we perform a similar calculation and find that the Einstein relation is violated. This analytic framework could be useful for a better understanding of the collective behavior of many biological systems such as bacterial colonies and other multicellular aggregates, in the context of dynamics and transport properties.

15 min. break

BP 20.6 Wed 16:30 H18

Shearing an Active Glass — •Rituparno Mandal and Peter Sollich — Institut für Theoretische Physik, Göttingen, Germany

Recent experiments and simulations have revealed glassy features of cytoplasm, tissues and dense assemblies of self propelled colloids. This prompts the fundamental question of whether non-equilibrium (active) amorphous materials are essentially equivalent to their passive counterparts, or whether they can present qualitatively different behaviour. To tackle this challenge we investigate the yielding and mechanical behaviour of a model active glass former, a Kob-Andersen glass in two dimensions where each particle is driven by a constant propulsion force whose direction varies diffusively over time. Using extensive Molecular Dynamics simulations, we focus in particular on the effects of the intermittent dynamics in the regime of highly persistent activity and reveal a novel type of shear induced orientational ordering in the system.

BP 20.7 Wed 16:45 H18

Active motion with varying self propulsion — Lorenzo Caprini[1], Alexander R. Sprenger[1], Umberto M. B. Marconi[2], Hartmut Löwen[1], and •René Wittmann[1] — [1]Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine Universität Düssel-

dorf, Germany — [2]School of Sciences and Technology, University of Camerino, Italy

Active Brownian Particles (ABPs), commonly perceived as the standard model for (dry) active motion, are characterized by a constant self-propulsion velocity along the direction of a unit vector which performs rotational diffusion. In nature, however, the swim velocity is usually not a constant in time and space. Here, we present a generic form of the equations of motion of active particles, which account for two aspects of varying self propulsion. First, we introduce a general stochastic process with fluctuating modulus of the self-propulsion vector, which defines a parental active model (PAM). We argue that the two well-known models of ABPs and Active Ornstein-Uhlenbeck Particles (AOUPs) emerge as limiting cases of the PAM [1], i.e., they are rather sisters than cousins. Second, we demonstrate that a position-dependent swim-velocity field can be consistently introduced for any self-propulsion mechanism [2]. Finally, we discuss the effects of varying self propulsion in external confinement [1,3] and predict the stationary probability distributions in terms of effective interactions [3].

[1] L. Caprini et al., J. Chem. Phys. 156, 071102 (2022).
[2] L. Caprini et al., Soft Matter, 18, 1412 (2022).
[3] L. Caprini et al., arXiv:2203.00603 (2022).

BP 20.8 Wed 17:00 H18

Perturbing the athermal jamming transition by activity — •Michael Schmiedeberg — Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany

By minimizing the interaction energy in a soft sphere system without crossing energy barriers the discontinuous athermal jamming transion can be observed at a packing fraction of about 0.64 in three dimensions [1]. We consider the jamming of active particles where the activity corresponds to a perturbation to the athermal jamming process. We find that due to the activity the transition becomes continuous and the transition packing fraction might occur at a different density [2]. The critical exponents agree to those of the universality class of directed percolation. As a consequence, athermal jamming of passive particles seems to be a (singular) limit of the jamming transition in an active system. Note that other perturbation like thermal fluctuations lead to a similar behavior [3]. Therefore, athermal active particles can be seen as a prototype system that leads to new insights how jamming with perturbations (as also studied in [2-5]) can be related to glassy dynamics.

[1] C.S. O'Hern et al., Phys. Rev. Lett. 88, 075507 (2002) and Phys. Rev. E 68, 011306 (2003).
[2] M. Maiti and M. Schmiedeberg, EPL 126, 46002 (2019).
[3] M. Maiti and M. Schmiedeberg, Scientific Reports 8, 1837 (2018); for 2D: Eur. Phys. J. E 42, 38 (2019).
[4] L. Milz and M. Schmiedeberg, Phys. Rev. E 88, 062308 (2013).
[5] S. Wilken et al., Phys. Rev. Lett. 127, 038002 (2021).

BP 20.9 Wed 17:15 H18

Non-equilibrium phase separation in mixtures of catalytically active particles: size dispersity and screening effects — •Vincent Ouazan-Reboul[1], Jaime Agudo-Canalejo[1], and Ramin Golestanian[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, D-37077, Göttingen, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, OX1 3PU, Oxford, UK

Biomolecular condensates in cells are often rich in catalytically active enzymes. This is particularly true in the case of the large enzymatic complexes known as metabolons, which contain different enzymes that participate in the same catalytic pathway. One possible explanation for this self-organization is the combination of the catalytic activity of the enzymes and a chemotactic response to gradients of their substrate, which leads to a substrate-mediated effective interaction between enzymes. These interactions constitute a purely non-equilibrium effect and show exotic features such as non-reciprocity. Here, we analytically study a model describing the phase separation of a mixture of such catalytically active particles. We show that a Michaelis-Menten-like dependence of the particles' activities manifests itself as a screening of the interactions, and that a mixture of two differently sized active species can exhibit phase separation with transient oscillations. We also derive a rich stability phase diagram for a mixture of two species with both concentration-dependent activity and size dispersity.

BP 21: Members' Assembly

Time: Wednesday 18:00–19:00 Location: H15

All members of the Biological Physics Division are invited to participate.

BP 22: Migration and Multicellular Systems

Time: Thursday 9:30–12:15 Location: H15

Invited Talk BP 22.1 Thu 9:30 H15

Cell and tissue mechano-plasticity in development — •Verena Ruprecht — Centre for Genomic Regulation (CRG), Barcelona, Spain

The development of a single fertilised cell into an embryo is a highly dynamic process that establishes the structural and functional architecture of the organism. The building of complex multicellular structures fundamentally emerges from the spatio-temporal coordination of dynamic behaviours at the single cell level. How this multi-scale process occurs with high fidelity and robustness is still a major open question. Here I will discuss how embryonic stem cells are able to sense and adapt to mechanical shape deformations in their 3D tissue environment. I will explore the function of the cell nucleus as an intracellular mechano-sensor and how it can act as a non-genetic controller of cell mechanics and migration plasticity. I will further discuss how cellular error correction is established in the earliest stages of embryo development by mechanical cell cooperation that promotes the efficient phagocytic clearance of aberrant apoptotic cells. Theoretical modelling of mechanical force fluctuations at the cell cortex and protrusive force generation in cell collectives will be presented to mechanistically describe the emergence of mechano-plasticity at the single cell and tissue level mediating robust embryo development.

BP 22.2 Thu 10:00 H15

Active T1 transitions in cellular networks — •Charlie Duclut[1,2], Joris Paijmans[1], Mandar M. Inamdar[3], Carl D. Modes[4,5,6], and Frank Jülicher[1,5,6] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 8, 01187 Dresden, Germany — [2]Université Paris Cité, Laboratoire Matière et Systèmes Complexes, Paris, France — [3]Department of Civil Engineering, Indian Institute of Technology Bombay, Powai, Mumbai 400076, India — [4]Max Planck Institute for Molecular Cell Biology and Genetics (MPI-CBG), Dresden 01307, Germany — [5]enter for Systems Biology Dresden, Pfotenhauerstrasse 108, 01307 Dresden, Germany — [6]Cluster of Excellence, Physics of Life, TU Dresden, Dresden 01307, Germany

In amorphous solids as in tissues, neighbour exchanges can relax local stresses and allow the material to flow. In this talk, I will use an anisotropic vertex model to study T1 rearrangements in polygonal cellular networks. We consider two different physical realization of the active anisotropic stresses: (i) anisotropic bond tension and (ii) anisotropic cell stress. Interestingly, the two types of active stress lead to patterns of oriented T1 transitions that are different. I will describe and explain these observations through the lens of a continuum description of the tissue as an anisotropic active material. I will furthermore discuss the energetics of the tissue and express the energy balance in terms of internal elastic energy, mechanical work, chemical work and heat. This allows us to define active T1 transitions that can perform mechanical work while consuming chemical energy.

BP 22.3 Thu 10:15 H15

Bistability between sessile and motile solutions in a nonlinear active gel model for cell migration — •Oliver M. Drozdowski,

Falko Ziebert, and Ulrich S. Schwarz — Institute for Theoretical Physics and BioQuant, Heidelberg University, 69120 Heidelberg, Germany

Cell motility is one of the hallmarks of life and often is based on flow in the actin cytoskeleton that is driven by myosin II motors. The standard model to describe such flows is active gel theory, in which myosin II contractility enters as active stress. Recently, we have shown how to include optogenetic control in a minimal active gel model [1]. Here we ask how active gel descriptions of motility need to be modified to explain the experimental observation that a cell's state can be switched between sessile and motile. We show that such bistability emerges in active gel theory if the myosin II motors are modeled as a supercritical van der Waals fluid, including volume exclusion and short-range attraction. We present phase diagrams in cell adhesion and contractility that include sessile, bistable and motile regimes in experimentally relevant parameter ranges. Including optogenetic perturbations of contraction, as done before for a simpler model [1], we find that such external activation can be used to control cell locomotion, in agreement with recent experiments [2].

[1] O. M. Drozdowski, F. Ziebert, and U. S. Schwarz, Phys. Rev. E 104, 024406 (2021),

[2] A. Hadjitheodorou, et al., Nat. Commun. 12, 6619 (2021).

BP 22.4 Thu 10:30 H15

Rotation of an aspherical organoid within its matrix - a continuum model — •Anne Materne[1], Charlie Duclut[1,2], and Frank Jülicher[1,3,4] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Université Paris Cité, Laboratoire Matière et Systèmes Complexes, Paris, France — [3]Center for Systems Biology Dresden, Dresden, Germany — [4]Cluster of Excellence Physics of Life, TU Dresden, Germany

Organoids and other 3D *in vitro* multicellular systems have frequently been observed to display rotational motion within their matrix. Collective rotational motion can also be witnessed *in vivo*, for example in the *Drosophila* egg chamber. We propose that this motion results from cell-matrix interactions. Cells are thought to move similarly to 2D migration - however, a (near-)spherical geometry of cell clusters can lead to the observed rotation in 3D. Here, we present a continuum mechanics descripion of an organoid rotating within its embedding matrix. We discuss the extreme cases of the matrix being either purely elastic or purely viscous. The organoid is considered to be a non-deformable solid with a surface polarity field, exerting traction forces on the matrix. Importantly, our study is not limited to perfectly spherical organoids but takes small shape deformations into account. This permits to distinguish between purely rotational and deformation-induced cell-matrix interactions. Our work clarifies how matrix material properties and cellular traction forces enable collective organoid rotation. Reciprocally, the rotating organoid can serve as an active rheology probe, revealing key information about the matrix properties.

15 min. break

BP 22.5 Thu 11:00 H15

Exploiting Onsager regression in passive measurements to reveal active mechanics of living systems — Till Münker, Gabriel Knotz, Matthias Krüger, and •Timo Betz — Faculty of Physics, Georg-August-University Göttingen

Understanding life is arguably among the most complex scientific problems faced in modern research. From a physics perspective, living systems are complex dynamic entities that operate far from thermodynamic equilibrium. This active, non-equilibrium behaviour, with its constant hunger for energy, allows life to overcome the dispersing forces of entropy, and hence drives cellular organisation and dynamics at the micrometer scale. Unfortunately, most analysis methods provided by the powerful toolbox of statistical mechanics cannot be used in such non-equilibrium situations, forcing researchers to use sophisticated and often invasive approaches to study the mechanistic processes inside living organisms. Inspired by Onsager's regression hypothesis, we introduce here a Mean Back Relaxation (MBR) observable, which detects active motion in purely passive measurements of particle fluctuations. The MBR, which is based on three point probabilities, is theoretically and experimentally shown to exhibit markers of non-equilibrium, i.e., of detailed balance breaking dynamics. We furthermore observe an astonishing relation between the MBR and the effective non-equilibrium energy in living cellular systems. This is used to successfully predict the viscoelastic response function and the complex shear modulus from a purely passive approach, hence opening the door for rapid and simple passive mechanics measurements even in active systems.

BP 22.6 Thu 11:15 H15

Redirecting early embryogenesis of the model organism *Caenorhabditis elegans* via altered mechanical cues — •Vincent Borne and Matthias Weiss — Experimental Physics I, University of Bayreuth, Universitätsstr. 30, D-95447 Bayreuth, Germany

During early development, somatic and germline precursor cells of the model organism *Caenorhabditis elegans* undergo an apparently predetermined and robust division scheme, suggesting early embryogenesis to run on autopilot. While the role of biochemical signaling in this process has long been recognized, the influence of mechanical forces for proper cell arrangement until gastrulation has only recently been revealed. Aiming to further explore, how mechanical cues contribute to proper embryogenesis, we have challenged the natural development at early stages via laser microsurgery and physical compression. As a result, we were able to significantly perturb the embryonic division scheme with both approaches, leading to catastrophic failures of cell divisions. While defects introduced by laser ablation remained mostly restricted to cells that had been challenged, compression frequently resulted in a global perturbation: Cytokinesis was compromised, leading to multinucleated cells or even a syncytium state in which nuclei kept on dividing up to stages of 60 nuclei or more with similar timing characteristics as observed in unperturbed embryos. Our data therefore underline the crucial role of properly adjusted mechanical cues during the early embryogenesis of *C. elegans*.

BP 22.7 Thu 11:30 H15

Active cell mechanisms reveal rich tissue-wide structures and dynamics in simulations — •Maxime Hubert[1], Lovro Nuić[2], Kevin Höllring[1], and Ana-Sunčana Smith[1,2] — [1]PULS group, FAU Erlangen-Nürnberg, Erlangen, Germany — [2]Group for Computational Life Sciences, Ruđer Bošković Institute, Zagreb, Croatia

Dissipative Particle Dynamics simulations provide a robust numerical platform of investigation to understand the dynamics of epithelial tissues. The technique allows to implement various properties at the cell level that can be related to tissue-wide structures and dynamics on various time scales, from hours to days in experiments. In this talk, we present our recent progresses in the field of epithelium numerical simulations by implementing different active ingredients that relate to the immediate neighbourhood of the cell within a tissue monolayer. We show, through comparisons with experiments performed with MDCK-II cells, that we are able to capture the formation of macroscopic compartments of the tissue, the complex relation between average cell velocity and cell density, and the rate of expansion of the tissue. These results highlight the importance of "nuclei"-based approaches along with "membrane"-based approaches in order to provide a complete numerical and mechanical perspective of epithelial tissues across various time- and length-scales.

BP 22.8 Thu 11:45 H15

'Forcing' changes in health and disease: New access into bioengineered skeletal muscle mechanics — •Arne Hofmeier[1,2], Till Muenker[2], Fabian Herkenrath[1], and Timo Betz[1,2] — [1]University of Muenster, Muenster, Germany — [2]University of Goettingen, Goettingen, Germany

Mechanical properties of skeletal muscles are tightly related to proper functionality, which makes experimental access to the biomechanics of skeletal muscle tissue a key requirement to advance our understanding of muscle function, development and disease. Recently devised in vitro culture chambers allow for raising 3D skeletal muscle tissues under controlled conditions and to measure global tissue force generation. However, these PDMS-based systems are inherently incompatible with high resolution microscopy. Here, we present a new chamber design that allows real-time high resolution 3D microscopy and simultaneous non-invasive quantification of global contractile forces and local tension during muscle formation for the first time. With this in hand, we observed an early mechanical homeostasis within mouse myoblast derived skeletal muscle tissues after one week of development, despite progressing myotube maturation. Additionally, we raised human in vitro skeletal muscles derived from patients suffering from Duchenne muscular dystrophy caused by loss of a functional membrane linker protein, called dystrophin. Interestingly, bioengineered Duchenne skeletal muscles displayed a disturbed mechanical homeostasis that correlates with functional impairment, suggesting a novel function of dystrophin

being a molecular tension sensor and regulator.

BP 22.9 Thu 12:00 H15

On multistability and constitutive relations of cell motion on Fibronectin lanes — Behnam Amiri[1], •Johannes Clemens Julius Heyn[2], Joachim Oskar Rädler[2], and Martin Falcke[1,3] — [1]Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Robert Rössle Str. 10, 13125 Berlin, Germany — [2]Ludwig-Maximilians-Universität München (LMU), Fakultät für Physik, Geschwister-Scholl-Platz 1, 80539 München, Germany — [3]Dept. of Physics, Humboldt University, Newtonstr. 15, 12489 Berlin, Germany

Migration of eukaryotic cells is a fundamental process for embryonic development, wound healing, immune responses, and tumour metastasis. Many cell types exhibit coexisting steady and oscillatory morphodynamics on flat substrates. There is, however, little quantitative understanding of how adhesion controls these dynamic states.

We study the motion of MDA-MB-231 cells on microlanes of a broad range of Fibronectin densities to address this topic and derive a biophysical model.

The experiments exhibit cells with steady or oscillatory morphodynamics and either spread or moving with spontaneous transitions between the dynamic states. Our biophysical model is based on the force balance at the protrusion edge, the noisy clutch of retrograde flow and a response function of friction and membrane drag to integrin signaling. The theory reproduces the experimentally observed cell states, characteristics of oscillations and state probabilities.

BP 23: Evolution

Time: Thursday 10:00–10:45 Location: H13

BP 23.1 Thu 10:00 H13

New phenotypes appear in an evolving population in non-Poissonian bursts — •Nora S. Martin[1], Steffen Schaper[1], Chico Q. Camargo[1,2], and Ard A. Louis[1] — [1]Department of Physics, University of Oxford, Oxford, UK — [2]Department of Computer Science, University of Exeter, Exeter, UK

For adaptive evolution, a central question is when and how frequently random mutations produce the specific rare adaptive phenotypes that have a selective advantage. A widely studied scenario is the following: a population starts with a given initial phenotype and accumulates neutral mutations, and new phenotypes are also introduced at a certain rate. Many theories implicitly assume that new phenotypes appear through simple stochastic processes which lead to Poissonian statistics. In this contribution, we use simulations on the biophysically motivated computational genotype-phenotype map from RNA sequences to secondary structures and show that new structures appear in highly non-Poissonian "bursts". In other words, if a new structure appears once, it is highly likely to appear multiple times in a relatively small number of generations. We show that there are several sources for this non-Poissonian behaviour, for example correlations in the mappings from genotypes to phenotypes, which may be a generic property of realistic genotype to phenotype maps. We find that these bursts can affect probabilities of fixation, especially when there are multiple competing adaptive phenotypes.

BP 23.2 Thu 10:15 H13

Proliferative advantage of specific aneuploid cells drives evolution of tumor karyotypes — •Lucija Tomašić[1], Ivana Ban[1], Marianna Trakala[2], Iva Tolić[3], and Nenad Pavin[1] — [1]Department of Physics, Faculty of Science, University of Zagreb, Croatia — [2]David H. Koch Institute for Integrative Cancer Research, Howard Hughes Medical Institute, Massachusetts Institute of Technology, Cambridge, Massachusetts 02142, USA — [3]Division of Molecular Biology, Ruder Bošković Institute, Croatia

Most tumors have abnormal karyotypes, which arise from mistakes during mitotic division of healthy euploid cells and evolve through numerous complex mechanisms. In a recent mouse model with high levels of chromosome missegregation, chromosome gains dominate over losses both in pretumor and tumor tissues, whereas tumors are characterized by gains of chromosomes 14 and 15. However, the mechanisms driving clonal selection leading to tumor karyotype evolution remain unclear. Here we show, by introducing a mathematical model based on a concept of a macro-karyotype, that tumor karyotypes can be explained by proliferation-driven evolution of aneuploid cells. In pretumor cells, increased apoptosis and slower proliferation of cells with monosomies lead to predominant chromosome gains over losses. Tumor karyotypes with gain of one chromosome can be explained by karyotype-dependent proliferation, while for those with two chromosomes an interplay with karyotype-dependent apoptosis is an additional possible pathway. Thus, evolution of tumor-specific karyotypes requires proliferative advantage of specific aneuploid karyotypes.

BP 23.3 Thu 10:30 H13

Data-driven modeling of social interactions in bats across time scales — •Frank Schweitzer[1], Pavlin Mavrodiev[1], and Gerald Kerth[2] — [1]Chair of Systems Design, ETH Zürich, Switzerland — [2]Applied Zoology and Nature Conservation, University of Greifswald, Germany

The study of bat's social and foraging behavior is of great relevance to forecast the outbreak and distribution of virus induced deseases. To analyze this behavior we use a large-scale data set from two colonies of Bechstein's bats over five years. From this data, we reconstruct the social interactions of bats at three different time scales: (a) At the scale of minutes: social influence and information transfer. This leads to the formation of leader-follower pairs, where an informed individual leads an uninformed one to a roost box. (b) At the time scale of days: fission-fusion dynamics. This leads to the formation and dissolution of roosting groups of different size, composed of different individuals. (c) At the time scale of months: Emergence of social structures. This leads to the formation of communities within a colony. While the analysis of (a) requires statistical data analysis and hypothesis testing, for (b) we employ agent-based models, and for (c) social network analysis. The combination of these approaches allows us to bridge time scales in social behavior, which cannot be observed together. With our models we are able to develop the bigger picture of how social interactions feed back to long-term social structures.

BP 24: Systems Biology, Gene Expression, Signalling

Time: Thursday 10:30–12:30 Location: H16

Invited Talk BP 24.1 Thu 10:30 H16

Actin waves as building blocks of cellular function — •Carsten Beta — Institute of Physics and Astronomy, University of Potsdam, Potsdam, Germany

Many cellular functions, such was motility, phagocytosis, and cell division, are driven by coherent patterns of activity in the actin cytoskeleton. Among them, actin waves are a recurrent motive that is commonly observed across different cell types. Here, we present experimental results demonstrating the rich variety of wave patterns in the actin cortex of motile amoeboid cells. We show that ring-shaped actin waves, commonly acting as precursors of macropinocytic cups, can mediate switches between different modes of motility, a pseudopod-based amoeboid mode, and a more persistent, wave-driven migratory mode, reminiscent of keratocyte motility. In multinucleate, oversized amoeboid cells, the same waves may also trigger spontaneous, cell cycle-independent cytofission events, resulting in mononucleated daughter cells of a well-defined size. We also demonstrate that a second wave pattern can coexist with the ring-shaped macropinocytic waves. It emerges in a cell-size dependent manner and consists of rapidly moving planar pulses that show typical signatures of an excitable system. Our experimental findings demonstrate the functional versatility of cortical waves patterns. They can be rationalized based on minimal reaction-diffusion models that mimic the evolution of cortical wave patterns and are coupled to a dynamic phase field to take the cell shape evolution into account. In addition, bifurcation analysis provides a more detailed understanding of how regimes of pattern coexistence may emerge.

BP 24.2 Thu 11:00 H16

Quantifying Dynamic Information Transfer in Stochastic Biochemical Networks — •Anne-Lena Moor[1,2] and Christoph Zechner[1,2] — [1]Max-Planck Institute of Molecular Cell Biology and Genetics, Dresden Germany — [2]Center for Systems Biology, Dresden, Germany

Transmission and encoding of information are fundamental processes for the functioning of biochemical systems. Information theoretical concepts, such as the mutual information, provide a rigorous mathematical framework to study intracellular signal transmission. In many biological systems, information is encoded in the time-trajectory of signalling components as opposed to instantaneous levels. However, performing information theoretical analysis on the trajectory-level is computationally demanding. In this work, we present an effective approach to calculate mutual information between complete trajectories of biochemical components. The resulting measure provides useful insights into the dynamic information transfer through networks of chemical reactions.

BP 24.3 Thu 11:15 H16

Optimal ligand discrimination by asymmetric dimerization of interferon receptors — •Patrick Binder[1,2,3], Nikolas D. Schnellbächer[1,2], Thomas Höfer[2,3], Nils B. Becker[2,3], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, 69120 Heidelberg, Germany — [2]BioQuant Center for Quantitative Biology, Heidelberg University, 69120 Heidelberg, Germany — [3]Theoretical Systems Biology, German Cancer Research Center, 69120 Heidelberg, Germany

In multicellular organisms, antiviral defense is mediated by ligands. These signaling molecules are usually characterized by highly inhomogeneous distributions due to scarcity of producer cells, diffusion and localized degradation. And yet, a molecular hub of the antiviral response, the interferon I receptor (IFNAR), discriminates between ligand types by their affinity regardless of concentration. In my talk, I address the long-standing question of how a single receptor can decode robustly ligand type. I frame ligand discrimination as an information-theoretic problem and systematically compare the major classes of receptor architectures: allosteric, homodimerizing, and heterodimerizing. As a result, asymmetric heterodimers achieve the best discrimination power over the entire physiological range of local ligand concentrations, enabling sensing of ligand presence and type. IFNAR exhibits this optimal architecture, suggesting that it has evolved the optimal design to detect and separate the presence of different ligand types in a noisy environment.

15 min. break

BP 24.4 Thu 11:45 H16

Rationalizing the optimality of the Drosophila gap gene system by ab-initio derivation of optimal solutions for morphogenetic patterns — •Thomas R. Sokolowski[1,2], Thomas Gregor[3,4], William Bialek[3], and Gašper Tkačik[1] — [1]IST Austria, Am Campus 1, A-4300 Klosterneuburg, Austria — [2]Present Address: Frankfurt Institute for Advanced Studies, Ruth-Moufang-Str. 1, D-60438 Frankfurt, Germany — [3]Department of Physics, Princeton University, Princeton, NJ 08540, U.S.A. — [4]Insitut Pasteur, Department of Developmental and Stem Cell Biology, 25 Rue du Dr. Roux, F-75015, Paris, France

Early fruit fly development is outstandingly precise in spite of the high level of stochasticity in the underlying biochemical processes. While the gap gene system driving fly embryo patterning has been shown to encode positional information optimally, the precise mechanisms that enable this remain elusive. We show that optimal solutions for the gap gene regulatory network can be obtained by optimizing a biophysically realistic spatial-stochastic embryo model, without inferring from data. Firstly, our predictions mechanistically explain how the observed developmental precision can be attained. Secondly, by exploring rich sets of optimal solutions, we elucidate the role of key components controlling early fly patterning. To our knowledge our work provides the first successful ab-initio derivation of a nontrivial biological network in a biophysically realistic setting. Our results suggest that even though real biological networks are hard to intuit, they may represent optimal solutions to optimization problems which evolution can find.

BP 24.5 Thu 12:00 H16

Stability of gene expression patterns in developmental systems with dynamic morphogen sources — •Maciej Majka — Jagiellonian University, Krakow, Poland

In developmental systems cells determine their fate by decoding chemical signals, called morphogens. In this presentation I will address the problem of gene expression patterns stability in the systems where two diffusible morphogens affect each other production and control the growth of their own source regions. Such systems are encountered in e.g. spinal cord development, limb formation and many others. The reaction-diffusion equation with bi-stable production term is employed as a generic model for this problem. The phase transition is found, between the phase of indeterminate patterning, where region of mixed gene expression is ever growing, and the phase of travelling gene expression patterns, where two expression domains form and preserve a well-defined contact zone. A sub-class of genuinely stationary patterns is then identified, alongside the exact conditions ensuring this stability. This allows me to classify the pattern stability for all possible two-gene regulatory motifs.

BP 24.6 Thu 12:15 H16

Conditions and trade-offs to enhance protein production in synthetic bacterial communities — •Marco Mauri[1,3], Jean-Luc Gouzé[2], Hidde de Jong[3], and Eugenio Cinquemani[3] — [1]Friedrich Schiller University, Jena, Germany — [2]University Côte d'Azur, Sophia-Antipolis, France — [3]Univ. Grenoble Alpes Inria, Grenoble, France

In nature, microorganisms occur in communities comprising a variety of mutually interacting species. To overcome the complexity of natural communities, a rapidly growing research field concerns the rational design and engineering of synthetic microbial consortia.

Here, based on a quantitative model of a prototypical synthetic microbial consortium, we discuss the precise conditions under which a consortium outperforms individual species in the production of a recombinant protein. Moreover, we identify the inherent trade-offs between productivity and efficiency of substrate utilization [1].

[1] Mauri M, Gouze' JL, de Jong H, Cinquemani E (2020) Enhanced production of heterologous proteins by a synthetic microbial community: Conditions and trade-offs. PLOS Computational Biology 16(4): e1007795. https://doi.org/10.1371/journal.pcbi.1007795

BP 25: Bioinspired Systems

Time: Thursday 11:00–12:00 Location: H13

BP 25.1 Thu 11:00 H13

Bottom-up assembly of synthetic cell-based tumor immune microenvironments in pancreatic cancer organoids — •Oskar Staufer — University of Oxford, Kennedy Institute of Rheumatology, Oxford, United Kingdom

Understanding the communication and interactions between tumour and immune cells is pivotal for holistic understanding of tumour biology and therapy. I present strategies to recreate immune cells, the defining elements of the tumor immune microenvironment (TIME), as synthetic cells by bottom-up assembly from their single molecular building blocks. The programmable synthetic cells are introduced into tumor organoids to function as lifelike leukocyte mimics presenting immune effector functions. By this, a molecularly defined artificial TIME (ART-TIME) is created inside tumor models. The central objective of this approach is to reduce the complexity of the intricate TIME composition to a comprehensible and systematic level by applying a novel bioinspired systems approach. This strategy links TIME architectures to cancer adaptation and immune evasion for quantitative description of therapy resistance. ART-TIME strive to de-convolute the dynamic complexity of the tumor immune microenvironment towards a rational dissection. Strategies for stable incorporation of synthetic cells into organoids, chemical, biophysical and ultrastructural characterizations of the synthetic immune cells as well as their molecular interactions with cancer cells inside the organoids are presented.

BP 25.2 Thu 11:15 H13

Frustrated frustules: geometrical frustration in *Coscinodiscus* diatom frustules — •Maria Feofilova and Eric Dufresne — Vladimir-Prelog-Weg 5, 8093 Zürich, Switzerland

Diatoms are single-celled organisms with a cell wall made of silica, called the frustule. Their elaborate patterns have fascinated scientists for years, however little is known about the biological and physical mechanisms involved in their organizations.

In this work, we take a top-down approach and examine the micron-scale organization of diatoms from the *Coscinodiscus* family. We find two competing tendencies of organization, which appear to be controlled by distinct biological pathways. On one hand, micron-scale pores organize locally on a triangular lattice. On the other, lattice vectors tend to point globally toward a center of symmetry. This competition results in a frustrated triangular lattice, populated with geometrically necessary defects whose density increases near the center.

BP 25.3 Thu 11:30 H13

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) may potentially serve as human fingernail substitute, which is especially relevant for the medical and cosmetics 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 complementary techniques, including SEM, confocal microscopy, contact angle (CA) measurements, XPS, ATR-FTIR and SAXS. In terms of composition, the prepared films show 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 structured KFs fit the nail's component composition better. 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 25.4 Thu 11:45 H13

Memory effect of red blood cells in a 3D microfluidic chip — •Amirreza Gholivand[1,2] and Minne Paul Lettinga[1,2] — [1]Forschungszentrum Jülich, IBI-4, Jülich, Germany — [2]KU Leuven, Laboratory of Soft Matter and Biophysics, Leuven, Belgium

The significance of healthy blood vessels and blood flow for proper brain functioning is becoming more recognized, for example due to its involvement in the development of human neurodegenerative disorders, notably Alzheimer's disease. Therefore, it is of interest to develop a platform to investigate blood flow and blood cell behavior through the brain vasculature.

Here we present model 3-D microfluidic channels to study the RBCs flow through different vessels geometry and their flow dynamics. RBCs in microcirculation and at bifurcation may attain different memory effect, which we studied systematically varying the interaction strength between the red blood cells and the complexity of flow geometries. To this end, we make use of a novel technique, Selective Laser-induced Etching (SLE), which can produce 3D structures in glass with any desirable shape. To study the shape memory of the vessels the second generation of the bifurcation has been implemented with a parallel and perpendicular orientation relative to the first bifurcation. Using ultrafast microscopy in combination with velocimetric analysis, we identify a new memory effect, where there is a shift in the maximum velocity, depending on the orientation of the downstream bifurcation.

BP 26: Focus Session: Bioinspired Systems

organized by Isabella Guido (MPI for Dynamics and Self-Organization, Göttingen) and Kerstin Göpfrich (MPI for Medical Research, Heidelberg)

Time: Thursday 15:00–17:30 Location: H15

Invited Talk BP 26.1 Thu 15:00 H15

Molecular robots working cooperatively in swarm — •Akira Kakugo — Hokkaido University, Sapporo, Japan

Cooperation is a strategy that has been adopted by groups of organisms to execute complex tasks more efficiently than single entities. Cooperation increases the robustness and flexibility of the working groups and permits sharing of the workload among individuals. Here, we demonstrate molecular transportation through the cooperative action of a large number of artificial molecular machines, photoresponsive DNA-conjugated microtubules driven by kinesin motor proteins. Mechanical communication via conjugated photoresponsive DNA enables these microtubules to organize into groups upon photoirradiation. The groups of transporters load and transport cargo, and cargo unloading is achieved by dissociating the groups into single microtubules. The group formation permits the loading and transport of cargoes with larger sizes and in larger numbers over long distances compared with single transporters. We also demonstrate that cargo can be collected at user-determined locations defined by ultraviolet light exposure.

BP 26.2 Thu 15:30 H15

Self-organization of microtubule filaments in energy dissipative evaporating droplet — •Vahid Nasirimarekani, Olinka Ramirez-soto, Stefan Karpitschka, and Isabella Guido — Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany

Cytoskeletal assemblies such as microtubule networks and motor proteins of the kinesin family drive vital cellular processes that, together with cargo delivery and cell division, also include providing mechanical stability when cells are exposed to external stresses. How these self-organising structures can orchestrate such response is not yet well understood. In this study, we develop a bioinspired system resembling intracellular cytoskeletal networks and characterise its activity under the influence of external stress. For this purpose, we confine an active network of microtubules and kinesin motors in an evaporating

aqueous droplet. This setup serves as a bioreactor that enables to apply forces to the active system. Namely, the flow field generated by the Marangoni and capillary flow couples with the active stress of the microtubule-motor protein network. We observe that this coupling influences the spatio-temporal distribution of the driving forces and the emergent behaviour of the system, which shows contracting and relaxing behaviour. By analysing such non-equilibrium systems, our study can contribute to understand the response of biological structures to cues from the external environment.

BP 26.3 Thu 15:45 H15

Amphiphile-stabilized microemulsions formed from synthetic DNA-nanomotifs — Xenia Tschurikow[1], Mai Tran[2], Rakesh Chatterjee[3,4], Vasily Zaburdaev[3,4], Kerstin Göpfrich[2], and •Lennart Hilbert[1] — [1]Karlsruhe Institute of Technology — [2]Max Planck Institute for Medical Research — [3]Friedrich-Alexander-Universität Erlangen — [4]Max-Planck-Zentrum für Physik und Medizin

DNA in the nuclei of pluripotent cells exhibits a unique, finely dispersed microdomain pattern. This pattern is formed from DNA and RNA, which behave as two separating phases, and is stabilized in a microemulsified configuration by amphiphiles forming at sites where DNA is transcribed into RNA. Here, we synthetically reproduce such an amphiphile-stabilised microemulsion using DNA oligo-based nanomotifs. Specifically, we implemented a droplet phase in the form of DNA-nanomotifs with three self-affine "sticky ends", to which we add amphiphile particles that additionally harbour negative charges that are repelled from DNA-dense droplets. We confirmed behaviors expected upon amphiphile addition in titration experiments, time-lapse microscopy, and by mapping the amphiphile distribution within droplets. We are currently carrying out lattice simulations with multi-ended particles, which explicitly capture the interaction rules that are encoded via the different DNA-nanomotif ends. Our work provides an avenue towards the model-guided design of more complex multi-phase systems, to reproduce, for instance, the multitude of nuclear bodies observed in biological cells.

15 min. break

BP 26.4 Thu 16:15 H15

Bottom-up assembly of synthetic cells with bio-inspired DNA-based cytoskeletons — •Kevin Jahnke[1], Pengfei Zhan[2], Maja Illig[1], Na Liu[2], and Kerstin Göpfrich[1] — [1]Max Planck Institute for Medical Research — [2]Stuttgart University

The bottom-up assembly of synthetic cells with a functional cytoskeleton sets a major milestone to understand cell mechanics and to develop man-made cellular machines. However, the combination of multiple elements and functions remained elusive, which stimulates endeavors to explore entirely synthetic bio-inspired and rationally designed solutions towards engineering life. To this end, DNA nanotechnology represents one of the most promising routes. Here, we demonstrate functional DNA-based cytoskeletons operating in microfluidic cell-sized compartments and lipid vesicles. The synthetic cytoskeletons consist of DNA tiles self-assembled into filament networks (Zhan*, Jahnke* et al., in press at Nat. Chem. 2022; Jahnke et al., ACS Nano 2022). These synthetic cytoskeletons can be rationally designed and controlled to imitate features of natural cytoskeletons, including ATP-triggered polymerization, morphology control and vesicle transport in cell-sized confinement. Also, they possess engineerable characteristics, including assembly and disassembly powered by DNA hybridization, light or aptamer-target interactions. Moreover, we incorporate membrane-spanning DNA origami signalling units to allow for mechanochemical signal transduction across the GUV membrane (Jahnke, Illig et al., biorxiv 2022). This work underpins DNA nanotechnology as a key player in building synthetic cells from the bottom up.

BP 26.5 Thu 16:30 H15

Synchronization, enhanced catalysis of mechanically coupled enzymes and how to design them — •Michalis Chatzittofi[1], Jaime Agudo-Canalejo[1], Tunrayo Adeleke-Larodo[2], Pierre Illien[3], and Ramin Golestanian[1,2] — [1]Department of Living Matter Physics, MPI -DS, D-37077 Göttingen, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, OX1 3PU, UK — [3]Sorbonne Universite, CNRS, Laboratoire Physicochimie des Electrolytes et Nanosystemes Interfaciaux, 75005, France

Enzymes are the catalysts of the chemical processes that take place in living organisms. These processes, during which chemical energy is converted to mechanical energy and heat, occur stochastically as a result of a noise-activated barrier-crossing event. Despite this stochasticity, it has been shown recently that two mechanically coupled enzymes can synchronize their catalytic reaction [1]. Even more interestingly, the coupling enhances the catalysis of the two enzymes. This effect can be understood as arising from a bifurcation in the deterministic dynamics of the system. In this work, we use a similar approach to describe the dynamics of an enzyme by assuming that the enzyme is attached to a passive molecule. The goal is to design the properties of the enzyme so that its motion favours a chemical reaction, for example dissociation or a shape switch of the molecule. A bifurcation in the deterministic dynamics can cause a change in the molecules state after one enzymatic reaction. The stochastic simulations, also show that the enzyme's activity affects the state of the molecule.

[1] J. Agudo-Canalejo, et al., Phys. Rev. Lett. 127, 208103 (2021).

BP 26.6 Thu 16:45 H15

Dynamic formation and size control of cell-like compartments — •Sebastian W. Krauss, Pierre-Yves Gires, Mithun Thampi, and Matthias Weiss — Experimental Physics I, University of Bayreuth, Germany

A fundamental feature of living matter is its spatial organization into individual units, with the replication of template-like entities during cell division supposedly being the most familiar process linked to this feature. Yet, spatially ordered arrays of cell-like compartments ('protocells') also emerge spontaneously in homogeneous, isotropic Xenopus egg extracts in the absence of template structures and genetic material. We show that the geometry of these patterns has properties of a random-packing problem, i.e. randomly placed seeds grow at a uniform rate until competition for material becomes limiting. We also show that the pattern undergoes a coarse-graining over time while maintaining its overall organization. Moreover, fluorescence imaging reveals the cytoskeleton to be the driving force behind the compartmentalization. In line with this notion, a perturbed dynamics of microtubules is observed to result in strongly reduced protocell areas. Altogether, our experimental observations suggest that space compartmentalization in living matter relies on few but robust generic physico-chemical principles.

BP 26.7 Thu 17:00 H15

New insights into the DNA origami silicification reaction mechanism by in situ small angle X-ray scattering — •Amelie Heuer-Jungemann[1,3], Martina Ober[2], Lea Wassermann[1], Anna Baptist[1], and Bert Nickel[2,3] — [1]Max Planck Institut für Biochemie, Am Klopferspitz 18, 82152 Martinsried — [2]Ludwig-Maximilians-Universität, Geschwister-Scholl-Platz 1, 80539 München — [3]Center for Nanoscience, LMU München, Geschwister-Scholl-Platz 1, 80539 München

DNA origami allows for the formation of arbitrarily shaped nanostructures with nm precision control. Yet, many potential real-life applications have been hampered due to the biologicL instability of DNA origami: Silicification provides an excellent way of increasing DNA origami stability. However, so far, it remains unclear how silicification affects the internal structure of the DNA origami and whether the whole DNA framework is embedded or if silica just forms an outer shell. By using in situ small angle x-ray scattering (SAXS), we were able to show that silica growth is not restricted to the outer origami surface, but also occurs on the inner surface, penetrating the whole structure and induces substantial condensation of the structure at early reaction times. Remarkably, we found that thermal stabilization of the origami up to 60°C as well as resistance towards degradation by nucleases could already be observed for sub-nm silica deposition in the highly condensed state. In this state DNA origami addressability could also be retained, resulting in the first fully site-specifically addressable silica nanostructure.

BP 26.8 Thu 17:15 H15

Energy transfer between coupled colloidal clusters — •Andreas Ehrmann and Carl Goodrich — Institute of Science and Technology Austria, Am Campus 1, 3400 Klosterneuburg, Austria

Can biology-inspired complexity be obtained without biochemical components? Can we replicate ubiquitous biological processes using only model physical building blocks like DNA-coated colloids that have simple but programmable interactions? The last decades have seen tremendous progress in understanding the self-assembly mechanisms that enable the formation of complex, sub-micron scale structures, but

embedding these structures with bio-inspired functional behaviors remains a considerable challenge. Here, we demonstrate a scheme for transferring energy between two colloidal clusters, in analogy to ATP hydrolysis. By coupling the two clusters, we show how the one acting as a receiver catalyzes a structural transition in the one acting as a fuel source, releasing energy that drives the receiver into a higher energy structural state. The coupled system shows a significantly reduced mean-first passage time. This work demonstrates that a fundamental and enabling biological process can be replicated without complex biochemical reactions. In contrast, theories of active matter often focus on the effect of energy consumption, not on the mechanism itself. However, the mechanism is intimately connected to the type of physical phenomena that can result. In a next step, we extend the scheme to convert energy into work by driving a net flux in the receiver, which is not possible in equilibrium and requires a fuel source.

BP 27: Statistical Physics of Biological Systems 2 (joint session BP/DY)

Time: Thursday 15:00–16:30 Location: H16

BP 27.1 Thu 15:00 H16

Sensing and making sense of fluctuating cellular states — •Felix J. Meigel[1], Lina Hellwig[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 self-organisation of cells into complex tissue relies on the tight regulation of cellular responses to fluctuating cues. Typically, the regulation of cell decisions is attributed to pathways controlling the concentration of molecular species in response to intrinsic or extrinsic signal. Here, by contrast, we show in the paradigmatic example of cell death that cells manipulate how fluctuations propagate across spatial scales to regulate cellular behavior. Specifically, we find that the feedback between molecular and mesoscopic organelle fluctuations gives rise to a quasi-particle degree of freedom whose intriguing kinetic properties construct a kinetic low-pass filter of time-dependent concentrations of signaling molecules. We show that the collective dynamics of the quasi-particle degree of freedom exhibits different kinetics on different temporal scales. This allows cells to distinguish between fast fluctuations and slow, biologically relevant changes in environmental signals. We demonstrate an order of magnitude effect of this phenomenon on the quality of the cell death decision and validate our predictions experimentally by dynamically perturbing the intrinsic apoptosis pathway. Our work reveals a new mechanism of cell fate decision making.

BP 27.2 Thu 15:15 H16

Guidance and optimization in branching morphogenesis — •Mehmet Can Ucar and Edouard Hannezo — Institute of Science and Technology Austria, Am Campus 1, 3400 Klosterneuburg, Austria

The development of branched, tree-like biological structures such as lung, kidney, or the neurovascular system has been a pivotal question in biology, physics and mathematics. Recently, many studies based on combinatorial, mechanical, or stochastic models explored local, selforganizing rules leading to branched morphologies in specific systems. However, in addition to local interactions, the growth of branched structures is also regulated globally by external chemical or mechanical guidance cues. In this talk, we present our recent theoretical framework that integrates local and global regulatory mechanisms of branching morphogenesis. Combining analytical theory and numerical simulations, we show that branch orientations follow a generic scaling law that depends on the strength of global guidance. Local interactions such as self-avoidance of branches, on the other hand, lead to denser, efficiently space-filling networks, with a minimal influence on the overall shape and territory. These quantitative predictions of the model are corroborated by experimental data on sensory neurons in the zebrafish caudal fin. Finally, we discuss effects of local interactions on optimal tiling of space in branched distribution networks such as in lymphatic vasculature.

BP 27.3 Thu 15:30 H16

Random force yielding transition in spherical epithelia — Aboutaleb Amiri[1], Charlie Duclut[2], Frank Jülicher[1], and •Marko Popović[1] — [1]Max Planck Institute for Physics of Complex Systems, Dresden — [2]Université Paris Diderot, Paris

Developing biological tissues are often described as active viscoelastic fluids on long time-scales, due to fluidization by cell division and apoptosis. However, on shorter time-scales they can behave as amorphous solids with a finite yield stress [Mongera et al., Nature, 2018]. Under shear stress beyond the yield stress value amorphous solids begin to flow. This yielding transition is a dynamical phase transition characterized by a diverging correlation length and a set of critical exponents. Developing tissues are active matter systems whose constitutive cells can propel themselves by exerting traction forces. Recently, a remarkable correspondence has been proposed between uniformly sheared amorphous solids and dense self-propelled particle systems [Morse et al., PNAS, 2021] based on the identical scaling of non-linear properties of their energy landscapes. Here, we use a vertex model of epithelial tissues to study how randomly oriented traction forces fluidize a spherical epithelial tissue. In particular, we identify a sharp transition between quiescent and randomly flowing states separated by the critical value of the traction force magnitude, analogous to the yield stress. Moreover, we show that this transition is characterized by the same set of exponents as the classical yielding transition, and the corresponding scaling relations provide a non-trivial relation between cell geometry, cell rearrangement dynamics and tissue flow.

BP 27.4 Thu 15:45 H16

Biological tissues as living amorphous solids — •Ali Tahaei and Marko Popović — Max Planck Institute for Physics of Complex Systems, Dresden

Biological tissues are often described as viscoelastic fluids on long time-scales. However, on shorter times-scales, tissues can behave as amorphous solids, such as clay, changing shape only when exposed to a shear stress above the material yield stress Σ_c. Amorphous solids near Σ_c display critical behaviour with a diverging correlation length-scale characterising dynamics of plastic activity. Here, we ask how would this critical behaviour be affected by active processes present in biological tissues, such as cell divisions.

In order to model yielding of biological tissues we employ the mesoscopic elasto-plastic model, commonly used to describe yielding of amorphous solids. Here, we extend the classical elasto-plastic model by introducing cell divisions as an additional source of plastic activity. We find that cell divisions strongly fluidise the solid phase of the system at stresses lower than Σ_c, consistent with literature. Furthermore, we find that critical behaviour is strongly suppressed, leading to localised dynamics of plastic activity nucleated by cell divisions. Finally, in our model we can describe how well is the cell division orientation aligned with local shear stress. We find that low alignment strength leads to less mechanically stable tissues where, consequently, most of the plastic flow arises from cell rearrangements, and vice versa.

BP 27.5 Thu 16:00 H16

Order-disorder transition in epithelial tissues — •Kartik Chhajed, Marko Popović, and Frank Jülicher — Max Planck Institute for Physics of Complex Systems, Dresden

Two dimensional packings of cells in developing epithelial tissues are commonly found to be disordered. However, highly organised packings can emerge during development, such as hexagonal pattern of ommatidia in the eye epithelium of the fruit fly. Here, we observe a disorder to order transition in the packing of the fruit fly pupal wing epithelium. In particular, we find a sudden increase in the hexatic order parameter ψ_6, which suggests a presence of hexatic and crystalline phases in two dimensional systems, as described by the classical KTHNY theory. The melting transition scenario with the intermediate hexatic phase has been reproduced in a model of epithelial tissues [Pashupalak et al. Soft Matter, 2020] where the stochastic active forces generated by the cells play the role of an effective temperature. However, both KTHNY theory and recent literature on packings of epithelial tissues assume uniform properties of particles and cells, respectively. In a proliferating tissue cells grow and divide, which inevitably leads to a heterogeneity of cell sizes. Here, we use the vertex model of epithelial

tissues to study how the disorder to order transition is affected by the heterogeneity of cell sizes. We find that reducing cell heterogeneity as a control parameter drives the system through an ordering transition. We compare our results with the experimental data of the fruit fly wing to identify the role of cell size heterogeneity in the observed disorder to order transition.

BP 27.6 Thu 16:15 H16

The Influence of Contact Maps on RNA Structure Prediction — •Christian Faber[1] and Alexander Schug[1,2] — [1]Jülich Supercomputing Centre, FZ Jülich — [2]Steinbuch Centre for Computing, KIT

The 3d structure of Proteins and non coding RNA are essential for their function, but hard to determine via NMR or x-ray crystallography. Therefore an effective way of simulation with the knowledge of the sequence only would be a huge improvement. Impressive progress has been made in recent years, most notably AlphaFold2 for protein structure prediction using Machine Learning techniques. Such a break through is still missing for RNA.

For RNA, there are folding programs such as SimRNA, that simulate the structure with a physical force field [1]. The outcome can be improved by incorporating evolutionary data from homologous sequences. From the evolutionary data, we can make predictions about possible contacts in the form of contact maps [2].

We investigate how contact maps can influence prediction quality and what are particularly valuable contacts. From these insights we develop new measures for machine learning algorithms.

[1] Boniecki, M. J. et al. *SimRNA: a coarse-grained method for RNA folding simulations and 3D structure prediction.* Nucleic Acids Research 44, e63 (2016).

[2] Weigt, M., White, R. A., Szurmant, H., Hoch, J. A., Hwa, T. *Identification of direct residue contacts in protein-protein interaction by message passing.* PNAS 106, 67-72 (2009).

BP 28: Biopolymers, Biomaterials and Bioinspired Functional Materials (joint session CPP/BP)

Time: Friday 9:30–11:15 Location: H39

Invited Talk BP 28.1 Fri 9:30 H39

New biobased material concepts using scattering techniques to elucidate and control nanoscale assembly — •Daniel Söderberg — KTH Royal Institute of Technology, Department of FIbre and Polymer technology, Stockholm, Sweden

Cellulose, the most abundant biopolymer on earth, can be crucial in mitigating fossil-based resources to more sustainable solutions. It is used as an engineering material, e.g. sawn timber, pulp for papermaking or as a polymer as a basis for plastic materials.

Cellulose nanofibres (CNF) constitute the structural component of plants, it is a semi-crystalline, semi-flexible rod-like nanoparticle having cross-sections in the order of 4-5 nm and lengths around one micrometre. Based on technical developments during the last decades, it is today possible to extract the CNF in large quantities, which has promoted significant research efforts aiming at new material concepts and devices based on cellulose.

Small and wide-angle x-ray scattering have been used to understand nanoscale assembly during fibre spinning from a CNF dope using microfluidics, allowing the tuning of the hierarchical structure, resulting in 100% bio-based filaments with exceptional properties. Furthermore, to develop scalable engineering processes, an in-depth understanding of nanoscale diffusion and the effects of nanoparticle interaction in low-concentration crowded systems has been pursued by combining light-scattering, X-ray Photon Correlation Scattering and coarse-grain modelling.

BP 28.2 Fri 10:00 H39

A Semisynthetic Superparamagnetic Nanoprobe for Protein Targeting and Manipulation — •Andreas Neusch[1], Iuliia Novoselova[1], Nikolaos Tetos[2], Michael Farle[2], Ulf Wiedland[2], and Cornelia Monzel[1] — [1]Heinrich-Heine University Düsseldorf, Germany — [2]University of Duisburg-Essen, Germany

Probing and manipulating biological functions requires tools to target and modify the proteins involved in the respective process. In recent years Magnetogenetics emerged as an approach where magnetic nanoparticles (MNPs) and external magnetic fields are used to realize such manipulation (Lisse et al., Adv. Mater., 29, 1700189 (2017)). The advantages of this combination lies within the deep tissue penetration of magnetic fields and the possibility to apply stimuli on nanoscales leading to spatial redistribution, force application, or heat generation of proteins. However, a precise active perturbation requires MNPs to be monodisperse, biocompatible, tunable with regard to their magnetic properties, as well as exhibiting a modifiable molecular shell (Monzel et al., Chem. Sci. 8, 7330-7338 (2017)). Here, we synthesize a bioinspired semisynthetic MNP - Magnetoferritin (MFt) -, which fulfils these demands. MFt is based on the globular iron storage protein complex ferritin that converts iron ions to a ferrihydrite core but can be synthetically loaded with a magnetic iron oxide core (Novoselova et al., Nanomaterials, 11, 2267 (2021)). MFt was chemically, physically and magnetically characterized both in vitro and in vivo. We demonstrate how MFt can be used to target proteins on living cells as well as to spatially manipulate MFts in a single cell environment.

BP 28.3 Fri 10:15 H39

Bioinspired electrodes for brain wave detection — •Volker Körstgens[1], Gökay Erbil[1], Andreas Zheng[1], Hsin-Yin Chiang[2], and Peter Müller-Buschbaum[1] — [1]TU München, Physik-Department, LS Funktionelle Materialien, 85748 Garching — [2]Cephalgo, 67000 Strasbourg, France

With increasing demands in brain computer interfaces (BCI) measuring biosignals non-invasively becomes more important. Applications like measuring brain waves via electroencephalography (EEG) with dry electrodes remains challenging as for a steady biosignal acquisition adhesion to the skin has to be maintained all the time. We present two different approaches inspired by nature for such electrodes. In our first approach we developed micro-structured dry adhesive electrodes based on polydimethylsiloxane (PDMS) with conductive fillers. The EEG-performance and adhesive properties of these electrodes will be discussed and compared to the concept of mussel-inspired hydrogels we follow in our second approach.

BP 28.4 Fri 10:30 H39

Anionically functionalized glycogens efficiently encapsulate cationic peptides — Hanna Zhukouskaya[1], •Pablo M. Blanco[2], Zulfiya Černochová[1], Lucie Čtveráčková[1], Roman Staňo[3], Ewa Pavlova[1], Miroslav Vetrík[1], Peter Černoch[1], Miroslav Šlouf[1], Marcela Filipová[1], Miroslav Štěpánek[2], Martin Hrubý[1], Peter Košovan[2], and Jiří Pánek[1] — [1]Institute of Macromolecular Chemistry, Czech Academy of Sciences, Heyrovského nám. 2, 162 06 Prague 6, Czech Republic — [2]Department of Physical and Macromolecular Chemistry, Faculty of Science, Charles University, Hlavova 8, 128 40 Prague 2, Czech Republic — [3]Faculty of Physics, University of Vienna, Kolingasse 14-16, 1090 Vienna, Austria

We developed and tested novel acid-functionalized glycogen conjugates as supramolecular carriers for efficient encapsulation and inhibition of a model cationic peptide melittin, which is the main component of honeybee venom. Systematic investigation of this model system allowed us not only to test its potential application as honeybee venom antidote but also to assess the role of the degree of substitution and solution pH in the interactions of these anionic carriers with multivalent cationic cargos. Our results demonstrate that the concept of electrostatically driven encapsulation by acid-functionalized glycogens should be applicable not only to the model case of melittin but also to other multivalent cationic biomolecules.

BP 28.5 Fri 10:45 H39

Dissipative Assembly: Controlling Changes of Membrane Topology by Reaction Cycles — •Gregor Ibbeken and Marcus Müller — Institut für Theoretische Physik, Georg-August Universität, Friedrich-Hund-Platz 1, 37075 Göttingen

Coupling a self-assembling system to a reaction cycle, we go beyond equilibrium self-assembly toward systems that dissipate energy and

thus exhibit new, unique features of dynamic self- organization. We consider polymers which can switch between a hydrophilic and an amphiphilic state and in the latter self-assemble to form vesicles in aqueous solution. This can occur either by macromolecular or monomeric reactions. In both cases a precursor reacts with a fuel to a product, which itself can decay back to the precursor. We perform particle-based simulations using a soft, coarse grained model for polymers. For the macromolecular reactions we find two drastically different scenarios depending on the fuel volatility: (i) For high fuel volatility, the coupling of inactivated to activated polymers introduces a length scale which dictates the maximal vesicle size and prevents fusion beyond this. This results in an interplay between the architecture- and the reaction-rate-determined length and time scales. (ii) For less volatile fuel, a fuel gradient arises in the system. This results in the compartments moving within the fuel gradient to approach the source. In doing so the moieties gain material over long times which drastically changes the formation mechanism of the vesicles. Finally, we show that the above reaction mechanism can be mimicked by monomeric reactions by the use of multiple, inhomogeneously distributed fuels.

BP 28.6 Fri 11:00 H39

Influence of molecular weight of polycation polydimethyldiallylammonium and carbon nanotube content on the electric conductivity of layer-by-layer films — •Sven Neuber[1], Annekatrin Sill[1], Peter Nestler[2], Heiko Ahrens[1], and Christiane A. Helm[1] — [1]Universcity of Greifswald, Institut of Physics, Greifswald, Germany — [2]TÜV NORD EnSys GmbH & Co. KG, Greifswald, Germany

For biological and engineering applications, nm-thin films with high electrical conductivity and tunable sheet resistance are desirable. Multilayers of polydimethyldiallylammonium chloride (PDADMA) with two different molecular weights (322 and 44.3 kDa) and oxidized carbon nanotubes (CNTs) were constructed using the layer-by-layer technique. Both the film thickness and the surface coverage of the CNTs increased linearly with the number of CNT/PDADMA bilayers deposited (dfilm up to 80 nm). Atomic force microscopy images showed a predominantly surface-parallel orientation of CNTs. Ohmic behavior with constant electrical conductivity of each CNT/PDADMA film and conductivity up to 4*10^3 S/m was found. A change in PDADMA molecular weight by almost a factor of ten does not affect the film thickness and electrical conductivity, only the film/air roughness is reduced. However, increasing CNT concentration in the deposition dispersion from 0.15 up to 0.25 mg/ml results in an increased thickness of a CNT/PDADMA bilayer (by a factor of three). The increased bilayer thickness is accompanied by a decreased CNT coverage and a decreased electrical conductivity (by a factor of four).

BP 29: Active Matter 5 (joint session DY/BP/CPP)

Time: Friday 10:00–12:45 Location: H18

BP 29.1 Fri 10:00 H18

Anomalous cooling and overcooling of active colloids — •Fabian Jan Schwarzendahl and Hartmut Löwen — Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, 40225 Düsseldorf, Germany

The phenomenon that a system at a hot temperature cools faster than at a warm temperature, referred to as the Mpemba effect, has been recently realized for trapped colloids. Here, we investigate the cooling and heating process of a self-propelling active colloid using numerical simulations and theoretical calculations with a model that can directly be tested in experiments. Upon cooling activity induces a Mpemba effect and the active particle escapes an effective temperature description. At the end of the cooling process the notion of temperature is recovered and the system can exhibit even smaller temperatures than its final temperature, a surprising phenomenon which we refer to as activity-induced overcooling.

BP 29.2 Fri 10:15 H18

Active Ornstein-Uhlenbeck model for self-propelled particles with inertia — •Gia Huy Philipp Nguyen, René Wittmann, and Hartmut Löwen — Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, Germany

Self-propelled particles, which convert energy into mechanical motion, exhibit inertia if they have a macroscopic size or move inside a gaseous medium, in contrast to micron-sized overdamped particles immersed in a viscous fluid. We have studied an extension of the active Ornstein-Uhlenbeck model, in which the self-propulsion is described by colored noise, to access these inertial effects affecting their translational motion [1]. In this talk, analytical solutions of the mean displacement, mean-squared displacement and velocity autocorrelation function will be discussed for a free active particle and in more general settings including an active dimer, a time-dependent mass and various external forces.

[1] G. H. P. Nguyen, R. Wittmann, H. Löwen, J. Phys.: Condens. Matter 34, 035101 (2021)

BP 29.3 Fri 10:30 H18

A quantitative scattering theory of active particles — •Thomas Ihle[1], Rüdiger Kürsten[1], and Benjamin Lindner[2] — [1]Institute for Physics, University of Greifswald, Greifswald — [2]Institute for Physics, Humboldt University of Berlin, Berlin

We consider a particular model of self-propelled particles with Kuramoto-type alignment interactions. Starting from the N-particle Fokker-Planck equation we observe that the usual factorization Ansatz of the probability density, often called Molecular Chaos approximation, predicts a relaxation behavior which qualitatively disagrees with agent-based simulations. Therefore, we develop a scattering theory which resolves the time-evolution of the two-particle correlation function, i.e. goes beyond the mean-field approximation. The theory does not require input from agent-based simulations; it is self-consistent and leads to analytical expressions. We show that this theory predicts the relaxation behavior of the system and the transport coefficients with high precision in certain parameter ranges.

BP 29.4 Fri 10:45 H18

Hierarchical self-organization in communicating polar active matter — •Alexander Ziepke[1], Ivan Maryshev[1], Igor S. Aranson[2], and Erwin Frey[1] — [1]Ludwig-Maximilians-Universität München, München, Germany — [2]Pennsylvania State University, University Park PA, USA

Self-organization in active matter plays an important role for various biological and artificial systems. In numerous cases, inter-agent communication is a key mechanism for the formation and localization of critical structures, such as the fruiting body in Dictyostelium discoideum or aggregation clusters in quorum-sensing bacteria. Despite its importance, the specific role of communication and its interplay with self-propulsion remains largely unexplored.

We propose a model for communicating active matter that endows self-propelled polar agents with information processing and signal relaying capabilities. We show that information processing greatly enriches the ability of these systems to form complex structures, allowing them to self-organize through a range of different collective dynamical states at multiple hierarchical levels. This provides insights into the role of self-sustained signal processing for self-organization in biological systems and opens pathways for applications using chemically driven colloids or microrobots.

BP 29.5 Fri 11:00 H18

Collective transport of microparticles by active cells — •Robert Grossmann[1], Kevin Meissner[1], Fernando Peruani[2], and Carsten Beta[1] — [1]University of Potsdam, Potsdam, Germany — [2]CY Cergy Paris Université, Cergy-Pontoise, France

Motivated by the challenge of targeted delivery of micron-sized objects, we investigate a novel type of bio-hybrid active matter, composed of motile cells acting as autonomously moving agents that transport passive cargoes. The transport process is a collective phenomenon: a bead can be lost by one cell and may picked up by another one, or multiple cells transport one bead together, thereby giving rise to an intermittent, stochastic stop-and-go dynamics. Combining experiment and active matter theory, we investigate the emerging transport properties of this system. We first deduce the waiting time distributions of active and passive transport episodes from experiments with the amoeba

Dictyostelium discoideum: whereas the duration of actual transport phases – determined by the time that cells and cargoes are in contact – are exponentially distributed, the waiting time distribution for passive periods exhibits power-law characteristics which results from the search of cells looking for immobile colloids. We predict displacement distributions and the mean-squared displacement of colloids based on the statistics of waiting times and particularly point out a crossover from normal to subdiffusive scaling. These results provide the basis for the future design of cellular micro-carriers and for extending our findings to more advanced transport tasks in complex, disordered environments, such as tissues.

BP 29.6 Fri 11:15 H18

Odd viscosity and active turbulence of hydrodynamic microrotors — •Joscha Mecke[1], Yongxiang Gao[2], Dirk G.A.L. Aarts[3], Alberto Medina[1], Gerhard Gompper[1], and Marisol Ripoll[1] — [1]Institute of Biological Information Processing, Forschungszentrum Jülich, Germany — [2]Institute for Advanced Study, Shenzhen University, China — [3]Department of Chemistry, University of Oxford, UK

Suspensions of rod-like silica colloids with a ferromagnetic head are considered in a rotating magnetic field applied parallel to a substrate. The magnetic moment is oriented perpendicular to the rod axis which implies a non-equilibrium vertical orientation to the substrate and synchronous spinning in the rotating field. We combine experiments and simulations to study the collective properties of these rotors. The hydrodynamic flows generated by the colloid rotations induce a cascade of translational motions in the neighbouring colloids. Thus, the rotors can be regarded as active matter with transport coefficients varying with local configuration and thus rotor density. The competition between hydrodynamic and steric interactions renders the translational dynamics non-monotonous in rotor density. The ensemble dynamics shows the emergence of eddies of various sizes reminiscent of turbulence. Furthermore, the rotor fluid is a realisation of a chiral active fluid with odd viscosity, that manifests itself in stress forces orthogonal to the direction of shear. In vortex flow, the stress acts like an effective pressure leading to density-vorticity correlations. Our experimental and numerical results are found to be in agreement.

BP 29.7 Fri 11:30 H18

Two-temperature activity drives liquid-crystal and crystalline order in soft repulsive spherocylinders — •Jayeeta Chattopadhyay, Sindhana Pannir-Sivajothi, Kaarthik Varma, Sriram Ramaswamy, Chandan Dasgupta, and Prabal K. Maiti — Centre for Condensed Matter Theory, Department of Physics, Indian Institute of Science, Bangalore 560012, India

We study the scalar activity induced phase separation and liquid crystal ordering in a system of Soft Repulsive Spherocylinders (SRS) of various aspect ratios (L/D). Activity was introduced by increasing the temperature of half of the SRS (labeled 'hot') while maintaining the temperature of the other half constant at a lower value (labeled 'cold'). The difference between the two temperatures scaled by the lower temperature provides a measure of the activity. We find that activity drives the cold particles through a phase transition to a more ordered state and the hot particles to a state of less order compared to the initial equilibrium state. For L/D = 5, the cold components of a homogeneous isotropic (I) structure acquire nematic (N) and, at higher activity, crystalline (K) order. Similarly, the cold zone of a nematic initial state undergoes smectic (Sm) and crystal ordering while the hot component turns isotropic. Interestingly, we observe liquid crystal ordering for the spherocylinders having aspect ratio below Onsager's limit. The hot particles occupy a larger volume and exert an extra kinetic pressure, confining, compressing and provoking an ordering transition of the cold-particle domains.

Ref:Phys. Rev. E104, 054610 (2021).

BP 29.8 Fri 11:45 H18

Spontaneous trail formation in populations of communicating active walkers — Zahra Mokhtari[1], Robert I. A. Patterson[2], and •Felix Höfling[1,3] — [1]Dept. Mathematics and Computer Science, Freie Universität Berlin — [2]WIAS Berlin — [3]Zuse Institute Berlin

How do ants form long stable trails? Despite abundant evidence that trail formation in colonies of insects or bacteria originates in their sensing of and responding to the deposits of chemicals that they produce, there is no consensus on the minimum required ingredients for this phenomenon. To address this issue, here, we develop an agent-based model in terms of active random walkers communicating via pheromones, which can generate trails of agents from an initially homogeneous distribution [1]. Based on extensive off-lattice computer simulations we obtain qualitatively the non-equilibrium state diagram of the model, spanned by the strength of the agent-chemical interaction and the number density of the population. In particular, we demonstrate the spontaneous formation of persistent, macroscopic trails, and highlight some behaviour that is consistent with a dynamic phase transition. We also propose a dynamic model for few macroscopic observables, including the sub-population size of trail-following agents, which captures the early phase of trail formation. At high densities and for strong alignment, we observe that rotating clusters ("ant mills") are more stable than trails and can swallow them up.

[1] Z. Mokhtari, R. I. A. Patterson & F. Höfling, New J. Phys. **24**, 013012 (2022).

15 min. break

BP 29.9 Fri 12:00 H18

Dynamics of microalgae in a porous environment — •Florian von Rüling, Liubov Bakhchova, Dmitry Puzyrev, Ulrike Steinmann, and Alexey Eremin — Otto von Guericke University Magdeburg, Germany

The navigation through complex environments is a task the microalgae *Chlamydomonas reinhardtii* are frequently confronted with in their natural habitats, where they encounter suspended and sedimented particles as well as rough surfaces. To investigate the motion in heterogeneous surroundings, we observe dilute and crowded active colloidal suspensions of *Chlamydomonas* in quasi-two-dimensional microstructured PDMS-channels. Arrays of cylindrical or elongated pillars with varying lattice spacing and obstacle orientation serve as artificial porous environments. The swimmer behaviour is characterised by means of velocity and orientation autocorrelation functions, trajectory straightness, velocity distributions and the reflection/transmission coefficients for the porous segments.

BP 29.10 Fri 12:15 H18

Extending the active Phase Field Crystal model to describe motility-induced condensation and crystallization — •Max Philipp Holl[1] and Uwe Thiele[1,2] — [1]Institut für Theoretische Physik, Universität Münster — [2]Center for Nonlinear Science, Universität Münster

The passive conserved Swift-Hohenberg equation (or phase-field-crystal [PFC] model) corresponds to a gradient dynamics for a single order parameter field related to density [1]. It provides a microscopic continuum description of the thermodynamic transition between liquid and crystalline states. A recent extension allows one to investigate both, vapour-liquid and liquid-solid transitions [3]. We first discuss the bifurcation and phase structure of this passive, i.e., thermodynamic model. Our subsequently introduced extension of the standard active PFC model [2] is able to describe passive and active (motility-induced) vapour-liquid and liquid-solid transitions. This is shown through a bifurcation and phase analysis based on path continuation supplemented by time simulations.

[1] H. Emmerich, H. Löwen, R. Wittkowski, T. Gruhn, G. I. Tóth, G. Tegze, and L. Gránásy. Phase-field-crystal models for condensed matter dynamics on atomic length and diffusive time scales: an overview. Adv. Phys., 61:665-743, 2012 [2] A. M. Menzel and H. Löwen. Traveling and resting crystals in active systems. Phys. Rev. Lett., 110:055702, 2013 [3] Z.-L. Wang, Z. Liu, Z.-F. Huang, and W. Duan. Minimal phase-field crystal modeling of vapor-liquid-solid coexistence and transitions. Phys. Rev. Materials, 4:103802, 2020

BP 29.11 Fri 12:30 H18

Engines driven by active fields — •Patrick Pietzonka[1] and Michael E. Cates[2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Department of Applied Mathematics and Theoretical Physics, University of Cambridge, United Kingdom

On macroscopic scales, where trajectories of individual particles cannot be observed, active matter may appear like matter in thermal equilibrium. We discuss how the non-equilibrium character of active matter can nonetheless be revealed by using it as a working medium of engines delivering mechanical work in an isothermal environment. We focus on scalar active field theories such as the active model B as minimal continuum models for active matter undergoing a phase separation. The

shape and chemical potential of droplets can be controlled through external potentials and activity patterns. We show how an asymmetric periodic activity pattern can drive a flow of active matter against an external force, thus acting as an autonomous engine. Moreover, we calculate and optimise the work that can be extracted by a cyclic engine that manipulates the activity and the potential landscape.