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Overview of Invited Talks and Sessions

(Lecture halls BAR/SCHÖ, BAR/0205, and BAR/0106; Poster P2 and P5)

Invited Talks

BP 1.7	Mon	11:15–11:45	BAR/SCHÖ	**Modeling and inference of magnetotactic motility in complex environments** — •Stefan Klumpp
BP 3.1	Mon	9:30–10:00	BAR/0205	**The unreasonable effectiveness of computational models in biological patterning and morphogenesis** — •Michel Milinkovitch
BP 4.1	Mon	15:00–15:30	BAR/SCHÖ	**The Multi-faceted Role of Cholesterol in Cellular Membranes and Lipid Nanoparticles** — •Rainer Böckmann
BP 8.3	Mon	17:15–17:45	BAR/0106	**Constructing synthetic life-like vesicle systems by integration of artificial metabolic reaction networks** — •Laura Heinen
BP 9.1	Mon	16:45–17:15	BAR/0205	**Breaking the photobleaching limit in single-molecule FRET with nanophotonic DyeCycling.** — Benjamin Vermeer, Dong Hoon Shin, Alexander Vogel, Fabian Zundel, Sabina Caneva, •Sonja Schmid
BP 11.7	Tue	11:15–11:45	BAR/0106	**Physics of bacterial adhesion: heterogeneity, patchiness, and surface interactions** — •Karin Jacobs
BP 12.1	Tue	9:30–10:00	BAR/0205	**Tuning the Tracks: Functional Diversity Encoded in Microtubule Lattice States** — •Lukas Kapitein
BP 16.1	Wed	9:30–10:00	BAR/0205	**Illuminating mitochondrial permeabilisation in apoptosis** — •Ana J. Garcia Saez
BP 18.1	Wed	10:30–11:00	BAR/0106	**Protein complex structure prediction, state-of-the-art and challenges** — •Ezgi Karaca
BP 18.4	Wed	11:45–12:15	BAR/0106	**From Sparse Restraints to All-Atom Models: Integrative Reconstruction of Hidden GPCR Conformations** — •Matthias Elgeti
BP 20.4	Wed	15:45–16:15	BAR/0106	**Solution scattering and MD simulation as quantitative probes of protein-specific and temperature-dependent hydration** — •Jochen S Hub
BP 21.1	Wed	15:00–15:30	HÜL/S386	**Microbial Behavior in Context** — •Fernanda Pinheiro
BP 21.4	Wed	16:15–16:45	HÜL/S386	**The navigability of fitness landscapes shaped by global and universal epistasis** — •Joachim Krug
BP 26.7	Thu	11:15–11:45	BAR/SCHÖ	**Directed evolution of material-producing bacteria** — •André Studart
BP 27.1	Thu	9:30–10:00	BAR/0205	**Tissue interplay and the coordination of morphogenesis** — •Elias Barriga
BP 30.1	Thu	10:15–10:45	BAR/0106	**Mechanogenetics for Cell ImmunoTherapy** — •Yingxiao Wang
BP 30.4	Thu	11:30–12:00	BAR/0106	**Recent theoretical progress on sound-propelled microsystems** — •Raphael Wittkowski
BP 33.1	Thu	15:00–15:30	BAR/0205	**Expanding the Bag of Optical Tricks for (Neuro)Biology** — •Fabian F. Voigt
BP 36.1	Fri	9:30–10:00	BAR/SCHÖ	**Swimming in complex environments** — •Christina Kurzthaler

BP 41.1	Fri	11:30–12:00	BAR/0205	**Probing spatiotemportal electrochemical dynamics on single bacterial cells** — Anaïs Biquet-Bisquert, Baptiste Carrio, Nathan Meyer, Thales Fernandes, Manouk Abkarian, Farida Seduk, Axel Magalon, •Ashley Nord, Francesco Pedaci

Invited Talks of the joint Symposium SKM Dissertation Prize 2026 (SYSD)

See SYSD for the full program of the symposium.

SYSD 1.1	Mon	9:30–10:00	HSZ/0002	**Stochastic-Calculus Approach to Non-equilibrium Statistical Physics** — •Cai Dieball
SYSD 1.2	Mon	10:00–10:30	HSZ/0002	**Nonuniform magnetic spin textures for sensing, storage and computing applications** — •Sabri Koraltan
SYSD 1.3	Mon	10:30–11:00	HSZ/0002	**Anomalous Quantum Oscillations beyond Onsager's Fermi Surface Paradigm** — •Valentin Leeb
SYSD 1.4	Mon	11:00–11:30	HSZ/0002	**Coherent Control Schemes for Semiconductor Quantum Systems** — •Eva Schöll
SYSD 1.5	Mon	11:30–12:00	HSZ/0002	**On stochastic thermodynamics under incomplete information: Thermodynamic inference from Markovian events** — •Jann van der Meer

Invited Talks of the joint Symposium The Sustainability Challenge: A Decade of Transformation (SYSC)

See SYSC for the full program of the symposium.

SYSC 1.1	Mon	15:00–15:30	HSZ/AUDI	**Open-Endedness and Community-Based Approaches to Sustainability Challenges** — •Hiroki Sayama
SYSC 1.2	Mon	15:30–16:00	HSZ/AUDI	**Education as a Social Tipping Element: Evidence from Climate and Physics Education Research** — •Thomas Schubatzky
SYSC 1.3	Mon	16:00–16:30	HSZ/AUDI	**Mechanistic and Material Perspectives on Enzymatic Hydrolysis of Semicrystalline Polyesters** — •Birte Höcker
SYSC 1.4	Mon	16:45–17:15	HSZ/AUDI	**Decarbonization Options for Industry** — •Uwe Riedel
SYSC 1.5	Mon	17:15–17:45	HSZ/AUDI	**Impacts of Cosmic Dust and Space Debris in the Terrestrial Atmosphere** — •John Plane

Invited Talks of the joint Symposium France: Soft, Active and Alive: Emergent Properties in Living Matter (SYGF)

See SYGF for the full program of the symposium.

SYGF 1.1	Wed	15:00–15:30	HSZ/AUDI	**Liquid crystal geometries in type I collagen-based tissues** — •Nadine Nassif
SYGF 1.2	Wed	15:30–16:00	HSZ/AUDI	**Self-organization of the cytoplasm by physical instabilities** — •Jan Brugues
SYGF 1.3	Wed	16:00–16:30	HSZ/AUDI	**From morphogenesis to space partitioning by microtubules and molecular motors.** — •Manuel Thery
SYGF 1.4	Wed	16:45–17:15	HSZ/AUDI	**More than the sum: how composite interfaces govern function** — •Alba Diz-Muñoz
SYGF 1.5	Wed	17:15–17:45	HSZ/AUDI	**Swimming and Swarming of Intelligent Active Particles** — Segun Goh, Priyanka Iyer, Rajendra Singh Negi, •Gerhard Gompper
SYGF 1.6	Wed	17:45–18:15	HSZ/AUDI	**Perturbing the collective motion of fish with challenging environments** — •Aurélie Dupont

Invited Talks of the joint Symposium AI and Data Challenges behind Emerging Self-Driving Laboratories (SYAI)

See SYAI for the full program of the symposium.

SYAI 1.1	Thu	9:30–10:00	HSZ/AUDI	**Data and Experimental Foundations for Reliable Self-Driving Laboratories** — •Dr. Marcus Tze-Kiat Ng

SYAI 1.2	Thu	10:00–10:30	HSZ/AUDI	**Digital Catalysis - AI for Experiment Planning and Control** — •Christoph Scheurer
SYAI 1.3	Thu	10:30–11:00	HSZ/AUDI	**Autonomous, Data-Driven Workflows for Materials Acceleration Platforms with pyiron** — •Jan Janssen, Joerg Neugebauer
SYAI 1.4	Thu	11:15–11:45	HSZ/AUDI	**Machine Learning for Autonomous Optimization and Discovery of Materials** — •Pascal Friederich
SYAI 1.5	Thu	11:45–12:15	HSZ/AUDI	**Transforming Our View on Transformers in the Sciences** — •Kevin Maik Jablonka

Sessions

BP 1.1–1.11	Mon	9:30–12:45	BAR/SCHÖ	**Active Matter I (joint session BP/CPP/DY)**
BP 2.1–2.12	Mon	9:30–12:45	BAR/0106	**Computational Biophysics I**
BP 3.1–3.11	Mon	9:30–12:45	BAR/0205	**Tissue Mechanics I**
BP 4.1–4.5	Mon	15:00–16:30	BAR/SCHÖ	**Computational Biophysics II**
BP 5.1–5.6	Mon	15:00–16:30	BAR/0205	**Membranes, Vesicles and Synthetic Life-like Systems I**
BP 6.1–6.12	Mon	15:00–18:30	ZEU/0160	**Active Matter II (joint session DY/BP/CPP)**
BP 7.1–7.56	Mon	15:00–17:00	P5	**Poster Session I**
BP 8.1–8.6	Mon	16:45–18:30	BAR/0106	**Systems and Networks Biophysics**
BP 9.1–9.6	Mon	16:45–18:30	BAR/0205	**Single Molecule Biophysics**
BP 10.1–10.12	Tue	9:30–12:45	BAR/SCHÖ	**Active Matter III (joint session BP/CPP/DY)**
BP 11.1–11.11	Tue	9:30–12:45	BAR/0106	**Franco-German Session: Bacterial Biophysics I**
BP 12.1–12.11	Tue	9:30–12:45	BAR/0205	**Cytoskeleton I**
BP 13.1–13.5	Tue	14:00–15:30	ZEU/0160	**Active Matter IV (joint session DY/BP/CPP)**
BP 14.1–14.96	Tue	18:00–21:00	P2	**Poster Session II**
BP 15.1–15.11	Wed	9:30–12:45	BAR/SCHÖ	**Computational Biophysics III**
BP 16.1–16.11	Wed	9:30–12:45	BAR/0205	**Membranes, Vesicles and Synthetic Life-like Systems II**
BP 17.1–17.12	Wed	9:30–12:45	ZEU/0114	**Statistical Physics of Biological Systems I (joint session DY/BP)**
BP 18.1–18.6	Wed	10:30–12:45	BAR/0106	**Focus session: Integrative Structural Modeling**
BP 19.1–19.1	Wed	11:45–12:45	ZEU/LICH	**Round Table Discussion: The Future of Neutrons in France and Germany (joint session CPP/BP)**
BP 20.1–20.9	Wed	15:00–17:45	BAR/0106	**Protein Structure and Dynamics**
BP 21.1–21.7	Wed	15:00–17:30	HÜL/S386	**Focus Session: Sequence Spaces, Populations and Evolution**
BP 22.1–22.5	Wed	15:00–16:30	ZEU/0114	**Statistical Physics of Biological Systems II (joint session DY/BP)**
BP 23.1–23.6	Wed	15:00–16:45	ZEU/0255	**Biopolymers, Biomaterials and Bioinspired Functional Materials I (joint session CPP/BP)**
BP 24.1–24.7	Wed	17:00–18:45	ZEU/0255	**Biopolymers, Biomaterials and Bioinspired Functional Materials II (joint session CPP/BP)**
BP 25	Wed	18:30–20:00	BAR/0205	**Members' Assembly**
BP 26.1–26.11	Thu	9:30–12:45	BAR/SCHÖ	**Biomaterials and Biopolymers (joint session BP/CPP)**
BP 27.1–27.11	Thu	9:30–12:45	BAR/0205	**Cell Mechanics I**
BP 28.1–28.11	Thu	9:30–12:45	ZEU/0160	**Active Matter V (joint session DY/BP)**
BP 29.1–29.6	Thu	9:30–11:15	ZEU/0260	**Focus Session: Theoretical Modeling and Simulation of Biomolecular Condensates I (joint session CPP/BP)**
BP 30.1–30.7	Thu	10:15–12:45	BAR/0106	**Focus Session: Controlling Microparticles and Biological Cells by Ultrasound (joint session BP/CPP/DY)**
BP 31.1–31.5	Thu	11:30–12:45	ZEU/0260	**Focus Session: Theoretical Modeling and Simulation of Biomolecular Condensates II (joint session CPP/BP)**
BP 32.1–32.12	Thu	15:00–18:15	BAR/SCHÖ	**Statistical Physics of Biological Systems III (joint session BP/DY)**
BP 33.1–33.12	Thu	15:00–18:30	BAR/0205	**Bioimaging**
BP 34.1–34.8	Thu	15:00–18:00	ZEU/0160	**Focus Session: Emergent Transport in Active Systems (joint session DY/BP)**
BP 35.1–35.5	Thu	15:15–17:45	ZEU/LICH	**Focus Session: 75 Years Division Polymer Physics: From Curiosity to Smart Materials (joint session CPP/BP)**
BP 36.1–36.11	Fri	9:30–12:45	BAR/SCHÖ	**Statistical Physics of Biological Systems IV (joint session BP/DY)**

BP 37.1–37.12	Fri	9:30–12:45	BAR/0106	**Tissue Mechanics II**
BP 38.1–38.9	Fri	9:30–12:15	ZEU/0160	**Active Matter VI (joint session DY/BP)**
BP 39.1–39.6	Fri	9:30–11:15	ZEU/0260	**Focus Session: Theoretical Modeling and Simulation of Biomolecular Condensates III (joint session CPP/BP)**
BP 40.1–40.5	Fri	10:00–11:15	BAR/0205	**Cell Mechanics II / Cytoskeleton II**
BP 41.1–41.4	Fri	11:30–12:45	BAR/0205	**Franco-German Session: Bacterial Biophysics II**
BP 42.1–42.1	Fri	13:15–14:00	HSZ/0002	**Closing Talk (joint session CPP/BP/DY)**

Members' Assembly of the Biological Physics Division

Wednesday 18:30–20:00 BAR/0205

- Report
- Elections
- Miscellaneous

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

Time: Monday 9:30–12:45 Location: BAR/SCHÖ

BP 1.1 Mon 9:30 BAR/SCHÖ

Bayesian inference of magnetosensing in a magnetotactic bacterium — •Sascha Lambert[1], Emilie Gachon[2], Damien Faivre[2], and Stefan Klumpp[1] — [1]University of Göttingen, Institute for the Dynamics of Complex Systems, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany. — [2]Aix Marseille Université, CEA, CNRS, BIAM, 13115 Saint-Paul-Lez-Durance, France.

Magnetotactic bacteria are often assumed to align only passively with external magnetic fields, yet recent observations of the magnetotactic bacterium SS-5 reveal a pronounced increase in swimming speed under geomagnetic conditions. Because flagellated microorganisms typically follow helical paths, magnetic torques could, in principle, straighten their trajectories and create an apparent increase in speed, offering a purely mechanical explanation. We test this hypothesis using a physical swimming model based on Active Brownian Particles that incorporates magnetic torques, rotational propulsion, and helical motion, and we explore the relevant parameter space using Bayesian inference constrained by three-dimensional trajectory data. Posterior predictive simulations demonstrate that the mechanically induced increase in apparent speed is far too small to account for the experimental observations, even under extreme parameter choices. The results quantitatively rule out swaying as a sufficient explanation for the behaviour of SS-5 and instead support the presence of an active magnetic sensing mechanism.

BP 1.2 Mon 9:45 BAR/SCHÖ

Vorticity-induced surfing and trapping in porous media — •Pallabi Das[1], Mirko Residori[1], Axel Voigt[2,3,4], Suvendu Mandal[5], and Christina Kurzthaler[1,3,4] — [1]Max Planck Institute for the Physics of Complex Systems, Germany — [2]Institute of Scientific Computing, TU Dresden, Germany — [3]Center for Systems Biology Dresden, Germany — [4]Cluster of Excellence, Physics of Life, TU Dresden, Germany — [5]TU Darmstadt, Germany

Microorganisms often encounter strong confinement and complex hydrodynamic flows while navigating their habitats. Combining finite-element methods and stochastic simulations, we study the interplay of active transport and heterogeneous flows in dense porous channels. We find that swimming always slows down the traversal of agents across the channel, giving rise to robust power-law tails of their exit-time distributions. These exit-time distributions collapse onto a universal master curve with a scaling exponent of $\approx 3/2$ across a wide range of packing fractions and motility parameters, which can be rationalized by a scaling relation. We further identify a new motility pattern where agents alternate between *trapping* along fast streams and extended *surfing* phases, the latter determining the power-law exponent. Unexpectedly, trapping occurs in the flow backbone itself – not only at obstacle boundaries – due to vorticity-induced reorientation in the highly-heterogeneous flow environment. These findings provide a fundamentally new active transport mechanism with direct implications for biofilm clogging and the design of novel microrobots capable of operating in heterogeneous media.

BP 1.3 Mon 10:00 BAR/SCHÖ

Adhesion Patterns in Gliding Filamentous Cyanobacteria — •Elias Fischer[1], Paul Nieschwitz[2], Stefan Karpitschka[2], and Holger Stark[1] — [1]Institute of Physics and Astronomy, TU Berlin, Germany — [2]Department of Physics, Universität Konstanz, Germany

Filamentous cyanobacteria play an important role in many ecosystems and the carbon cycle of our planet. They exhibit gliding motility when in contact with solid surfaces or each other. Despite their ecological relevance and increased use in biotech applications, the exact nature of the force-generating process remains not fully understood.

Our recent measurements of filamentous cyanobacteria gliding across flat surfaces and visualized in kymographs show spatio-temporal adhesion regions along the filament, indicating an intrinsic helical shape. Based on our a novel approach for modeling the mechanical aspects of individual cyanobacteria filaments, we are able to interpret the complex kymograph patterns. Each filament is modeled as a helical chain of thin cylindrical segments in 3D with bending and twisting elasticity. The filaments interact with nearby surfaces and filaments via a hard-core repulsion and an exponentially decaying adhesion force. Importantly, the propulsion forces that push the filament forward are only applied locally at surface-contacting segments.

Our simulated kymographs reveal how both the helical shape and the adhesion strength strongly influence the filament's gliding speed and the dynamics of the surface-attachment regions. Thereby, we crucially contribute to the understanding of how real filamentous cyanobacteria generate their propulsion forces.

BP 1.4 Mon 10:15 BAR/SCHÖ

The 3D chirality of malaria parasites determines their motion patterns in 2D and originates at the apical pole — •Leon Lettermann[1], Mirko Singer[2], Smilla Steinbrück[2,3], Falko Ziebert[1], Sachie Kanatani[3], Photini Sinnis[3], Friedrich Frischknecht[2], and Ulrich Schwarz[1] — [1]Institute for Theoretical Physics & BioQuant, Heidelberg University — [2]Parasitology, Center for Infectious Diseases, Heidelberg University — [3]School of Public Health and Malaria Research Institute, Johns Hopkins University

Plasmodium sporozoites, the slender forms of the malaria parasite injected by mosquitoes into the skins of their vertebrate hosts, provide a medically highly relevant model system for active chiral particles. Using 3D tracking in synthetic hydrogels, we show that sporozoites consistently move on right-handed helical trajectories. When they encounter a two-dimensional substrate, they switch to clockwise circular motion, whereas circling on glass in medium occurs with the opposite sense of rotation, suggesting on glass they try to invade the medium above. Using a sandwich assay, we demonstrate that chirality also determines the reverse transition from two-dimensional to three-dimensional motion. Combining these measurements with a theory for gliding motility allows us to identify the likely origin of chirality, namely an asymmetric distribution of adhesins. After confirming this via two-sided traction force microscopy, we finally use STED super-resolution microscopy to reveal a corresponding tilt in the apical ring complex. In summary, our analysis thus uncovers both the biological relevance and the molecular basis of chirality in the movement of malaria parasites.

BP 1.5 Mon 10:30 BAR/SCHÖ

Squirmer dynamics in porous environments — •Mirko Residori[1], Christina Kurzthaler[1], and Sebastian Aland[2] — [1]Max Planck Institute for the Physics of Complex Systems — [2]TU Freiberg

We introduce a computational framework for simulating the dynamics of micro-swimmers in complex porous environments. Specifically, we adopt a diffusive domain approach to represent the surface of a microswimmer, modeled as a squirmer. This method ensures accurate and stable finite-element simulations, even in highly confined geometries. Validation against analytical and numerical benchmarks confirms the model*s accuracy and robustness. We then apply it to explore squirmer motion in heterogeneous porous media, revealing how hydrodynamic interactions lead to behaviors such as dynamic trapping due to hydrodynamically induced re-orientations. Moreover, we demonstrate that the squirmer parameter and the repulsive potential critically influence a squirmer's ability to navigate and escape confinement. The proposed framework offers a versatile and efficient tool for studying active motion in complex fluids and provides new insights into micro-swimmer transport and control in natural and engineered systems.

BP 1.6 Mon 10:45 BAR/SCHÖ

Dynamics of passive tracers in active dumbbell suspension — •Chandranshu Tiwari and Sunil P. Singh — Department of Physics, Indian Institute of Science Education and Research, Bhopal 462066, India.

The transport of passive tracers in active fluids exhibits rich dynamics arising from persistent interactions between active agents and the tracer. In our work, we employ Brownian dynamics simulations to investigate the dynamical behaviour of both isotropic(circular) and anisotropic(elliptical) tracers in active dumbbell suspension, considering only steric interactions. For circular tracers, we find that the speed shows a crossover from monotonically decreasing to increasing with tracer size as the dumbbells' speed is increased. The tracer's effective diffusion also displays a non-monotonic dependence on area fraction: the diffusivity first increases and then decreases at higher area fractions.

For anisotropic tracers, the characteristic non-monotonic trend per-

sists. Moreover, their motion along the major and minor axes differs significantly. Anisotropic accumulation of active particles around the tracer generates direction-dependent forces and fluctuations, favouring motion along the major axis. Consequently, both the speed and diffusivity along the major axis exceed those along the minor axis.

15 min. break

Invited Talk BP 1.7 Mon 11:15 BAR/SCHÖ

Modeling and inference of magnetotactic motility in complex environments — •Stefan Klumpp — Institute for the Dynamics of Complex Systems, University of Göttingen, Göttingen, Germany

Magnetotactic bacteria orient themselves and swim along field lines of the geomagnetic field. Their magnetically directed self-propelled motion makes them an instance of dipolar active matter. Here we focus on the interaction of these bacteria with walls or obstacles. Experiments in microfluidic systems show that interactions with walls result in (possibly transient) alignment parallel to the wall, which may compete with the alignment with the magnetic field. The dynamic behavior arising from the competition of the two alignments includes U-turn trajectories in circular chambers and trapping and escape dynamics in channels with overlapping cylindrical obstacles. In a phenomenological picture, the resulting motion can be described in an Active Brownian Particle model by introducing a wall torque that competes with the magnetic torque, which results in good agreement with experimental observations. Systematic Bayesian inference of the wall torque from observations shows that only a part of the torque function (dependence on incident angle) can be learned reliably from the data.

BP 1.8 Mon 11:45 BAR/SCHÖ

Quantifying aggregation behaviour of filamentous cyanobacteria — •Elias Illing and Stefan Karpitschka — Fachbereich Physik, Universität Konstanz

Cyanobacteria are ubiquitous in nature, frequently causing ecological and economic harm by explosive growth, so called blooms.

We investigate the collective dynamics of entangled filamentous cyanobacteria in open liquid media, reminiscent of their aggregates found during later stages of blooms. We investigate the impact of illumination on the clustering and spreading of the bacteria and quantify the morphology of the bacterial aggregates by image analysis. We determine the critical density necessary for initial clustering and track the evolution of the subsequent stages, ranging from stable clusters to spreading mats. These states can be modulated by light intensity variations, potentially allowing for control of the morphological evolution of cyanobacterial aggregates.

BP 1.9 Mon 12:00 BAR/SCHÖ

Dynamically Induced Spatial Segregation in Multi-Species Bacterial Bioconvection — •Mingqi Yan[1,2], Chenxi Wang[3], Oscar Gallardo-Navarro[4], Rinat Arbel-Goren[4], Joel Stavans[4], and Erwin Frey[1,2] — [1]Department of Physics, Ludwig-Maximilians-Universität München, Theresienstraße 37, 80333 München, Germany — [2]Max Planck School Matter to Life, Hofgartenstraße 8, 80539, München, Germany — [3]School of Science, Harbin Institute of Technology, 518055, Shenzhen, China — [4]Department of Physics of Complex Systems, Weizmann Institute of Science, 7610001, Rehovot, Israel

Bacterial bioconvection is a classic example of collective behavior in active matter, where upward-swimming bacteria create density instabilities leading to large-scale fluid flows. While this phenomenon is well-studied in single-species suspensions, natural environments are typically inhabited by diverse microbial communities. Here, we investigate the collective dynamics of multi-species bacterial suspensions. Combining experiments with a continuum model, we show that different bacterial species can spontaneously segregate into stable, spatially interlocked domains. Our theoretical analysis reveals that this segregation is not driven by biochemical antagonism but rather by the interplay between species-specific motility characteristics and the self-generated hydrodynamic flows. This work provides new insights into how physical interactions alone can drive the spatial organization of complex microbial communities.

BP 1.10 Mon 12:15 BAR/SCHÖ

Light-switchable microbial rafts at air-liquid interfaces — •Gustav F. Nolte, Alexandros A. Fragkopoulos, Timo Völkl, Mechthild Rappold, and Oliver Bäumchen — University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany

In biological active matter, clustering occurs across a wide range of time and length scales, from molecular assemblies such as actomyosin networks to macroscopic systems like fire ant rafts. Here, we report on a fast, light-switchable, and fully reversible clustering phenotype on the microscale, observed at air-liquid interfaces: the raft formation of the biciliated microalga *Chlamydomonas noctigama*.

C. noctigama is a relative of the model organism *Chlamydomonas reinhardtii*, which exhibits light-switchable adhesion and subsequent clustering at solid-liquid interfaces [1,2]. We show how the cluster morphology depends on cell density and discuss potential growth mechanisms by analyzing dynamics of individual clusters. Furthermore, we characterize the dependence of raft formation on the light spectrum and interfacial free energy. Using micropipette force spectroscopy [3], we show that single cells exploit capillary forces for light-switchable ciliary adhesion to the air-liquid interface, enabling raft formation. In their natural habitats, reversible clustering may provide an advantage by allowing cells to accumulate in locations optimal for photosynthesis while increasing resilience to environmental stress.

[1] C. T. Kreis, et al., *Nat. Phys.* **14**, 45 (2018).
[2] S. Till, et al., *Phy. Rev. Res.* **4**, L042046 (2022).
[3] M. Backholm and O. Bäumchen, *Nat. Protoc.* **14**, 594-615 (2019).

BP 1.11 Mon 12:30 BAR/SCHÖ

Circadian gravitaxis: Photosynthetic microswimmers remodel local pH to actively tune vertical migration — Arkajyoti Ghoshal[1], Soumitree Mishra[1], Jayabrata Dhar[2], Hans-Peter Grossart[3,4], and •Anupam Sengupta[1,5] — [1]Physics of Living Matter, Department of Physics and Materials Science, University of Luxembourg, Luxembourg — [2]Department of Mechanical Engineering, National Institute of Technology Durgapur, India — [3]Department of Plankton and Microbial Ecology, Leibniz Institute of Freshwater Ecology and Inland Fisheries, Stechlin, Germany — [4]Institute of Biochemistry and Biology, Potsdam University, Germany — [5]Institute for Advanced Studies, University of Luxembourg, Luxembourg

Motile phytoplankton shuttle between bright surface waters and deeper nutrient rich layers, usually controlled by internal circadian clocks. Yet many species show irregular movements, defying the expected circadian rhythm. Studying a bloom forming photosynthetic species, we found that cells adjust their vertical migration by altering local pH, mediated by a shift in their gravitactic behavior. This self-modulation of pH generates sub-populations which are physiologically similar but swim differently, remaining vertically separated even under uniform conditions. Supported by a cell-level analysis and mathematical model, we confirm that the pH-mediated circadian shift is underpinned by morphological adjustments. Our results support a circadian gravitactic model in which diurnal pH control drives diversified migration, enhancing fitness particularly in acidifying oceans.

BP 2: Computational Biophysics I

Time: Monday 9:30–12:45 Location: BAR/0106

BP 2.1 Mon 9:30 BAR/0106

Topology driven spatial organization of DNA-polymers in geometric confinement — •Debarshi Mitra[1], Shreerang Pande[2], and Apratim Chatterji[2] — [1]Leibniz Institute of Polymer Research Dresden, Hohe Strasse 6, 01069 Dresden, Germany — [2]Dept. of Physics, Indian Institute of Science, Education and Research-Pune (IISER-Pune), India-411008

The mechanism of chromosome segregation and organization in the bacterial cell cycle is one of its least understood aspects. The bacterial chromosome is often modeled as a bead spring ring polymer. We introduce cross-links in the DNA-ring polymer, resulting in the formation of loops within each replicating bacterial chromosome. We use simulations to show that the chosen polymer-topology ensures its self-organization along the cell long-axis, such that various chromosomal loci get spatially localized as seen in-vivo, in various growth conditions [1,2]. The organization arises only due to entropic repulsion between polymer loops of each daughter chromosome. We also reconcile observations from complementary experimental techniques probing the organization of the chromosome [1]. We further establish organizational principles for topologically modified polymers in various kinds of geometric confinement and discuss possible relevance to eukaryotic chromosomes.

[1] Debarshi Mitra Shreerang Pande, Apratim Chatterji. Soft Matter, 2022.

[2] Shreerang Pande, Debarshi Mitra, and Apratim Chatterji. Phys. Rev. E, 110(5), November 2024.

BP 2.2 Mon 9:45 BAR/0106

An extended boundary integral method for viscoelastic cells — •Thomas Mayr and Stephan Gekle — University Bayreuth, Bayreuth, Germany

The boundary integral method is a powerful method for modeling soft objects such as capsules, vesicles or red blood cells in flows at low Reynolds numbers. The beauty of this method lies in its effective two-dimensional description of the boundaries making fluid-structure interaction simple in comparison to other methods. So far, the boundary integral method is restricted to cells with a viscoelastic membrane and a purely viscous interior, whereas most biological cells contain a complex cytoskeleton and a nucleus in addition to their membrane. Here, we develop an extended three-dimensional boundary integral method, that can handle such cells, which are treated as a homogeneous viscoelastic material surrounded by a viscoelastic membrane. We use our method to study systematically the influence of bulk and membrane viscoelasticity on the dynamics of a cell in shear flow closely corresponding to recent experiments [1].

[1] Gerum et al., Elife 11, e78823 (2022)

BP 2.3 Mon 10:00 BAR/0106

Synchronization of both microtubule ends facilitates robust spindle length control — •Shane Fiorenza[1], Sheba Cheeran[2], Elena Doria[2], Iva Tolić[3], Patrick Meraldi[2], and Nenad Pavin[1] — [1]Faculty of Science, University of Zagreb — [2]Faculty of Medicine, University of Geneva — [3]Rudjer Bošković Institute, Zagreb

The mitotic spindle is a biomechanical structure that relies on a well-controlled geometry to accurately segregate genetic material, and so the mechanisms responsible for setting spindle length have been extensively studied both in vivo and in vitro. One of these myriad mechanisms, microtubule poleward flux, has proven difficult to characterize, with experiments showing that decreasing poleward flux can lead to spindle length increasing, decreasing, or remaining constant. How the spindle regulates its length and the role of poleward flux in this process remains unclear. Here we show that length-dependent regulation at both microtubule ends constitutes a fundamental mechanism of spindle length control through poleward flux. Our model demonstrates that length-dependent mechanisms at both microtubule ends allow plus- and minus-end dynamics to synchronize with one another, resulting in perturbations at either end having opposite effects on poleward flux for increasing spindle size. We predict that spindle length and poleward flux can be uncoupled via simultaneous perturbations, which we confirm with in vivo depletion experiments of KIF18A, KIF2A, and KATNB1 proteins. Our results provide a new way of understanding spindle length control and resolve a long-standing paradox of how poleward flux relates to spindle length.

BP 2.4 Mon 10:15 BAR/0106

A coarse-grained model for investigating the ejection of ds-DNA from a viral capsid — •Adrian John Pinto[1], Klara Strobl[2], Carmen San Martin[3], Mar Alcazar Hutardo[2], Paul van der Schoot[4], Pedro J. de Pablo[2], Horacio V. Guzman[5], and Peter Virnau[1] — [1]Institute of Physics, JGU, Mainz, Germany — [2]Autonomous University of Madrid, Madrid, Spain — [3]Spanish National Center for Biotechnology, Madrid, Spain — [4]Eindhoven University of Technology, Eindhoven, Netherlands — [5]Institute of Material Science of Barcelona, Barcelona, Spain

Viruses are microscopic infectious agents that hijack the metabolic machinery of their hosts to replicate. They consist of genetic material, DNA for adenovirus, enclosed within a protein shell called a capsid. Adenoviruses are associated with respiratory diseases, gastroenteritis, conjunctivitis, and urinary tract infections. In this work, we investigate the denaturation of the viral capsid in the presence of urea as a chemical denaturant and analyze how increasing urea concentration affects capsid stability. To model the experimental system in simulations, we propose a coarse-grained representation of viral DNA based on a Kratky-Porod chain, which allows us to incorporate solvent conditions and obtain realistic length scales. Additionally, we model the capsid as a spherical confinement composed of discrete beads and introduce openings of various sizes to map changes in urea concentration to the simulation environment. Our findings indicate that the lag time observed in intensity curves can be explained by differences between partial and complete capsid opening.

BP 2.5 Mon 10:30 BAR/0106

Multi-Scale Computational Framework for Modeling Metabolic Pathways — •Miljan Dašić, Ashwathi Poolamanna, Mehrnoosh Khodam Hazrati, and Štěpán Timr — J. Heyrovský Institute of Physical Chemistry of the Czech Academy of Sciences, Dolejškova 2155/3, 182 00 Prague 8, Czech Republic

Spatial organization of enzymes (clustering, assemblies, and substrate channeling) has been increasingly recognized as a key determinant of metabolic efficiency. Recent studies suggest that non-specific enzyme-substrate interactions and molecular crowding can further impact the performance of metabolic pathways. However, the combined effect of these factors remains insufficiently quantified.

To address this gap, we developed a multi-scale computational framework connecting molecular-level enzyme-substrate interactions with emergent pathway-level kinetics. We first perform extensive coarse-grained Molecular Dynamics (MD) simulations with LAMMPS to quantify substrate transition kinetics at varying crowding levels. Resulting trajectories are analyzed using Markov State Models (MSMs) to extract the relevant states and transition rates. These kinetic parameters are then used to parameterize stochastic Reaction-Diffusion (RD) simulations in Smoldyn, enabling the study of large enzyme assemblies, different reaction orders, and multi-step metabolic pathways.

Our results reveal how molecular interaction strengths, crowding conditions as well as enzyme spatial organization impact pathway efficiency across scales: from nanometers and nanoseconds (MD) to micrometers and seconds (RD).

BP 2.6 Mon 10:45 BAR/0106

Coexistence in competition for shared resources with fluctuating fitness — •Angelique Burdinski and Dirk Brockmann — Center Synergy of Systems (Synosys), TUD Dresden University of Technology, 01069, Dresden, Germany

Understanding how species coexist in competitive scenarios has long been a central question in ecology and evolution. The contradiction between the competitive exclusion principle and the observed diversity of species has puzzled researchers for decades. Fluctuating environmental factors that selectively change species fitness have been proposed to stabilize coexistence, but theoretical results remain inconclusive. How competitive forces and temporal variability shape evolutionary outcomes remains debated, with model-specific results and few universal insights. We compare species dynamics under two generic but qualitatively different mechanisms. One model captures direct competition via the standard replicator equation; the other represents a

consumer-resource system, yielding the adjusted replicator model. Under uniform fitness, both show identical asymptotics, diverging sharply when fitness fluctuates. The standard replicator leads to quasi-fixation of a single species, whereas the adjusted replicator exhibits stable coexistence below a critical timescale. We derive coexistence bounds based on the mean and variance of fitness, showing that higher mean and lower variability favor fixation, while coexistence may persist even in disadvantaged situations. This contrast reflects direct versus indirect competition and supports coexistence as a generic outcome of shared-resource interactions in temporally varying environments.

15 min. break

BP 2.7 Mon 11:15 BAR/0106

Dielectric response of graphene and MoS_2 nanopores in the detection of single amino acids — •Longlong Li and Maria Fyta — Computational Biotechnology, RWTH Aachen University, Germany

Recent advances in two-dimensional (2D) material nanopores have opened new opportunities for biosensing with single-molecule precision. In this work, we investigate the interaction of single amino acids with graphene and MoS_2 nanopores using density-functional theory (DFT), combined with dielectric response calculations and non-equilibrium Green's function (NEGF) transport simulations. After identifying the most stable conformations of selected amino acids residing inside the nanopores, we calculate both the electronic transport and optical response of the nanopores in the absence and presence of these biomolecules. While electronic current-voltage characteristics reveal only modest amino-acid-dependent variations, the optical response, characterized by frequency-dependent dielectric functions and optical absorption spectra, exhibits distinct material-specific signatures. In particular, MoS_2 nanopores exhibit strong and broadband optical sensitivities, which are significantly larger than those of graphene and thus enable more distinct discrimination of single amino acids across multiple photon energies. Our simulations reveal an enhancement in the optical read-out of nanopores and an even stronger signals in the case of MoS_2 nanopores highlighting the possibility of a broadband optical detection for protein detection platforms and biosensors.

BP 2.8 Mon 11:30 BAR/0106

From Bioanalytics to Neuromorphic Computing: Graphite-Based Nanopores for Protein Sequencing and Iontronic Memristors — •Chandan K. Das and Maria Fyta — Computational Biotechnology, RWTH Aachen University, Worringerweg 3, 52074 Aachen, Germany

Protein sequencing with single amino acid resolution using ionic current signatures is a rapidly advancing technique, yet challenges persist in maintaining protein linearity and controlling their translocation through solid state nanopores. We introduce a graphite-based nanopore featuring a constriction inspired by alpha-hemolysin. All atom MD simulations show that the positively charged pore lumen promotes strong anion selectivity and drives electro-osmotic flow (EOF), which generates hydrodynamic drag opposing the electrophoretic force (EPF). Balancing these forces straightens proteins during translocation and increases their residence time within the constriction, substantially improving sequencing accuracy. This design enables detection of all 20 proteinogenic amino acids and their post-translational modifications. Beyond sequencing, the graphite-based architecture supports diverse iontronic applications. In a graphite-hydrogel-graphite nanofluidic memristor, a neutral hydrogel selectively traps cations, inducing ion concentration polarization. Simulations reveal characteristic memristive behavior, including a hysteretic current-voltage response. Overall, graphite nanopores offer a versatile platform for sequencing and neuromorphic computing.

BP 2.9 Mon 11:45 BAR/0106

Protein Translocation in Two Dimensional Nanopores from Molecular Dynamics and Free Energy Calculations — •Peijia Wei, Mayukh Kansari, Santiago López Páramo, and Maria Fyta — Computational Biotechnology, RWTH Aachen University, Worringerweg 3, 52074 Aachen, Germany

Nanopores, nanometer scale openings in materials, offer strong potential for ultra fast, cost effective and real time next generation sequencing technologies. These pores can electrophoretically drive charged biomolecules through and detect them. Using computer simulations, we compare two dimensional nanopores, graphene and MoS_2, to evaluate their effectiveness in protein detection. Protein translocation and dynamics are being controlled by varying the surrounding solvent, using both a typical monovalent salt solution and a molecular solution. Atomistic simulations assess the ability of each nanopore to thread proteins, on the basis of the ionic current signals through the pore. We also perform free energy calculations to quantify the thermodynamic factors that influence protein entry and passage through the pores. Our results show that graphene nanopores interact strongly with proteins, which hinders translocation under physiological conditions. This can be overcome by adding a denaturant that forms a hydrophilic and cation rich layer on the surface and enables linearized threading. In contrast, MoS_2 nanopores allow protein passage even in physiological solutions and offer inherent control of the translocation. By combining molecular dynamics with free energy analysis, we reveal how the complex interactions among all components shape translocation behavior.

BP 2.10 Mon 12:00 BAR/0106

Extending quantum-mechanical benchmark accuracy to biological ligand-pocket interactions — •Mirela Puleva[1], Leonardo Medrano Sandonas[2], Balázs D. Lorincz[3], Jorge Charry[4], David M. Rogers[5], Péter R. Nagy[3], and Alexandre Tkatchenko[1] — [1]University of Luxembourg, Luxembourg — [2]TUD Dresden University of Technology, Germany — [3]Budapest University of Technology and Economics, Hungary — [4]Luxembourg Researchers Hub asbl, Luxembourg — [5]Oak Ridge National Laboratory, USA

Predicting the binding affinity of ligands to protein pockets is key in the drug design pipeline, yet accurate capture of interactions in the flexible ligand-pocket motifs requires robust quantum-mechanical (QM) benchmarks, which are scarce. Disagreement between "gold standard" Coupled Cluster (CC) and Quantum Monte Carlo (QMC) methods further challenges large non-covalent benchmarks. We introduce the QUantum Interacting Dimer (QUID) benchmark framework modeling diverse ligand-pocket motifs. CC and QMC agree within 0.5 kcal/mol for QUID, which spans key non-covalent binding motifs and energetic contributions from symmetry-adapted perturbation theory. Benchmark results shows several dispersion-inclusive density functional approximations predict energies accurately but differ in atomic van der Waals forces, while semiempirical and empirical methods need improvements for non-covalent interactions (NCIs) in out-of-equilibrium geometries. With a wide span of NCIs, highly accurate interaction energies, and further molecular properties, QUID goes beyond the "gold benchmark" QM benchmark of ligand-protein systems.

BP 2.11 Mon 12:15 BAR/0106

Insights into Quantum Decoherence in Biological Light Harvesting from First-Principles Simulations — Thomas Trepl, •Ingo Schelter, Johannes M. Foerster, and Stephan Kümmel — University of Bayreuth, Bayreuth, Germany

Photosynthesis is a fascinating process of outstanding importance since it provides the energy for most life on Earth. Considering the remarkable quantum efficiency with which the energy of absorbed photons is transferred in the initial light-harvesting step, there exists a long-standing speculation about the role of quantum coherence.

In this talk, I show the decoherence and localization of excitation energy that evolves from the coupled electron and nuclear dynamics in the B850 ring at room temperature after an initial Laser excitation as typically used in an experiment. The electron dynamics of the whole multichromophoric system is described by the real-time formulation of time-dependent density functional theory. The nuclear dynamics is treated by Ehrenfest dynamics, allowing for a non-adiabatic coupling between electrons and nuclei. The simulations show that nuclear dynamics starts to trigger quantum decoherence after only a few tens of femtoseconds.

BP 2.12 Mon 12:30 BAR/0106

Human breathing pattern dominates the effective diffusivity of droplets emitted while speaking — •Lars Natusch and Roland Netz — Fachbereich Physik, Forschungsgruppe Roland Netz, Freie Universität Berlin, Berlin, Germany

For understanding airborne viral infection pathways, the prediction of the effective diffusivity of saliva droplets emitted from a person while speaking and breathing is crucial.

In enclosed non-ventilated indoor spaces the diffusivity of tracer particles or molecules emitted by a person is governed by the complex interplay of various physical transport mechanisms. By comparison of lattice-based simulations of the three-dimensional compressible Navier-Stokes equation with experiments measuring the spreading of

carbon-dioxide emitted from a person, we demonstrate that molecular diffusion and convection due to body heat and temperature gradients at walls and windows are present, but that the main spreading mechanism is related to the periodic breathing pattern of a person, which induces long-range advection.

Our results identify breathing as the dominant mechanism for particle transport in stagnant indoor air.

BP 3: Tissue Mechanics I

Time: Monday 9:30–12:45 Location: BAR/0205

Invited Talk BP 3.1 Mon 9:30 BAR/0205

The unreasonable effectiveness of computational models in biological patterning and morphogenesis — •Michel Milinkovitch — Dept. of Genetics & Evolution, University of Geneva, Geneva, Switzerland

I will discuss how vertebrate skin colours and skin appendages (scales, feathers, hairs) are spatially patterned through Turing and mechanical instabilities. First, I will show that Reaction-diffusion (RD) models are particularly effective for understanding skin colour patterning at the macroscopic scale, without the need to parametrise the profusion of variables at the microscopic scales. I suggest that the efficiency of RD is due to its intrinsic ability to exploit continuous colour states and the relations among growth, skin-scale geometries, and the (Turing) pattern intrinsic length scale. Second, I will show how drug treatments can permanently trigger transitions between scale appendage types or even between chemical and mechanical self-organisation. Third, I will show that a three-dimensional mechanical model, integrating growth and material properties of embryonic skin layers, captures most of the dynamics and steady-state pattern of head scales in crocodiles and tortoises. Fourth, I will show that the spectacular morphogenesis of the strongly overlapping snake scales can be recapitulated with a mechanical model integrating tissue plasticity and active material properties. These studies indicate that Biology, despite its 'messy' nature (with its unmanageable profusion of cellular and molecular variables) can be efficiently and quantitatively investigated mathematically, including with simple phenomenological models.

BP 3.2 Mon 10:00 BAR/0205

Mechano-chemical stabilisation of topological defects in an elasto-nematic sheet — •Suganthan Senthilkumar[1], Kinneret Keren[2], and Marko Popović[1,3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Technion-Israel Institute of Technology, Haifa, Israel — [3]Ruder Bošković Institute, Zagreb, Croatia

Self-organisation of patterns during animal development involves a complex interplay of various biophysical and biochemical mechanisms. A striking example is *Hydra*, where ordered arrays of nematic actin fibers give rise to orientational order on animal-scale with +1 topological defects at the head and foot of an adult animal. To study the nematic patterns observed during *Hydra* regeneration we recently proposed a mechano-chemical feedback loop that involves orientational order, tissue strain and morphogen gradients[1]. Here we develop a continuum formulation of the same feedback loop in 2d and show that it can stabilise aster shaped +1 topological defects in a self organised manner. We obtain a phase diagram for +1 defect stability using analytical calculations and compare it with vertex model simulations that employ the feedback loop. Finally, we calculate the correction to the mobility coefficient of the +1 defect due to the morphogen field associated with it.

References:

1. Maroudas-Sacks *et al* Development, (February 2025) 152; doi: https://doi.org/10.1242/dev.204514

BP 3.3 Mon 10:15 BAR/0205

What jellyfish teach us about tissue mechanics and shape programming — •Anne Materne[1,2], Zhiqi Shen[1,2,3], Daniel Font-Martín[4], Vladislav Koren[5], Ulyana Shimanovich[5], Chiara Sinigaglia[4], and Carl D. Modes[1,2] — [1]MPI of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Center for Systems Biology Dresden, Germany — [3]Southern University of Science and Technology, Shenzhen, China — [4]CNRS Languedoc-Roussillon, France — [5]Weizmann Institute of Science, Israel

Jellyfish are little-studied marine organisms with astounding regenerative capacities. Their rapid wound closure has been implicated to rely, at least partially, on the mechanical properties of the individual tissues in the jellyfish umbrella. In particular, this includes the mesoglea, a thick extracellular matrix structure essential for jellyfish shape and body function. Here, we model the mesoglea's role in wound closure using a coarse-grained spring lattice approach. In this way, we can capture essential material processes without knowledge of all molecular- and cellular-scale underpinnings. Our work shows that simple mesoglea pre-strain is sufficient to initiate closure in a broad spectrum of wound shapes. This finding is in line with previous experimental work in the hydrozoan jellyfish *Clytia hemisphaerica* and confirms the essential role of tissue mechanics in the life history of marine invertebrates. It will be interesting to explore this role more systematically in the future. Furthermore, our results presented here also provide unexpected insights for the field of 3D shape-programmable materials.

BP 3.4 Mon 10:30 BAR/0205

Apical extracellular matrix regulates fold morphogenesis in the Drosophila wing disc — •Vincenzo Maria Schimmenti[1], Jana F. Fuhrmann[2], Natalie A. Dye[3,4], and Marko Popovic[1] — [1]Max Planck Institute for Physics of Complex Systems, Dresden, Germany — [2]Aix Marseille Univ, CNRS, IBDM, Marseille, France — [3]Mechanobiology Institute, National University of Singapore, Singapore — [4]Biomedical Engineering Department, National University of Singapore, Singapore

Tissue folding is a fundamental process in animal organ development. We investigate how fold shape and mechanics change during Drosophila wing disc morphogenesis, from larval stages (when folds deepen and grow) to early pupa, when the tissue unfolds into a bilayer. Using 3D apical surface segmentation, we introduce quantitative metrics for fold depth and width on a curved surface. We also identify a fibrous apical extracellular matrix (aECM) that physically links the two sides of each fold. A lateral vertex model with an adhesive aECM layer predicts that unfolding requires aECM removal. Genetic perturbations confirm that aECM adhesion stabilizes folds: its loss distorts fold shape and dynamics, while failure to remove it prevents unfolding. These perturbations produce adult wing defects, demonstrating that larval fold morphology influences adult wing shape. Together, our work highlights a central mechanical role for aECM in stabilizing epithelial folds during animal development.

BP 3.5 Mon 10:45 BAR/0205

Elastic coupling between nucleus and cell shape drives a mechanical transition in epithelial architecture — •Ian D. Estabrook[1], Anne Rosfelter[2], Yu-Chiun Wang[2], and Anna Erzberger[1] — [1]European Molecular Biology Laboratory (EMBL), Heidelberg, Germany — [2]RIKEN Center for Biosystems Dynamics Research, Kobe, Japan

As the largest organelle, the cell nucleus can affect the shape, spatial organisation and mechanics of cells in a variety of tissue contexts. Despite extensive studies on the molecular mechanisms underlying nuclear positioning and mechanics, it remains unclear whether the nucleus actively controls tissue architecture.

Here, we combine elasticity theory and the Drosophila blastoderm stage embryo as a generic experimental model to investigate the mechanical role of nuclei on epithelial organisation.

By developing a general method that integrates mechanical and geometrical properties extracted from imaging data, we show that from elastic coupling between nuclei and the cell surface, a mechanically driven phase transition emerges between simple columnar and pseudostratified tissue architectures. Genetic and optogenetic experimental perturbations provide evidence supporting such coupling and confirm the predicted transitions following changes in mechanical and geometric parameters.

Our work identifies a novel mechanical role of nuclear elasticity, independent of specialised machineries and may represent a general, generic mechanism controlling emergence of tissue level structures.

15 min. break

BP 3.6 Mon 11:15 BAR/0205

Mechanical regulation of neuroepithelial development — •Niklas Gampl[1,2], Alex Kingston[3], Caren Norden[4], and Kristian Franze[1,2,5] — [1]Max-Planck-Zentrum für Physik und Medizin, Erlangen, DE — [2]Medical Institute of Biophysics, FAU Erlangen-Nürnberg, DE — [3]Cambridge Stem Cell Institute, University of Cambridge, UK — [4]Gulbenkian Institute for Molecular Medicine, Oeiras, PT — [5]Department of PDN, University of Cambridge, UK

During embryonic development, initially flat neuroepithelial tissues remodel themselves into complex 3D structures such as the brain or retina. This process is driven by intrinsically generated forces that depend on the cells' mechanical environment. However, how accumulated tension in the tissue feeds back on individual cells to influence their fate or migration patterns is not well understood. To address this, we downregulated the cellular force sensor Piezo1 in zebrafish and *Xenopus laevis* embryos, thereby reducing local mechanosensing capabilities. Piezo1 downregulation led to impaired retinal lamination, deformed retinae and nuclear rounding. Additionally, live imaging of Piezo1-deficient zebrafish eye primordia revealed defects in retinal progenitor migration during optic cup morphogenesis. These finding suggest that Piezo1 activity contributes to coordinating force generation and tissue level tension in the developing neuroepithelium, thus leading to nuclear and tissue shape changes. Combining laser ablation to locally perturb force propagation with direct measurement of tissue tension will clarify how Piezo1-dependent mechanical feedback links nuclear shape, cell fate decisions and tissue morphogenesis.

BP 3.7 Mon 11:30 BAR/0205

Emergence of hyperuniform tiling in the developing retina — •Mehmet Can Ucar[1] and Sandra Siegert[2] — [1]University of Sheffield, Sheffield, UK — [2]Institute of Science and Technology Austria, Klosterneuburg, Austria

Efficient tiling and space-filling are fundamental design principles of living systems: from neurons and immune cells to vascular networks, these structures must optimize spatial coverage for proper function. Yet how cells collectively achieve non-redundant coverage during growth remains largely unexplored. Here, we combine a theoretical model of growing, branched cells with tunable local interactions and experimental analysis of developing retinal microglia. Our model shows that simple neighbor repulsion during growth is sufficient to drive non-redundant tiling, yielding a substantial increase in coverage with minimal territory overlap. Strikingly, this mechanism also leads to the emergence of a hyperuniform organization, where density fluctuations are progressively suppressed. Consistent with these predictions, microglia in the developing retina exhibit both efficient tiling and suppressed fluctuations, supporting the proposed mechanism for retinal patterning. Together, these findings reveal how local interactions can generate both efficient tiling and hyperuniform order, suggesting a general principle for tissue-wide optimization.

BP 3.8 Mon 11:45 BAR/0205

Reshaping morphogen gradients through porous tissue architecture — •Diana Khoromskaia[1,2], Mohit Dalwadi[4], and Zena Hadjivasiliou[2,3] — [1]Universität Münster, Germany — [2]Francis Crick Institute, London, UK — [3]University College London, UK — [4]University of Oxford, UK

The morphogenesis of tissues during embryonic development is controlled by concentration gradients of morphogens – signalling molecules whose readout determines cell fate decisions. How the spread of morphogens is affected in tissues with complex geometry and spatially heterogeneous architecture is not well understood. To address this question, we introduce a porous vertex model, by explicitly considering the network of extracellular spaces between the cells. Morphogens produced by source cells disperse through the tissue via three modes of transport: extracellular diffusion, membrane-bound diffusion, and cell-based transport through recycling. With this model we investigate how cell-scale geometry, such as cell size, cell shape anisotropy, and cell distance, influences effective diffusion and degradation of morphogens at tissue-scale, employing numerical and semi-analytical upscaling methods. A non-linear coupling between cell packing and morphogen concentration renders the morphogen gradient robust to perturbations by locally buffering fluctuations in the production. Our characterisation of tissues as active porous materials provides new insights into how morphogenesis and cell fate determination may interact during embryonic development.

BP 3.9 Mon 12:00 BAR/0205

Mechanics and hydraulics of the *C. elegans* germ line — •Chandraniva Guha Ray[1,2,3], Jonathan Jackson[2], Jonas Neipel[1,2,3], Julia Pfanzelter[2], Stephan W. Grill[2,3,4], and Pierre A. Haas[1,2,3] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute of Molecular Cell Biology and Genetics — [3]Center for Systems Biology Dresden — [4]Cluster of Excellence Physics of Life, TU Dresden

In the cylindrical germ line of the nematode *Caenorhabditis elegans*, germ cells surround a tube called the rachis, to which all germ cells are connected via openings in the cells called rachis bridges. These rachis bridges allow exchange of cytoplasm between the rachis and the germ cells, which mature as they move towards the proximal end of the germ line where a hydraulic instability decides germ cell fate [1]. However, cortical contractility would collapse static germ cells by releasing their cytoplasm into the rachis through the rachis bridges. Here, we explain how the hydraulic flows in the germ line prevent this collapse and thus stabilise the germ line mechanically: We present a coarse-grained vertex model of a steady-state germ line that couples these hydraulic effects to cell mechanics. We compare the model to experimental observations and thus show how the interplay of fluid pumping and cell contractility can build a dynamically stable germ line.

[1] N. T. Chartier *et al.*, Nat. Phys. **17**, 920 (2021)

BP 3.10 Mon 12:15 BAR/0205

Hydrodynamic theory of two-dimensional human gastruloid development — •Oliver M. Drozdowski[1], Chloé Roffay[2], Sarah Jay[2], Diana Pinheiro[2], and Edouard Hannezo[1] — [1]Institute of Science and Technology Austria, Klosterneuburg, Austria — [2]Research Institute of Molecular Pathology, Vienna, Austria

Gastrulation is a crucial stage of embryonic development, as it entails the formation of the three germ layers. Two-dimensional in-vitro systems derived from human embryonic stem cells, so-called gastruloid discs, recapitulate the underlying patterning mechanisms, resulting in the formation of concentric rings of extraembryonic amnion-like cells at the edge and the three germ layers. Starting from experimental data of flattening amnion-like cells at the gastruloid edge, we developed a cross-sectional bubbly vertex model to describe the observed columnar to squamous transition. In agreement with experimentally measured morphometrics and mechanical properties, cell flattening is shown to be driven by local active wetting. Since gastruloids display fluid-like tissue properties, we developed a hydrodynamic description of the tissue-scale dynamics derived from the vertex model. This model predicts a gastruloid morphology consistent with experimental observations, suggesting that local cellular mechanics contribute to human gastruloid shape dynamics.

BP 3.11 Mon 12:30 BAR/0205

A mechanical origin for implantation defects in embryos from aged females — Kate E. Cavanaugh[1,2], •Maria-Jose Franco-Oñate[3,4], Diana J. Laird[5], Patrick W. Oakes[6], Ricard Alert[3,4,7], and Orion D. Weiner[1,2] — [1]Cardiovascular Research Institute, University of California, San Francisco, USA — [2]Department of Biochemistry and Biophysics, University of California, San Francisco, USA — [3]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [4]Center for Systems Biology Dresden, Germany — [5]Department of Obstetrics, Gynecology, and Reproductive Sciences, University of California, San Francisco, USA — [6]Department of Cell and Molecular Physiology, Loyola University Chicago Stritch School of Medicine, IL USA — [7]Cluster of Excellence Physics of Life, TU Dresden, Germany

Women over 35 experience reduced fertility, linked to impaired embryo implantation. In mouse embryos from aged mothers, we observe defective spreading of the extra-embryonic tissue. To uncover the mechanism, we use a continuum model that treats the tissue as a droplet of active polar fluid. Fitting the model to experimental data shows that increased tissue surface tension and viscosity in aged embryos account for the impaired spreading. Experimental measurements of forces and spreading dynamics confirm that these mechanical changes are sufficient to explain the implantation defect. This work shows how physical modeling of embryo mechanics can quantitatively predict implantation success and guide embryo selection in Assisted Reproductive Technologies.

BP 4: Computational Biophysics II

Time: Monday 15:00–16:30 Location: BAR/SCHÖ

Invited Talk BP 4.1 Mon 15:00 BAR/SCHÖ

The Multi-faceted Role of Cholesterol in Cellular Membranes and Lipid Nanoparticles — •Rainer Böckmann — Computational Biology - Theoretical & Computational Membrane Biophysics, Friedrich-Alexander-Universität Erlangen-Nürnberg

Cellular membranes serve as dynamic interfaces regulating numerous biological processes, with cholesterol playing a central role in shaping their structure, dynamics, and function. Likewise, cholesterol is crucial for stabilizing lipid nanoparticles (LNPs) in pharmaceutical applications and for enhancing their therapeutic efficacy. Here, we elucidate the multifaceted functions of cholesterol in both biological membranes and LNPs using atomistic molecular dynamics simulations, including constant-pH approaches.

Our findings challenge conventional views of membrane organization by revealing that thermal membrane bending and local cholesterol distribution can collaborate to soften membranes [1], even though cholesterol is widely associated with membrane thickening and reduced permeability. Turning to lipid nanoparticles, we demonstrate that cholesterol is significantly enriched in the LNP shell [2], resulting in shifts of the pK_a of aminolipids by 2-4 units, contingent on the specific lipid composition [3]. This insight underscores the importance of cholesterol-lipid interactions in modulating the physicochemical properties of LNPs, with direct implications for the design and optimization of cholesterol-containing nanocarriers in drug delivery. [1] Pöhnl et al. Nat.Commun. 14, 8038 (2023) [2] Trollmann, Böckmann. Biophys.J. 121, 3927 (2022) [3] Trollmann, Böckmann. Small (2026)

BP 4.2 Mon 15:30 BAR/SCHÖ

Transient interactions between cationic ionizable lipids and anionic lipids foster lamellar to hexagonal phase transition — •David Noel Zimmer[1,2], Friederike Schmid[1], and Giovanni Settanni[1,2] — [1]Physics Department Johannes-Gutenberg University Mainz — [2]Faculty of Physics and Astronomy Ruhr University Bochum

RNA-based therapeutics have demonstrated remarkable efficacy and hold great promise for future applications. The most common delivery systems for these drugs are lipid-based nanoparticles (LNPs), which incorporate ionizable cationic lipids (ICLs) as key components. ICLs are believed to facilitate endosomal escape of the cargo by interacting with anionic lipids in the endosomal membrane, although the underlying molecular mechanism remains unclear. One proposed model suggests that the membrane is destabilized by cone-shaped complexes formed between ICLs and endosomal anionic lipids; clear evidence of stable complexes is still missing. Here[1], we re-examine the problem through equilibrium and nonequilibrium simulations of model membrane systems containing DODMA (ICL), DOPS (anionic lipid) and DOPE (helper lipid). Our results confirm absence of co-localization at equilibrium, but reveal a transient formation of cone-shaped complexes during lamellar-to-inverted-hexagonal phase transitions, which considerably accelerates the transition process. These findings may open new ways for controlling endosomal escape through the rational design of ICLs optimized to interact with cell- or stage-specific endosomal anionic lipids. [1] Zimmer DN, Schmid F, Settanni G. ChemRxiv. 2025; doi:10.26434/chemrxiv-2025-rwb18

BP 4.3 Mon 15:45 BAR/SCHÖ

Osmolyte Effects on Protein Stability: Charge-Regulation is Essential — •Julia Keil and Nico F. A. van der Vegt — Technische Universität Darmstadt, Germany

Osmolytes such as glycine modulate protein stability through differences in their preferential interactions with folded and unfolded states. In this work, we revisit glycine's influence on protein stability by explicitly incorporating charge-regulation effects - protonation and deprotonation of titratable groups - into our study of glycine-protein interactions. Using constant-pH molecular dynamics simulations[1], we develop a titratable glycine model. This pH-dependent model predicts that at pH 7 glycine is depleted from nonpolar elastin-like polypeptides (ELPs) but enriched near acidic and basic ELP residues. It also shows a pH-dependent accumulation of glycine around ELPs and the miniproteins Trp-cage and GB1, both consistent with prior experimental and computational observations[2-4]. Notably, charge regulation produces systematically stronger preferential binding of glycine to ELPs and mini-proteins at neutral pH than predicted by fixed-charge models. Although glycine is zwitterionic in bulk solution at pH 7, acid-base interactions with NH_3^+ and COO^- protein groups alter its protonation state within biomolecular hydration shells. The corresponding shifts in apparent pKa values promote electrostatically favorable combinations of protonation states, providing a mechanistic explanation for the enhanced preferential binding. [1] J. Chem. Theory Comput. 2022, 18, 10,6148-6160 [2] PNAS 2017, 114, 10, 2479-2484 [3] J. Phys. Chem. B 2020, 124, 30, 6565-6574 [4] Biochem. 1987, 26, 16, 5147-5153

BP 4.4 Mon 16:00 BAR/SCHÖ

Is helicity cooperative? Mechanistic insights from IM30 folding-unfolding dynamics — •Tika Ram Bhandari[1,2], Kurt Kremer[1], Friederike Schmid[2], and Martin Girard[1] — [1]Polymer Theory, Max Planck Institute for Polymer Research, Mainz, Germany — [2]Institute of Physics, Johannes Gutenberg University, Mainz, Germany

Helical transitions help regulate protein behavior, but how different chain segments influence each other's helicity is not well understood. Using coarse-grained molecular dynamics with Hamiltonian Replica Exchange, we examine the disordered-to-helical transition of IM30, the bacterial homolog of ESCRT-III. By tuning hydrogen-bond strengths, we show that the coiled-coil region is more helical than other domains, while overall helicity stays stable due to secondary-structure interactions. Fragments behave differently inside the full chain, revealing cooperative coupling without changing total helicity. Analysis shows both positive and negative links between helicity and chain extension, and identifies four main conformational states. These results clarify how segment interactions control helical transitions and maintain global helicity stability.

BP 4.5 Mon 16:15 BAR/SCHÖ

Grand canonical simulations of micellization in intrinsically disordered proteins — •Rodrigo F. Dillenburg[1,2], Martin Girard[1,5], Friederike Schmid[2], and Edward A. Lemke[3,4] — [1]Max Planck Institute for Polymer Research, Mainz, Germany — [2]Institute of Physics, Johannes Gutenberg University, Mainz, Germany — [3]Biocenter, Johannes Gutenberg University, Mainz, Germany — [4]Institute of Molecular Biology, Mainz, Germany — [5]Institute for quantitative and computational biosciences, Mainz, Germany

Molecular dynamics (MD) simulations with coarse-grained force fields have been the gold standard in the computational modeling of liquid-liquid phase separation (LLPS) and biomolecular condensates. While much attention has been focused on large droplets, very little is known about the formation of microphases, such as micelles, in such systems. There is evidence that such assemblies arise from intrinsically disordered proteins (IDPs) with a block co-polymer architecture. However, due to their finite size they are highly sensitive to the periodic boundary conditions of the simulation box. The commonly implemented slab geometry is thus unfit to tackle such systems. To overcome this we have implemented a semi-grand canonical monte carlo (SGCMC) algorithm that significantly speeds-up MD simulations. Our implementation is compatible with implicit solvent 1-bead-per-amino acid force fields such as Calvados and HPS. We show that such approach allows one to run simulations efficiently in a cubic box, at very low densities typical of biological systems. We also highlight the advantages of SGCMC in simulating micelles compared to regular MD.

BP 5: Membranes, Vesicles and Synthetic Life-like Systems I

Time: Monday 15:00–16:30 Location: BAR/0205

BP 5.1 Mon 15:00 BAR/0205

Toward programmable microrobots: DNA-based molecular communication between hydrogel microbeads — •Alexandra Bienau, Alexander Wietfeld, Wolfgang Kellerer, and Friedrich C. Simmel — Technical University Munich, Germany

Emerging applications in biomonitoring and smart therapeutics require materials that can sense biochemical cues, process and transfer information, and respond accordingly. In nature, such capabilities are often achieved through chemical communication, for example in bacterial quorum sensing or immune-cell signaling, where diffusing molecules enable coordinated behavior across many units.

DNA-based hydrogels offer a programmable platform for engineering similar functions, supporting sensing, logic operations, and responsive cargo release. Their porous structure enables molecular diffusion and biochemical exchange. Here, we establish DNA-based molecular communication between hydrogel microbeads. Using emulsion-based droplet microfluidics, we fabricate uniformly sized microbeads that can be modularly loaded with molecular cargo. We immobilize photo-initiated transmitter (TX) and fluorescence-based receiver (RX) systems within them. Communication occurs through diffusing DNA strands, and we characterize signal propagation using experiments and a comprehensive modeling framework.

Looking ahead, this platform enables the design of more sophisticated communication protocols and provides a step toward programmable hydrogel microrobots capable of collective information processing and dynamic interaction with biological environments.

BP 5.2 Mon 15:15 BAR/0205

Microfluidic Micropipettes: A Chip-Based Platform for Membrane Mechanics at Scale — •Sebastian W. Krauss[1], Megan Wong[2], Sepideh Razavi[3], Lorenzo Di Michele[1], and Pietro Cicuta[2] — [1]Department of Chemical Engineering and Biotechnology, University of Cambridge, UK — [2]Cavendish Laboratory, University of Cambridge, UK — [3]School of Sustainable Chemical, Biological and Materials Engineering, University of Oklahoma, USA

The mechanical properties of lipid membranes play an important role in diverse processes, from cell interactions to diseases. Established techniques, however, often suffer from low throughput or provide only bulk mechanical readouts, such as overall stiffness, making it challenging to obtain statistically robust measurements of membrane mechanics. Here, we present a microfluidic platform incorporating hundreds of micropipette like confinements on a single chip, enabling parallel mechanical characterisation of giant unilamellar vesicles (GUVs) in a single experiment. The forces acting on the membrane can be precisely tuned via the applied flow rates and the custom channel geometries, allowing well-defined, controllable mechanical testing. The platform also enables in situ exposure of GUVs to membrane-active compounds, such as surfactants, facilitating direct observation of their impact on membrane mechanics, including the dynamics and reversibility of these effects. This high-throughput approach opens the possibility for systematic screening of compound libraries, providing a quantitative framework to study the interactions between solutes and their impact on membranes.

BP 5.3 Mon 15:30 BAR/0205

Supported DPPC/DPPG Bilayers on Oxide Substrates as a Versatile Platform for Protein*Membrane Studies and Future FRET-Based Sensing — •Daniel Saavedra[1], Benjamin Ruz[1], Marcelo Cisternas[2], Susana Rojas[2], and Ulrich Volkmann[1] — [1]Institute of Physics, Pontificia Universidad Católica de Chile, Santiago, Chile — [2]School of Industrial Engineering, University of Valparaíso, Santiago, Chile

We develop a dry-processed supported lipid platform to study how membrane composition and substrate chemistry modulate protein-lipid interactions. Following the dry two-step self-assembly method for DPPC on silicon [1], we prepare DPPC bilayers with gramicidin A on SiO2 and characterize them by temperature ramps using very-high-resolution ellipsometry, AFM, FTIR, and SERS. Ellipsometry resolves DPPC pre- and main-phase transitions and peptide-induced shifts in thermal stability, which correlate with AFM domain morphology and FTIR amide I changes. In parallel, DPPC/DPPG bilayers are deposited on SiO2 and TiO2 and probed by AFM, FTIR, and ellipsometry to disentangle the influence of lipid charge and oxide surface on bilayer continuity and phase behavior, consistent with previous studies on lipid oxide interfaces [2]. Together, these results establish a solvent-free, thermally robust lipid architecture compatible with multimodal read-out and future integration of carbon quantum dots for FRET-based sensing. Acknowledgements: ANID Fellowship (DS) References 1.Cisternas MA et al. Int J Mol Sci. 2020;21:6819. 2.Tero R et al. Proc SPIE. 2007;6769:67690J.

BP 5.4 Mon 15:45 BAR/0205

Hexagonal and Lamellar Superstructure in DSPE-PEG1000 Monolayers at the Air/Water Interface — •Issam Assi, Heiko Aherns, and Christiane A. Helm — Institute of Physics, University of Greifswald, Germany

Inspired by diblock copolymer self-assembly, we investigate lipopolymer monolayers at the air/water interface. We studied DSPE-PEG1000 monolayers with alkyl chains in the liquid-condensed phase in dependence of the molecular area. Due to its conformational entropy, the moderately hydrophilic PEG has a larger area requirement than the alkyl chains in all-trans conformation. Small-angle grazing incidence X-ray diffraction (GID) measurements identified a hexagonal superstructure. The ordered alkyl chains form hydrophobic domains that are embedded in dissolved PEG. These domains consist of the alkyl chains of ca. 200 PEGylated lipid molecules. During monolayer compression, the number of alkyl chains in a domain remains constant, while their area fraction increases. At an area fraction of 50%, a transition to a lamellar superstructure occurs. During this transition, the alkyl chain domains merge. This transition is attributed to the entropy loss of the laterally compressed PEG chains. Wide-angle GID reveals that the alkyl chains in the liquid-condensed phase possess the same small cross-sectional area, as those in DSPE monolayers, indicating that PEG has little influence on the liquid-condensed phase. The hexagonal superstructure was confirmed with AFM images.

BP 5.5 Mon 16:00 BAR/0205

Numerical simulation of wetting of biomembranes — •Mokbel Marcel and Aland Sebastian — TU Bergakademie Freiberg

Biological cells utilize membranes and liquid-like droplets, known as biomolecular condensates, to structure their interior. The interaction of droplets and membranes, despite being involved in several key biological processes, is so far little understood. Here, we present a first numerical method to simulate the continuum dynamics of droplets interacting with deformable membranes via wetting. The method combines the advantages of the phase-field method for multiphase flow simulation and the arbitrary Lagrangian-Eulerian method for an explicit description of the elastic surface. The model is thermodynamically consistent, coupling bulk hydrodynamics with capillary forces, as well as bending, tension, and stretching of a thin membrane. Its capabilities are illustrated in several two- and three-dimensional axisymmetric scenarios.

BP 5.6 Mon 16:15 BAR/0205

Theory of Michaelis-Menten kinetics in phase-separated systems — •Gaetano Granatelli[1], Samuel S. Gomez[1], Sudarshana Laha[2], and Christoph A. Weber[1] — [1]Faculty of Mathematics, Natural Science, and Materials Engineering, Institute of Physics, University of Augsburg, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Phase-separated systems can regulate chemical reactions through spatial organization. Motivated by their biological relevance, we develop a mean-field theoretical framework for enzymatic kinetics within liquid condensates formed by phase separation. Building on a model that decouples the phase separation dynamics of scaffold components from the chemical kinetics of dilute clients, we generalize the classical Michaelis-Menten theory of enzyme kinetics to spatially heterogeneous systems with coexisting phases. In our framework, the dynamics of client concentrations are governed by scaffold-controlled parameters such as condensate size, partitioning, relative kinetic coefficients, and diffusion. We explore how they modulate the initial reaction rate across regimes set by the interplay of diffusive and reactive timescales, and we derive explicit expressions for the local reaction rate constants in each phase, allowing direct experimental measurement of how condensates

modulate reaction kinetics. We find that, compared to homogeneous conditions, phase-separated liquid condensates can mediate either optimal enhancement or suppression of the initial rate. Our results provide experimentally testable predictions to quantify how phase separation modulates enzymatic activity in living and synthetic systems.

BP 6: Active Matter II (joint session DY/BP/CPP)

Time: Monday 15:00–18:30 Location: ZEU/0160

BP 6.1 Mon 15:00 ZEU/0160

Field-controlled self-organization in an active spin system — Mintu Karmakar[1,2,3], •Matthieu Mangeat[4], Swarnajit Chatterjee[5,4], Heiko Rieger[4], and Raja Paul[3] — [1]WIUCAS, Beijing, China — [2]Universitat de Barcelona, Barcelona, Spain — [3]IACS, Kolkata, India — [4]Saarland University, Saarbrücken, Germany — [5]CY Cergy Paris Université, Cergy-Pontoise, France

We investigate the collective response of active Potts particles to an external magnetic field and uncover three striking nonequilibrium phenomena. We first examine how the flocking transition is reshaped for a homogeneous and unidirectional field: the coexistence regime between an apolar gas and a polar liquid is replaced by a phase separation between two polar-ordered phases, a low-density, weakly polarized background and a high-density, strongly polarized band, both moving along the field. Second, when the particles self-organize into a high-density longitudinal lane whose long axis is perpendicular to the field, the lane slowly treadmills against the field direction, driven by the weakly polarized background. Finally, we identify a field-induced interface pinning regime that arises when the domain is divided into two regions with opposite field directions, causing particles to accumulate and perform a back-and-forth motion at the interface. This pinning phenomenon also leads to the emergence of a disordered state in the presence of a random field orientation. A coarse-grained hydrodynamic theory supports and confirms the phenomena observed in our microscopic simulations.

BP 6.2 Mon 15:15 ZEU/0160

Nucleation kinetics in two-dimensional polar active fluids — •Yuta Kuroda and Thomas Speck — Institute for Theoretical Physics IV, University of Stuttgart, Germany

Polar active fluids constitute one of the most important classes of active matter. These systems possess alignment interactions that cause the local polarization to align with that of neighboring particles, leading to a flocking transition in which global polar order emerges. Extensive numerical and analytical studies have established that the flocking transition is discontinuous, and consequently, the phase diagram possesses a coexistence region in which propagating polar bands appear. Despite intensive studies on flocking transitions, the nucleation mechanism responsible for the formation of these bands remains poorly understood. In this work, we numerically investigate the nucleation kinetics of polar bands using a particle model, namely active Brownian particles with a Kuramoto-type alignment interaction, and we report the behavior of the nucleation rate over a wide range of parameters.

BP 6.3 Mon 15:30 ZEU/0160

Collision dynamics of active Brownian hard disks — •Jonas Buba — Soft Matter Theory Group, Theoretical Physics: Lab for Emergent Phenomena, Friedrich-Alexander-Universität Erlangen-Nürnberg, 91058 Erlangen, Germany

Active matter systems, composed of self-driven agents, display emergent behaviors such as collective motion, clustering, and motility-induced phase separation (MIPS). To better understand the microscopic origin of MIPS, we study collisions of active Brownian hard disks within the framework of dynamical density functional theory (DDFT). The particle interactions are modeled using fundamental measure theory (FMT). Each particle is represented by a Gaussian density peak, which allows us to quantify the mean delay from collisions for different configurations. The post-collision density resulting from the simulation can be described by a convolution of the pre-collision density, enabeling the analysis of different contributions to the delay.

BP 6.4 Mon 15:45 ZEU/0160

Active Ornstein-Uhlenbeck Particles: A Stochastic Path Integral Approach — •Carsten Littek, Mike Brandt, and Falko Ziebert — Institut für Theoretische Physik, Universität Heidelberg, Germany

In a recent publication (arXiv:2509.26296) we have developed a path integral formulation of the stochastic dynamics of a single active Brownian particle (ABP), with or without a constant torque, confined by a harmonic trap. This approach is based on the particle's microscopic degrees of freedom and we have derived exact analytic time-dependent expressions for key observable quantities such as the mean position and mean square displacement without the necessity of solving the Fokker-Planck equation. Here we present the application of this approach to the dynamics of active Ornstein-Uhlenbeck particles (AOUP). In particular, we generalize our formulation to systems of many AOUPs interacting via a suitable two-particle potential and derive the statistical quantities relevant in the context of collective phenomena, such as motility-induced phase separation (MIPS).

BP 6.5 Mon 16:00 ZEU/0160

Self-alignment and chirality in dense active matter: from flocking to circling crystals — •Marco Musacchio[1], Alexander Antonov[1], Hartmut Löwen[1], and Lorenzo Caprini[2] — [1]Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, Universitätsstraße 1, D-40225 Düsseldorf, Germany — [2]Physics Department, University of Rome La Sapienza, P.le Aldo Moro 5, IT-00185 Rome, Italy

Several experimental systems in active matter are characterized, at the single-particle level, by an effective torque that aligns particle orientation with their instantaneous velocity. This mechanism, known as self-alignment, appears in both biological and granular active systems. In dense active systems, a sufficiently strong self-alignment can suppress mips and drive the system from a clusterized flocking state to an homogeneous one, where all particles move collectively, with aligned velocities. This flocking transition is approached for a broad range of densities, even close to maximal packing, where the system is in a crystalline configuration. Specifically, in the crystal case, the flocking transition can be predicted analytically since the dynamics can be mapped onto a velocity-dependent Landau*Ginzburg free energy, revealing that this disorder*order transition is second order. The onset of chirality drives the system from collective flocking to a circling crystal phase, characterized by coherent circular motion of all the system. Further increasing chirality suppresses the global rotation, leading to a vortex-like structure in the velocity field. These findings are experimentally testable in systems governed by self-alignment and chirality.

BP 6.6 Mon 16:15 ZEU/0160

Number fluctuations distinguish different self-propelling dynamics — •Tristan Cerdin[1,2], Sophie Marbach[2], and Carine Douarche[1] — [1]Université Paris-Saclay, CNRS, FAST, 91405, Orsay, France — [2]CNRS, Sorbonne Université, Physicochimie des Electrolytes et Nanosystèmes Interfaciaux, F-75005 Paris, France

In nonequilibrium suspensions, static number fluctuations N in virtual observation boxes reveal remarkable structural properties, but the dynamic potential of $N(t)$ signals remains unexplored. Here, we develop a theory to learn the dynamical parameters of self-propelled particle models from $N(t)$ statistics.

Theoretical plots of the mean-squared number difference $\langle \Delta N^2(t) \rangle$ exhibit 3 scaling regimes in time corresponding to the 3 regimes of self-propelled particles: diffusive, advective and effectively diffusive again at long times. By expanding the theory in each of these regimes, we recover limiting laws for the number fluctuations, which can be used in practice to quantify self-propulsion properties.

Additionally, unlike traditional trajectory analysis, $N(t)$ statistics distinguish between models, by sensing subtle differences in reorientation dynamics that govern re-entrance events in boxes. This paves the way for quantifying advanced dynamic features in dense, out-of-equilibrium suspensions.

BP 6.7 Mon 16:30 ZEU/0160

Flocking transitions in dense mixtures of active self-aligning and passive particles — •Weizhen Tang[1], Amir Shee[2],

Zhangang Han[1], Pawel Romanczuk[3,4], Yating Zheng[3,4], and Cristián Huepe[1,5,6] — [1]School of Systems Science, Beijing Normal University, Beijing, China — [2]Department of Physics, University of Vermont, USA — [3]Department of Biology, Humboldt Universität zu Berlin, Unter den Linden 6, Berlin, Germany — [4]Research Cluster of Excellence 'Science of Intelligence', Berlin, Germany — [5]Northwestern Institute on Complex Systems and ESAM, Northwestern University, Evanston, USA — [6]CHuepe Labs, 2713 West Augusta Blvd #1, Chicago, USA

We investigate the passivity-driven flocking transition in a dense mixture of self-aligning active particles and passive particles, using a minimal model of active polar disks. We show that anisotropic damping leads to a discontinuous flocking transition as a function of the fraction of passive components, whereas isotropic damping produces a smooth transition where the final ordered state can display sustained oscillations and remain trapped in a metastable state, depending on the exact spatial arrangement of the passive particles. We also explore in detail the emergence of metastable oscillatory ordered states and their relation to the spatial distribution of passive particles and interstitial voids. Our findings demonstrate that heterogeneous activity and mobility anisotropy can result in a rich variety of self-organized states in various biological systems, synthetic active materials, and robotic swarms.

15 min. break

Invited Talk BP 6.8 Mon 17:00 ZEU/0160

Topological transition in filamentous cyanobacteria: from motion to structure — •Marco Mazza — Loughborough University, Loughborough, UK

Many active systems are capable of forming intriguing patterns at scales significantly larger than the size of their individual constituents. Cyanobacteria are one of the most ancient and important phyla of organisms that has allowed the evolution of more complex life forms. Despite its importance, the role of motility on the pattern formation of their colonies is not understood. Here, we investigate the large- scale collective effects and rich dynamics of gliding filamentous cyanobacteria colonies, while still retaining information about the individual constituents' dynamics and their interactions. We investigate both the colony's transient and steady-state dynamics and find good agreement with experiments. We furthermore show that the Péclet number and aligning interaction strength govern the system's topological transition from an isotropic distribution to a state of large-scale reticulate patterns. Although the system is topologically non-trivial, the parallel and perpendicular pair correlation functions provide structural information about the colony, and thus can be used to extract information about the early stages of biofilm formation. Finally, we find that the effects of the filaments' length cannot be reduced to a system of interacting points. Our model proves to reproduce both cyanobacteria colonies and systems of biofilaments where curvature is transported by motility.

BP 6.9 Mon 17:30 ZEU/0160

Novel Phase Coexistence in a Multi-Species Vicsek Model — •Eloise Lardet[1], Letien Chen[1,2], and Thibault Bertrand[1] — [1]Imperial College London, UK — [2]University of Edinburgh, UK

A hallmark in natural systems, self-organization often stems from very simple interaction rules between individual agents. While single-species self-propelled particle (SPP) systems are well understood, the behavior of mixtures of self-propelled particles with general alignment interactions remains largely unexplored with a few scattered results hinting at the existence of a rich emergent phase behavior. Here, we first present a generalization of the two-species Vicsek model with reciprocal intra- and interspecies (anti-)alignment couplings, uncovering a rich phenomenology of emergent states. Notably, we show that rather than destroying polar order, anti-aligning interactions can promote phase separation and the emergence of global polar order. Secondly, we derive a kinetic theory for the system, finding good agreement between theoretical predictions and particle simulations. This includes a novel mechanism for microphase separation, as predicted by a Turing instability. We finally show that these coexistence patterns can be generalized to multi-species systems with cyclic alignment interactions.

BP 6.10 Mon 17:45 ZEU/0160

Flocking in weakly nonreciprocal mixtures — •Charlotte Myin — Max Planck Institute for Dynamics and Self-Organization (MPI-DS), 37077 Goettingen, Germany

We show that weakly nonreciprocal alignment leads to large-scale structure formation in flocking mixtures. By combining numerical simulations of a binary Vicsek model and the analysis of coarse-grained continuum equations, we demonstrate that nonreciprocity destabilizes the ordered phase formed by mutually aligning or anti-aligning species in a large part of the phase diagram. For aligning populations, this instability results in one species condensing in a single band that travels within a homogeneous liquid of the other species. When interactions are anti-aligning, both species self-assemble into polar clusters with large-scale chaotic dynamics. In both cases, the emergence of structures is accompanied by the demixing of the two species, despite the absence of repulsive interactions. Our theoretical analysis allows us to elucidate the origin of the instability, and show that it is generic to nonreciprocal flocks.

BP 6.11 Mon 18:00 ZEU/0160

Collective behavior in nonreciprocal multi-species Vicsek model with permutation symmetry — •Jae Dong Noh[1], Chul-Ung Woo[2], and Heiko Rieger[2] — [1]Department of Physics, University of Seoul, Seoul 02504, Korea — [2]Department of Theoretical Physics and Center for Biophysics, Saarland University, Saarbrücken, Germany

Nonreciprocal systems are typically built upon asymmetric roles among interacting agents, such as a pursuer-evader relationship. We propose a multi-species nonreciprocal active matter model that is invariant under permutations of the particle species. The nonreciprocal, yet symmetric, interactions emerge from a constant phase shift in the velocity alignment interactions, rather from an asymmetric coupling matrix. This system displays rich collective behaviors, including a species-mixed chiral phase with quasi-long-range polar order and a species-separated vortex cell phase. We present numerical evidence for these phases using particle-based Monte Carlo simulations and analytic evidence using continuum Boltzmann and hydrodynamic equations. Our work demonstrates that multi-species chiral fluids can be realized by a nonreciprocal but symmetric alignment interaction, where the rich collective behavior is a consequence of the interplay between nonreciprocity and permutation symmetry.

BP 6.12 Mon 18:15 ZEU/0160

Flocking with random non-reciprocal interactions — •Jiwon Choi[1], Jae Dong Noh[2], and Heiko Rieger[1] — [1]Department of Physics & Center for Biophysics, Saarland University, Campus E2 6, 66123 Saarbrücken, Germany — [2]Department of Physics, University of Seoul, Seoul, 02504, Korea

Flocking is ubiquitous in nature and emerges from alignment interactions among self-propelled agents. Two species that anti-align or interact non-reciprocally exhibit complex collective phenomena, ranging from parallel and anti-parallel flocking and run-and-chase behavior to chiral phases. Whether such behavior survives in the presence of many species with random non-reciprocal interactions has remained unclear. As a first step, we study a continuous-time Vicsek-like model with fully random non-reciprocal interactions between particles. For infinite-range interactions, flocking emerges once the alignment bias becomes comparable to the non-reciprocal interactions, and deep inside this phase random non-reciprocity can still support slow global chiral and oscillating states. For short-range interactions, even without alignment bias, self-organized cliques form, where medium-sized clusters with predominantly aligning interactions remain stable over long times. We further investigate the robustness of clique formation and the coexistence phase under angular noise using a discrete-time Vicsek model with random non-reciprocal interactions. These results provide a basis for studying multi-species flocking with complex nonreciprocal interactions.

BP 7: Poster Session I

Biomaterials and biopolymers, cytoskeleton, cell mechanics and tissue mechanics; FS controlling biological cells by ultrasound

Time: Monday 15:00–17:00 Location: P5

BP 7.1 Mon 15:00 P5

Eco-Friendly PEGylated Iron Oxide Nanoparticles for In Vitro Targeted Delivery and Controlled Release of Docetaxel in SK-OV-3 Ovarian Cancer Cells — •Romesa Soomro[1], Che Azurahanim Che Abdullah[1,2], and Halima Alem Marchand[3] — [1]1Biophysics Lab, Department of Physics, Faculty of Science, Universiti Putra Malaysia, 43300, Selangor, Malaysia — [2]2Cancer Research Lab, Institute of Bioscience, Universiti Putra Malaysia, 43300, Selangor, Malaysia — [3]3Department of Matériaux, Métallurgie, Nanosciences, Université de Lorraine, Nancy, France

Iron oxide nanoparticles were green-synthesized using oolong tea extract as a natural reducing and stabilizing agent. A Taguchi L9 design was applied to optimize reaction parameters and obtain stable nanoparticles with reduced hydrodynamic size. The optimized particles were PEG-coated to improve biocompatibility and subsequently loaded with docetaxel for targeted cancer therapy. Characterization using spectroscopy, diffraction, magnetic measurements, and electron microscopy confirmed successful synthesis and coating, with superparamagnetic behavior and particle sizes below twenty nanometers. Drug release studies showed sustained, pH-responsive release under acidic conditions. Cytotoxicity evaluation using SK-OV-3 ovarian cancer cells demonstrated high biocompatibility of PEG-coated nanoparticles and strong anticancer activity of the docetaxel-loaded system. The results indicate that green-synthesized PEGylated iron oxide nanoparticles provide a promising and sustainable platform for controlled anticancer drug delivery.

BP 7.2 Mon 15:00 P5

The Potential Impact of a Novel Chitosan-Titanium dioxide Nanoparticles against Hepatocellular Carcinoma in Rat Model — Omnia Ahmed Mohamed Elbakary[1], Eman Ibrahim Kandil[1], Sawsan Mohamed Elsonbaty[2], Shaimaa El-saied Mohamed[1], and •Nermeen Mohamed Elbakary[3] — [1]Faculty of Science, Biochemistry department, Ain Shams University, Cairo, Egypt — [2]Radiation microbiology department, National center for radiation research and technology, Egyptian Atomic Energy Authority, Cairo, Egypt — [3]Radiation biology department, National center for radiation research and technology, Egyptian Atomic Energy Authority, Cairo, Egypt

Hepatocellular carcinoma (HCC) the most common type of liver cancer, is the fifth most common malignant tumor type worldwide and the second leading cause of cancer-related death. This study investigates the potential therapeutic effects of novel chitosan-titanium dioxide nanoparticles (Cs-Ti NPs) against hepatocellular carcinoma (HCC) in a rat model. The experimental design included five groups: a healthy control group, a group administered with diethylnitrosamine (DEN) to induce liver carcinogenesis, a group treated with Cs-Ti NPs, a DEN group subsequently treated with 5-Fluorouracil (5-FU), and a DEN group treated with Cs-Ti NPs. DEN was administered orally at 20 mg/kg body weight five times weekly for six weeks to induce tumor formation. Therapeutic interventions with Cs-Ti NPs and 5-FU were applied post-induction. The study evaluated apoptotic markers (Bcl-2, Bax, p53, Caspase-3, Cytochrome C), signaling pathways (MAPK, ULK1, mTOR), and serum tumor markers (AFP, NF-κB, COX-2) via ELISA. Results are expected to elucidate the molecular mechanisms involved and assess the efficacy of Cs-Ti NPs in mitigating HCC progression, potentially offering a new nanotherapeutic avenue for liver cancer treatment.

BP 7.3 Mon 15:00 P5

Viscous and Plastic Energy Dissipation Processes of Native Collagen Fibrils in AFM-based Nanoindentation Measurements under Controlled Humidity — •Martin Dehnert, Paul Zech, Mario Zerson, and Robert Magerle — Fakultät für Naturwissenschaften, Technische Universität Chemnitz, Germany

Collagens, lipids, and water are among the major molecular components of connective tissue, yet surprisingly little is known about their interactions in vivo. Here, we use AFM-based nanoindentation experiments to measure the mechanical response of collagen fibrils to deformation under constant strain (relaxation) or constant stress (creep) at different humidity levels and at different deformation speeds. The measured data are evaluated using a power-law analysis, in which the detailed indentation history, including the different indentation velocities, is taken into account. An in-depth analysis reveals that the phenomena of stress relaxation and creep compliance can be described by a time-scaled power law. Furthermore, we show that energy dissipation is primarily caused by plastic deformation during tip indentation and can be quantified with the ductility index. This parameter can also be used for high-resolution imaging of connective tissues. The ductility index provides additional information about the nanomechanical changes in collagen fibrils during development, aging, and disease.

BP 7.4 Mon 15:00 P5

Cyanobacteria as biological actuators — •Paul Nieschwitz and Stefan Karpitschka — Department of Physics, Universität Konstanz, Germany

Filamentous cyanobacteria are highly resilient, light-responsive organisms whose robustness and availability makes them ideal candidates for building engineered living materials (ELMs), that can adapt to or be controlled by external cues.

Here, we present a simple actuator composed of entangled filament assemblies wrapped around elastic PDMS-pillars. Contraction of the network generates a net resultant force that deflects the pillars. By calibrating the compliance of the pillars, we quantify this force. Varying the actuator geometry, filament density and illumination conditions, allows us to characterize the force output and dynamic response of the actuator.

Without requiring the need for genetic modification or sophisticated culture conditions, this platform offers a simple and robust approach to create light-controlled biological machines.

BP 7.5 Mon 15:00 P5

LactiFilm: Hydrogel supported co-culture biofilms of lactobacilli and phytoplankton for sustainable production of lactic acid — •Carina Schneider and Regine von Klitzing — TU Darmstadt, 64289 Darmstadt, Germany

Lactic acid is an essential bulk chemical used across the food, pharma, and cosmetics industry. Recently, its demand has been rising as the monomer for synthesizing polylactic acid, a major biodegradable alternative to conventional plastic. Hence, biological synthesis of lactic acid offers a greener production option. In this work, we develop a biofilm-inspired strategy by immobilizing lactobacilli and algae in smart hydrogels.

The algae immobilization matrix is formed from crosslinkable PNIPAM (Poly N-Isopropylacrylamide) microgels containing the UV-sensitive comonomer HMABP (2-Hydroxy-4-(methacryloyloxy)benzophenone), enabling microgel crosslinking into a stable hydrogel film. Due to the volume phase transition temperature of PNIPAM, the matrix exhibits controllable swelling and deswelling behavior. This responsiveness allows for regulated partial lysis of the algae to release nutrients that support lactic-acid production. To assess the mechanical strength of the hydrogel, we perform atomic force microscopy (AFM) indentation measurements.

BP 7.6 Mon 15:00 P5

Multi-phase coexistence of charged condensates — •Chengjie Luo, Yicheng Qiang, and David Zwicker — MPI-DS, Göttingen, Germany

Biomolecular condensates are complex droplets whose formation is believed to be primarily driven by short-range attractive interactions between diverse molecules. However, charges that mediate long-range interactions can also strongly affect phase separation. Using a mean-field theory, we demonstrate that electrostatic interactions can drive rich phase separation behavior. In a simple system of three charged components, these interactions can lead to the coexistence of multiple phases, including homogeneous phases with different compositions and patterned phases with finite-sized droplets. Furthermore, applying an external electric field can dramatically alter these coexistence states:

weak fields cause charged droplets to move like colloidal particles, while stronger fields stretch droplets, leading to the formation of striped patterns. Our work establishes electrostatics and electric fields as potent controllers of phase coexistence, with implications for understanding biological condensates and designing synthetic patterned materials.

BP 7.7 Mon 15:00 P5

Density and viscosity Measurements of the cytosol of human red blood cells — •Thomas John, Karin Kretsch, and Christian Wagner — Experimental Physics, Saarland University

We present a method to determine the viscosity of the intracellular liquid - the cytosol - of human red blood cells (RBCs). Our method combines the measurement of the mass density distribution of RBCs and the viscosity of the cytosol as a function of the water content. The density distribution is measured through buoyant density centrifugation combined with cell counting. By correlating this distribution of cell population densities with the viscosity-density relation of the cytosol, we obtain a log-normal distribution of the cytosol viscosity of healthy RBCs. The viscosity contrast λ, defined as the ratio of viscosities between the RBC cytosol and the blood plasma under physiological conditions, is determined to have a log-normal distribution with a mean value of $\bar{\lambda} = 10$. This value is significantly larger than those used in the literature for numerical simulations. The wide distribution of the viscosity values results from the loss of a small amount of water from the RBCs over their 120-day lifespan. We find that the viscosity of the cytosol in older cells is more than twice as high as in younger cells, a fact that should be taken into account in future theoretical investigations.

BP 7.8 Mon 15:00 P5

Model particles to study interaction of microplastic particles — •Kai Gossen, Andreas Fery, and Günter Auernhammer — IPF Dresden, Dresden, Germany

Microplastic in the environment is typically coated by natural organic matter forming an ecocorona. We present an approach to model ecocorona on parti- cles with well-defined polymers, synthetic and derived from natural polymers. Polystyrene particles were coated with fluorescent polyelectrolyte multilayer systems, PS(Chitosan/Hyaluronic acid) and PS(Poly(dimethyldiallylammonium chloride) /Polystyrene sulfonate) by the layer-by-layer method. Systems with 2, 4 and 6 bilayers were synthesized. The second layers were fluorescently labelled with SNARF conjugated dextran. It was found that zeta potentials of the PS(Chi/HS)2/4/6 systems assume val- ues (-20 mV to -35 mV) that are similar to those of PS-ecocorona particles (-40 mV to -5 mV). The pH-dependent fluorescence of particle suspensions and indi- vidual particles were measured at pH values between pH 3 and pH 8. A well mea- surable pH dependence between pH 4.5 and 8 for the PS(Chi/HS) systems and the PS(PDADMAC/PSS) system could be measured. Automating particle synthesis via cross-flow filtration produces particle batches of up to 5 g. The system could serve to selectively study effects of surface properties of ecocorona coated particles such as surface stiffness or zeta potential.

BP 7.9 Mon 15:00 P5

Controlled Spray coating of Bacterial Nanocellulose Thin films revealed by Surface-Sensitive X-ray Scattering — •Joanne Neumann[1], LI Li[2], Edina Klein[1,3], Jan Rubeck[1], Ute Römling[2], Holger Sonderrmann[1,3], and Matthias Schwartzkopf[1] — [1]DESY, Photon Science, Notkestr. 85, D-22607 Hamburg — [2]Department of Microbiology, Tumor and Cell Biology, Biomedicum, KI, Karolinska Institutet, Nobels väg 6, S-17177 Stockholm — [3]CSSB, Center for Structural Systems Biology, Notkestr. 85, D-22607 Hamburg

Bacterial nanocellulose (BNC) is a sustainable biomaterial valued for its purity, nanoscale fibrillar structure, and biocompatibility. Its properties can be tailored through genetic engineering, growth conditions, and processing. Here, we fabricate thin films from BNC produced by *S. typhimurium*, *Komagataeibacter*, and *Klebsiella* using airbrush spray deposition of aqueous dispersions as a green, reproducible method. We examine how different extraction procedures (acidic, alkaline, surfactant-based) affect nanoscale organization and film adaptability. High-resolution X-ray scattering (μGIUSAXS/μGIWAXS) is used to probe fibril orientation, aggregation, and hierarchical ordering. Our results show extraction-dependent structural variations that influence film homogeneity and functional performance. By refining spray-coating and scattering protocols, this work links chemical treatment history to structural adaptability and supports sustainable strategies for controlled BNC thin-film fabrication in materials science and bioengineering.

BP 7.10 Mon 15:00 P5

Engineering Shear-Thinning Hydrogels: A Dynamic Scaffold for 3D Tissue Culture — •Bruno Schmelz[1], Fen Li[2], Kai Zhang[2], and Timo Betz[1] — [1]Third Institute of Physics, University Göttingen — [2]Sustainable Materials and Chemistry, University Göttingen

Extracellular matrix scaffolds are essential for advanced 3D cell culture systems, providing structures for cell movement as well as physical and chemical cues that promote migration, proliferation, and differentiation. Hence, the extracellular matrix is crucial for functional tissue formation. However, natural extracellular matrix materials used in vitro, such as collagen and elastin, are difficult to control regarding elastic properties, polymer mesh size, and homogeneity. Our objective is to design a dynamic hydrogel, tailored to meet the specific requirements of 3D tissue culture, such as viscoelastic properties and cell-binding sites, that initially supports tissue formation but can be dissolved and replaced by cell-generated extracellular matrix. We propose a hydrogel with dynamic cross-links that allows for reorganization by embedded cells, resembling processes in physiological tissues. We present the rheological properties of the hydrogel and the initial findings of cellular migration and reorganization of cell-gel systems. When subjected to stress, the hydrogel exhibits a transition to a more liquid-like state, with the potential to solidify again upon stress relaxation. This behavior allows cells to remodel their surrounding matrix and shape their environment, as evidenced by experiments with cells cultured in the hydrogels.

BP 7.11 Mon 15:00 P5

Atomic-Scale Probing of Aluminum Distribution in Catalysts and Peptide COM Fidelity — •Sakshi Sinha — Department of Materials Physics, Institute of Material Science, University of Stuttgart, Heisenbergstr. 3, 70569 Stuttgart

Atom Probe Tomography (APT) enables three-dimensional, atomic-scale mapping of inorganic and biomolecular materials. Using conventional lift-out specimen preparation, we study aluminum distribution in microporous aluminosilicate catalysts with varying Al content. The frequency distribution with considering different sphere sizes N in order to investigate size-dependent effects for segregating or clustering behavior of the Al atoms. APT reveals atomic-scale clustering and uniformity of Al, providing direct insight into acid site density and strength, and complements bulk techniques such as ICP-OES by resolving localized compositional variations. For biomaterials, cryogenic quench-freezing is used to prepare aqueous specimens. Mass spectra indicate that fragmentation behavior is concentration-dependent and influenced by hydration shell disruption during field evaporation. Experimental interfragment distances closely match theoretical center-of-mass distances within 1 Å, demonstrating that APT can preserve biomolecular subunit spatial relationships with sub-angstrom fidelity. These studies demonstrate the versatility of APT in probing both inorganic and biomolecular systems with unprecedented atomic precision, opening pathways for understanding structure*function relationships across material classes.

BP 7.12 Mon 15:00 P5

Decoupling Crosslink Stability and Network Connectivity in Coiled Coil Crosslinked Hydrogels — Stefanie Lenzeder[1], Geonho Song[1,2], Isabell Tunn[2], Alberto Sanz de Leon[2], Tanja D. Singewald[1], and •Kerstin G. Blank[1,2] — [1]Johannes Kepler University, Linz, Austria — [2]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Biomimetic hydrogels serve as a powerful platform for investigating how cells sense and respond to the mechanical cues in their environment. Despite significant progress, the precise mechanisms how cells evaluate the elastic and viscoelastic properties of their surroundings remain incompletely understood. While hydrogels are typically characterized based on their bulk material properties, cells probe these materials on the molecular scale through receptor-ligand interactions. Bridging the gap between molecular-scale interactions and macroscopic material behavior is thus essential for advancing our understanding of cell-material interactions. Inspired by proteins found in the extracellular matrix, we are investigating biomimetic hydrogels crosslinked with coiled coil forming peptides. These modular building blocks enable precise control over their molecular characteristics, such as thermodynamic, kinetic and mechanical stability as well as oligomerization

state. Our findings show that the bulk material properties are governed more strongly by network connectivity than crosslink stability. These insights deepen our understanding of how molecular design impacts the macroscopic behavior of hydrogels, opening new avenues for tailoring materials for specific biological applications.

BP 7.13 Mon 15:00 P5

Development and investigation of coarse-grained particle models for alginates. — •Hensi Gandhi, Rudolf Weeber, and Christian Holm — Institute for Computational Physics, University of Stuttgart, Stuttgart, Germany

Alginates form ion-mediated gel networks whose mesoscale structure and mechanical properties depend on monomer sequence, charge distribution, and environmental conditions. We aim to develop coarse-grained models that capture these molecular features while remaining computationally efficient. Our ongoing work combines all-atom molecular dynamics with systematic coarse-graining to derive bonded interactions, electrostatics, and ion-mediated cross-linking rules. The models will be implemented in ESPResSo [1] using implicit solvent, with extensions for multivalent ions and shear via Lees Edwards or lattice Boltzmann coupling. We will study how monomer sequence, salt concentration, and pH influence chain flexibility, persistence length, gelation kinetics, and network topology, and compare structural and mechanical observables with experiments to assess model transferability. This framework is intended to support mesoscale predictions within the GRK SusGel program [https://www.susgel.kit.edu/24.php] and link molecular design to macroscopic gel properties.

[1] F. Weik, R. Weeber, K. Szuttor, K. Breitsprecher, J. de Graaf, M. Kuron, J. Landsgesell, H. Menke, D. Sean, C. Holm, ESPResSo 4.0 - An extensible software package for simulating soft matter systems, European Physical Journal-Special Topics, 227 (2019), 1789-1816, DOI: 10.1140/epjst/e2019-800186-9.

BP 7.14 Mon 15:00 P5

Cytoskeletal Networks in 3D Cysts Under Strain — •Greta Höhndorf[1], Ruth Meyer[1], Ruben Haag[1], Ulrike Rölleke[1], Ulla Unkelbach[2], Nicole Schwarz[3], Andreas Janshoff[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen — [2]Institute of Physical Chemistry, University of Göttingen — [3]Institute of Molecular and Cellular Anatomy RWTH Aachen University

The cytoskeleton of eukaryotic cells mainly consists of actin filaments, microtubules and intermediate filaments (IFs). Unlike actin and microtubules, IFs are cell-type specific. Epithelial cells express keratin IFs, which form a layer close to the membrane in certain cell types. This layer is referred to as the "IF-cortex" and is hypothesized to adopt a "rim-and-spokes" structure with radial spokes supporting mechanotransduction properties of the cell. This structure raises questions about how the actin and IF cortices complement each other and how the mechanical properties of keratin influence force transmission in cells under high strain. To address these questions, we show a 3D approach where epithelial cells form polarized cysts and are stretched by injecting mineral oil into the lumen. When comparing wild-type (WT) and keratin knock-out (KO) cysts, we find that KO cysts deform more easily at low strains and respond more sensitively at high strains than WT cysts, indicating a stabilizing role of keratin under increased mechanical load. Furthermore, by staining actin, keratin, and the nuclei and performing fluorescence imaging pre and post stretching, we investigate strain dependent network changes and deformations.

BP 7.15 Mon 15:00 P5

Interactions between single actin and vimentin filaments — •Pallavi Kumari[1], Kristian Pajanonot[1,2], Komal Bhattacharyya[2], Stefan Klumpp[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Germany

The cytoskeleton plays a crucial role in maintaining cellular structure, mechanics, and function. Recent advances suggest that the diverse tasks of the eukaryotic cytoskeleton depend on the interactions between its filamentous components–microtubules, actin filaments, and intermediate filaments. Despite a growing number of studies aimed at a better understanding of these interactions, it remains unclear whether actin and intermediate filaments interact directly in the absence of an auxiliary protein. Previous *in vitro* studies on reconstituted mixed filament networks have reported inconclusive results. To clearly resolve this inconclusiveness, it is essential to further simplify the system down to the single filament level. Here, we present a study on the direct interactions between actin and vimentin intermediate filaments at the single filament level. Using quadruple optical tweezers combined with confocal microscopy and microfluidics, we precisely control the interaction conditions, visualize the interactions in real time, and measure the forces involved. Our research provides direct evidence of actin-vimentin interactions, together with a quantification of the interaction forces they exert on each other.

BP 7.16 Mon 15:00 P5

Mechanical Properties of Intermediate Filament Networks — •Jonas Penning, Komal Bhattacharyya, and Stefan Klumpp — Institut für Dynamik komplexer Systeme, Georg-August-Universität Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

The mechanical strength and dynamics of cells are essential for sustaining life. For instance, during simple activities such as breathing or walking, cells experience significant tensile stresses as they are stretched, sheared, or compressed. The cytoskeleton - a cross-linked composite network of actin, microtubules, and intermediate filaments - plays a central role in determining the cells' mechanical properties. This work focuses primarily on intermediate filaments, with particular emphasis on vimentin. Compared to actin, intermediate filaments exhibit much smaller persistence lengths, but are much more stretchable with highly nonlinear elasticity. A simplified, lattice-based model of fibrous networks with variable connectivity has been developed to investigate the mechanical and physical properties of such vimentin filament networks, as the model allows for the corresponding nonlinear behavior of individual vimentin filaments under strain. Analogous to experimental approaches, the mechanical properties of the model are tested by applying normal and shear strains or stresses and analyzing the resulting responses. Stretching the networks isotropically and comparing linear and nonlinear strain-behavior of individual filaments, the model shows an internal energy decrease for nonlinear elasticity and a strain-softening quantified by a turning point in the bulk modulus with increasing network-strain.

BP 7.17 Mon 15:00 P5

Phosphorylation-induced softening of vimentin networks revealed by optical tweezers microrheology — •Yuzhen Feng, Shanay Zafari, and Sarah Köster — Institute for X-Ray Physics, University of Göttingen, Germany

Phosphorylation is a key post-translational modification regulating intermediate filament (IF) organization and cell mechanics. While phosphorylation-induced softening of single vimentin filaments has been reported, its impact on network-level mechanics remains unclear. Here, we employ optical tweezers-based active microrheology to quantify the mechanical properties of vimentin IF networks containing defined fractions of the phosphomimetic vimentin mutant S72E. Both unmodified and phosphomimetic vimentin networks exhibit a viscoelastic response with partial stress relaxation after deformation. Increasing the phosphomimetic content reduces the overall stiffness, indicating phosphorylation-induced softening at the network level. These findings extend the understanding of how biochemical regulation at the molecular level translates into mechanical remodeling of IF across scales from the single-filament to the network level.

BP 7.18 Mon 15:00 P5

Microtubule networks exhibit amorphous material behavior — •Claudia Marcelli[1], Raffaele Mendozza[2], Shanay Zafari[1], Ruben Haag[1], Peter Sollich[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]Institute for Theoretical Physics, University of Göttingen, Germany

Microtubules (MTs), together with intermediate filaments and actin, are the main components of the cytoskeleton. Among these filaments, MTs are the stiffest. They can form a rigid cellular scaffold and transmit forces across the cell while remaining extremely dynamic and able to assemble into specific cell structures (e.g. mitotic spindles). While MTs have been extensively characterized at the single-filament level, it is still not fully resolved how they collectively behave at the network-scale level. Here, we present a comprehensive characterization of the linear and nonlinear mechanical responses of stabilized MT networks at the microscale by using optical tweezers. To this aim, we employ both strain-ramp and large-amplitude oscillatory strain protocols, applying a range of deformations that allows us to probe both regimes. Our results show that MTs can withstand high stress and behave as an amorphous material, exhibiting a yielding transition from an elastic response at small strains to a viscous response at large strains.

These findings provide us with a deeper understanding of the mechanics of MT networks while setting the stage for future studies in which dynamic or active elements can be incorporated into the network to understand how activity modifies material mechanical properties.

BP 7.19 Mon 15:00 P5

MatrixModel: Building a Computational Model of the HSPC niche — •Julia Käsehagen and Sophia Rudorf — Institute for Cell Biology and Biophysics, Leibniz Universität Hannover, Germany

Haematopoietic stem and progenitor cells (HSPCs) rely on finely tuned adhesion to extracellular matrix (ECM) proteins within the bone marrow niche to balance quiescence, self-renewal, and differentiation. As part of the research consortium Matrix Evolution [1], MatrixModel develops a multiscale computational framework to predict how ECM composition, architecture, and mechanics regulate HSPC behavior, including adhesion and motility. We implemented two pipelines to use and adapt models by other goups: (i) a mechanochemical ODE model of integrin-talin-vinculin adhesion dynamics (by Honasoge et al. [2]) and (ii) a hybrid Cellular-Potts-Bead-Spring model of ECM fiber networks (by Tsingos et al. [3]).

For (i), we will parameterize the ODE model for HSPCs to predict adhesion lifetimes and tractions per adhesion. In (ii), the Cellular-Potts-Model (CPM) governs HSPC shape and contract energies, while a nonlinear fiber network captures density, crosslinking, and anisotropy. Cell-fiber links inherit rate laws from results of the ODE model.

[1] https://www.cell.uni-hannover.de/en/research/main-research-areas/matrix-evolution
[2] Honasoge et al., 2023, PLoS Comput Biol.
[3] Tsingos et al., 2023, Biophysical Journal.

BP 7.20 Mon 15:00 P5

Stiffness Characterization of Microtentacles: an optical tweezers study — •Kirill Korneev[1], Thomas John[1], Franziska Lautenschläger[1,2], and Christian Wagner[1,2] — [1]Department of Experimental Physics, Saarland University, Saarbrücken, Germany — [2]Center of Biophysics, Saarland University, Saarbrücken, Germany

Laser tweezers (LT) are devices used for manipulating, trapping, and measuring forces on particles within optical traps, and they are commonly used in biophysics. Microtentacles (McTNs) are membrane protrusions supported by bundles of microtubules produced inside cells. These McTNs appear in circulating tumor cells and are thought to play a key role in facilitating the cells adhesion and extravasation process from the blood vessel. Although the biological mechanisms underlying McTN formation have been partially characterized, their characterization by physical material parameters is still lacking. The objective of this work is to study the deformation of McTNs using optical trap force measurements. We will show how McTNs behave under the action of external forces in the piconewton range and suggest a method to extract their Young's moduli

BP 7.21 Mon 15:00 P5

Determination of the Human Red Blood Cell Mass Density Distribution — •Luca Hastenteufel[1], Thomas John[1], Karin Kretsch[1], and Christian Wagner[1,2] — [1]Dynamics of Fluids, Experimental Physics, Saarland University, 66123 Saarbrücken, Germany — [2]Physics and Materials Science Research Unit, University of Luxembourg, L-1511 Luxembourg, Luxembourg

Red blood cells (RBCs) survive in circulation for approximately 120 days, during which their mass density increases, leading to the formation of a density distribution (DD). This distribution is commonly used as a diagnostic marker and as an indicator of individual cell age. However, few studies have examined the detailed form of the DD, with only few datapoints. In this study, the DD of erythrocytes was quantitatively derived using microscopic imaging approaches in controlled linear density gradients. Linear gradients were created using Percoll and Optiprep, common density media used for the density separation of cells or subcellular compounds. A custom microscopic scanning setup was developed to image RBC distributions along the gradient with a micrometre spatial resolution over several cm. Through image analysis, the vertical positions of individual cells were detected and by single cell counting, the DD was constructed in high resolution. The measured DD revealed significant deviations from Gaussian behaviour.

BP 7.22 Mon 15:00 P5

Integration of environmental stimuli into the contraction dynamics of *Physarum polycephalum* — •Nora Deiringer and Karen Alim — School of Natural Sciences, Technical University of Munich, Garching, Germany

In many organisms, behaviour and decision-making are guided by environmental stimuli. However, the internal dynamics linking stimuli to behaviour are often complex and not fully understood. Additionally, an organism's response to a stimulus can depend on its past stimulus history. In the unicellular, network-shaped organism *Physarum polycephalum*, migration results from the redistribution of cell mass driven by self-organised rhythmic tube contractions. In this study, we mimic environmental stimuli by exposing the cell's contraction dynamics to patterns of harmful blue light. Through live recordings, we observe the imprints of these patterns in the cell's dynamics and investigate how dynamic stimulus memories arise and decay. By varying the time span between two consecutive stimuli, we aim to elucidate how past stimulus history influences responses to future ones. Our findings provide insight into the mechanisms by which simple, non-neural organisms can organise adaptive behaviour.

BP 7.23 Mon 15:00 P5

Coordination of Migration by Adaptive Mechanics — •Diana Lenski, Lucas Troeger, and Karen Alim — School of Natural Sciences, Technical University of Munich, Germany

Unicellular organisms navigate and adapt to their environment using characteristic migration strategies, among them chemotaxis, the ability to detect and respond to chemical gradients. Although numerous models exist for amoeboid migration, the mechanisms governing directional sensing and movement in dynamical systems with complex morphologies across various size scales remain partially characterised. Besides continuous locomotion, migration strategies can involve dynamic regulatory phases that modulate the migratory behaviour. One such example in the slime mould *Physarum polycephalum* are stationary oscillations that repeatedly interrupt persistent migration.
This project involves the analysis and modelling of experimentally observed stationary oscillations in *P. polycephalum* across macroscopic and intermediate scales. These oscillations manifest as the periodic, opposing formation of protrusions that define the direction of migration, making them a key observable across spatial and temporal scales. First, we will statistically evaluate the chemotactic efficiency of large and small plasmodia on the macroscopic scale. Subsequently, we will examine oscillation dynamics by tracking contraction patterns to evaluate their contribution to migration phases and energy efficiency.
Integrating both perspectives will provide a deeper understanding of oscillatory migration phases as a fundamental element of amoeboid migration strategies.

BP 7.24 Mon 15:00 P5

Deep learning architecture combining Vision Transformers and U-Nets for robust traction force microscopy — •Yunfei Huang[1], Elena Van der Vorst[2,3], and Benedikt Sabass[1,2,3] — [1]Faculty of Physics, Technical University Dortmund, Dortmund, 44227, Germany — [2]Faculty of Physics and Center for NanoScience, Ludwig Maximilian University of Munich, Munich, 80752, Germany — [3]Department of Veterinary Science, Ludwig Maximilian University of Munich, Munich, 80752, Germany

Traction force microscopy (TFM) quantifies cellular forces on the extracellular matrix. Although deep learning has advanced TFM analysis, challenges remain in achieving reliable inference across spatial scales, estimating uncertainty, and integrating biological information such as cell type. In this study, we propose a robust deep learning architecture, ViT+UNet, which integrates a U-Net with a Vision Transformer. Our results show that this hybrid model outperforms either U-Net or ViT alone in predicting traction force fields. In addition, ViT+UNet achieves superior generalization across a wide range of scales, which allows one to use the algorithm for TFM with different setups and equipment. We extend the model with an uncertainty estimation module that enables simultaneous prediction of traction forces and confidence levels. Incorporating cell-type information further improves accuracy. Simulated results show that the algorithm effectively reconstructs 3D traction fields in non-linear elastic matrices.

BP 7.25 Mon 15:00 P5

Identifying the proteins controlling the intracellular active mechanics — •Noemie Veyret, Till Muenker, and Timo Betz — Third institute of Physics, University of Göttingen, Germany

Over the past few years, the study of cell mechanical properties has allowed new insights on the understanding of biological processes and life

complexity. According to previous work, intracellular mechanical properties can be narrowed down to a fingerprinting of only 6 parameters. Through the use of active and passive microrheology measurements via optical tweezers, frequency dependent viscoelastic properties and intracellular activity were found to vary for different cell types. The aim of this project is to find a correlation between changes in protein expressions and mechanical fingerprint of cells. To do so optical tweezers measurements will be performed during the differentiation process of induced Pluripotent Stem Cells (iPSC) into different cell types such as skeletal muscles or cardiac fibroblasts. This measurement allows the characterization of the mechanics during the iPSC differentiation process. In parallel, the cell proteome will be studied using mass spectroscopy. Combining both, we hope to find the connection between proteins and their mechanical role, the intracellular "mechanome".

BP 7.26 Mon 15:00 P5

Characterization of filamentous cyanobacteria using force-sensing micropipettes — •Paul Dufke and Stefan Karpitschka — Fachbereich Physik, Universtität Konstanz

Filamentous cyanobacteria strongly influence nearly all ecosystems, sometimes with harmful impacts. It is believed that their dominance is based on collective traits such as aggregation, entanglement and dispersal, but the details remain elusive. To understand the collective behaviour that arises in ensembles of many filaments, it is necessary to quantify the mechanical properties of individual filaments. We characterize their bending stiffness using force-sensing micropipettes with nanonewton resolution, quantifying three different species across various growth stages, which affect the filament diameter and thus their bending stiffness. The observed diameter dependence of the bending modulus suggests that most of the structural rigidity emerges from a thin region near the cell wall. The connection between culture age and mechanical properties indicates that modulations of flexural rigidity may also influence the collective behaviour at different stages in the life cycle of a colony.

BP 7.27 Mon 15:00 P5

Passive vs active shells: from spectrin to actin cortex — •Tim Kutz[1], Bart Vos[1], Bart Jan Ravoo[2], Andreas Janshoff[3], and Timo Betz[1] — [1]Third Institute of Physics, Georg August Universität Göttingen, Göttingen, Germany — [2]Institute of Physical Chemistry, Georg August Universität Göttingen, Göttingen, Germany — [3]Organic Chemistry Institute and Center for Soft Nanoscience, University of Münster

The viscoelastic and tensile properties of the cell surface are key regulators of processes such as migration, division, and shape control, yet the respective roles of membrane and cortex remain only partially understood. Here, we use a combined experimental approach integrating atomic force microscopy (AFM) and micropipette (MPA) aspiration to dissect surface mechanics in two paradigmatic systems: red blood cells (RBCs) and Xenopus tadpole cells (XTCs). RBCs provide a membrane-dominated reference state with a passive spectrin network, while XTCs feature an active actomyosin cortex coupled to the plasma membrane. AFM-based tether pulling and creep compliance measurements yield local effective tension and viscoelastic response, whereas MPA reports global surface tension and large-scale deformation behaviour. From the combined data, we identify clear differences in relaxation behavior and tension build-up between RBCs and XTCs, reflecting the presence of active contractile elements in the cortex. Our results demonstrate how multi-modal micromechanical probing can disentangle membrane- versus cortex-dominated contributions to cell surface tension.

BP 7.28 Mon 15:00 P5

Deciphering the role of flagellar membrane glycoproteins in ciliary adhesion of *Chlamydomonas reinhardtii* — •Lea Rupprecht[1], Adrian Nievergelt[2], Rodrigo Catalan[1], Lara Hoepfner[3], and Oliver Bäumchen[1] — [1]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [2]Max Planck Institute of Molecular Plant Physiology, 14476 Potsdam, Germany — [3]Human Technopole, 20157 Milan, Italy

Elucidating the physical mechanisms of microbe-surface interactions is essential for developing novel technologies to control the formation of microbial biofilms. While most studies focus on bacteria as model systems, the adhesion of eukaryotic photosynthetic microorganisms to surfaces remains rather elusive. *Chlamydomonas reinhardtii* has been shown to adhere to surfaces with its two cilia under blue light [1], yet the underlying molecular mechanism remains unclear. For decades, the N-glycosylated proteins FMG1-B were considered the main adhesive components of the ciliary glycocalyx, with FMG1-A also contributing to its organization and function. We performed *in vivo* single-cell micropipette force spectroscopy [2] and adsorption/desorption [3] experiments on CRISPR/Cas9-generated FMG1-B-, FMG1-A-, and double-knockouts of *C. reinhardtii*. Thereby we examine how the absence of specific glycocalyx components affects ciliary adhesion forces in different light conditions.

[1] Kreis *et al.*, *Nature Physics* **14**, 45-49 (2018).
[2] Backholm and Bäumchen, *Nature Protocols* **14**, 594-615 (2019).
[3] Catalan *et al.*, *Soft Matter* **19**, 306-314 (2023).

BP 7.29 Mon 15:00 P5

Probing the micromechanics and fluidity of cellular spheroids — •Tom Sosniok[1], Antoine Girot[1], Gabriel de Barros Righes[2], Rodrigo Catalán[1], Ada Cavalcanti-Adam[2], and Oliver Bäumchen[1] — [1]University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany — [2]University of Bayreuth, Cellular Biomechanics, 95447 Bayreuth, Germany

Characterizing the mechanical properties of multicellular spheroids is crucial to elucidate the dynamics of biophysical processes such as pathological tissue development, tumor metastasis and disease progression. Spherical cellular aggregates often serve as valuable tissue models, yet, they cannot be readily characterized with conventional techniques that are optimized for single cells. By combining micropipette force spectroscopy [1] with optical shape tracking, we provide an experimental approach to measure the mechanical properties of spheroids. Here, we first applied this technique to the model organism *Volvox globator*, a photosynthetic microbe that naturally forms spherical aggregates. We show that the compression and relaxation dynamics of *Volvox* can be described by a viscoelastic model, with the viscous component exhibiting a shear-thinning behaviour that is accurately described by a power-law fluid. We find that the viscoelasticity of the aggregates as well as their elastic modulus depend on their life stage. Finally, we applied the same methodology and modelling to aggregates of human colorectal adenocarcinoma cells with epithelial morphology and analysed their mechanical properties.

[1] M. Backholm and O. Bäumchen, *Nat. Protoc.* **14**, 594 - 615 (2019).

BP 7.30 Mon 15:00 P5

Intracellular mechanics in migrating cells — •Jannis Fischer[1], Mohammad Amin Eskandari[1], Sarah Louisa Lädke[1], Till Moritz Münker[1], Matthias Krüger[2], and Timo Betz[1] — [1]Third Institute of Physics, Göttingen, Germany — [2]Institute for Theoretical Physics, Göttingen, Germany

To fulfill their incredibly large number of different tasks, biological cells have developed mechanisms to adapt their physical properties and appearance, for example cell shape variation or cell migration. It is still not clear whether the changes in these mechanical properties are due to passive or active processes. Investigating and understanding these processes is the core of this work. For this, I will analyze the behavior of migrating cells, which are induced to move alternately on adhesive patterns. To connect the observed dynamics with the underlying mechanical properties and activities, I will use the new quantity of mean back relaxation (MBR). This can not only overcome the low throughput of optical tweezers, but also determine activity and mechanical properties through purely passive observations. With the MBR, we want to answer the question of how cellular shape influences mechanical properties.

BP 7.31 Mon 15:00 P5

Passive microrheology reveals anisotropic intracellular activity — •Sarah Louisa Lädke[1], Till Moritz Münker[1], Matthias Krüger[2], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics, Georg August Universität Göttingen — [2]Institute for Theoretical Physics, Georg August Universität Göttingen

To investigate intracellular activity and the associated deviations from thermodynamic equilibrium, we study the fluctuations of endogenous vesicles and phagocytosed beads in various cell types and conditions. Experimentally, we combine darkfield microscopy with high-speed imaging and advanced image post-processing techniques, enabling the acquisition of trajectories with spatial and temporal resolution in the order of nanometers and milliseconds, respectively. We apply a novel observable, termed Mean Back Relaxation (MBR) [Münker et al., Nature Materials, 2024], to these trajectories. The MBR quantifies non-equilibrium in confined systems and establishes a link between intracellular particle fluctuations and their effective energies.

In doing so, we aim to extend the principles of passive microrheology to non-equilibrium environments. The MBR derived from our trajectories breaks time-reversal symmetry and exhibits pronounced anisotropies, indicating not only heterogeneous cellular structures but also anisotropic activity.

BP 7.32 Mon 15:00 P5

Forces in oocyte deformation analyzed via shear flow deformability cytometry — •Merle Duchêne[1], Bart Vos[1], Jordan Dieter Groh[1], Pratima Sawant[2], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics, Georg August University Göttingen — [2]Institute for X-Ray Physics, Georg-August-Universität Göttingen

Oocytes form the origin of many developing organisms and display distinct mechanical responses compared to smaller somatic cells. Their nuclei are unusually deformable, mimicking whole-cell shape during external compression. Apart from chemical signaling, mechanosensing in the nucleus plays a central role in gene expression. However, the forces involved in oocyte deformation are not quantified and still poorly understood.

Here, we aim to employ microfluidic methods to investigate deformations of cells and nuclei in a well-controlled, high-throughput method via shear flow deformability cytometry, commonly referred to as real-time deformability cytometry (RT-DC). We modified this method for oocytes, by first generating a preliminary channel design using COMSOL simulations. To evaluate device performance after fabrication, polyacrylamide beads are studied and provide a reference for estimating oocyte behavior in the same geometry. Finally, oocyte deformation is recorded to obtain mechanical properties. This helps us to better understand forces involved oocyte development and migration on its journey from the ovaries to an embryo.

BP 7.33 Mon 15:00 P5

Linking Theory and Experiment: RBC Deformation in a Cross-Shaped Microfluidic Channel — •Clara Gremmelspacher[1], Stephan Gekle[1], and Manouk Abkarian[2] — [1]Universität Bayreuth — [2]Centre de Biologie Structurale, Montpellier

Red blood cells (RBCs) must deform significantly to pass through narrow capillaries, a process governed by membrane mechanics such as shear elasticity and membrane viscosity. We use a combined experimental and computational approach to study RBC stretching under extensional flow. The investigated setup consists of two opposing inflow channels and two perpendicular outflow channels arranged in a cross shaped geometry creating a stagnation point at the intersection. By comparing deformation patterns and timescales between microfluidic experiments and Bounday-Integral-Simulations, we extract key mechanical properties of the RBC membrane. This approach links theoretical descriptions to observed dynamics, providing insights into microcirculatory behavior.

BP 7.34 Mon 15:00 P5

Mechanistic Insights into PFAS Interactions with Biological Membranes — •Samuel Türken[1], Doreen Biedenweg[2], Janet Krüger[1], Stefanie Spiegler[2], Bob Fregin[2], Wibke Busch[1], and Oliver Otto[2] — [1]Helmholtz Centre for Environmental Research - UFZ, Leipzig, Germany — [2]Institute of Physics - University of Greifswald, Greifswald, Germany

Per- and polyfluoroalkyl substances (PFAS) are widely used, highly persistent organic chemicals that accumulate in humans and the environment. PFAS exposure is associated with a range of adverse health and environmental effects, yet their mechanisms of action in human cells remain poorly understood. Molecular simulation studies show that PFAS integrate into phospholipid membranes and alter membrane fluidity in a structure-dependent manner.

To investigate how PFAS influence whole-cell mechanics, we used real-time deformability cytometry (RT-DC), which provides single-cell, millisecond-scale measurements of deformation and cell elasticity, i.e., the Young's modulus. This approach captures the mechanical response of HL60 cells after 1 minute PFAS exposures, reducing the contribution of slower cellular adaptive processes. Complementing this, we quantified PFAS-induced changes in membrane order using a Laurdan-based assay. We found that PFAS exposure decreased cell deformability and increased cell stiffness, detectable even at environmentally relevant concentrations in a dose- and structure-dependent manner. Combined membrane-order and RT-DC results show that PFAS alter membrane physical state and thereby modulate whole-cell mechanics.

BP 7.35 Mon 15:00 P5

Bat thermomechanics of red and white blood cells as a blueprint for human hibernation — •Bob Fregin[1,2], Doreen Biedenweg[1], Gerald Kerth[3], and Oliver Otto[1,2] — [1]Institute of Physics, University of Greifswald, Greifswald, Germany — [2]German Center for Cardiovascular Research, Greifswald, Germany — [3]Applied Zoology and Nature Conservation, Zoological Institute and Museum, University of Greifswald, Greifswald, Germany

Hibernation lets mammals conserve energy by sharply slowing metabolism during cold or resource-poor periods. A key challenge is sustaining blood flow at low body temperatures ($\leq$ 10 °C). Here, the mechanical properties of red (RBCs) and white blood cells (WBCs) could play a crucial role, which we studied for the hibernating common noctule bat, the non-hibernating Egyptian fruit bat, and humans. Using dynamic real-time deformability cytometry, RBC and WBC elasticity and viscosity were measured at physiologically-relevant time scales (Milliseconds) and temperatures (37 °C, 23 °C, and 10 °C).

Our analysis revealed a temperature-driven increase in RBC elasticity and viscosity, which is mainly influenced by membrane properties and not the cytosol. This effect is significantly enhanced in bats. Finally, our data demonstrate that RBC membranes of both bat species display a transition to a viscous-like state at lower temperatures, which is not explained by seasonal variations of environmental factors but seems to originate from physical properties of the cell membrane. Our results suggest blood cell thermomechanics as a target for future research on human hibernation.

BP 7.36 Mon 15:00 P5

Enhancing optical parameters of platelets in real-time deformability cytometry — •Tristan Franke, Bob Fregin, Doreen Biedenweg, Lucia Wegbünder, and Oliver Otto — Institute of Physics, University of Greifswald, Greifswald, Germany

Real-time deformability cytometry (RT-DC) is a high-speed, label-free cytometric method for imaging and analyzing cell mechanical properties. Cells are flushed through a narrow microfluidic channel and deform by hydrodynamic stresses, while being illuminated by a stroboscopic high-power LED and imaged by a high-speed CMOS camera.

Using RT-DC allows for investigating platelet mechanics, which are key to blood coagulation and may help explain underlying causes of, e.g., coagulopathy and thrombosis. However, with a cell size of only a few micrometers, platelets appear to be difficult to analyze optically, resulting in low image quality, often characterized by motion blurring, low brightness, and a low level of morphological detail.

We investigated the interplay between various parameters, including LED exposure time (brightness), hydrodynamic flow rate, objective magnification, numerical aperture, and camera settings, to identify optimal imaging parameters. To further enhance image quality, we inserted a 2.18x intermediate lens in our inverted microscope setup to increase image magnification, previously not possible to achieve, while preserving the depth of focus. In combination with an extended exposure time of 9.3 μs, and a 2x digital gain our results demonstrate a balance between image brightness and motion blurring while achieving improved contrast and resolution in RT-DC.

BP 7.37 Mon 15:00 P5

Microparticle traction force microscopy for DNA microparticles based on experimental and computational advances — •Bastian K. Kraus[1,2], Simon Brauburger[1,2], Tobias Walther[3], Tobias Abele[3], Kerstin Göpfrich[3], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics (ITP), Heidelberg University — [2]BioQuant, Heidelberg University — [3]Center for Molecular Biology (ZMBH), Heidelberg University

Traction force microscopy quantifies cellular forces by inferring traction fields from the displacements of fiducial markers embedded in soft elastic substrates. Microparticle traction force microscopy extends this concept by employing elastic spherical microparticles as finite-sized force sensors. Traction fields can be recovered by two methods: the volume method, which tracks nanoparticles inside the microparticle, and the surface method, which only considers the deformed microparticle surface. Here, the two approaches are compared systematically, each as a pipeline combining image processing and elasticity theory. Moreover, they are both implemented in the same experimental system, using soft DNA microparticles with different fluorescent labels, which are held and deformed in micropatterned wells. We find that the two methods can lead to similar results, but have different advantages. While the volume method requires fewer assumptions in the elasticity

equations, the surface method is less sensitive to imaging artifacts.

BP 7.38 Mon 15:00 P5

A fast & quantitative method to study membrane elasticity of suspended cells — •Eric Sündermann, Bob Fregin, Doreen Biedenweg, Jan Wilder, Stefanie Spiegler, and Oliver Otto — Institute of Physics, University of Greifswald, Greifswald, Germany

Current research acknowledges the importance of bulk and membrane mechanics for understanding cell state and function under pathophysiological conditions. While microfluidic technologies allow for measuring bulk mechanical properties at rates exceeding 1,000 cells per second, traditional approaches for assessing membrane elasticity lack the throughput required to screen entire cell populations.
Here, we utilise membrane tension cytometry (MTC), a microfluidic method combining shear-induced deformation of cells with the capabilities of Flipper-TR, a fluorophore with fluorescence lifetime proportional to the cell membrane elasticity. We established a calibration procedure using thousands of osmotically stressed red blood cells, and confirmed a quantitative relation between surface area and membrane elasticity introduced earlier for different cell models. Next, we focused on HL60 cells, a myeloid precursor cell line. We disturbed cholesterol and filamentous actin, and demonstrated that MTC is sensitive to changes in lipid composition, while being insensitive to cytoskeletal alterations. Finally, we directly measured the mitochondrial membrane elasticity inside living cells using Mito Flipper-TR. Interestingly, mitochondria seem to respond to an external hydrodynamic stress by an increase in membrane elasticity, which might be relevant to understand fission and fusion processes from a mechanical perspective.

BP 7.39 Mon 15:00 P5

The nature of correlations in the fractional Kelvin-Voigt model — •Dorian Marx[1], Raffaele Mendozza[2], Till Moritz Münker[1], Peter Sollich[2], and Timo Betz[1] — [1]Third Institute of Physics - Biophysics, Georg-August-University Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [2]Institute for Theoretical Physics, Georg-August-University Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

The inside of cells is a complex, non-equilibrium system. We are interested in the mechanics of this intracellular space, which typically are phenomenologically well described by a complex double-power law (fractional Kelvin-Voigt model). There have been multiple studies on intra- and extracellular systems using different measurement methods that indicated a correlation in the model parameters. We present an analytical and numerical analysis of the complex double-power law model, uncovering the nature of such a correlation and its dependency on measured frequency range. This results in a tool to judge experimental findings and to discern significant, possibly meaningful correlations from those stemming from the nature of the model. As complex double-power law models (or a subclass of them) seem to continue being used in the study of intracellular mechanics, we expect this theoretical investigation to be relevant going forward.

BP 7.40 Mon 15:00 P5

The biophysical response of HL60 cells to a millisecond osmotic stress — •Lucia Wegbünder[1], Eric Sündermann[1], Lea Graichen[1], Doreen Biedenweg[1], Marta Urbanska[2], and Oliver Otto[1] — [1]Institute of Physics, University of Greifswald, Greifswald, Germany — [2]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, United Kingdom

Local differences in the concentration of osmolytes within the human body require cells to consistently regulate their water in- and efflux. While cells are known to change their volume and mechanical properties on the timescale of seconds to minutes, their millisecond response to an osmotic stress has been, so far, unexplored.

Here, we leverage real-time deformability cytometry to apply osmotic challenges to cells and measure their physical properties including size and elastic modulus 0.5 to 10 milliseconds after exposure. We focus on HL60 cells (a myeloid precursor cell line), which are flushed through a microfluidic channel and in which they are in contact with a sheath fluid of varying osmolality. Similar to longer timescale regimes, we observe swelling under hypoosmotic, and shrinkage under hyperosmotic conditions. Independent of stress direction there is a decrease in the Young's modulus of cells. This is in contrast with long timescale findings, where cells are consistently reported to increase their stiffness under hypertonicity. The ability of cells to physically respond to osmotic stress within milliseconds can be of physiological consequences in situations where cells are exposed to steep osmotic gradients, as is the case for immune cells migrating through changing environments.

BP 7.41 Mon 15:00 P5

Mechanical and Viscoelastic Characterisation of *Giardia duodenalis* Trophozoites Using SCFS and nDMA — •Johannes Mischo[1,2], Maike Derenek[1], Markus Bischoff[1], Karin Jacobs[2], Chistian Klotz[3], Anton Aebischer[3], and Philipp Jung[1] — [1]Institute of Medical Microbiology and Hygiene, Saarland University, Homburg, Germany — [2]Experimental Physics, Saarland University, Saarbrücken, Germany — [3]Department of Infectious Diseases, Unit 16, Robert Koch-Institute, Berlin, Germany

Giardia duodenalis trophozoites use a ligand-independent, mechanically dominated suction or clutching mechanism mediated by the ventral disc to resist intestinal shear [1]. Little is known about the mechanical and viscoelastic properties of the cell. We used single-cell force spectroscopy (SCFS) on individual trophozoites to record detachment force-distance profiles. These datasets provide mechanical information of whole-cell deformation during pull-off, including contributions from the cell body, ventral disc and ventrolateral flange. Complementarily, we measured cell-body elasticity by nano-dynamic mechanical analysis (nDMA). Ventral disc and flange are inaccessible to nDMA because stationary cells keep them in surface contact. We observed single-digit kPa storage and loss moduli with a negative correlation between stiffness and approach speed. Together, SCFS and nDMA provide complementary mechanical information and a framework for understanding how *Giardia* balances elasticity and structural rigidity during its adhesion cycle and survival in the small intestine.

[1] Gunaratnam et al. Nanoscale, 2024, 16 (14), 7145-7153.

BP 7.42 Mon 15:00 P5

Dynamics of confined immune cell migration — •Santiago Kuhl and Joachim Rädler — Ludwig-Maximilians-Universität, München, Germany

Immune cells must invade tissue to reach their targets, but the dynamics and mechanics of their invasiveness are not well understood at the single cell level. Photolithographically fabricated 3D hydrogel micro-structures provide a promising platform for probing cellular invasiveness. Here we use nonadhesive 3D dumbbell-microcavities to enforce repeated encounters between single cells and pores of varying dimensions, simulating migration in a dense extracellular matrix. This platform enables us to record trajectories of macrophages and dendritic cells and measure dwell times and transmigration probabilities as a function of confinement.

BP 7.43 Mon 15:00 P5

Structural changes of sarcomeres in iPSC-derived 3D engineered skeletal muscle after laser-induced injury — •Lisa-Marie Scharfenstein[1,2], Daniel Härtter[1], Mahboubeh Farajian[2], Mattias Luber[2], Timo Betz[2], Wolfram Zimmermann[1], and Arne Hofemeier[1] — [1]Department of Pharmacology and Toxicology, University Medical Center Göttingen, Göttingen, Germany — [2]Third Institute of Physics, University of Göttingen, Göttingen, Germany

Skeletal muscle injury models are employed to study mechanisms of muscle repair and regeneration. Commonly used muscle injury models such as cryo-injury, crush-injury and cardiotoxin-treatment do not allow for precisely localized muscle damage. Here, we introduce precise laser-based injury in human iPSC-derived 3D engineered skeletal muscle (ESM) tissue grown in a custom-made culture platform. Using high-resolution live microscopy and a sarcomere reporter model (ACTN2-Citrine), we monitor Z-band morphology on timescales of seconds to several days using the previously by our group introduced AI-based Sarcomere Analysis Multi-tool (SarcAsM). In doing so, we find an average sarcomere elongation of (0.45 +- 0.061) mum (mean +- sem) within 50 mum distance from the injury, that further decays exponentially from the location of injury towards the periphery, suggesting local impaired tensional homeostasis in myofibers surrounding the injury. Taken together, we report first data obtained in a novel human iPSC-based skeletal muscle injury model, which we intend to use for repair and regeneration inducing drugs.

BP 7.44 Mon 15:00 P5

What we learned from 6000 patient blood samples measured with deformability cytometry: age, biomarkers, and disease mechanotypes — •Markéta Kubánková[1,2], Lena Summa[1,2], Maximilian Schlögel[1,2], Martin Kräter[1,2], Manfred Rauh[3], Markus Metzler[3], and Jochen Guck[1,2] — [1]Max Planck Institute

for the Science of Light, Erlangen, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [3]Department of Pediatric and Adolescent Medicine,University Hospital Erlangen, Germany

Deformability cytometry is a label-free microfluidic imaging technique that quantifies mechanical and morphological properties of single cells at ~1000 cells/s directly from brightfield images. Here we analyse >6000 whole-blood measurements from a clinical cohort ranging from newborns to adults. We developed an automated analysis pipeline combining feature extraction with clustering and classification of the main blood cell populations, replacing manual gating. Using this framework, we established age-dependent baselines of size and deformation for the major cell classes. We correlated the features with routine biomarkers such as CRP, IL-6 and PCT. Specific mechanotypes, particularly of neutrophils and monocytes, showed associations with these markers and provided information beyond simple cell counts. We also quantified the impact of pre-analytical confounders, such as the time between blood draw and measurement. Finally, by stratifying samples according to clinical information, we identified disease-related patterns in cell mechanotypes, providing a biophysical basis for future diagnostic applications.

BP 7.45 Mon 15:00 P5

Investigating the role of the membrane-associated cytoskeleton in neuronal action potential propagation — •Julia Butzke[1] and Kristian Franze[1,2,3] — [1]Chair of Neuronal Mechanics, Medical Institute of Biophysics, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [3]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK

During maturation, neuronal axons develop submembraneous F-actin rings as a part of the membrane-associated periodic skeleton (MPS). The MPS has been shown to regulate axon diameter, provide mechanical support and contribute to axonal transport. However, the role of the MPS in successful action potential propagation in single axons is not yet fully understood. In this project, we investigate the impact of submembraneous F-actin rings on the mechanical aspects of action potentials. Using super-resolution microscopy, we study the effect of different F-actin-disrupting drugs on the presence and periodicity of F-actin rings in primary hippocampal mouse neurons. We then use atomic force microscopy to measure the mechanical waves that accompany action potentials in axons with different levels of F-actin ring periodicity. By analysing the possible correlation between F-actin ring periodicity and the propagation properties of the mechanical waves, we will contribute to a better understanding of the mechanical aspects of neuronal signal transmission.

BP 7.46 Mon 15:00 P5

Characterizing the Effective Membrane Tension Response to Substrate Stiffness Using AFM and Optical Tweezers — •Tina Borić[1,2], Maria Villamarin[1,2], Julia Butzke[1,2], Eva Kreysing[4], and Kristian Franze[1,2,3] — [1]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [2]Friedrich-Alexander-Universität, Erlangen-Nürnberg, Erlangen, Germany — [3]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK — [4]University of Warwick, Coventry, UK

Cellular membranes change their physical properties in response to mechanical stimuli, such as changes in tissue stiffness. Membrane tension transduces these mechanical signals into intracellular responses via mechanosensitive ion channels. However, how and if a change in tissue stiffness affects the surface mechanics of the cell, which in turn would contribute to the activation of mechanosensitive ion channels, is not yet known. To investigate the dependence of the effective membrane tension on substrate stiffness, we culture HEK293T cells and hippocampal neurons on custom made compliant substrates, and measure tether forces using optical tweezers and AFM. Furthermore, we use pharmacological treatments that primarily affect the actin cortex and membrane composition to characterize their contributions to the effective membrane tension. Ultimately, our aim is to understand how stiffness induced changes in membrane tension lead to the activation of the mechanosensitive ion channel Piezo1. Our work will contribute to the understanding of how mechanosensitive ion channels are gated, which may have important implications for drug design in the future.

BP 7.47 Mon 15:00 P5

Topologically invariant coordinates for dynamic epithelia undergoing morphogenesis — •Paweł Korzeb[1], Marko Popović[1,4], and Frank Jülicher[1,2,3] — [1]Max Planck Institute for Physics of Complex Systems, Dresden, Germany — [2]Center for Systems Biology, Dresden, Germany — [3]Cluster of Excellence Physics of life, Technische Universität Dresden, Dresden, Germany — [4]Rudjer Bošković Institute, Zagreb, Croatia

Epithelia are two-dimensional tissues, sheets of tightly connected cells that form many structures in organs. Such tissues acquire their shape and function through morphogenesis, a process that involves changes in both their geometry and cellular network topology. A key question in morphogenesis is to understand how cellular processes, such as cell division or T1 transitions, contribute to tissue morphology by changing its geometry and topology. For a curved epithelium, this problem can be formulated in a continuous covariant description on the tissue surface. In this work, we propose two sets of topologically invariant coordinates, describing cellular networks, obtained by embedding a graph representation of the network into $\mathbb{R}^2$ using only its connectivity, without the need to take into account the underlying tissue geometry. We construct these embeddings using the spectrum of the graph Laplacian and a spring-meshwork representation. Local changes of these topologically invariant coordinates allow us to identify the cellular processes occurring during tissue development. This formalism provides a framework to investigate the coupled evolution of epithelial geometry and topology.

BP 7.48 Mon 15:00 P5

BeadBuddy: Multiscale shape analysis of in-vivo stress sensors for force inference — •Alejandro Jurado Jiménez[1], Jonas Isensee[3], Arne Hofemeier[2], Lea Johanna Krüger[4], Raphael Wittkowski[5], Ramin Golestanian[3], Philip Bittihn[3], and Timo Betz[1] — [1]Third Institute of Physics-Biophysics, University of Göttingen — [2]Institute of Pharmacology and Toxicology, University Medical Center Göttingen — [3]Max-Planck-Institute for Dynamics and Self-Organization, Göttingen — [4]Institute of Theoretical Physics, University of Münster — [5]Department of Physics, RWTH Aachen University, DWI - Leibniz Institute for Interactive Materials

The measurement of stresses and forces at the tissue level has proven to be an indispensable tool for the understanding of complex biological phenomena such as cancer invasion, embryo development, or wound healing. One of the most versatile tools for force inference at the cell and tissue level are elastic force sensors, whose biocompatibility and tunable material properties make them suitable for many different experimental scenarios. The evaluation of those forces, however, is still a bottleneck due to the numerical methods seen in the literature until now, which are usually slow and render low experimental yield. Here, we present BeadBuddy, a ready-to-use platform for the evaluation of deformation and stresses from fluorescently labeled sensors within seconds. The strengths of BeadBuddy lie in the precomputed analytical solutions of the elastic problem, the abstraction of data into spherical harmonics, and a simple user interface that creates a smooth workflow for force inference.

BP 7.49 Mon 15:00 P5

Mechanics of reconstituted cardiac microtissues — •Polina Malova, Mattias Luber, Noemie Veyret, Anna Mukhina, Till Münker, and Timo Betz — Georg-August Universität Göttingen

Cardiovascular diseases remain the leading cause of mortality in Western countries [1]. Heart failure, which characterized by reduced cardiac output, myocardial thickening, and diminished contractile strength is among them and is highly prevalent. Human induced pluripotent stem cells (hiPSCs) are widely used for cardiac disease modelling and drug screening due to a preservation of patient-specific genetic backgrounds [2]. hiPSC-derived engineered human myocardium (EHM) microtissues provide an opportunity for *in vitro* research of the cardiac environment in a three-dimensional (3-D) system. Despite extensive characterization of the heart as a complex 3-D system, the mechanics of cellular interactions within the cardiac tissue still require detailed clarification. This work examines how cells within EHM microtissues mechanically interact with neighbouring cells and the extracellular environment to generate observed load curves. We compare contraction profiles of tissues composed of cardiomyocytes with cardiac fibroblasts to those containing cardiomyocytes with human foreskin fibroblasts. In addition, we investigate the contribution of extracellular matrix homeostatic tension to the mechanics of the 3-D system. These findings support the further development of 3-D tissue models for patient-specific drug screening.

[1] World Health Organization, 2022
[2] Takahashi K, Yamanaka S., 2006

BP 7.50 Mon 15:00 P5

Connecting tissue stiffness and glycosylation patterns in the developing brain — •Sarah Fritsche[1,2], Sebastián Vásquez-Sepúlveda[1,2], Leonhard Möckl[3,4], and Kristian Franze[1,2,5] — [1]Medical Institute of Biophysics, FAU Erlangen-Nuremberg, Germany — [2]MPZPM, Erlangen, Germany — [3]Department of Medicine 1/CITABLE, University Hospital Erlangen, FAU Erlangen-Nuremberg, Germany — [4]MPL, Erlangen, Germany — [5]Department of Physiology, Development and Neuroscience, University of Cambridge, United Kingdom

Mild malformation of cortical development with oligodendroglial hyperplasia and epilepsy (MOGHE) is a pathological entity leading to drug resistant epilepsy that is characterised by increased density of oligodendroglial cells, hypomyelination, and heterotopic neurons in the white matter. This malformation has been linked to mutations of the galactose transporter SLC35A2. At the same time, processes like brain folding involve motion and must therefore be driven by large scale forces. This is why, in order to comprehend this disease to a greater extent, we are investigating the connection between the physical properties of brain tissue and its glycosylation patterns to emulate brain malformations in the Xenopus laevis embryo. The physical properties are measured via atomic force microscopy and the glycosylation patterns via super-resolution microscopy of metabolically labelled galactose, as well as antibody- and lectin stainings. With this approach we aim to understand the relation between the mechanical properties of brain tissue and developmental pathologies.

BP 7.51 Mon 15:00 P5

Cellular shape anisotropy couples to morphogen transport to drive pattern formation — •Stefan Nienhaus[1] and Diana Khoromskaia[1,2] — [1]Institut für Theoretische Physik, Universität Münster, 48149 Münster, Germany — [2]Center for Soft Nanoscience, Universität Münster, 48149 Münster, Germany

To attain their intended structures, many tissues have been shown to rely on morphogens that induce concentration-dependent changes in cell fate and in cellular mechanical properties. These changes can alter the transport properties of the morphogen within the affected tissue. Hence, a feedback loop may arise in which tissue patterning influences morphogen distribution, which in turn influences tissue patterning (bioRxiv:658228). This concept also applies to tissues with nematic order, which has been shown to be crucial to certain morphogenetic processes that predominantly occur at topological defects.

In this work, we explore the complex couplings between morphogens and nematics and aim to investigate the role of topological defects in localising cellular signalling for morphogenesis. Previous work has shown that cellular shape anisotropy may lead to anisotropic diffusion (bioRxiv:683494). Here, through numerical simulations of a reaction-diffusion system coupled to a nematic order parameter, we study how locally anisotropic diffusion affects the observed patterns. Introducing a concentration-dependent nematic alignment as a next step, we will investigate mechanisms of self-organisation that arise from this inherent coupling of morphogens and nematic order in tissues.

BP 7.52 Mon 15:00 P5

Quantifying vascular morphology on a chip — •Leonie Karr — TUM, Munich, Germany

Our human vasculature is dynamic, growing and reorganising not only in development but also continuously adapting its morphology. Yet, what determines vessel formation and branching in healthy and disease states seems complex, given the multitude of contributing factors. Our focus lies in growing a human vasculature within the controlled environment of a chip, with the goal of quantifying the flow properties of self-organised in vitro networks. Employing image analysis techniques in conjunction with flow simulation methods, our objective is to accurately quantify how flow and related properties, such as shear stress and absorption determine network architecture. The results obtained from our analyses will significantly contribute to the development of next-generation therapeutics aimed at targeting vessel development.

BP 7.53 Mon 15:00 P5

Mechanics of spinal cord regeneration in Xenopus laevis — •Maria Tarczewska[1,2] and Kristian Franze[1,2,3] — [1]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [2]Medical Institute of Biophysics, Friedrich-Alexander- Universität Erlangen-Nürnberg, Erlangen, Germany. — [3]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK

In mammals, spinal cord injury (SCI) often leads to paralysis due to the limited regeneration of damaged neurons in the central nervous system (CNS). The African clawed frog (Xenopus laevis) can regenerate CNS neurons during its early life stages - pre-metamorphosis. However, this ability is lost post-metamorphosis, in frogs adult form. Biochemical differences between pre- and post-metamorphosis frog spinal cord tissue identified so far cannot fully explain the differences in their regenerative capacity, suggesting that other signals may contribute to the regeneration. Following SCI, the composition of the extracellular matrix changes, and scar tissue forms. In mammals, this scar tissue, which is softer than healthy tissue, inhibits axon regeneration. In zebrafish, whose CNS neurons regenerate after SCI, tissue stiffens after injury. Mechanical properties of frog spinal cord tissue have not been measured yet. Because mechanosensing of tissue stiffness is critical for axon growth, we test the hypothesis that tissue stiffness is a critical factor in axon regeneration after SCI. We investigate the mechanical differences in the SCI lesion environment in Xenopus. By examining both tissue stiffness and molecular changes, we will illuminate the relationship between these factors and the regenerative capabilities.

BP 7.54 Mon 15:00 P5

Dimensionality and confinement reshape competition in cellular renewing active matter — •Patrick Zimmer[1,2], Philip Bittihn[1,2], and Yoav G. Pollack[1,2] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, Göttingen University, Germany

Cellular renewing active matter—assemblies of proliferating and apoptotic cells—underlies tissue homeostasis, morphogenesis, and clonal competition. Previous work in one-dimensional periodic systems identified a fitness advantage associated with rapid dead-cell clearance, an "opportunistic" competition mechanism. Extending this framework, we study two-dimensional cellular aggregates and show that dimensionality modifies the interplay between competition mechanisms for clones with different clearance rates: in 2D, opportunistic and homeostatic-pressure-based competition jointly shape clonal selection. We introduce an explicit circular confinement to probe how boundaries modulate this interplay. While opportunistic competition persists, distinct timescale-dependent behaviors emerge through weakened homeostatic-pressure-based competition near boundaries. Structural analysis reveals that confinement promotes tangential alignment and spatially heterogeneous homeostatic pressure, thereby reshaping competitive outcomes at tissue edges. Our study connects newly discovered competition mechanisms with more realistic biological contexts, highlighting how dimensionality and spatial constraints influence tissue structures and modulate competition in heterogeneous cell populations, with implications for tumor growth dynamics and tissue development.

BP 7.55 Mon 15:00 P5

Remotely Actuated Elastic Meta-Lattices using Bjerknes Forces — •Laurin Sartori[1], Peer Fischer[1,2], and Athanasios G. Athanassiadis[1,2] — [1]Heidelberg University, Heidelberg, Germany — [2]Max-Planck Institute for Medical Research, Heidelberg, Germany

Acoustically-responsive elastic structures have recently gained interest as tools for gentle, wireless manipulation of biological materials. By combining acoustic effects with elastic structures, they can be actuated dynamically to even manipulate single cells in fluidic chambers. However, there is currently a large gap between existing manipulators designed for single cells and larger-scale acoustically-actuatable materials that could be integrated with larger biological tissues or organoids.

Here, we introduce a dynamic acoustic metamaterial that can be change both its geometric configuration and elastic properties in response to sound. The metamaterial consists of an elastic lattice with embedded gas bubbles, and is actuated leveraging the secondary radiation forces between embedded bubbles. By tuning the driving or the microscopic structures the specific response of the material can be tailored. We introduce a numerical model to predict the response of arbitrary lattices, and validate the model experimentally using carefully designed structures that achieve the desired motion.

The engineered lattices shown in this work can be used as building blocks for metamaterials with a remotely tunable stiffness, auxetic properties and memory behavior, providing new interaction paradigms for applications in bio-interfaced soft robotics.

BP 7.56 Mon 15:00 P5

Direct Measurement and Enhancement of Piezoelectric Fields around Microparticles in an Ultrasound Field — •Mareike Stoll[1,2], Honorata Kazimierczak[1,2], Peer

Fischer[1,2], and Athanasios Athanassiadis[1,2] — [1]Institute for Molecular Systems Engineering and Advanced Materials, Heidelberg University, Heidelberg, Germany — [2]Max Planck Institute for Medical Research, Heidelberg, Germany

There is growing interest in designing ultrasound-responsive materials that broaden the possibilities for non-invasive, remotely controlled therapies. In this context, piezoelectric micro- and nanoparticles are emerging as promising mediators, generating electric fields and reactive chemical species that can interact with biological tissues. Despite growing evidence suggesting macroscopic effects, a direct measurement of the piezoelectric response of individual particles under an applied ultrasound field has not yet been demonstrated. This knowledge gap presents a hurdle to further design and targeting of piezoelectric particle-mediated therapies. In this work, we introduce a new methodology and provide the first direct measurements of electric potential generated by piezoelectric microparticles during ultrasonication. By mapping the time-varying potential around microparticles we are able to quantify the ultrasound-induced fields and identify enhancement strategies. These results provide a first step to disentangling the contributions of different physical processes involved in sonopiezoelectric therapies, and provide insights into the feasibility and design strategies for therapies based on ultrasound-activated piezoelectric materials.

BP 8: Systems and Networks Biophysics

Time: Monday 16:45–18:30 Location: BAR/0106

BP 8.1 Mon 16:45 BAR/0106

Origins of the Fittest: Clonal interference in the World Aviation Network — •Adrian Zachariae, Pascal Klamser, and Dirk Brockmann — Technische Universität Dresden, Dresden, Deutschland

Clonal interference, the competition between strains carrying different beneficial mutations, plays a crucial role in shaping evolutionary outcomes in asexual populations. Since the spread of new mutations is critical for CI, it is strongly influenced by the structure of the population. For example, long-range connections can rapidly distribute new mutations, reducing CI. We investigate how this phenomenon unfolds in the the World Aviation Network, which shapes the population structure of microorganisms that use humans as hosts, including pathogens. We developed a novel analytical framework that models the succession of adaptive mutations as a Markov Renewal Process. The process is built by leveraging epidemic modeling methods to model mutation spread in the network. Or approach reveals how the interplay between mutation rate and network topology gives rise to distinct evolutionary regimes: At low mutation rates, strains originating from globally central nodes have higher fixation probabilities, while at higher mutation rates, meso-scale and local properties become more important. Applied to the WAN, affluent, western regions are most likely origins of high-fitness lineages in the low-rate regime, shifting to more populous nations in Asia at high rates. The framework provides valuable insights how spatial structure shapes evolutionary outcome, with particular relevance for pandemic preparedness.

BP 8.2 Mon 17:00 BAR/0106

Polymerization of prebiotic building blocks in a wet-dry cycling system — •Almuth Schmid — LMU, Geschwister-Scholl-Platz 1, München

When it comes to the question on how life could have emerged on an early Earth, not only the setting plays an important role but also the chemistry that helped forming the first building blocks of life. Prebiotic chemistry is limited in multiple ways since many of the common catalysts life uses nowadays are too complex to have been present in such an early stage. In addition, the existing compounds were diluted and only available in low concentration. To overcome these problems, systems like wet-dry cycles can help accumulating molecules while at the same time lowering the reaction activation barrier.[1] In addition, amino acids promote RNA copolymerization more than 100-fold via acid-base catalysis, starting from prebiotically plausible ribonucleoside-2',3'-cyclic phosphates.[2] MD simulations and X-ray crystallography confirmed that water is still present in the dry state, limiting the condensation reaction and hydrolyzing the material. Preliminary experiments showed that by using ammonium salts instead of sodium salts, including nucleotides and hydroxide to adjust the pH, overall longer polymers and yields 5-fold higher than before were obtained. Expanding this adapted wet/dry cycling system with an NH3/CO2 enriched atmosphere [3] would re-create a day and night rhythm on the early Earth, providing a prebiotic way to synthesize RNA.

Invited Talk BP 8.3 Mon 17:15 BAR/0106

Constructing synthetic life-like vesicle systems by integration of artificial metabolic reaction networks — •Laura Heinen — DWI - Leibniz Institut für interaktive Materialien, Aachen, Germany

Life emerges as a systemic property of the interplay of complex chemical reaction networks out of equilibrium. Living cells, for example, need energy to grow, divide, process information and synthesize their own constituent building blocks. In my group we develop minimal metabolic reaction networks to fuel out of equilibrium behavior in synthetic lipid vesicles, to finally, build active cell-like compartments bottom-up, called synthetic cells. In my talk I will demonstrate the construction of autonomous, active behavior in vesicles by the example of cross-feeding in between synthetic vesicles. Key to such sustained out-of-equilibrium behavior is the selective transport of energy molecules across the lipid membrane. One population of vesicles produces and exports adenosine triphosphate (ATP) while a second population of vesicles takes up the ATP and uses this chemical energy to fuel ATP-consuming reactions. The hydrolyzed ATP feeds back into the first vesicle population where it will be recycled, and the interdependent metabolic cycle can be sustained. The vesicles are a platform to enable active behavior in synthetic systems in a continuous, autonomous and adaptive fashion. Fundamentally, they allow us to study non-equilibrium processes in an energy-controlled environment and will promote our understanding of constructing life-like materials and systems.

BP 8.4 Mon 17:45 BAR/0106

Living Network Dynamics: From pH-Stimulated Growth to Resistance Optimization — •Mathieu Le Verge-Serandour, Alexandra Bienau, Karen Alim, and Friedrich Simmel — School of Natural Sciences, Technical University of Munich

In this work, we explore how vascular-like functionality can be integrated into bioelectronic interfaces using the unicellular slime mold Physarum polycephalum. This organism forms a dynamic, self-organized tubular network that exhibits emergent behaviors such as optimization, adaptation, and self-healing, making it an ideal model for studying decentralized, stimulus-responsive growth. By leveraging electrochemically induced pH gradients, we experimentally translate designed network layouts into biological structures and characterize the key dynamics underlying their responses to pH stimuli.

We further analyze Physarum morphological evolution, where the network reorganizes over several hours to evacuate a defined area by sequentially pruning competing parallel veins, ultimately forming a tree-like architecture. Drawing an analogy with power-grid networks, we investigate how sequential pruning depends on the ratio of tube to network resistance. Analytical and numerical results show that regular graphs undergo pruning until the average node degree falls below four, a finding that remains robust in simulations of random networks. Incorporating mass redistribution into this process leads to resistance homogenization, revealing fundamental physical constraints that shape adaptive transport networks.

BP 8.5 Mon 18:00 BAR/0106

Simulation of autoimmune and autoinflammatory diseases: the novel mechanism of psoriasis progression. — •Nadezhda Esenkova[1,2], Lukas Pöschl[1,2], Gerard C. L. Wong[3], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Germany — [3]University of California, Los Angeles, USA

Autoimmune and autoinflammatory diseases (AIIDs) still remain an unsolved problem. One of the most studied diseases which carries features of both types is psoriasis. In this study, we are focusing on the novel mechanism of disease enhancement, driven by antimicrobial

peptides (AMPs) and AMP-like fragments organizing innate immune ligands for enhanced binding to Toll-Like Receptors in immune cells. These fragments have a diverse origin: there is strong recent evidence that serine proteases can digest viral and host proteins into AMP-like fragments. In order to explore the effect of this emerging pathway, we developed a new unified interaction network model for psoriasis, based on the current extant measurements. The model was reduced to a system of nonlinear differential equations, which were studied by using dynamical system theory and numerical methods. Importantly, we find that the proposed model can reproduce the full spectrum of disease progression from healthy response to uncontrolled inflammation and allows comparison of different therapeutic interventions. Finally, by expanding the model to include diffusion, we can successfully predict the geometry of psoriatic plaques, the precise measurements of which may inform modulation of treatment.

BP 8.6 Mon 18:15 BAR/0106

Network-induced control of sustained oscillations in SIRS epidemics — •Samuel Ropert[1,2], Tomas Perez-Acle[2], and Dirk Brockmann[1] — [1]Technische Universität Dresden, Dresden, Germany — [2]Universidad San Sebastián, Santiago, Chile

Sustained oscillations in SIRS epidemic models are well understood in well-mixed populations when infectious and immune periods deviate from exponential waiting times. In contrast, the role of contact network structure in generating or suppressing such oscillations has received little attention. Existing work on small-world networks reports oscillations but does not relate them to effective transition-time distributions. This work investigates how network topology shapes oscillatory SIRS dynamics by simulating a stochastic SIRS process on self-similar modular hierarchical (SSMH) networks. These networks interpolate between random-like graphs and strongly modular, hierarchical structures while preserving system size and mean degree. A single structural parameter controls edge placement across hierarchical levels, reshaping effective distances between communities. Preliminary results show that random-like networks support robust, coherent oscillations in global prevalence, whereas increasing hierarchical modularity desynchronizes outbreaks across communities and gradually destroys the global limit cycle, leading to damped or irregular fluctuations. These findings support an interpretation of epidemic oscillations as a synchronization phenomenon of individual SIRS cycles, where network topology promotes or inhibits global coherence by reshaping the time-to-infection distribution through changes in effective distances.

BP 9: Single Molecule Biophysics

Time: Monday 16:45–18:30 Location: BAR/0205

Invited Talk BP 9.1 Mon 16:45 BAR/0205

Breaking the photobleaching limit in single-molecule FRET with nanophotonic DyeCycling. — Benjamin Vermeer[1], Dong Hoon Shin[2,3], Alexander Vogel[4], Fabian Zundel[1], Sabina Caneva[2], and •Sonja Schmid[1,4] — [1]University of Basel, Basel, Switzerland — [2]Delft University of Technology, Delft, The Netherlands. — [3]Korea University, Sejong, Republic of Korea — [4]Swiss Nanoscience Institute, Basel, Switzerland

Paradoxically, single-molecule FRET studies rely on ensemble averaging during data analysis, because early photo-bleaching prohibits sufficient sampling of single molecules. As a result, the FRET-based study of inter- and intra-molecular heterogeneity in biomolecular function - a specific hallmark of single-molecule techniques - is hardly possible, preventing insights into dynamic disorder, the effects of post-translational and other modifications, of rare but decisive states, etc. Here, we demonstrate hour-long single-molecule FRET observations using DyeCycling in zero-mode waveguides, which circumvents photobleaching through reversible fluorophore binding. We detect the conformational dynamics of single molecules over four orders of magnitude in time (milliseconds-hour), enabling us to directly observe slow kinetic regime changes within individual molecules that were intractable previously. Moreover, we demonstrate the versatility of DyeCycling with DNA and protein molecules. Together, these advances establish DyeCycling/FRET as a powerful new approach that vastly expands the information gain of single-molecule FRET, enabling the study of important biological questions that were previously inaccessible.

BP 9.2 Mon 17:15 BAR/0205

Monitoring the ribosome dynamics at the single molecule level — •Baptiste Bouhet[1], Sandra Blanchet[2], Charles Truong[3], Olivier Namy[2], and Karen Perronet[1] — [1]Light, Matter and Interactions lab, Gif/Yvette, France — [2]Institute for Integrative Biology of the Cell, Gif/Yvette, France — [3]Centre Borelli, Gif/Yvette, France

Protein synthesis is a complex multi-step process involving factors that need to interact in a coordinated manner to properly translate mRNA. As translating ribosomes cannot be synchronized over many elongation cycles, single molecule studies, mainly using total-internal-reflexion fluorescence microscopy, have been introduced to better understand translation dynamics. We decided to monitor the passage of individual, unmodified eukaryotic ribosomes from wheat germ extracts at specific fluorescent primers hybridized along mRNA. Because of the ribosome helicase activity, the double strand formed by the oligonucleotide and the mRNA is opened while the ribosome translates this region of the mRNA. Thus, the consecutive loss of fluorescence signal of two oligonucleotides allows us to measure the translation speed distribution of single ribosomes. We use this system to measure simultaneously the initiation and the elongation kinetics for linear mRNA and during -1 frameshifting, which is induced by a secondary structure on mRNA. We are also currently developing a magnetic tweezers assay to get complementary information on the opening dynamics of these structures. Thanks to its versatility, this method is a valuable tool to investigate translation machinery modifications in human diseases.

BP 9.3 Mon 17:30 BAR/0205

Single-molecule force and torque spectroscopy reveals conformational transitions in DNA and proteins — •Jan Lipfert — Universität Augsburg

Magnetic tweezers are a powerful tool to probe single molecules under precisely controlled forces, down to well below 1 pN, and, in addition can control twist and torque. Here, I highlight recent developments and applications of magnetic tweezers. In particular, I will present how we use magnetic tweezers to probe regulatory conformational changes in protein complexes, including pathogen-cell adhesion and the initiation of primary hemostasis by von Willebrand factor. In addition, I will show how we use the capabilities of magnetic tweezers to precisely measure DNA helicity under changes in environmental conditions and upon small-molecule binding.

BP 9.4 Mon 17:45 BAR/0205

Direct measurement of ultra-weak plant kinesin steps using silicon nanospheres as optical tweezers probes — •Aleksandr Kostarev[1], Shu Yao Leong[1], Anita Jannasch[1], Minoru Fujii[2], Hiroshi Sugimoto[2], and Erik Schäffer[1] — [1]Eberhard Karls Universität Tübingen, Tübingen, Germany — [2]Kobe University, Kobe, Japan

Kinesin motor proteins are essential for transport along cytoskeletal microtubules and cell division. In plants, cytokinesis relies on phragmoplast orienting kinesins (POKs). The kinesin-12 paralog POK2 can generate only about 300 fN of force. This low force is consistent with the idea that POK2 does not transport cargo, similar to weak kinesin-8 motors, the function of which is unknown in plants. To understand the function and mechanochemistry of these ultra-weak motors, it is necessary to detect their individual steps during ATP hydrolysis. However, the spatiotemporal resolution achieved with conventional probes in optical tweezers is insufficient for detecting fast steps at such low forces. To overcome this limitation, we used high refractive-index silicon nanospheres for optical trapping. With these nanospheres, we achieved an unprecedented force resolution of 60 aN at room temperature in liquids with a force sensitivity of 2.7 fN Hz^(-1/2). We bound single POK2 or plant kinesin-8 motors to the nanospheres and were able to detect individual 8-nm steps with 4-nm substeps within a force range of 100-400 fN. These in vitro measurements establish a path toward identifying plant kinesin function and demonstrate the potential of silicon nanospheres for studying ultra-weak molecular machines.

BP 9.5 Mon 18:00 BAR/0205

Ultrafast sensing of single nanoparticles with an optoflu-

idic microcavity — •Shalom Palkhivala[1], Larissa Kohler[1], Christian Ritschel[1], Christoph Pauer[2], Tim Liedl[2], Claus Feldmann[1], and David Hunger[1] — [1]Karlsruhe Institute of Technology, Karlsruhe — [2]Ludwig Maximilian University, Munich

The characterisation of single, unlabelled particles in water is of much interest in biophysics and chemistry, where most processes occur in an aqueous environment. We report measurements of single nanoparticles in aqueous suspension using a fibre-based Fabry-Perot microcavity. For quantitative analysis of the nanoparticles' diffusion dynamics, we developed an analytical autocorrelation function to model diffusion in a standing wave field. This enabled the accurate sizing of nanoparticles having diameters down to 3 nm. [1]

Additionally, the rotational dynamics of anisotropic particles were investigated. Via the polarization modes of the cavity, the orientation of a nanorod was tracked with high temporal resolution ($\sim$ 20 ns), orders of magnitude faster than most other current techniques. As an application of our sensor to biosensing, we demonstrate measurements of individual DNA "origami" structures and of few protein molecules, which already enabled their hydrodynamic sizes to be determined.

We further expect our nanosensor to give an insight into the structural properties and conformation of single bioparticles, and to become a powerful tool for diagnosis in biomedicine and for biochemical and environmental assays.

[1] Palkhivala *et al.* (2025), *ACS Nano*, 19, 45, 39320-39326

BP 9.6 Mon 18:15 BAR/0205

Indications for Ultrafast Energy Transfer and Subsequent Disulfide Bond Cleavage in Lysozyme upon Ultrafast Excitation of Aromatic Residues — •Philip Wehling[1], Jessica Harich[1], Antonia Freibert[1], Ru-Pan Wang[2], Tae Gyun Woo[3], Junho Lee[3], Seonghyeon Jeong[3], Sungin Yu[3], Haneol Oh[3], Migel Ochmann[1], Victoria Kabanova[4], Emma Beale[4], Philip Johnson[4], Claudio Cirelli[4], Camila Bacellar[4], Briony Yorke[5], Tae Kyu Kim[3], and Nils Huse[1] — [1]University of Hamburg, Hamburg, Germany — [2]DESY, Hamburg, Germany — [3]KAIST, Daejeon, Republik of Korea — [4]Paul Scherrer Institute, Villigen, Switzerland — [5]University of Leeds, Leeds, U.K.

Disulfide bonds play a crucial role in stabilizing the tertiary structure of proteins. Ultraviolet (UV) radiation leads to S-S bond cleavage, possibly compromising the functionality of proteins. Femtosecond X-ray absorption spectroscopy at the sulfur K-edge revealed ultrafast geminate disulfide bond reformation in aliphatic disulfides [1]. These findings raise the question how disulfide bridges behave in proteins upon UV irradiation. Disulfide photochemsitry in Lysozyme by UV excitation across the dominant absorption of the aromatic residues leads to efficient sulfur radical formation which must stem from energy transfer. We discuss yields and possible mechanisms of energy transfer in competition with direct photocleavage of disulfide bridges, and implications for energy dissipation and structural integrity of proteins.

[1] M. Ochmann et al, Nat. Commun. 15, 8838 (2024).

BP 10: Active Matter III (joint session BP/CPP/DY)

Time: Tuesday 9:30–12:45 Location: BAR/SCHÖ

BP 10.1 Tue 9:30 BAR/SCHÖ

inertia-driven re-entrant coil-Globule transition of active ring polymers — •Sunil P Singh[1], Roland G Winkler[2], Rakesh Palariya[1], and Arindam Panda[1] — [1]Indian Institute of Science Education and Research Bhopal, India — [2]Theoretical Physics of Living Matter, Institute for Advanced Simulation, Forschungszentrum Jülich, 52425 Germany

The role of inertia in the collective dynamics of active systems has been a subject of increasing interest in recent studies. The present study investigates the inertial effects on active agents. We present the conformational and dynamical characteristics of an active Brownian ring polymer using Langevin dynamics simulations. We show that a long active ring polymer shrinks into globular-like structures even in the absence of attractive interactions. This transition becomes sharper and the structures more compressed as the reduced moment of inertia of the monomers increases, particularly in the intermediate range of activity. We demonstrate that the ring polymer undergoes a coil-globule-coil transition, which is modulated by both activity and rotational inertia. The coil-to-globule transition is mapped in the inertial parameter space (J-M) using the radius of gyration. Additional physical quantities, including bond-bond correlations, scaling behavior in the compressed state, monomer contact probability, geometric distances, coordination number, and effective temperature, further elucidate the physical mechanism driving the collapse. Finally, we show that the effective diffusivity of the ring polymer increases with the reduced moment of inertia as $D_p \sim \sqrt{J}$.

BP 10.2 Tue 9:45 BAR/SCHÖ

Shape selectivity by complex buckling dynamics in poroelastic active gels — •Kinjal Dasbiswas[1], Subhaya Bose[1], Arnab Roy[1], Michael Vennettilli[1], and Anne Bernheim[2] — [1]University of California, Merced, USA — [2]Ben Gurion University, Israel

Shape change in animal cells is prototypically driven by active forces, generated by myosin molecular motors bound to the actin cytoskeleton. Inspired by experiments on disc-shaped extracts of crosslinked actomyosin gels, we aim to show how a family of 3D shapes can arise from buckling caused by non-uniform active stresses. Although synthesized with identical composition of actin, myosin and the crossliker fascin, these gels contract and buckle into different shapes depending on the initial aspect ratio of the disc: thinner gels tend to wrinkle, while thicker gels tend to form domes. By incorporating active stresses, actin alignment, and stress-dependent myosin binding kinetics into a 2D poroelastic gel model, we qualitatively capture trends in gel contraction dynamics observed from quantitative particle image velocimetry (PIV). Next, we carry out numeric simulations of a geometric elastic model for thin sheets to obtain 3D buckled shapes from the strain rates predicted by the poroelastic model. Our results show that the coupling of elasticity to solvent flow, motor binding and fiber alignment play an important role in shape changes in living matter. Our studies have implications for shape changes during tissue morphogenesis and cell migration.

BP 10.3 Tue 10:00 BAR/SCHÖ

The energy cost to build a spindle — •Dongliang Zhang[1], Xingbo Yang[4], Jan Brugués[2,1,3,4], and Frank Jülicher[1,3,4] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]Center for Systems Biology Dresden, Dresden, Germany — [4]Physics of Life, Cluster of Excellence, TU Dresden, Dresden, Germany

Spindle is a structure actively build from microtubules (MTs), and plays an important role for chromosome segregation during cell cycle. It's observed in experiments that the spindle size and shape depends on the cell level metabolic rate. In this work, we developed a minimal model that captures the active, energy-consuming processes such as MT turnover and active stress generation, which shows the energy cost for spindle mass maintenance and spindle-shape formation. We show that a spindle can be self-organized through these active processes. We aim to predict how the size and shape of the spindle depends on the energy input, and explain relative experimental phenomena, e.g. spindle shrinkage when the metabolism level is reduced.

BP 10.4 Tue 10:15 BAR/SCHÖ

Cytoskeletal oscillations drive large-scale flows and nuclear organization in early embryonic systems. — •Lara Koehler, Elissavet Sandaltzopoulou, and Jan Brugués — Physics Of Life, TU Dresden

Synchronization drives early embryonic development, enabling simultaneous cell divisions and the spatial organization of nuclei within the embryo. In organisms such as Xenopus, Drosophila, and zebrafish, mitotic waves coordinate cell cycles across distances that exceed diffusion limits, guided by a chemical oscillator. At the same time, global cytoplasmic flows in these syncytial tissues contribute to the large-scale self-organization of nuclei, yet the coupling between biochemical signaling and cytoskeletal mechanics that underlies these directed flows remains poorly understood. Here, we relax the geometric constraints

of the embryo and investigate nuclear dynamics in Xenopus egg extracts and complementary simulations. We show that the periodic polymerization and depolymerization of microtubule asters are sufficient to generate robust large-scale directed flows, even though the asters are intrinsically isotropic. Furthermore, we demonstrate that cell division stabilizes short-range order in a global synchronized system. Together, these findings reveal a minimal physical mechanism by which cytoskeletal dynamics and biochemical oscillations jointly organize flows and patterns, with implications for understanding the emergent principles that shape early development across species.

BP 10.5 Tue 10:30 BAR/SCHÖ

Geometric control of cell migration in disordered porous media — •Laeschkir Würthner[1] and Frederik Graw[2] — [1]European Molecular Biology Laboratory, Heidelberg, Germany — [2]Friedrich-Alexander-Universität Erlangen-Nürnberg and Universitätsklinikum Erlangen, Erlangen, Germany

Cell migration is a dynamic process that plays a central role in development, wound healing, and immune responses. Active cell movement is controlled by several biochemical and mechanical cues, including chemokine gradients and the mechanical properties of the extracellular matrix (ECM). Although the biochemical pathways underlying directed cell motion are increasingly well understood, the influence of the porous structure of the ECM on active cell motion remains largely unexplored. Using a combination of computational modeling and theory, we investigate how active cells move through 3D disordered porous environments. We show that cell migration in disordered porous media can be understood as a generalized random walk among "traps", with the effective diffusivity determined by the geometry of the microenvironment. A key implication of our work is that spatial heterogeneities in porosity effectively direct cell motion, revealing a guidance mechanism that we refer to as porotaxis. Overall, our work connects geometry with cell motility and underscores the microenvironment as a key regulator of cell migration.

BP 10.6 Tue 10:45 BAR/SCHÖ

Motility-induced mixing transition in exponentially growing multicellular spheroids — •Torben Sunkel[1,2], Lukas Hupe[1,2], and Philip Bittihn[1,2] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Germany

Growth drives cellular dynamics in various dense aggregates, but its effects on other relevant activities have only received limited attention. Here, we investigate the interplay of unconstrained growth, steric repulsion and motility in a minimal agent-based model of exponentially growing, three-dimensional spheroids. Our results reveal a diverging mixing time scale at a critical motility threshold, below which mixing of cells is completely suppressed. Above the threshold, large-scale mixing is enabled. Using an effective phenomenological model parameterized from full simulations, we identify two fundamental mechanisms governing this transition: On the cell scale, weak motility-induced active motion is locally suppressed by growth-induced steric repulsion, consistent with an Active Brownian Particle type description of single-cell dynamics. Beyond this, the expanding nature of the system inhibits global mixing purely geometrically by limiting the exploration range of diffusive cell motion. Both mechanisms naturally scale with the growth rate, highlighting the nature of the transition as an interplay between proliferation and motility. The results provide a baseline for identifying additional biological mechanisms in experiments and could be relevant for competition, heterogeneous tumor evolution and other manifestations of motile proliferating active matter.

15 min. break

BP 10.7 Tue 11:15 BAR/SCHÖ

Fluctuation-Response Theory of Non-Equilibrium Complex Fluids — •Ryota Takaki[1] and Frank Jülicher[1,2,3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Center for Systems Biology Dresden, Dresden, Germany — [3]Cluster of Excellence Physics of Life, TU Dresden, Dresden, Germany

Active soft materials such as cytoplasm and tissues are constantly driven by chemical reactions and often retain long-lived mechanical memory. In this work, we develop a generalized hydrodynamic framework applicable to non-equilibrium fluids with memory at finite wavevectors and frequencies. Our approach is based on exact correlation-function identities, leading to a fluctuation-response relation for steady states, including non-equilibrium. Applying the theory to chemically driven active fluids, we uncover Active Viscoelastic Memory, in which reaction cycles dynamically renormalize the viscous response and can generate negative storage moduli at finite frequency, absent in conventional viscoelastic materials. Our results provide a first-principles basis for modeling memory-dependent dynamics in a broad class of biological and synthetic active systems, and suggest concrete rheological signatures of chemical driving that can be tested experimentally.

BP 10.8 Tue 11:30 BAR/SCHÖ

Chemically Active Liquid Bridges Generate Repulsive Forces — •Noah Ziethen — DAMTP, University of Cambridge, UK

Intracellular droplets help organize cells by compartmentalizing biomolecules and mediating mechanical interactions. When such droplets bridge two structures, they generate capillary forces that depend on the surface properties and the separation between the structures. While the forces exerted by passive liquid bridges are well understood, the impact of active chemical reactions, ubiquitous in biological condensates, remains unclear.

Here, we investigate a single liquid bridge with continuous chemical turnover, in which the production and degradation of droplet material maintain a non-equilibrium steady state. In this active bridge, the reactions dynamically set the bridge radius, thereby controlling the force-distance relation. In striking contrast to passive systems, we find that activity can generate purely repulsive forces over a broad range of separations. These results show that chemical activity can qualitatively alter capillary forces generated by liquid bridges, suggesting a potential route for cells to actively regulate mechanical coupling via droplets.

BP 10.9 Tue 11:45 BAR/SCHÖ

Shared Laws of Pattern Formation in Reaction-Diffusion and Phase Separation — •Daniel Zhou[1] and Erwin Frey[1,2] — [1]Arnold Sommerfeld Center for Theoretical Physics — [2]Max Planck School Matter to Life

Many nonlinear field theories generate a strikingly similar repertoire of patterns: arrested coarsening, traveling waves, and spatiotemporal chaos appear both in phase-separating systems and in classical reaction-diffusion models. These descriptions have different physical origins, yet recent studies on Turing mixtures and foams in protein systems [1] and on chemotaxis-driven phase separation in cell populations [2] have already highlighted unexpected connections between these ostensibly different mechanisms, linking foam-like, phase-separating, and reaction-diffusion-type patterns. The present work revisits the relation between kinetic and phase-separating descriptions from a more general viewpoint. A unifying perspective is developed that places different modeling frameworks on comparable footing, identifies the conditions under which they yield effectively equivalent patterns, and suggests how stability criteria and design principles can be translated between them. This points toward a more systematic classification of pattern-forming dynamics that cuts across traditional divides between reaction-diffusion, chemotactic, and phase-separating systems.

[1] H. Weyer et. al, Deciphering the Interface Laws of Turing Mixtures and Foams, arXiv:2409.20070 (2024).

[2] H. Weyer et. al, Chemotaxis-Induced Phase Separation, Physical Review Letters 135, 208402 (2025).

BP 10.10 Tue 12:00 BAR/SCHÖ

Spatial self-organization of enzymes in complex reaction networks — •Vincent Ouazan-Reboul[1,2], Ramin Golestanian[2,3], and Jaime Agudo-Canalejo[2,4] — [1]LPTMS, CNRS, Université Paris-Sud, 91400, Orsay, France — [2]Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, D-37077, Göttingen, Germany — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, OX1 3PU, Oxford, UK — [4]Department of Physics and Astronomy, University College London, WC1E 6BT, London, UK

Living systems contain intricate biochemical networks whose structure is closely related to their function and allows them to exhibit robust behavior in the presence of external stimuli. Such networks typically involve catalytic enzymes, which can have non-trivial transport properties, in particular chemotaxis-like directed motion along gradients of substrates and products. Here, we find that taking into account enzyme chemotaxis in models of catalyzed reaction networks can lead to their spatial self-organization in a process similar to biomolecular condensate formation. We develop a general theory for arbitrary reaction networks, and systematically study all closed unimolecular reac-

tion networks involving up to six chemicals. Importantly, we find that network-wide propagation of concentration perturbations can be key to enabling self-organization, in a manner which is highly sensitive on the global network structure.

BP 10.11 Tue 12:15 BAR/SCHÖ

Spatial organisation of the cell's metabolic power plant via phase separation — •Kathrin S. Laxhuber[1,2] and Frank Jülicher[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck School Matter to Life

Cell metabolism is the power plant that fuels the active processes essential to life. Recent experimental results show that glycolytic enzymes, central to sugar metabolism, phase-separate to form foci under energetic stress and can localise to sites of demand. To understand this phenomenon, we build and study a minimal theoretical model. We show that droplet formation can act as a metabolic switch that enables the system to maintain energetic homeostasis at higher output power. Notably, the metabolic droplets that emerge from this switch can self-organise to colocalise with demand. We discuss the non-equilibrium features and spatial energetic profiles in this system.

BP 10.12 Tue 12:30 BAR/SCHÖ

Emergent interactions lead to collective frustration in robotic matter — •Onurcan Bektas[1,3], Adolfo Alsina[2,3], and Steffen Rulands[1,3] — [1]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoSciences, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München, Germany — [2]GISC, Universidad Rey Juan Carlos, Tulipán, 28933, Móstoles, Spain — [3]Max-Planck-Institute for the Physics of Complex Systems, Noethnitzer Str. 38, 01187 Dresden, Germany

Current artificial intelligence systems show near-human-level capabilities when deployed in isolation. Systems with intelligent agents are deployed to perform tasks collectively. This raises the question of whether robotic matter, where many learning and intelligent agents interact, shows emergence of collective behaviour. And if so, what kind of phenomena would such systems exhibit? Here, we study a paradigmatic model for robotic matter: a system composed of a large collection of stochastic interacting particles where each particle is endowed with a deep neural network that optimizes its transitions based on the particles' environments. For a 1D model, robotic matter exhibits complex phenomena arising from emergent interactions, including transitions between long-lived learning regimes, the emergence of particle species, and frustration. We also find an abrupt, density-dependent change in the behaviour of particles. Using active matter theory, we show that this phenomenon is a reflection of a phase transition with signatures of criticality. Our model captures key phenomena observed in more complex forms of robotic systems.

BP 11: Franco-German Session: Bacterial Biophysics I

Time: Tuesday 9:30–12:45 Location: BAR/0106

BP 11.1 Tue 9:30 BAR/0106

Monitoring of biofilms formation using a QCM-D — •Philipp Sievers[1], Andreas Böttcher[1], Günther Räcker[2], Felix Bosch[2], and Diethelm Johannsmann[1] — [1]Institute of Physical Chemistry, Clausthal University of Technology, Arnold-Sommerfeld-Str. 4, 38678 Clausthal-Zellerfeld, Germany — [2]Feindrahtwerk Adolf Edelhoff GmbH & Co. KG, Am großen Teich 33, 58640 Iserlohn, Germany

Biofilms formed by bacteria are a severe problem in many industries. Biofilm formation leads to biofouling, which limits the heat transfer (e.g. in heat exchangers) or contaminates process water. Regular biofilm removal often is necessary. In order to reduce cost, an online detection of biofilm formation is highly desirable.

An instrument is described, which monitors biofilm formation based on a quartz crystal microbalance with dissipation monitoring (QCM-D). In contrast to a conventional gravimetric QCM, which would rely on the shift in the resonance frequency, the most useful parameter to quantify biofouling was found to be the increase in the resonance bandwidth. This is due to the fact that biofilms consist of soft material loosely attached to the resonator, mostly leading to the dissipation of energy. This behavior is recognized based on a specific overtone dependence of the bandwidth, namely increased bandwidth (**) being the same on the different overtones. This feature is best explained with a mechanical equivalent circuit containing a single dashpot coupled to the resonator surface.

BP 11.2 Tue 9:45 BAR/0106

Following bacterial biofilm formation with X-rays: From scanning gradients towards real-life studies. — •Matthias Schwartzkopf[1], Joanne Neumann[1], Edina Klein[1,2], and Holger Sondermann[1,2] — [1]Deutsches Elektronen-Synchrotron (DESY), Notkestr. 85, D-22607 Hamburg, Germany — [2]Centre for Structural Systems Biology (CSSB), Notkestr. 85, D-22607 Hamburg, Germany

Bacterial biofilm formation is a complex multi-step process yielding microbial communities encapsulated in an extracellular matrix of polymeric substances. Biofilms are a significant problem in treating bacterial infections and are one of the main reasons for the persistence of infections. Their increased resistance to classical antibiotics poses a severe threat to global health issues. Therefore, following and understanding the process of biofilm formation are essential for early detection and suppressing biofilm-associated infections. In this context, surface-sensitive X-ray scattering (GI-SAXS) is successfully applied to observe initial thin film growth morphologies and kinetics at various metal/organic interfaces [Schwartzkopf and Roth, Nanomaterials, 6, 239 (2016)]. In this contribution, we present the capabilities and first results of our combinatorial X-ray study on *Pseudomonas aeruginosa* biofilms aiming to provide nanoscale insight into the structure and dynamics of growing biofilms.

BP 11.3 Tue 10:00 BAR/0106

Nonlinear rheology of biofilm streamers: An eDNA-driven stress-hardening mechanism — Giovanni Savorana[1,2] and •Eleonora Secchi[1] — [1]ETH Zurich, Switzerland — [2]Princeton University, US

Biofilms are aggregates of microorganisms embedded in a self-secreted polymeric matrix that protects the community from physicochemical insults, enhancing their resilience across environmental, industrial, and medical settings. Because most biofilms develop in moist, flowing environments, they are constantly exposed to hydrodynamic forces. Yet how biofilms withstand strong or fluctuating flow conditions remains poorly understood.

Our work investigates how biofilms assemble under flow and how their morphology and rheology adapt across different flow regimes. Using a microfluidic platform enabling reproducible formation and in situ rheological testing, we show that biofilm streamers-filamentous assemblies that develop within the bulk of the flow-display stress-hardening: under flow-induced axial stress, both the differential elastic modulus and the effective viscosity increase linearly. This non-linear rheological response is conserved across several bacterial species. We develop a physical model showing that extracellular DNA (eDNA) is the key component enabling this stress-hardening behavior, allowing streamers to withstand both rapid and sustained variations in hydrodynamic load. Our work advances the physical understanding of biofilm development, reveals the molecular drivers of their mechanical resilience, and informs strategies for preventing biofilm-induced clogging.

BP 11.4 Tue 10:15 BAR/0106

Matrix-Microbe-Metabolite: Re-thinking transport phenomena in microbially-active soft matrices — •Juan Pablo Carmona Almazán[1] and Anupam Sengupta[1,2] — [1]Physics of Living Matter, Department of Physics and Materials Science, University of Luxembourg, Luxembourg — [2]Institute for Advanced Studies, University of Luxembourg, Luxembourg

The diffusion of biological metabolites through soft matrices is central to microbial biophysics, mediating healthy microbe-host interactions as well as diverse infections and biodegradation. An interplay of mechano-chemical cues, together with the microbe-induced remodeling of the local environments, impacts the metabolite transport in these settings. Yet, currently, we lack a mechanistic model of the Matrix-Microbe-Metabolite interactions. Here, we use a combination of high resolution imaging and quantitative image analysis techniques

to study metabolite transport in diverse synthetic matrices with varying mechanical stiffness, composition, and biochemical complexity. Using suitable fluorescent probes as proxies, we quantify the transport kinetics in agarose as well as Matrigel, a model mammalian extracellular matrix. By interfacing atomic force microscopy, we map the results to the matrix structure, focusing on two key metabolites, formate and citrate. Finally, we embed bacterial cells to capture microbe-mediated impact on the diffusion kinetics, which together with the mechanochemical datasets, provide a biophysical framework for active metabolite distribution in soft environments.

BP 11.5 Tue 10:30 BAR/0106

Differential pili interactions trigger colony eversion and dissemination of bacteria — Stephan Wimmi[1], •Isabelle Wielert[1], Kai Zhou[2], Marc Hennes[1], Benedikt Sabass[2], and Berenike Maier[1] — [1]Institute for Biological Physics, and Center for Molecular Medicine Cologne, University of Cologne, Germany — [2]Institute for Infectious Diseases and Zoonoses, Ludwig-Maximilians-Universitaet Munich, Germany

Attractive forces between cells determine the shape and sorting behaviour of bacterial colonies. During colony development, chemical gradients form within the colony but it is unclear how they affect cohesion. Here, we discover global eversion of colonies formed by Neisseria gonorrhoeae. Like a jet, the inner core flows towards the periphery where it is partially dispersed and partially spreads around the core of the colony. Living dispersed cells leading to fast dissemination. The eversion depends on local oxygen depletion that reduces cellular attraction: prior to eversion the colony consists of a weakly cohesive spherical core surrounded by a strongly cohesive shell. A computational model reveals when the thickness of the strongly interacting shell falls below a critical value a non-linear instability initiates colony-wide eversion. Simulations predict that an increase of cohesion forces among the bacteria suppresses colony eversion. This was confirmed experimentally by a genetic modification that increases attractive forces among bacteria. Overall, we conclude that a gradient of oxygen pushes the colony out of its equilibrium state and that non-linear instabilities trigger cellular fluxes during relaxation to a new stationary state.

BP 11.6 Tue 10:45 BAR/0106

How substrate stiffness and roughness tune early biofilm development: designing platforms for in situ observation of bacterial behavior — •Mathieu Letrou[1], Sofia Gomes[1], Kennedy Chagua Encarnacion[2], Rebecca Matthias[1], Yeraldinne Carrasco Salas[1], Elena Murillo Vilella[1], Lionel Bureau[1], Karin John[1], Delphine Débarre[1], and Sigolène Lecuyer[2] — [1]Université Grenoble Alpes, CNRS, LIPhy, Grenoble, France — [2]Laboratoire de Physique, ENS de Lyon, CNRS, Lyon, France

Biofilm formation begins with bacterial colonization of substrates, a process that occurs across diverse living tissues and abiotic surfaces. Early bacterial exploration of solid-liquid interfaces, governed by adhesion and individual motility, is a known determinant of the subsequent development and persistence of bacterial colonies. Yet, how bacteria integrate environmental cues at these interfaces and adapt their behavior accordingly remains poorly understood. In this talk, I will present recent experimental approaches to generate microenvironments with precisely controlled properties, that also enable the in situ imaging of bacterial behavior within microfluidic channels. Using the pathogen Pseudomonas aeruginosa, I will show how substrate stiffness, rigidity gradients, and the presence of dispersed obstacles can alter surface exploration, thus modifying the onset of colony formation [1]. These results highlight how physical properties of solid-liquid interfaces can regulate early biofilm development and suggest new avenues for controlling surface colonization.

[1] Letrou et al., Eur Phys J E Soft Matter, 48(10-12):70 (2025)

15 min. break

Invited Talk BP 11.7 Tue 11:15 BAR/0106

Physics of bacterial adhesion: heterogeneity, patchiness, and surface interactions — •Karin Jacobs — Saarland University, Experimental Physics & Center for Biophysics, Saarbrücken, Germany

Bacterial cells interact with solid interfaces through a heterogeneous cell envelope, giving rise to rich physical behavior at solid-liquid boundaries. From a physics perspective, bacteria can be regarded as soft objects whose adhesion is governed by collective interactions of many fluctuating macromolecules. In this talk, I summarize recent experimental and theoretical work on bacterial adhesion using concepts from soft matter and surface physics.

Using atomic force microscopy-based single-cell force spectroscopy, we determine interaction forces between individual microbial cells and well-defined substrata. These experiments reveal heterogeneity of adhesion across the surface of single bacteria [1,2]. In particular, Gram-positive bacteria such as S. aureus exhibit a patchy adhesion landscape, reminiscent of patchy colloids, where a small number of adhesive regions dominate surface interactions.

We further show how surface properties such as wettability and protein coatings control bacterial adhesion by modulating the accessibility of tethering macromolecules [3]. Overall, these results place bacterial adhesion in the framework of condensed matter physics and illustrate how physical principles can guide the design of bio-interactive materials, ranging from simple functional interfaces to artificial cells. [1] C. Spengler et al., Soft Matter 20 (2024) 484; [2] E. Maikranz et al., Nanoscale 12 (2020) 19267; [3] F. Nolle et al., ACS Omega 10 (2025).

BP 11.8 Tue 11:45 BAR/0106

Bacterial motility and chemotaxis in porous media: lophotrichously flagellated *Pseudomonas putida* exhibits run motility with mechanical trapping and active turning events that enable chemotaxis based on a turn-angle bias — •Sönke Beier[1], Agniva Datta[1], Veronika Pfeifer[1], Robert Grossmann[1], and Carsten Beta[1,2] — [1]University of Potsdam, Institute of Physics, Germany — [2]Kanazawa University, Nano Life Science Institute, Japan

Chemotaxis has been extensively studied in bulk liquid, particularly for the peritrichously flagellated *Escherichia coli* with its run-and-tumble motility, where navigation toward chemoattractants relies on a run-time bias, which extends runs when cells swim up nutrient gradients. Less is known about chemotaxis in environments, where confinement limits free swimming and reduces the effectiveness of a run-time bias. Previous studies suggest that *E. coli* also bias its turning angle, adjusting reorientations to favor subsequent runs toward the chemoattractant. By analyzing the soil bacterium *P. putida* in porous media, we identify run phases and active turning events -known from bulk liquid- and additional mechanical trappings caused by the environment[1]. We provide evidence that the bacterium performs chemotaxis by employing a turn-angle bias and show that the resulting directional preference of runs arises from the active, motor-induced turning events, while passive mechanical trapping in the porous matrix weakens the preference[2]. Agent-based simulations indicate that the turn-angle bias is the predominant chemotactic strategy[2]. [1] Datta et al.:Sci Rep 15, 20320 (2025), [2] Beier et al.:arXiv:2503.05286 (2025)

BP 11.9 Tue 12:00 BAR/0106

Patchy Adhesion of Staphylococcus aureus on Structured Surfaces Uncovered via Single Cell Force Spectroscopy — •Samer Alokaidi[1], Hannah Heintz[1], Michael A. Klatt[1], Markus Bischoff[2], and Karin Jacobs[1] — [1]Saarland University, Saarbrücken, Germany — [2]Institute for Microbiologie, Homburg/Saar, Germany

Investigating bacterial adhesion at the single-cell level provides critical insights into bio-film formation and the influence of surface properties on microbial attachment. This study examines the adhesion behavior of Stapylococcus aureus on wrinkled polydimethylsiloxane (PDMS) surfaces using single cell force spectroscopy (SCFS) [1]. While conventional SCFS typically evaluates a single contact point, our approach-utilizing structured surfaces-enables mapping of adhesion across the lower portion of the bacterial cell envelope. This method reveals considerable variation in adhesion strength at different points on the cell surface, supporting the "patchy colloid" model originally proposed for Escherichia coli. Simulations, incorporating angle-dependent molecule-substrate interactions, suggest that localized adhesive "hotspots" on S. aureus may arise from surface roughness, chemical composition, and the clustering of specific adhesive proteins. These findings emphasize the significance of surface structuring in bacterial attachment and provide insights that inform the design of antimicrobial materials.

[1] C. Spengler, E. Maikranz, et. al: "The adhesion capability of Staphylococcus aureus cells is heterogeneously distributed over the cell envelope", Soft Matter, 20 (2024) 484

BP 11.10 Tue 12:15 BAR/0106

Drug interactions between translation and transcription-targeting antibiotics result from differences in ribosome regulation — •Natawan Gadjisade and Tobias Bollenbach — Institute for Biological Physics, Cologne, Germany

Combining antibiotics has the potential to improve treatment efficacy and slow the evolution of resistance. When two antibiotics are combined, their effect on bacterial growth may be stronger or weaker than expected. Recent work has shown that such interactions between ribosome-targeting antibiotics can often be predicted using a biophysical model based on bacterial growth laws. Here, we aim to understand the interplay between translation and transcription inhibitors. We identified different types of drug interactions by measuring E. coli growth in two-dimensional concentration gradients of the transcription inhibitor rifampicin and several translation inhibitors. We systematically quantify proteome allocation and individual protein regulation using mass spectrometry-based proteomics measurements. Notably, some translation inhibitors, such as kasugamycin, exhibit signs of disrupted coordination between the two ribosomal subunits. The ribosome concentration does not increase in response, thus violating the usual growth law. The way ribosomes respond to each translation inhibitor influences drug interactions with rifampicin, which itself causes a decrease in ribosome concentration. Based on the quantification of these different responses, we aim to build a biophysical model of antibiotic action that can explain the interaction patterns. Our work has the potential to facilitate quantitative predictions of drug interactions.

BP 11.11 Tue 12:30 BAR/0106

How transformation affects evolution in changing environments — •Ariana Leu, Mona Förster, Melih Yüksel, and Berenike Maier — Institute for Biological Physics, Cologne

Horizontal gene transfer (HGT) is known to play a critical role in bacterial evolution. However, it is still poorly understood under which exact conditions it can confer a fitness advantage and how it affects the dynamics of an evolving bacterial population. We study the effect of transformation on the adaptation of a bacterial population to a new environment depending on cell history.

First, the laboratory strain is adapted to two different environments, exponential growth in liquid and to growth in a structured environment. The pre-adaptation is driven purely by mutation. By selecting one of the two environments for further evolution we compare the adaptation pathways of a well adapted and a poorly adapted strain. We evaluate the fitness of the evolved populations relative to their ancestor, taking into account the effect of HGT. For well-adapted strains growing exponentially in a liquid environment, we see that the distribution of fitness effects broadens for hybrid populations. In a structured environment the adaptation of a poorly adapted strain is accelerated by transformation. We also find that transformation opens up a new genotypic pathway for adaptation that is not available through mutation. In addition, each cell is labeled with a unique genetic barcode at the beginning of evolution. By analyzing the ratio of barcodes at different time points, we gain insight into the evolutionary dynamics within the population.

BP 12: Cytoskeleton I

Time: Tuesday 9:30–12:45 Location: BAR/0205

Invited Talk BP 12.1 Tue 9:30 BAR/0205

Tuning the Tracks: Functional Diversity Encoded in Microtubule Lattice States — •Lukas Kapitein — Utrecht University

Microtubules are active polymers that power intracellular transport and signaling. In cells, functionally distinct microtubule subsets are known to coexist, but the underlying mechanisms that specify these subsets have remained unclear. I will show that microtubule lattice conformation, specifically expanded and compacted states, acts as a tunable structural parameter that regulates both motor-driven transport and cytoskeletal signaling. Whereas expanded lattice states define tracks for Kinesin-1 driven transport, compacted states sequester specific signaling factors, both independently of tubulin chemical modification. These findings identify microtubule lattice plasticity as a fundamental mechanism by which active cytoskeletal matter encodes functional diversity.

BP 12.2 Tue 10:00 BAR/0205

Mechanical tension extends the microtubule lattice and modulates kinesin-1 binding in an isoform-dependent manner — Yannic Lurz[1], Benedikt Fischer[1], Laura Muras[2], Antoine Rittaud[3], Hevré Morhbach[4], Igor Kulic[3], E. Michael Ostap[5], Erik Schaffer[1], and •Serapion Pyrpassopoulos[1] — [1]University of Tübingen — [2]University of Uppsala — [3]ICS, Strassburg — [4]ICPM, Metz — [5]University of Pennsylvania

Recent work has shown that the microtubule lattice possesses remarkable structural plasticity, with its conformation modulated by MAPs and motor binding. However, how this plasticity responds to mechanical forces remains poorly understood. We developed assays to measure the effect of tensile forces on single microtubules using optical tweezers and fluorescence microscopy. Decorating microtubules with quantum dots enabled us to measure, with nm-precision, mechanical distortions of ~0.4% under changes in average tensile force $<\Delta F>$ = 10.4 pN, within the rage of Fmin = 1.29 pN to Fmax = 20.4 pN, forces comparable to those generated by one to three kinesin-1 motors. Under forces in this range, the average binding rate of KIF5B decreased by ~20%, while its dissociation rate increased by ~10%, reducing its average run length. In extreme cases, run length dropped by up to 46% under tension. By contrast, no statistically significant effects were observed for KIF5C at the same forces. Together, these experiments provide new insights into how microtubules can act as sensors and transducers of mechanical and biochemical cues across the cell.

BP 12.3 Tue 10:15 BAR/0205

Beyond the tip: lattice dynamics, seams, and the mechanism of microtubule fracture — •Amir Zablotsky[1], Subham Biswas[2], Laura Schaedel[2,3], and Karin John[1] — [1]Université Grenoble-Alpes, CNRS, Laboratoire Interdisciplinaire de Physique 38000 Grenoble, France — [2]Experimental Physics and Center for Biophysics, Saarland University, 66123 Saarbrücken, Germany — [3]PharmaScienceHub (PSH), 66123 Saarbrücken, Germany

The structural integrity of microtubules is paramount for cellular function. While tip behavior has been extensively studied, the dynamics of the microtubule lattice remain less explored. We present a theoretical analysis of lattice fracture mechanisms, focusing on the influence of multi-seam structures arising from monomer defects and aiming to provide a more accurate estimation of GDP lattice parameters.

Our findings reveal that seams function as pre-existing pathways that accelerate damage propagation. Consequently, monomer vacancies destabilize the lattice due to the inherent structural loss of tubulin-tubulin contacts and the additive acceleration of fracture through multiple seams. Furthermore, comparison of our simulations with experiments on lattice fracture suggests that the intrinsic ratio of longitudinal to lateral binding energies is bounded at approximately 1.5, challenging previous predictions of lattice anisotropy from tip-growth models.

These results emphasize the urgent need to revise current microtubule growth models to incorporate parameters obtained from lattice dynamics and reassess their implications for overall microtubule stability and tip dynamics.

BP 12.4 Tue 10:30 BAR/0205

Microtubule mechanics in actin network — •Komal Bhattacharyya, Sarah Köster, and Stefan Klumpp — University of Göttingen, Göttingen, Germany

The cytoskeleton provides structural support while enabling dynamic cellular processes such as growth and migration. Actin filaments and microtubules are key cytoskeletal components: actin is semiflexible, whereas microtubules are comparatively stiff and rod-like. The interplay between these two filament systems underlies many biological behaviors. For example, microtubules exhibit increased resistance to compressive forces when embedded within an actin network. In our work, we use the simulation package Cytosim to investigate composite actin-microtubule networks. In particular, we examine the buckling behavior of microtubules subjected to compressive loads and thermal fluctuations, and how these responses are altered by mechanical coupling to actin. Our results show that the mechanical response of a probe filament such as a microtubule is governed primarily by its immediate local interactions rather than by the bulk properties of the surrounding network. Indicating the actin network can not influence the microtubule dynamics as an uniform elastic medium but only through direct interactions through crosslinkers or molecular motors.

BP 12.5 Tue 10:45 BAR/0205

Polydispersity-Induced Traveling Waves in Microtubule-Motor Mixtures — •Katrina Wharam[1], Ivan Maryshev[1], Filippo De Luca[2], and Erwin Frey[1] — [1]Ludwig-Maximilians Universität München, Germany — [2]University of Cambridge, United Kingdom

Microtubule-motor mixtures are exemplary active systems that self-organize into a variety of non-equilibrium phases, including asters, bilayers, and active foams. While previous theoretical work has largely assumed monodisperse filament lengths, we investigate a mixture with two microtubule populations of distinct lengths and derive a continuum field theory using a Boltzmann-Ginzburg-Landau approach. Analytical and numerical analysis shows that, despite reciprocal microscopic interactions, the system develops emergent asymmetric behaviour at the macroscopic scale. We identify the filament length ratio as a key control parameter: small length ratios yield stationary nematic bands, whereas increasing the disparity leads to traveling waves - a pattern absent in monodisperse models. Our results reveal a generic, collective route to traveling states in non-self-propelling active matter and connect ad-hoc asymmetric-alignment theories with biologically realistic microtubule systems.

15 min. break

BP 12.6 Tue 11:15 BAR/0205

Hold on tight no matter what! How cholesterol and cytoskeletal fibers affect microtentacles formation. — •Enrique Colina Araujo[1,2], Lucina Kainka[1,2], and Franziska Lautenschläger[1,2,3] — [1]Department of Experimental Physics, Saarland University, Saarbrücken, 66123, Germany — [2]Center for Biophysics, Saarland University, Saarbrücken, 66123, Germany — [3]Max Planck School, Matter to Life, Heidelberg, 69120, Germany

Following the formation of a primary tumor, cancer cells in the outer areas may detach and undergo an epithelial-to-mesenchymal (EMT) transition, enabling them to migrate and colonize new tissues, ultimately leading to metastasis. Circulating tumor cells (CTCs) play a key role during this invasion. Invasion can only occur after CTCs have attached to the blood vessel wall and extravasated from the bloodstream. Recent work suggests that such adhesion is mediated by microtubule (MT)-based membrane protrusions, known as microtentacles (McTNs). However, it remains unclear how McTNs protrude from the CTC and how they facilitate cell adhesion. In this work, we analyzed McTN formation in MDA-MB-231 cells. Using the actin depolymerizing drug latrunculin A and the cholesterol-depleting drug methyl-β-cyclodextrin (MβCD), we show that McTNs growth results from a reorganization of the actin cortex into areas of high actin concentration as well as from variations in cholesterol distribution in the plasma membrane of CTCs. Furthermore, McTNs' adhesion is integrin-based. Integrin-β-2 is evenly distributed across the surface of McTN, enabling adhesion at every potential contact with the blood vessel walls.

BP 12.7 Tue 11:30 BAR/0205

Coexistence and selection of branched actin networks — •Valentin Wössner[1,2], Falko Ziebert[1,2], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, Philosophenweg 19, 69120 Heidelberg, Germany — [2]BioQuant, Heidelberg University, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany

The actin cytoskeleton is crucial for essential cellular processes such as division, migration, and shape regulation. Most cellular actin structures are continuously turned over while keeping similar sizes. However, they are coupled through a shared and finite pool of actin monomers, which begs the question of how they can control their sizes. For branched actin networks, we suggest that local depletion of actin monomers at the leading edge constitutes a generic negative feedback mechanism between the current state of a structure (filament density) and its growth rate (creation of new branches). We derive a single equation capturing this local feedback and the global competition between different networks. Our theory leads to well-defined steady states even in the case of multiple networks sharing the same pool of monomers, without any need for specific molecular processes, in agreement with recent experiments on reconstituted systems. We also present the phase diagram for the transition from coexistence to selection under increased competition.

BP 12.8 Tue 11:45 BAR/0205

Phase Separation Strength Controls Actin Filament Treadmilling — •Beatrice Nettuno[1], Davide Toffenetti[1], Timon Nast-Kolb[2], Moritz Striebel[1], Erwin Frey[1], and Andreas Bausch[2] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC), Department of Physics, Ludwig-Maximilians-Universität München, Theresienstrasse 37, München, D-80333, Germany — [2]Heinz Nixdorf Chair in Biophysical Engineering of Living Matter, Technical University of Munich, Ernst-Otto-Fischer Str.8, Garching bei München, D-85748, Germany

Actin treadmilling underlies diverse forms of cellular motility, yet the physical principles enabling stable, persistent turnover remain unclear. In our work, we reconstitute a minimal system in which phase-separated condensates of zyxin and VASP balance cofilin-driven severing to produce robust treadmilling and higher-order actin organization. To uncover the mechanistic basis of this emergent behavior, we develop agent-based simulations that quantitatively recapitulate the experimental dynamics. Our modeling reveals that persistent treadmilling requires an optimal condensate cohesion: phase separation must be strong enough to locally concentrate and crosslink filaments, yet sufficiently fluid to permit barbed-end growth and internal rearrangements. Too weak a cohesion fails to stabilize bundles, whereas overly cohesive condensates suppress filament dynamics and prevent sustained turnover. Together, experiments and theory identify a physical mechanism by which the material properties of multivalent protein condensates regulate cytoskeletal turnover.

BP 12.9 Tue 12:00 BAR/0205

Anisotropic stretch biases the self-organization of actin fibers in multicellular Hydra aggregates — •Anais Bailles, Giulia Serafini, Heino Andreas, Christoph Zechner, Carl Modes, and Pavel Tomancak — Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Hydra displays a striking planar pattern of actin fibers at the organism scale, and mechanics influence the morphogenesis of biological structures during its prepatterned regeneration. However, how mechanics participate in the formation of an ordered pattern from a totally disordered state remains unknown. To study this, we used cellular aggregates formed from dissociated Hydra cells, which initially lose all actin polarity yet regenerate a long-range actin pattern. We showed quantitatively that the actin meshwork evolves from a disordered symmetric state to an ordered state in which rotational symmetry is broken, and translation symmetry is partially broken, with the nematic and smectic order parameters increasing over days. During the first hours, the actin meshwork displayed spatial heterogeneity in the nematic order parameter, and ordered domains separated by line defects progressively grew and fused. This suggests that local cell-cell interactions drive the transition from disorder to order. To understand the mechanism of ordering, we perturbed the tissue's physical constraints. We showed that while topology and geometry do not have a direct effect, anisotropic stretch biases the emerging orientation of the actin meshwork within hours. This demonstrates the role of tissue mechanics in the alignment of the actin fibers during the disorder-to-order transition.

BP 12.10 Tue 12:15 BAR/0205

Bridging Scales in the Cytoskeleton: Towards a nonperturbative renormalization group framework — •Patrick Jentsch, Thomas Quail, Niccolò Banterle, and Anna Erzberger — European Molecular Biology Laboratory, Heidelberg, Germany

Microtubules (MTs) and their interactions are microscopically well characterized, yet the connection between these interactions and the emergent, functionally relevant collective behavior of the cytoskeleton remains incomplete. To develop an analytic framework that links these scales, we aim to explore the use of nonperturbative renormalization group (NPRG) methods to derive large-scale effective theories of MT networks from a microscopic model of interacting MTs. Using *Xenopus laevis* egg extract as a model system, we have begun inferring a phenomenological theory of interacting MTs at the micrometer scale based on TIRF microscopy data. In the next stage, this model will be coarse-grained using NPRG methods to obtain an effective description at the millimeter scale, enabling us to track the scale dependence of interaction couplings and the emergence of new dynamical processes. Ultimately, the resulting effective theory will be evaluated by comparing predicted correlation functions with experimental measurements of spontaneously formed MT asters which we are currently imaging using millimeter-scale widefield and confocal techniques.

BP 12.11 Tue 12:30 BAR/0205

Bayesian inference of bond parameters from interactions between single filaments — •Kristian Angeli Pajanonot[1,2], Sascha Lambert[1,2], Pallavi Kumari[1], Stefan Klumpp[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Germany

Interactions among cytoskeletal filaments-actin, microtubules, and intermediate filaments-regulate cell structure, movement, and transport. Single-filament direct interactions can be measured using a quadruple optical tweezers setup. In this approach, filaments are attached to two separate bead pairs held in optical traps and positioned in a cross configuration. As the vertical filament is pulled across the other one, the bond that forms between these filaments experiences increasing mechanical load until it breaks. Previous analysis using Kolmogorov-Smirnov (KS) tests allows for the estimation of bond parameters but lacks a probabilistic interpretation. Here, we present a Bayesian inference framework to estimate bond parameters from the interaction data. Using published data on the interaction between two vimentin filaments, we show that Bayesian inference provides consistent results with the KS test and with narrower parameter estimates. We then investigate how the pulling velocity influences the bond parameters and find that probing different pulling velocities improves inference compared to using a single velocity. Finally, we apply the method to other cytoskeletal filament interactions demonstrating broader applicability and offering guidance for future experimental optimization

BP 13: Active Matter IV (joint session DY/BP/CPP)

Time: Tuesday 14:00–15:30 Location: ZEU/0160

BP 13.1 Tue 14:00 ZEU/0160

Automated decision-making by chemical echolocation in active droplets — •Aritra K. Mukhopadhyay[1], Ran Niu[2], Linhui Fu[2], Kai Feng[2], Christopher Fujta[1], Qiang Zhao[2], Jinping Qu[2], and Benno Liebchen[1] — [1]Technische Universität Darmstadt, Darmstadt, Germany. — [2]Huazhong University of Science and Technology, Wuhan, China.

Motile microorganisms like bacteria and algae combine self-propulsion, cooperation, and decision-making at the micron scale. Inspired by these biological systems, synthetic microswimmers are emerging as human-made counterparts capable of self-propulsion. Recent breakthroughs provide a platform to integrate additional functionalities, bridging the gap between biology and synthetic systems. We propose and experimentally demonstrate a mechanism that enables synthetic microswimmers, including autophoretic colloids, droplet swimmers, and ion-exchange-driven modular swimmers, to make autonomous navigational decisions. These swimmers generate chemo-hydrodynamic signals that interact with boundaries, producing echoes that encode structural information about the environment. These echoes trigger automatic responses, such as synthetic chemotaxis, allowing swimmers to avoid dead ends and autonomously find paths through complex mazes. We show the mechanism remains robust across different maze geometries, ensuring reliable navigation without external cues. Our findings illustrate how simple physical principles can endow synthetic systems with advanced navigation functionalities.

BP 13.2 Tue 14:15 ZEU/0160

Dead or alive?—Probing scale-dependent liveliness in multiscale active matter — •Joscha Mecke[1] and Klaus Kroy[2] — [1]Institute for Advanced Study, Shenzhen University, Shenzhen, China — [2]Institut für Theoretische Physik, Universität Leipzig, Leipzig, Germany

If you have ever watched live and dead trouts swimming upstream, side by side, you may have wondered how closer inspection of their mesoscale activity might help to tell them apart. But probing spatially heterogeneous activity in living matter is a major challenge. We demonstrate the emergence of multiple effective ("active") temperatures in nonequilibrium molecular- and Brownian-dynamics simulations of an active polymer. Energy injection at different length scales leads to mode coupling, inter-modal energy transfer, and entropy production. We put forward a generalised Langevin equation for a labelled monomer, which, by application of a harmonic potential, can serve as a spectroscopic device. Upon varying the trap stiffness, we can selectively scan through the emergent effective temperatures and thereby resolve the scale-dependent activity. Our approach thus provides a minimally invasive spectroscopic tool to generate quantitative maps of liveliness, across multiple scales.

BP 13.3 Tue 14:30 ZEU/0160

Tuning the velocity of thermophoretic microswimmers with thermo-sensitive polymers — Franziska M. Braun, Aritra K. Mukhopadhyay, Samad Mahmoudi, Benno Liebchen, and •Regine von Klitzing — Institute for Condensed Matter Physics, TU Darmstadt, Hochschulstrasse 8, 64289 Darmstadt

Understanding and controlling the motion of self-propelled particles in complex fluids is crucial for applications in targeted drug delivery, microfluidic transport, and the broader field of active matter. Here, we investigate the thermophoretic self-propulsion of partially gold-coated polystyrene Janus particles (Au-PS) in temperature-responsive linear Poly(N-isopropyl acrylamide) (PNIPAM) solutions across various PNIPAM concentrations and temperatures. Particle velocities are examined at three representative temperatures: far below, near but below and above the LCST. In pure water, Au-PS Janus particles propel with the PS hemisphere leading, driven by their intrinsic thermophoretic response. Conversely, the positive Soret coefficient of PNIPAM results in depletion forces that induce motion of the Janus particle towards the hot Au side. The experiments reveal a non-monotonic dependence of particle velocity on temperature, with a maximum near the LCST. Interfacial processes like ion movement in the electric double layer and PNIPAM adsorption at the Au-PS particles are separated from processes that are coupled to the bulk solution. Theoretical calculations are in good agreement with the experimental findings and are essential for the understanding of the complex interplay of microswimmers with thermoresponsive polymers.

BP 13.4 Tue 14:45 ZEU/0160

Non-reciprocal multifarious self-organization — •Saeed Osat[1] and Ramin Golestanian[2] — [1]Institute for Theoretical Physics IV, University of Stuttgart, Heisenbergstraße 3, 70569 Stuttgart, Germany — [2]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Goettingen, Germany

Biological systems exhibit a unique ability to design diverse structures from a shared set of building blocks, with a plethora of proteins made from a limited set of amino acids as a prime example. Furthermore, these systems often use building blocks efficiently by introducing transformations between different structures. A structure might undergo structural transformations to form a new structure with different functional purposes, without the need to discard the current structure and start anew. To unravel this mystery, one must examine the underlying non-equilibrium processes that make this shape-shifting behavior feasible.

Here, we leverage non-reciprocal interactions between building blocks to provide a foundation for designing dynamic structures. We used a multifarious self-assembly (MSA) model, which is the molecular counterpart of the Hopfield associative memory. By upgrading the MSA model to its non-equilibrium counterpart with non-reciprocal interactions, we introduce the ability to not only self-assemble different structures on demand but also facilitate shifts and transformations that lead to shape-shifting behavior.

Invited Talk BP 13.5 Tue 15:00 ZEU/0160

Designing topological edge states in bacterial active matter — Yoshihito Uchida[1], Daiki Nishiguchi[2,1], and •Kazumasa A. Takeuchi[1] — [1]The University of Tokyo, Tokyo, Japan — [2]Institute of Science Tokyo, Tokyo, Japan

Besides its potential relevance to the life sciences, active matter also manifests as a novel, intrinsically non-equilibrium kind of matter, endowed with characteristic transport properties distinguished from conventional matter. A challenge is how to control and design transport in active matter. A potentially useful, emerging concept here is topological transport developed in condensed matter physics, which was extended to active matter successfully, but experimental realizations have thus far relied on the chirality of the active particles, which limits

design capabilities.

Here we report a controlled realization of topological edge states in dense bacterial suspension, induced by microfabricated geometry instead of the bacteria's chirality. First we demonstrate that we can rectify bacterial collective motion by a channel with asymmetric shape. Then we construct networks made of asymmetric channels and show that we can control the emergence of topological edge states through the network design. Through modelling and experiments, we discuss what properties of the network and the bacterial flow are crucial to the observed topological phenomenon. We expect our results may pave the way for establishing a control and design principle of topological transport in such active matter systems.

Ref) Y. Uchida, D. Nishiguchi, and K. A. Takeuchi, to appear.

BP 14: Poster Session II

Active matter; bacterial biophysics; bioimaging; computational biophysics; membranes, vesicles and life-like systems; protein structure and dynamics; single molecule biophysics; statistical physics of biological systems; systems and networks biophysics; FS integrated structural modelling; FS sequence spaces, populations and evolution

Time: Tuesday 18:00–21:00 Location: P2

BP 14.1 Tue 18:00 P2

Controlling Cell Motility and Morphology by Microscale Stripe Patterns — •Henrik Groh and Matthias Weiss — University of Bayreuth, Experimental Physics I, 95447 Bayreuth, Germany

Cells are highly responsive to the architecture of the substrate on which they adhere. In particular, cell morphology and motility can be influenced by providing microstructured adhesion patterns, e.g. fibronectin-coated lanes of varying width, as this determines how cellular adhesion sites form and organize. To study this in more detail, we generated fibronectin-coated lanes through the Primo technique with widths ranging from 2.5 μm to 40 μm on which highly migratory breast cancer cells (MDA-MB-231) adhered. As the lane width was changed, cells exhibited significant changes in their morphology, including alterations in aspect ratio and orientation angle relative to the lanes. In addition, the cells' motility, specifically velocity and migration mode composition, underwent pronounced changes as the lane width decreased. Our findings provide important insights into how cell migration might be guided with simple physico-chemical cues and highlight the potential of micro-patterned substrates as a tool for cancer cell migration analyses, possibly providing a core mechanism that underlies cell migration in development and disease.

BP 14.2 Tue 18:00 P2

Computational Modelling of Active-Polymer Dynamics in Gliding Filamentous Cyanobacteria — •Krishna Iyer Vadakkeputhanmadom Subramanian[1], Stefan Karpitschka[2], and Stefan Klumpp[1] — [1]Georg-August University, Göttingen, Germany — [2]University of Konstanz, Konstanz, Germany

Filamentous cyanobacteria such as *Oscillatoria lutea*, *Kamptonema animale* and *Nostoc commune* constitute a natural realization of active polymers: long, flexible filaments that self-propel by gliding motility and whose activity can be tuned with light. Dense colonies display a rich repertoire of collective phenomena—nematic lanes, topological-defects, spirals, clusters etc.—yet the physical mechanisms that connect single-filament properties (bending rigidity, propulsion force, reversal rates) to these emergent states remain largely unexplored. We develop a Browinan-dynamics framework, each filament represented as a chain of active particles with tangential self-propulsion and stochastic direction-reversal events, and explore the collective-state phase diagram in the space of activity, rigidity and length of filaments. Through comparisons with experiments, we seek to understand the mechanisms behind reversal events, both at collective and filament levels.

BP 14.3 Tue 18:00 P2

Filamentous cyanobacteria in model complex environments — •Jakob Gönnenwein, Elias Illing, and Stefan Karpitschka — Fachbereich Physik, Universität Konstanz

Cyanobacteria are pervasive throughout most ecosystems, ranging from open water bodies to porous media like soil or sandstone. Their accelerated growth in a warming climate constitutes rising ecologic and economic threats. Besides harmful blooms in natural water bodies, their degrading effect on buildings and sculptures has been identified as a threat to cultural heritage sites.

In our work we investigate the motility, individual behaviour and collective mechanics of filamentous cyanobacteria. We use well-controlled quasi-two-dimensional model porous media that mimic properties of natural habitats like soil or sandstone, while allowing direct observation of their dispersal characteristics. Using this system, we derive characteristic persistence scales of orientational order and density fluctuations in relation to the porosity parameters of the model medium.

Characterizing their collective behaviour in porous media allows us to understand and potentially mitigate their adverse effects on porous structural materials.

BP 14.4 Tue 18:00 P2

Motility Modes and Deformation Dynamics in *Trypanosoma brucei* — •Hannes Wunderlich[1], Marinus Thein[2], Lucas Brehm[2], Geena Eglmeier[2], Klaus Ersfeld[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth, Germany — [2]Laboratory of Molecular Parasitology, University of Bayreuth, Germany

Trypanosoma brucei is a unicellular parasitic microswimmer whose flagellum-driven motion and cell-body elasticity are essential for navigating host environments and maintaining immune evasion.

Although run-and-tumble dynamics have been described for both the procyclic and bloodstream forms of T. brucei, details of motility changes and cell deformation during locomotion remain poorly understood. To address this gap, we performed a comparative analysis of the motility of bloodstream- and procyclic-form trypanosomes in controlled microfluidic environments. Using high-resolution recordings in bulk and in confining single-emulsion droplets (allowing tracking over extended periods), we extracted and analyzed positional trajectories and cell-shape time series. As a result, we reveal marked differences in swimming efficiency and overall motion patterns between the two trypanosome forms. Our findings indicate that cell-body elasticity and deformation play a crucial role in motility and may be directly relevant for biological processes such as surface-protein exchange.

BP 14.5 Tue 18:00 P2

A microfluidic device for probing microbial adhesion phenotypes in light and flow gradients — •Florian Böhme and Oliver Bäumchen — University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany

The unicellular photosynthetic microbe *Chlamydomonas reinhardtii* has naturally evolved the ability to unspecifically adhere to surfaces under sufficient illumination with blue light [1]. Their natural habitats are porous, liquid-infused soil and temporary pools. Thus, the cells regularly experience spatiotemporal light variations as well as external flows. *Chlamydomonas* employs its two cilia to firmly attach to surfaces, a mechanism which is hypothesized to sustain a stable photosynthetic yield while providing protection from external flows at low energetic costs.

We mimic such complex natural habitats by creating artificial microscale flow systems with tailored light and fluid flow conditions. Our microfluidic devices entail sections featuring continuous light-intensity gradients of certain wavelengths. At the same time the cells may experience external flows through precise pressure control in the channels. This allows for quantifying population statistics of microbial adhesion phenotypes in terms of threshold intensities of individual light switches and adhesion strengths during exposure to external flows. Our microfluidic devices can be employed for the high-throughput screening of adhesion phenotypes of wild-type and genetically modified photosynthetic microorganisms.

[1] R. Catalan et al., *Soft Matter* **19**, 306 - 314 (2023).

BP 14.6 Tue 18:00 P2

Active stresses induce bending instabilities and oscillatory dynamics in semiflexible filaments — •Sreehari Choorikkat, Jonas Bosche, Ludger Santen, and Reza Shaebani — Theoretical Physics and Center for Biophysics, Saarland University, 66123 Saarbrücken, Germany

Despite their high structural rigidity, cytoskeletal filaments can undergo large deformations driven by active stresses generated by motor proteins. We investigate this phenomenon by developing a two-dimensional model in which a discretized filament interacts with an underlying array of molecular motors. Using Monte Carlo simulations, we show that stochastic motor binding and unbinding events can produce a wide range of deformation patterns, including bending, buckling, knot formation, and oscillatory motion. We characterize these dynamical regimes by analyzing the time-resolved mean curvature and by determining how the frequency and amplitude of oscillations depend on key physical parameters such as filament length, bending stiffness, and motor density. Our results delineate the parameter space that supports robust, sustained oscillations and clarify how the coupling between motor activity and filament mechanics generates dynamical instabilities.

BP 14.7 Tue 18:00 P2

Modeling host-pathogen interactions via stochastic simulations and neural network-driven Bayesian inference — •Soham Mukhopadhyay[1], Jonathan Pollock[2], David Voehringer[2], and Vasily Zaburdaev[1] — [1]MPZPM, Erlangen, Germany — [2]Department of Infection Biology, University Hospital Erlangen, Friedrich-Alexander University Erlangen, Germany

Helminth infections affect a large proportion of the world's population and cause significant morbidity. There are no vaccines against helminths, and the mechanisms of anti-helminth immune responses are often not well-understood. Taking the murine hookworm *N. brasiliensis* as our experimental system, we develop a mechanistic model that describes the parasite load in different host organs — which the parasite migrates through over the course of its lifecycle — as a function of time. We abstract infection progression as a state-transition process and simulate it via kinetic Monte Carlo, thereby linking the infective dose of larvae to the number of eggs shed to the environment by adult worms from the host intestines, which can then be compared to experimental data. To infer model parameters — the various transition rates — from experimental data, we employ emerging techniques from the domain of neural network-driven Bayesian inference to infer the posterior probability distribution of parameters conditioned on data. Using this model and inference framework, we plan to compare the population dynamics for different immune perturbations.

BP 14.8 Tue 18:00 P2

Structural Analysis of Cyanobacterial Monolayers — •Rodewald Lars and Karpitschka Stefan — Department of Physics, University of Konstanz, Germany

Cyanobacteria are interesting organisms from several perspectives e.g., due to their ecological importance and biotechnical potential but also as model active matter systems as they constitute active polymers that exhibit a wide variety of collective behavior.

Here we investigate dense quasi-2-dimensional layers of filaments and analyze the patterns that emerge from their motility and mutual interactions. In contrast to molecular systems here the complete microstate of the system can be accessed by optical microscopy, which allows for a more complete understanding and description of the global dynamics and structures including nematic and polar order parameters and defect formation.

In this contribution we discuss the design of a confining structure to generate monolayers while providing a healthy environment allowing for long term experiments. Using this structure we investigate the impact of light intensity on the behavior of the individual cyanobacteria and therefore the structures present the associated emerging order in the monolayer.

BP 14.9 Tue 18:00 P2

Mathematical modeling of larvae motility in complex environments — •Sreya Chatterjee[1], Jhanvi H. Patel[2], David Voehringer[2], and Vasily Zaburdaev[1] — [1]MPZPM, Erlangen,Germany — [2]Department of Infection Biology,University Hospital Erlangen,Friedrich-Alexander University,Erlangen.Germany

N. brasiliensis is one of the most widely-studied helminth parasites due to the relatively simple life cycle for parasite production and its ability to be used in animal models, especially rodents. The larvae mature into adult worms in the lumen of the small intestine, which is composed of mucus produced by goblet cells. Studying their interactions with the surrounding host tissue will help us understand how helminths trigger and modulate immune responses. The mucus layer of the extracellular matrix is viscoelastic which influence their motility. We model these adult worms as active agents exhibiting persistent motion within this viscoelastic environment. To capture their dynamics, we formulate the problem using the well-established framework of Active Brownian Particles (ABPs). As a first step, we study the behavior of a simple system of two ABPs connected by a spring through analytical approaches as well as numerical simulations. Next we will extend this model to simulate N-particles connected by springs to capture a more realistic model of the movement of the worm in viscoelastic environment.

BP 14.10 Tue 18:00 P2

Modeling the aging dynamics of confluent endothelial cells — •Anselm Hohlstamm, Andreas Deussen, Stephan Speier, and Peter Dieterich — Institut für Physiologie, TU Dresden

Coordinated movements of endothelial cells are essential for maintaining the barrier function of blood vessels while adapting to disturbances. Understanding the underlying dynamics of these movements can provide valuable insights into the complex biological processes and help to detect changes under pathophysiological conditions. Therefore, we cultured human umbilical vein endothelial cells and stained their nuclei to enable cell tracking. We obtained several tens of thousands of cell paths with durations of up to 48 hours (dt=10 min). Bayesian inference was applied to estimate model parameters and probabilities. Our analysis revealed an age-dependent reduction of mean cell velocities, with cells never coming to a complete standstill. Furthermore, the velocity autocorrelation function indicated correlated movement patterns that persist for approximately 1-2 hours and may be linked to the movements of neighboring cells. The active motion is further influenced by strong repulsive cell-cell interactions, which become particularly relevant shortly after cell division. By combining elements of generalized stochastic processes and cell-cell-interactions, we constructed models that integrate these characteristics and generate collective dynamics in simulations similar to those observed in experiments. In summary, our study provides a comprehensive characterization of endothelial cell movement dynamics and develops a stochastic model that can be used for future simulations and predictions.

BP 14.11 Tue 18:00 P2

Mechanosensing by active singularities — •Fabian Knüpfer[1], Jonas Neipel[1,2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute for Molecular Cell Biology and Genetics, Dresden, Germany

During the development of an animal, the self-organized formation of chemical patterns establishes the body plan, defining body axes as well as the midline. However, the overall symmetry of an embryo is typically broken before, in particular due to environmental cues. Here we investigate how mechanical cues can control pattern formation. Motivated by the egg-shell that confines various embryos, we consider a rigid heterogenous substrate coupling to an active fluid surface. We focus on localized centers of mechanical activity, i.e. multipoles and topological defects of the active stress field. We ask how variations in friction and substrate curvature impact on the movement of such active singularities. We show that monopoles of isotropic active tension are advected towards maxima in friction. We then discuss how on a curved surface gradients in Gaussian curvature map to friction gradients to explain the localization of stress multipoles in anisotropic geometries. Finally, we explore how in an active nematic, topological defects move along gradients in friction and substrate curvature.

BP 14.12 Tue 18:00 P2

Swimming With and Against Confined Microscale Flows — •Vishu Saini and Marisol Ripoll — Theoretical Physics of Living Matter (IAS-2), Institute for Advanced Simulation, Forschungszentrum Jülich , Germany

Bacteria in real-world settings are typically navigating heterogeneous porous media, such as soil [1]. Such environments involve a complex interplay between geometric confinement and fluid flow [2], which can be understood as networks of channels with varying cross sections [3]. By means of Brownian Dynamics simulations, we investigate the properties of microswimmers in the presence of both confinement and flow to identify universal mechanisms that microorganisms employ to traverse

complex environments. Since self-propelled particles tend to accumulate at the walls, the strength of the flow will determine the upstream or downstream nature of swimming. This will be importantly modified by the intrinsic rotational noise of the self-propelled and the channel width, which is known to vary together with the geometric characteristics of the media. The interaction between self-propelled particles will also importantly affect the dynamics with the formation of percolating clusters. We systematically characterize these dynamics for varying flow strengths and channel sizes, as often encountered in soil-like porous environments.

[1] Bhattacharjee et al (2019). Nature communications, 10(1), 2075. [2] Conrad, J. C et al. Annual review of chemical and biomolecular engineering, 9(1), 175-200. [3] Monteiro et al. Commun Biol 8, 662 (2025).

BP 14.13 Tue 18:00 P2

Synthesis and characterization of platinum (pt)-decorated se-tio2@fcnts nanocomposite and their photocatalytic antibacterial mechanism — •Asif kamal[1], Akhtar munir[2], Jinguang yang[3], and Yingwen wang[4] — [1]Department of Plant Sciences Quaid-i-Azam University Islamabad, 45320 Islamabad, Pakistan. — [2]Department of Chemistry, Quaid-i-Azam University Islamabad, 45320 Islamabad, Pakistan. — [3]Key Laboratory of Tobacco Pest Monitoring, Controlling and Integrated Management, Tobacco Research Institute of Chinese Academy of Agricultural Sciences, Qingdao 266101, China: — [4]Key Laboratory of Tobacco Pest Monitoring, Controlling and Integrated Management, Tobacco Research Institute of Chinese Academy of Agricultural Sciences, Qingdao 266101, China:

The development of efficient and sustainable antibacterial agents is crucial to address the growing threat of multidrug-resistant pathogens. In this study, we report the synthesis and characterization of a novel nanocomposite Pt-decorated selenium-doped titanium dioxide supported on functionalized carbon nanotubes (Pt/Se-TiO2@FCNTs) with enhanced photocatalytic antibacterial performance under visible light. This new material was synthesized through sol gel method by in situ pt NPs decoration to achieved uniform dispersion and strong interfacial coupling between the components. Comprehensive characterization using XRD, TEM, SEM-EDS, FTIR, Raman, XPS and UV confirmed successful Se doping, Pt decoration, and improved optical absorption in the visible range. The photocatalytic antibacterial activity was evaluated against E. coli and Ralstonia solanacearum.

BP 14.14 Tue 18:00 P2

Laser-cell interactions in a microorganism model: Influence of irradiation with 1064 nm on *E. coli* — •Katja Schmitz and Beatrix Konermann — Trier University of Applied Sciences, Trier, Germany

Lasers are being used more and more in sensor technology, including in biotechnological applications such as fermentation monitoring. However, the biological impact of laser radiation on microorganisms is not clarify understood. Depending on the wavelength, the radiation can induce DNA damage, protein denaturation, or thermal effects, which can inhibit growth or kill cells. Additional parameters, such as irradiation duration and intensity, also influence these interactions.

This study investigates the effects of a 1064 nm laser on the growth and metabolism of *E. coli* under different irradiation conditions. An *E. coli* culture was exposed to a 100 mW laser radiation with variable irradiation times. After treatment, the samples were either cultivated immediately or returned to the culture medium. Growth behavior was evaluated by determining total and viable cell counts, which were then compared to those of untreated reference samples.

Initial results showed no detectable influence of 1064 nm irradiation on cell growth or metabolic processes. A literature review was conducted to contextualize these findings and summarize the reported positive, negative, and neutral effects of laser exposure on microorganisms. These results contribute to a more detailed understanding of laser-cell interactions and highlight the need for further research, particularly regarding wavelength- and organism-specific effects.

BP 14.15 Tue 18:00 P2

Agent-based modeling of short range cell-cell communication — •Ricardo Santander[1,3], Noam Golan[2], Lior Kreindler[2], Avigdor Eldar[2], and Vasily Zaburdaev[1,3] — [1]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [2]School of Molecular Cell Biology & Biotechnology Tel Aviv University, Israel — [3]Friedrich-Alexander-Universität, Erlangen, Germany

We use agent-based simulations to model synthetic gene regulatory networks that mediate short-range cell-cell communication in bacterial monolayers. These circuits couple intracellular dynamics of transcription factors and inhibitors with extracellular concentration fields driven by diffusion, secretion, and uptake of signaling peptides. Individual bacteria are represented as elongating, dividing capsules that act as point-like sources and sinks shaping the extracellular concentration field. The model is nondimensionalized to expose key parameter groups that govern the balance between secretion, import, diffusion, and dilution. Simulations reproduce the influence of nearby inhibitor-producing cells on their neighbors observed in microfluidic experiments and provide detailed insight into how spatial organization and transporter-driven accumulation control signaling range, spatial patterns, and circuit behavior in dense bacterial populations

BP 14.16 Tue 18:00 P2

Effects of extracellular DNA on material properties of bacterial biofilms — •Mandus Aldag, Isabelle Wielert, Stephan Wimmi, and Berenike Maier — Institute for Biological Physics, University of Cologne

Many bacterial species form spatially structured biofilms that protect the bacteria from external stresses. In *Neisseria gonorrhoeae*, a human pathogen, early biofilms are characterized by the formation of spherical colonies with liquid-like local order via active attractions between single cells. An important component of biofilms is extracellular DNA (eDNA), that is predominantly released from lysed cells and is proposed to have biofilm-stabilizing properties. Here, we use a combination of confocal microscopy, laser tweezers and tolerance assays to explore the spatial distribution of eDNA and how it affects structure, dynamics and attractive forces in gonococcal colonies. We find that after 16h of growth, *N. gonorrhoeae* colonies show filamentous, network-like eDNA structures, that can span over large parts of the colony and often interconnect lysed cells. Treatment with DNase prevents the formation of the eDNA network while the spherical colony shape is maintained. Furthermore, we find that the presence of eDNA is associated with a lower bacterial within-colony motility, compared to DNase-treated colonies. The results suggest that even though gonococcal colonies can still form in DNase presence, eDNA affects the cohesive properties of cells within biofilms which potentially influences the biofilm's susceptibility to antibiotics.

BP 14.17 Tue 18:00 P2

Probing Bacterial Adhesion on Functionalized Silicon Surfaces Using AFM-Based Single-Cell Force Spectroscopy — •Hannah Heintz, Hendrik Hähl, and Karin Jacobs — Experimental Physics & Center for Biophysics, Campus E2 9, 66123 Saarbrücken, Germany

Understanding bacterial adhesion to solid surfaces is crucial for biomedical as well as technical applications ranging from implants to antifouling strategies. In this study, we investigate how chemical functionalization and nanoscale roughness influence microbial attachment. We employed silicon surfaces that were modified by (i) coating with octadecyltrichlorosilane (OTS) to render them hydrophobic, (ii) preconditioning with a protein film of the hydrophobin HFBI from *Trichoderma reesei*, and (iii) controlled etching with hydrofluoric acid to introduce varying roughness levels. Adhesion forces of *Staphylococcus aureus* and *Shewanella oneidensis* were quantified using Atomic Force Microscopy (AFM)-based Single-Cell Force Spectroscopy (SCFS), employing both polydopamine-mediated and FluidFM vacuum-based cell immobilization. Complementary AFM and confocal microscopy enabled simultaneous characterization of topography, elasticity, and cell wall architecture. Our results reveal distinct adhesion profiles depending on surface chemistry and bacterial species, highlighting the interplay between hydrophobicity and roughness. These findings provide mechanistic insights into biointerface design and pave the way for tailored surface engineering to control microbial colonization.

BP 14.18 Tue 18:00 P2

Exploring Chemotaxis in Magnetotactic Bacteria: A Biophysical Approach — •Diego Roesch — nstitut de Biosciences et Biotechnologies d'Aix-Marseille, Aix en Provence, France

Magnetotactic bacteria (MTB) navigate complex microenvironments by integrating magnetic, chemical, and physical cues. Although magnetotaxis and aerotaxis have been extensively studied, the mechanisms governing chemotaxis in MTB remain largely unexplored, particularly at the level of the bacterial flagellar motor. This work aims to establish a quantitative steady-state model of motor dynamics in Magnetospirillum gryphiswaldense (MSR-1) as a foundation for studying how the

motor adapts to and integrates chemical stimuli.

Using tethered-cell assays, high-speed recording, and a custom Python analysis pipeline, individual MSR-1 motors were characterized, revealing three well-defined rotational states: counterclockwise (CCW), clockwise (CW), and pausing. MSR-1 motors exhibited frequent directional reversals and extensive time spent in transient failed-switch pauses, whereas genuine long pauses formed rare but highly persistent states following lognormal distributions, likely reflecting regulatory or mechanistic resets of the motor.

Switching intervals, long pauses, and most run durations follow non-Poissonian, lognormal-like statistics, suggesting structured rather than memoryless regulation. Since MSR-1 possesses two polar flagella, this framework also opens the way to investigate the synchronicity and coordinated behavior of both motors under chemical stimulation.

BP 14.19 Tue 18:00 P2

Controlling transport for RNA enrichment in alkaline hydrothermal vents at the emergence of life — •Mona B. Michelsen[1], Almuth Schmid[2], Dieter Braun[2], and Karen Alim[1] — [1]Theory of Biological Networks, School of Natural Sciences, Technical University of Munich, Garching, Germany — [2]Systems Biophysics, Ludwig Maximilians University, Munich, Germany

Reactive mineral surfaces within alkaline hydrothermal vents (AHVs) at the prebiotic ocean floor are compelling candidates for mediating the accumulation and stabilization of early biomolecules such as RNA. The intricate hierarchical architecture of AHVs, featuring central conduits branching into finely ramified networks, creates dynamic microenvironments that may promote selective adsorption of RNA onto mineral surfaces and enhance local concentrations through flow-driven accumulation. These mineral-RNA interactions could have influenced both the persistence and the catalytic potential of primitive RNA species, potentially facilitating steps toward replication and evolution.

In this project, we apply microfluidics to construct quasi-2D analogues of hydrothermal vents in the laboratory, enabling direct observation of mineral precipitation, flow patterns, and RNA transport under controlled chemical and physical conditions. This approach allows us to investigate how mineral surfaces and flow dynamics influence RNA accumulation and the potential for mineral-assisted RNA catalysis and replication in prebiotic environments.

BP 14.20 Tue 18:00 P2

Molecular Dynamics Simulations as a tool to investigate the impact of novel imidazole-based cholesterol analogs in lipid bilayers — •Clara Rickhoff and Andreas Heuer — Institut für Physikalische Chemie, Universität Münster, Münster, Germany

In biological membrane systems of eukaryotic cells, the cholesterol plays an important role, impacting for example the fluidity and structure of the membrane. To gain a deeper understanding of the behaviour of cholesterol a range of analogs were developed to add functionalities required for lab experiments such as fluorescence to the sterol. In order to investigate cholesterol via these tools, it is essential that the anaolgs show a similar behaviour to that of the wildtype molecule. In a previous study a similar behaviour was observed between a non-charged imidazole-based cholesterol analog (CHIM-N) and cholesterol itself [1].

The present study focuses on a novel group of imidazole-based cholesterol analogs with a more flexible linker between imidazolium and cholesterol and a fully retained cholesterol backbone. Via Molecular Dynamics (MD) Simulations it can be assessed how accurate these new analogs mimic cholesterol in terms of order parameter, tilt angle and position within the membrane. Furthermore, a comparison of the different new analogs as well as with the molecules already applied in cells can be made.

[1] M. Pierau et al, Langmuir 2025, 41 (17), 10991-11002

BP 14.21 Tue 18:00 P2

Modelling genome condensation and membrane bending in SARS-CoV-2 — •Nils O. Winkler, Sarah M. Seibert, Falko Ziebert, and Ulrich S. Schwarz — Institut Theoretische Physik & BioQuant, Uni Heidelberg

While many enveloped RNA-viruses use a rigid protein capsid to package and protect their genome, SARS-CoV-2 uses a high density of the transmembrane protein M to structurally reinforce its membrane, which then bends around the viral genome condensed by the cytosolic protein N. Interestingly, the RNA-genome seems to be further subdivided into smaller subunits, leading to a nested egg structure. We theoretically study the energetics of this situation by miminizing appropriate energy functions for genome condensation, membrane bending, droplet wetting and wrapping. In particular, we investigate which of these energy contributions can explain the nested egg structure as observed experimentally.

BP 14.22 Tue 18:00 P2

Modelling Wave Propagation on Monolayers — •Philipp Zolthoff and Jan Kierfeld — TU Dortmund University, Dortmund, Germany

Recent experimental advances have enabled precise studies of pressure wave propagation through monolayers at the air-water interface, triggered by light-induced conformation changes of embedded azobenzenes. We model wave generation and propagation using a fractional Lucassen-type wave equation and compare experimental results on pulse shape and pulse propagation in detail with numerical simulations in order to describe experiments quantitatively and unravel the influence of possible non-linearities and different rheological monolayer models. Particular attention is paid to the question how the influence of non-linearities and rheology changes for different states of the monolayer, i.e., in different regions along its Langmuir isotherm.

BP 14.23 Tue 18:00 P2

A synthetic flow system for modelling the vascular margination effect using microbeads — •Teresa M. Maunz, Alexandra Bienau, Friedrich Simmel, and Karen Alim — School of Natural Sciences, Technical University of Munich, Germany

The margination effect in the blood vasculature causes particles to migrate toward the blood vessel walls due to interactions with red blood cells (RBCs). Margination plays an important role in particle-based drug delivery targeted at the vascular endothelium, which requires contact with the endothelium for delivery. While margination has been studied with simulations and (some) experiments, how to control margination for synthetic particles is underexplored and requires thorough experimental testing of multiple variable parameters. Here, we present a synthetic microfluidic system dedicated to investigating the margination effect. The base system consists of a microfluidic channel carrying a binary suspension of beads, mimicking RBCs and marginating particles. Physiological conditions are emulated by tuning parameters that have been predicted to be crucial for the emergence and prominence of the margination effect, such as vessel diameter, RBC volume fraction, RBC deformability, the size ratio between RBCs and particles, and flow characteristics. We anticipate that our system will contribute to identifying key parameters that enable the margination effect, thereby improving our understanding of blood flow and facilitating the development of future drug delivery testing models.

BP 14.24 Tue 18:00 P2

Effects of perfluorocarbons on lipid monolayers and protein adsorption — •Jaqueline Savelkouls[1], Michael Paulus[1], Christian Thiering[1], Michelle Dargasz[2], Lena Friedrich[1], Mike George[1], Prashant Hitaishi[3], Svenja Hövelmann[3,4], Oleg Konovalov[5], Eric Schneider[1], Gordon Scholz[1], Chen Shen[4], and Metin Tolan[1] — [1]Technische Universität Dortmund, Germany — [2]Universität Siegen, Germany — [3]Christian-Albrechts-Universität zu Kiel, Germany — [4]DESY, Hamburg, Germany — [5]ESRF, Grenoble, France

Lipid monolayers serve as biomimetic models to study structural and functional aspects of protein-membrane interactions, which are essential for understanding physiological functions. Investigating how perfluorocarbon (PFC) effects on these interactions may aid new therapeutic strategies. This study examines the influence of various PFCs on structural changes of lung-surfactant-like DPPA and DPPC monolayers at different initial surface pressures, as well as on the adsorption behavior of surface-active proteins. Experiments were conducted at beamlines ID10 (ESRF, Grenoble) and P08 (PETRA III, Hamburg) under ambient conditions using a combined grazing incidence X-ray diffraction and X-ray reflectivity study. The results demonstrate that the effect of the PFCs on the lipid structure and protein adsorption depends on the chemical characteristics of the PFCs, the lipid type, and the lipid phase. This work will discuss how the adsorption of PFCs at the membrane promotes protein association.

BP 14.25 Tue 18:00 P2

Local dynamical properties of lipid bilayers using Scanning Ion Conductance Microscopy (SICM) — •Eric Lieberwirth[1], Franziska Dorn[1], Regina Lange[1], Una Janke[2], Mihaela Delcea[2], Ingo Barke[1], and Sylvia Speller[1] — [1]Physics of Sur-

faces and Interfaces, Institute of Physics & LLM, University of Rostock, Germany — [2]Biophysical Chemistry, Institute of Biochemistry, University of Greifswald, Germany

To determine dynamical properties of lipid bilayers, various experimental methods have been established, e. g. contour analysis and fluctuation spectroscopy. Based on Helfrichs theory from 1973 [1], bending rigidity and membrane tension of lipid bilayers can be derived. We demonstrate a local measurement approach by Scanning Ion Conductance Microscopy (SICM) on Giant Unilamellar Vesicles (GUVs) for evaluation of dynamic lipid bilayer properties. Using a nanopipette controlled via a feedback loop to maintain constant membrane-tip distance, we record time traces of local membrane height fluctuations with nanometer precision. In a contour analysis like approach [2], we obtain a bending rigidity of a few k_BT and membrane tension of a few $\mu\mathrm{Nm}^{-1}$. Computation of the power spectral density (PSD) based on [3] combined with a global-local fit provides a second evaluation route with same data set, yielding in similar results. Differences and limitations of both methods are discussed.

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[2] J. F. Faucon et al., J. Phys. France 50 (1989), p. 2389-2414
[3] T. Betz & C. Sykes, Soft Matter 8 (2012), p. 5317-5326

BP 14.26 Tue 18:00 P2

Influence of PLIN5 and Lipid Composition on Lipid Droplet Contact Sites with other Organelles — •Mahsa Mohammadian, Shima Asfia, and Ralf Seemann — Department of Experimental Physics and Center for Biophysics, Saarland University, Saarbrücken, Germany

Lipid droplets (LDs) maintain cellular lipid homeostasis through dynamic interactions with other organelles. Understanding how these contact sites form is crucial for uncovering the mechanisms of lipid exchange and signaling. In this study, we used an in vitro model to investigate how lipid composition and the LD-associated protein perilipin 5 (PLIN5) influence contact formation between an LD monolayer and a bilayer membrane. Artificial LDs consisting of triolein and coated with either a DOPE or DOPC monolayer containing PLIN5 or not were incubated with large unilamellar vesicles (LUVs) that mimic the bilayer membrane of the organelle. Using double fluorescence labeling of the LUV bilayer and the core, we can distinguish between fusion of the LUV bilayer with the LDs and stable attachment of LUVs to the LD's surface. Our results show that the probability of fusion between LDs and LUVs is greatly increased for DOPE-coated LDs, while PLIN5 promotes the stable attachment of LUVs to the LD's surface and prevents fusion. These observations illustrate how certain lipid and protein components can modulate contact formation between LDs and membranes in a controlled in vitro system, and provide a basis for future studies on the molecular mechanisms of organelle communication.

BP 14.27 Tue 18:00 P2

Elucidating the dynamics of DNA-based Transmembrane Receptors through Molecular Dynamics Simulations — •Cyrille Ngueldjou Tahabo[1], Doruk Baykal[2], Lorena Baranda Pellejero[2], Andreas Walther[2], and Lukas Stelzl[3,4] — [1]Institute of Physics,University of Johannes Gutenberg,Mainz,Germany — [2]Department of Chemistry,University of Johannes Gutenberg,Mainz,Germany — [3]Institute of Molecular Physiology, University of Johannes Gutenberg, Mainz, Germany — [4]Institut of Molecular Biology, Mainz (IMB), Germany

Building an artificial cell is an essential step to creating artificial life-like systems and a critical step in this endeavour is to design molecular systems which enable the communication of an artificial cell with its environment. Such artificial life-like systems hold great promise for biomedical engineering. By mimicking biological mechanisms to enable the transmission of information from the exterior of artificial cells across membranes to their interior, we will contribute to creating new artificial life-like systems and gain insights to essential biological information processing mechanisms and advance simulation method development, using an atomistic molecular dynamics and Coarse Grained simulations approaches, who can be synthesized to function as receptors in artificial life-like systems. we study DNA attached to an anchor insert in lipid membranes. In the simulations we investigate how Anchor interacts with the membranes and how DNA-Anchor changes local membrane structure.

BP 14.28 Tue 18:00 P2

Ray-based simulation and experimental analysis of red blood cell imaging in brightfield microscopy — •Aaron Kreis, Sarah Tabea Hermes, Thomas John, and Christian Wagner — Experimental Physics, Saarland University

The interpretation of brightfield microscopy images of red blood cells (RBCs) requires a quantitative understanding of how light propagates through their biconcave geometry. We present a numerical ray-tracing framework that models refraction and reflection at the cell–medium interface according to Snell's and Fresnel's laws, explicitly reproducing the optical configuration of a brightfield microscope. The simulated intensity distributions show excellent quantitative agreement with experimentally measured axial intensity profiles acquired using a conventional inverted microscope. This confirms that geometrical optics adequately describe light propagation through RBCs, as diffraction effects remain negligible for micrometer-scale objects. The approach enables label-free prediction of contrast and focus-dependent image formation, paving the way for future quantitative assays of single-cell oxygenation and advanced label-free imaging.

BP 14.29 Tue 18:00 P2

Photothermal imaging of autofluorescent retinal pigment epithelium (RPE) granules — •Sicheng Tian[1,2], Maryam Ali[1,2], Hanan Alderzy[1,3], Christoph Krafft[1,2], Martin Hammer[1,3], and Daniela Täuber[1,2] — [1]Friedrich Schiller University Jena — [2]Leibniz Institute of Photonic Technology, Jena — [3]Jena University Hospital, Jena, Germany

The retinal pigment epithelium (RPE) plays an important role in the photocycle. RPE cells contain varied amounts of micrometer-sized autofluorescent granules, including melanosomes (M), lipofuscin (L) and melanolipofuscin (ML), whose distribution varies throughout the RPE layer and with increasing age. Non-invasive fundus autofluorescence is used for clinically monitoring the distribution of L and ML. Specific alterations in the distribution of L, ML and M are linked to age-related macular degeneration (AMD)[Bermond et al., IOVS, 2020, 61, 35]. In spite of their importance, their chemical composition is not fully understood. Mid-IR Photo-induced Force Microscopy (PiF-IR) can provide a chemical evaluation of cell and organelle surfaces with less than 5 nm spatial resolution [Ali et al., Anal. Chem., 2025, 97, 23914] by combining powerful infrared illumination with mechanical detection using atomic force microscopy (AFM-IR). We utilized PiF-IR for the investigation of isolated M in a dried droplet. We complemented our study by sub-micron photothermal images using Optical Photothermal Infrared spectroscopy (O-PTIR) under illumination at visible wavelengths. We compare the results to PiF-IR spectra and conventional Fourier-transform IR spectra obtained on membrane phospholipids.

BP 14.30 Tue 18:00 P2

Multimodal imaging with light microscopes and scanning small angle X-ray scattering — •Boram Yu[1], Mangalika Sinha[1], Rita Mendes da Silva[1,2], Ulrike Rölleke[1], Manfred Burghammer[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]The European Synchrotron, Grenoble, France

Imaging biological cells using X-rays is a complementary approach to electron and fluorescence microscopy due to their high penetration depth and the possibility for label-free imaging. One such technique is scanning small angle X-ray scattering (SAXS), which enables the acquisition of a real-space overview image with moderate resolution and reciprocal-space information with high resolution of cells in aqueous environment. However, intracellular structures in aqueous environment are very sensitive to radiation; therefore, the investigation of such damage requires additional imaging techniques beyond scanning SAXS. We present a scanning SAXS configuration, which integrates a mobile fluorescence microscope and an on-axis bright field microscope with a microfluidic sample chamber. The microfluidic sample chamber is compatible with X-ray measurement, as well as two microscopes, owing to its very thin design. While the fluorescence microscope enables obtaining correlative images before and after X-ray scanning within a short time span, the bright field microscope produces bright field images simultaneously during the scan. Our approach provides complementary information on specimens to X-ray measurements, thereby demonstrating its applicability in various fields.

BP 14.31 Tue 18:00 P2

Receptor-Mediated Binding Kinetics of Ligand-Functionalized Lipid Nanoparticles for Targeted mRNA Delivery — •Tianyi Cao — Faculty of Physics and Center for NanoScience, Ludwig Maximilians University, Munich 80539, Ger-

many

For targeted mRNA delivery, lipid nanoparticles (LNPs) are functionalized with PEG-lipid tethers that display affinity ligands–such as full antibodies, Fab fragments, or peptides–to enable receptor-specific cell binding.

We establish a quantitative single-cell binding assay to characterize these receptor-mediated interactions using functionalized LNPs. Using time-lapse live-cell imaging on single-cell arrays (LISCA), we track individual particles via fluorophore-labeled lipid components incorporated directly into the LNP membrane. We systematically vary the molar fraction of functionalized PEG-lipids to quantify how ligand density influences binding probability and saturation behavior.

From these trajectories we extract apparent on-rates, binding capacities, and cell-to-cell variability arising from heterogeneous receptor expression. Under controlled shear flow, we distinguish diffusion-limited from reaction-limited binding and quantify how hydrodynamic forces modulate bond formation and stability.

We further extend the framework to multivalent LNPs carrying mixtures of different ligands that target distinct receptors on the same cell. This assay provides a mechanistic, single-cell-resolved readout of receptor-mediated LNP binding, enabling rational optimization of selective mRNA delivery formulations.

BP 14.32 Tue 18:00 P2

Optical properties of red blood cells and refractive index of hemoglobin — •Sarah Tabea Hermes, Agatha Belén Pinto Pino, Thomas John, and Christian Wagner — Experimental Physics, Saarland University

As the determination of the oxygen saturation of whole blood is common practice in medicine, the research of the oxygenation state of individual red blood cells (RBCs) remains challenging. When observing RBCs under a light microscope, the image is a composition of absorption as well as refraction (since the refractive index inside the RBC is higher than in the medium) and further depends on the focal plane, see Poster Aaron Kreis. This is important both for determining the composition of the cell via absorption as well as for edge detection because the refraction leads to "ghost edges". It is thus relevant to research the optical properties of RBCs and in particular the refractive index of the hemoglobin inside the RBCs. This allows for better comparison with numerical simulations and enables to precisely match the refractive index of the medium and the RBCs. We will present a detailed measurements about the refractive index of hemoglobin solutions in comparison with literature values.

BP 14.33 Tue 18:00 P2

Time resolved fluorescence anisotropy of single phalloidin-dye complexed F-Actin fibrils: MD simulation and experiments. — Phillip Seeber[1], •Shangjun Cheng[1,2], Lukas Spantzel[1,3], Rainer Heintzmann[1,2], and Daniela Täuber[1,2] — [1]Friedrich Schiller University Jena — [2]Leibniz Institute of Photonic Technology, Jena — [3]Jena University Hospital, Jena

Phalloidin conjugates are widely used to visualize actin filaments (F-Actin) due to their high binding affinity [1]. Fluorescence polarization imaging adds information on cellular structures known from other approaches [2, 3]. Moreover, super-resolution techniques such as STED and SIM often employ polarization optics. For aligned samples, such as actin filaments, insights in fluorophore orientation and wobbling dynamics will improve the interpretation of experimental results. Here, we apply quantum chemical methods including DFT, TD-DFT and ADC(2) to study the trajectory of the dye*s transition dipole moments during thermal fluctuations. We correlate the MD simulations with fluorescence anisotropy measurements acquired using time-resolved fluorescence lifetime imaging (FLIM) and 2D polarization fluorescence imaging (2D-POLIM) [3]. [1] Melak M., Plessner M., et al. Journal of cell science, 2017, 130, 525. [2] Rimoli, C. V., Valades-Cruz C.A., et al. Nat Commun 2022, 13, 301. [3] Camacho R., Täuber D., et al. Communications Biology, 2018, 1, 157.

BP 14.34 Tue 18:00 P2

Nanomechanical ultrastructure of native skin — •Mario Zerson[1], Martin Dehnert[1], Paul Zech[1], Melanie Knaak[2], Korinna Jöhrens[2], Martin Kaatz[3], and Robert Magerle[1] — [1]Fakultät für Naturwissenschaften, TU Chemnitz — [2]Institut für Pathologie, Klinikum Chemnitz gGmbH — [3]Hautklinik, DRK Krankenhaus Chemnitz-Rabenstein

Native skin has a complex, layered structure across the epidermis and dermis. In this study, we explore the use of atomic force microscopy (AFM) to examine the nanomechanical morphology of skin under controlled relative humidity conditions that maintain water content close to physiological levels. We examined cryosections of native, unfixed rabbit skin with tapping mode AFM and AFM-based nanoindentation measurements. This enables imaging the nanomechanical ultrastructure of the stratum basale in the epidermis and of collagen fibrils in the dermis with 20 nm spatial resolution. The results are compared with optical micrographs of adjacent stained sections of the same specimen and with scanning electron micrographs reported in the literature.

BP 14.35 Tue 18:00 P2

Red Blood Cell shape classification using curvature flow and spherical harmonics — •Nikolas Lerch, Felix Maurer, Diana Örüm, and Thomas John — Universität des Saarlandes

The morphological characterization of erythrocytes deformed due to pathology or disease has traditionally relied on manual assessment, which introduces subjective sources of error and hampers the differentiation of closely related morphologies such as echinocytes and acanthocytes. We present an automated method for the objective classification of deformed erythrocytes. The approach employs a bijective mapping of surface curvature onto a reference sphere via curvature flow and decomposes the resulting features into spherical harmonics. The resulting spectral signatures enable the assignment of cells to morphologically distinct clusters. The method is quantitative and reproducible, explicitly identifies transient shapes and transition regions between morphologies, recognizing them as such and distinguishing them from clearly defined class expressions, and thereby opens new perspectives for computer-assisted hematology.

BP 14.36 Tue 18:00 P2

Diffusion and deoxygenation/oxygenation of hemoglobin solutions in microfluidics — •Agatha Belén Pinto-Pino, Sarah Tabea Hermes, Thomas John, and Christian Wagner — Experimental Physics, Saarland University

The observation of red blood cells (RBCs) under bright field microscopy allows the study of how absorption and refraction combine to form image contrast. In this work, we use the absorption of light to investigate the diffusion of hemoglobin in water in microfluidic channels. By analyzing how intensity profiles evolve over time, we characterize the diffusion behavior of hemoglobin in water. The setup will also be used to study the transition from deoxygenated to oxygenated hemoglobin, because the absorptions differ strongly for those states, in particular for different wave length of the light. This study helps for a better understanding of the mechanisms that govern oxygen transport in blood.

BP 14.37 Tue 18:00 P2

Implementation of NIR excitation and detection in 2D-POLIM setup — Shangjun Cheng[1,2], •Zilong Huang[1], Rainer Heintzmann[1,2], and Daniela Täuber[1,2] — [1]Friedrich Schiller University Jena — [2]Leibniz Institute of Photonic Technology, Jena

Two-dimensional polarization fluorescence imaging (2D-POLIM) has been used to probe the orientation/rotation of molecules and the Förster resonance energy transfer between closely located chromophores [Camacho et al., Adv. Mat. 2019, 31, 1805671; Camacho et al., Commun. Biol. 2018, 1, 157]. 2D-POLIM can provide full in-plane information on the polarization state of the sample through synchronized control of the excitation and detection polarizations. Near-infrared (NIR) excitation reduces the background from intrinsic autofluorescence in cells and tissue samples. Here, we show a stable, precisely controllable excitation polarization of a 785 nm laser. We also demonstrate the potential of 2D-POLIM in imaging and analysis of molecular orientation in the NIR range.

BP 14.38 Tue 18:00 P2

Metasurfaces for Oblique Plane Microscopy — •Maike Kreutz[1,2], Martijn Moorlag[1], Ibnun Nur Akash[3], Stephan Daetwyler[4], Sara Lelek-Greskovic[5], Ibnun Nur Akash[3], Yijun Wang[3], Chih-Yao Hsu[6], Yu-Chuan Chang[6], Yao-Wei Huang[6], Reto Fiolka[4], Florian Engert[1], Maryna L. Meretska[3], and Fabian F. Voigt[1] — [1]MCB, Harvard University — [2]RWTH Aachen University — [3]INT, Karlsruhe Institute of Technology (KIT) — [4]UT Southwestern Medical Center — [5]SCRB, Harvard University — [6]Department of Photonics, National Yang Ming Chiao Tung University

A promising emerging bioimaging technique is oblique plane light-sheet microscopy (OPM), which allows volumetric imaging using a single scan mirror but suffers from significant losses due to its complex optical path. To enhance the light-collection efficiency of OPMs, we propose to integrate optical metasurfaces into the optical path of an OPM. Metasurfaces utilize sub-wavelength nanostructures for manipulation of electromagnetic fields and can be produced with CMOS-compatible technology. By implementing tailored metagrating designs, we aim to reduce losses in single-objective light-sheet setups.

BP 14.39 Tue 18:00 P2

Lens-free lab-on-chip fluorescence microscopy using angle-stable polariton filters — •Anja Lindenau[1], Andreas Mischok[1], and Malte Gather[1,2] — [1]Humboldt Centre for Nano- and Biophotonics, Department of Chemistry, University of Cologne, Germany — [2]School of Physics and Astronomy, University of St Andrews, Scotland

Fluorescence microscopy is an essential tool in biomedical research but typically relies on complex optical setups with high-numerical-aperture objectives and specialised colour filters, which results in a large footprint and high acquisition costs. Here, we present a modified commercial CMOS image sensor for lens-free fluorescence microscopy. Lens-free imaging enables compact, low-cost systems with a large field-of-view (> 20 mm) and pixel-limited resolution (1.4 micrometer). To overcome the limitations of conventional colour filters, in particular their strong angular dispersion, we integrate a polariton-based filter directly on the sensor. This novel filter design exploits ultra-strong light-matter coupling between photons and material excitons, maintaining a stable long-pass cut-off below 540 nm over a broad range of incidence angles and thereby drastically improving the signal-to-noise ratio. Initial results highlight the potential for high-resolution on-chip lens-free fluorescence microscopy with significantly enhanced image quality.

BP 14.40 Tue 18:00 P2

Construction of Mueller Matrix Polarimeter with a Polarization Camera — •Kathrin Rott — Georg August Universität, Göttingen, Deutschland

A Mueller matrix polarimeter based on a division-of-focal-plane polarization camera has been developed for microscopy. The setup enables spatially resolved measurements of Mueller matrix elements in a single image acquisition, allowing the extraction of polarization parameters such as retardance, diattenuation and depolarization. The setup includes a polarization state generator (PSG) consisting of a linear polarizer and a rotating compensator, and a polarization state analyzer (PSA) implemented through the micro-polarizer array of the camera. This design allows fast measurement of Mueller matrix images with micrometer-scale resolution. Initial work focused on characterizing the camera, including calibration of nonlinear response, sensor homogeneity, polarization angle accuracy and pixelwise extinction ratio. The aim is to enable label-free imaging of biological cell cultures and to investigate whether polarization-based contrast can provide information about microstructures such as the cytoskeleton or nucleus. Unlike tissue samples, which typically exhibit polarization effects, the focus here lies on exploring polarization contrast in single cells. The project combines optical component development with a potential biophysical application and forms the basis for further studies on polarization contrast in cell culture imaging.

BP 14.41 Tue 18:00 P2

Quantification of in vivo flow of blood cells - adhesion cascade — •Khadija Larhrissi[1], Felix Maurer[1], Selina Wrublewsky[2], Alexis Darras[3], and Christian Wagner[1] — [1]Department of Experimental Physics, University Campus, Saarland University, 66123 Saarbrucken, Germany. — [2]Institute for Clinical and Experimental Surgery, Saarland University, 66421 Homburg, Germany — [3]School of Physics, University of Bristol, Bristol, United Kingdom)

Red blood cells (RBCs) constitute the majority of cells in the blood and play a key role in transporting oxygen to tissues and organs. On the other hand, leukocytes, also known as white blood cells (WBCs), make up approximately 1% of the total blood volume in most mammals. The flow of these cells ensures the body's defense against various viral and bacterial infections. The WBCs exhibit two modes of motion: a fast flow mode where they move with the surrounding fluid, and a slower rolling mode where they partly adhere to the wall, whereas RBCs simply flow with the surrounding fluid. In this study, our objective is to examine the influence of geometry and distribution on the flow of WBCs. To achieve this, we used Golden Syrian Hamsters as a model system to quantify the flow of cells by fluorescence microscopy and compare their behavior in different networks of vessels. Additionally, since some WBCs are larger in size than the capillaries they pass through, we will examine the impact of this size difference on their flow.

BP 14.42 Tue 18:00 P2

Visualizing Immune Cell Behaviour in 3D: An Ex Vivo Lattice Lighsheet Microscopy and Analysis Framework — •Anna Schepers[1], Joannah Fergusson[1], Edward Wheeler[1], Jacky Ko[1], Robert Kochl[2], and Marco Fritzsche[1] — [1]Kennedy Institute of Rheumatology, University of Oxford, UK — [2]King's College London, UK

The inherently multiscale immune response is regulated by diverse cell interactions, relying on cues from tissues down to single cells and subcellular structures. The intricate dynamics of the immune system present challenges for the observation of the immune response. A technological advance has been achieved with the introduction of lattice light sheet microscopy (LLSM), allowing fast and gentle imaging of live samples while achieving subcellular resolution. By complementing LLSM-based volumetric imaging with advanced sample handling of ex vivo tissue samples and perfusion imaging chambers, we provide a system that preserves critical physiological complexity. We present a complex data processing and analysis framework for robust 3D segmentation and tracking cells in the complex tissue environment allowing cell profiling from live cell behaviour. We show that in our setup, we can follow single cells and their interactions in volumes several cell layers deep in living samples within their environment, providing nuanced insights into the immune response.

BP 14.43 Tue 18:00 P2

Large-area AFM SmartMapping for contact lens characterization and mechanobiological tissue analysis — •Jörg Barner, Andre Körnig, Joan-Carles Escolano, and Thomas Henze — BioAFM, Bruker Nano Surfaces, Am Studio 2D, 12489 Berlin, Germany

Atomic force microscopy (AFM) provides quantitative nanoscale characterization of soft materials and biological systems, enabling analysis of surface topography, elasticity, and viscoelasticity under physiologically relevant conditions. We applied AFM to two distinct systems: ophthalmic contact lenses and highly corrugated tissues. For lenses, SmartMapping was used to acquire large-area curvature maps (up to several millimeters) combined with localized high-resolution measurements of nanomechanical properties. Silicone hydrogel lenses were analyzed, revealing heterogeneities in elasticity critical for balancing oxygen permeability and comfort. For biological samples, SmartMapping enabled automated imaging of rough, heterogeneous specimens such as 3D tumor spheroids (>100 um) and brain tissue sections (>300 um), capturing stiffness gradients relevant to mechanotransduction and transport. The synchronized XYZ-piezo and AFM head movement ensured reproducible mapping across extended areas without manual intervention, overcoming limitations of conventional AFM in lateral range and throughput. These results demonstrate that SmartMapping integrates large-scale imaging with nanoscale precision, establishing AFM as a robust platform for material optimization in ophthalmology and spatially resolved mechanobiological studies.

BP 14.44 Tue 18:00 P2

X-ray holo-tomography reveals 3D structure of protein networks and lipid globules in heat-treated egg yolk — •Felix Wittwer[1,2], Nimmi Das Anthuparambil[2], Frederik Unger[2], Randeer Pratap Gautam[2], Silja Flenner[3], Imke Greving[3], Christian Gutt[2], and Peter Modregger[1,2] — [1]Deutsches Elektronen-Synchrotron DESY, Hamburg, Germany — [2]Universität Siegen, Siegen, Germany — [3]Helmholtz-Zentrum Hereon, Geesthacht, Germany

Egg yolk is a versatile ingredient for cooking and food processing. As a natural emulsifier, it allows to bind fats and water. Under heating, the texture and consistency of egg yolk changes due to denaturation, aggregation, coagulation and gelation. By using X-ray holo-tomography, we could study the heat-induced changes in egg yolk on the micron to sub-micron length scale. In contrast to other techniques such as electron microscopy, X-ray holography can be used without sample staining, fixation, or drying, which potentially alter or damage the sample. Our results reveal a developing separation between proteins and lipids with fatty components rapidly aggregating into large globules around 40 micrometer in size.

BP 14.45 Tue 18:00 P2

Realignment and realization of polarization-resolved confocal FLIM — •Lizhong Mou[1], Shangjun Cheng[1,2], Subham Adak[1,2], Maryam Ali[1,2], Daniela Täuber[1,2], and Rainer Heintzmann[1,2] — [1]Friedrich Schiller University Jena — [2]Leibniz Institute of Photonic Technology, Jena

Fluorescence lifetime imaging microscopy (FLIM) is an attractive technique in the life sciences that enables quantitative mapping of excited-state lifetimes in the regime of nanoseconds within microscopic images [Le Marois et al., J. Biophot. 2017, 10,1124]. Conventional fluorescence polarization is widely used to assess the orientation and rotation of molecules but typically relies on millisecond acquisition times [Camacho et al., Adv. Mat. 2019, 31, 1805671]. Here, we present an alignment protocol for polarization-resolved confocal FLIM that delivers nanosecond temporal resolution and high-quality imaging. We further investigate time-resolved polarization states of dye molecules from cell and tissue samples.

BP 14.46 Tue 18:00 P2

Physics Informed Neural Networks for Microbial Interaction Network Inference — •Luca Battiston[1,2] and Frank Cichos[1] — [1]Universität Leipzig, Linnestr. 5, 04103, Leipzig, Germany — [2]Helmholtz Centre for Environmental Research GmbH (UFZ), Permoserst. 15, 04318, Leipzig, Germany

Recent advances in machine learning have enabled data-driven modeling of complex dynamical systems, with growing interest in methods that extract meaningful information about the underlying physical laws. Among these, Physics-Informed Neural Networks (PINNs) have emerged as a powerful tool for system identification, particularly in settings where data are scarce or noisy. On the other hand, generalized Lotka-Volterra (gLV) equations are widely used to model microbial community dynamics, provided that the underlying interaction matrix is known. In this work, we aim to reconstruct these interactions by combining PINNs with Least Squares Regression for inference of the interaction network. We evaluate our method using extensive gLV simulations covering a range of interaction matrix complexities and noise levels. Our results demonstrate high accuracy in network recovery and show that the approach retains robustness under measurement noise. This provides a step toward developing a robust and flexible framework for identification of complex interaction patterns in microbial communities.

BP 14.47 Tue 18:00 P2

Experimental Setup for the Irradiation of Organoids with High-Energy Electron Beams — •Laura Andrea Pastor Luque[1], Natascha Thomas[2], Victor Emde[2], Carla Sprengel[1], Antonio Tarzikhan[2], Constantin Aniculaesei[2], Thomas Heinemann[2], Mirela Cerchez[2], and Thomas Heinzel[1] — [1]Condensed Matter Physics Laboratory, Heinrich Heine University, Düsseldorf, Germany — [2]Institut für Laser- und Plasmaphysik, Heinrich Heine University, Düsseldorf, Germany

Organoids are three-dimensional cell systems that mimic key physiological and structural characteristics of human tissues, making them highly relevant models for studying biological responses to ionizing radiation. However, experimental platforms for irradiating organoids with high-energy electron beams remain limited, particularly regarding precise dose control and sample handling. In this work, we present the design and development of an experimental irradiation setup specifically adapted for organoid cultures. The system integrates a high-energy electron beam source with a setup to irradiate organoids samples at different energy ranges (MeV).

BP 14.48 Tue 18:00 P2

Evolution-inspired exploration of pattern formation in reaction diffusion systems — •Ming Hong Lui[1,2] and Erwin Frey[1,2] — [1]Faculty of Physics, Ludwig Maximilian University of Munich, Germany — [2]Max Planck Schools Matter to Life, Max Planck Institute for Medical Research, Heidelberg, Germany

Protein reaction networks often contain complex network topology. Modelling them involves numerous variables such as concentrations, diffusion rates and kinetic coefficients. Each variable adds an additional dimension to the phase space that made sweeping parameters challenging and impedes comprehensive understanding of the full dynamics by demanding assumptions or simplifications of biological systems.

Here, we present an alternative pipeline to full parameter sweeps, to characterize pattern-forming regimes, by applying an evolutionary algorithm. We iteratively bootstrapped parameter combinations that demonstrated instability using linear stability analysis. Together with applying mutations, represented by random displacements on the high-dimensional phase space, we could focus our attention in the vicinity of instabilities to reconstruct a heuristic phase diagram more effective than evenly-spaced parameter sweeps.

We shall demonstrate how this algorithm can be applied to various reaction-diffusion models, where it provided more informed choices of diverse systems to run full numerical simulations on, bridging the gap bewteen analytical and numerical solutions.

BP 14.49 Tue 18:00 P2

Pancreatic Network Morphogenesis — •Yasmin Abdelghaffar[1], Coline Schewin[2], Szabolcs Horvát[3], Monalisa Mishra[2], Lydie Flasse[2], Carl Modes[2,4], Anne Grapin-Botton[2], and Benjamin M. Friedrich[1,4] — [1]Cluster of Excellence Physics of Life, Technical University Dresden, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]Reykjavik University, Reykjavik, Iceland — [4]Center for Systems Biology Dresden, Dresden, Germany

During the course of development, the mammalian pancreatic ductal network remodels from a fully connected plexus to a tree-like branched network optimized for fluid transport. Previous in silico modeling suggested that this remodeling could be guided by flow through the network [1]. However, the physical mechanism of flow sensing in the developing pancreas remains open.

We quantitatively analyze duct network morphology at subsequent developmental time-points, to reverse-engineer putative physical mechanisms of network remodeling. This includes a spatial zonation of statistical network properties and an empirical Murray's law relating duct diameter to hierarchy level (Strahler number). We put forward theoretical descriptions, e.g., of cilia-based flow sensing, which reproduce distinct variants of Murray's law, which could be distinguished by future experiments.

[1] Dahl-Jesen et al., PLoS Biology, 2018.

BP 14.50 Tue 18:00 P2

A Mathematical Model of Microlesion-Driven Calcium Signalling in Fibroblast Networks — •Kara Nachtnebel[1,2,3,5], Eric Greto[1,2,3], Anna Möller[1,2,3,6], Christian Maueröder[1,2,3], David B. Blumenthal[6], Vasily Zaburdaev[4,5], and Stefan Uderhardt[1,2,3] — [1]Department of Medicine 3 - Rheumatology and Immunology, FAU und Universitätsklinikum Erlangen — [2]Deutsches Zentrum für Immuntherapie, FAU — [3]Exploratory Research Unit, Optical Imaging Centre Erlangen, FAU — [4]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU) — [5]Max-Planck-Zentrum für Physik und Medizin, Erlangen — [6]Department of Artificial Intelligence in Biomedical Engineering, FAU, Erlangen, Germany

Resident tissue macrophages (RTMs) maintain tissue homeostasis by continuously sensing and integrating local environmental signals. The interstitial fibroblast network, an omnipresent, self-interconnected system capable of generating intracellular calcium signals and transmitting them to neighbouring cells, provides signals that RTMs can detect and respond to. For example, in response to calcium elevations associated with tissue lesions, macrophages initiate rapid cloaking behaviour. Disruption of fibroblast networks can amplify unwanted immune activation and may contribute to the development of autoimmune diseases. We present a mathematical model of microlesion-induced calcium signalling in gap-junction-coupled fibroblast networks. It shows how microlesions drive signal propagation via intra- and extracellular pathways and quantifies the factors that shape this process.

BP 14.51 Tue 18:00 P2

Equal Partitioning of the Min Proteins at Cell Division — •Natan Dominko Kobilica[1], Nora Deiringer[2], Vitalii Grigorev[3], Antonia Winter[1], Robin Köhler[4], Sean Murray[5], Viktor Sourjik[3], Henrik Weyer[6], and Erwin Frey[1] — [1]ASC, LMU München, Munich, Germany — [2]Technical University of Munich, Garching, Germany — [3]Max Planck Institute for Terrestrial Microbiology, Marburg, Germany — [4]Geomagic, Leipzig, Germany — [5]IMESO-IT, Giessen, Germany — [6]Kavli Institute for Theoretical Physics, University of California, Santa Barbara, Santa Barbara, USA

The pole-to-pole oscillation of the Min proteins in Escherichia coli plays a crucial role in the process of cell division. The oscillation facilitates the formation of the FtsZ ring, which determines the division site.

It is essential that the Min proteins are distributed equally between daughter cells to ensure precise determination of the division site in subsequent divisions. Previously, experiments and stochastic particle-based simulations have linked protein equipartition to the splitting of the pole-to-pole oscillation. Importantly, the splitting is already triggered before the division is fully completed. The goal of this study is to explain the mechanism underlying the splitting of oscillations using the well-known reaction-diffusion equations for the Min System. We model the constriction during cell division as a reduced diffusion rate between the two parts of the mother cell. This already captures the oscillation splitting and agrees well with realistic simulations of the constricting cell. Additionally, we conduct high-throughput microfluidic experiments which align well with the predicted protein dynamics.

BP 14.52 Tue 18:00 P2

Information Processing and Scaling of Spatially Coupled Complex Networks — •Ambar Neel[1,2,3] and Carl Modes[1,2,3] — [1]Max Planck Institute for Molecular Cell Biology and Genetics (MPI-CBG), Dresden 01307, Germany — [2]Center for Systems Biology Dresden (CSBD), Dresden 01307, Germany — [3]Cluster of Excellence, Physics of Life, TU Dresden, Dresden 01307, Germany

Biological adaptive spatial networks are constantly grappling with increasing the efficiency of the network while minimising the metabolic costs. Simulations demonstrate that incorporating fluctuations in a system's sinks/sources leads to the onset of topological complexity in the network. Additionally, it has recently been shown that coupling two spatial networks also results in topological complexity categorised by the existence of loops. This framework is very well suited to investigating information processing in such spatially coupled networks and is thus the focus of this presentation. Along with organ systems such as the pancreas, kidney and bone marrow, the liver is a prime candidate for this analysis as it consists of bile and blood capillary systems that are interwoven. Another challenge is to understand the packing limit of these complex spatial networks by scaling them until a critical point is reached. This provides a meaningful length-scale for the system, allowing for further investigation into fundamental questions regarding geometrical aspects of these spatially embedded complex networks as well as setting up the template to compare these results to experimentally acquired datasets of sinusoids in the liver lobules of mice.

BP 14.53 Tue 18:00 P2

Chimeric RNA-DNA Oligomers Overcome Template-Product Inhibition in Prebiotic Ligation — •Lena Mühlschlegel, Ludwig Burger, and Ulrich Gerland — Physics of Complex Biosystems, School of Natural Sciences, Department of Bioscience, Technical University of Munich, Garching, Germany

The RNA world hypothesis proposes that DNA-based life evolved from a precursor living system that used RNA alone to store genetic information. However, it is unclear how the transition from a system purely based on RNA to one incorporating DNA could have occurred. At the transition, a lack of specificity in the synthesis of genetic polymers in prebiotic systems likely led to the simultaneous emergence of RNA and DNA, involving molecules comprising RNA-DNA nucleotides, which we refer to as chimeric RDNA strands. Because homogeneous RNA-RNA and DNA-DNA duplexes are highly stable, template-product inhibition can impede template-directed ligation. Experimental data show that RDNA-DNA or RDNA-RNA duplexes tend to be less stable than RNA-RNA and DNA-DNA duplexes, suggesting that RDNA strands might overcome template-product inhibition. We developed a nearest neighbor model parametrized by experimental data to predict RDNA hybridization energies as a function of sequence and used it to simulate template-directed ligation of RNA and DNA in the presence and absence of RDNA strands. We found a hybridization free energy regime in which RDNA strands enable the efficient replication of RNA and DNA, providing a potential pathway for the early evolutionary transition from RNA to DNA.

BP 14.54 Tue 18:00 P2

FRET-guided selection of RNA 3D structures — •Mirko Weber[1], Felix Erichson[1], Maciej Antczak[2,3], Vanessa Schumann[1], Josephine Meitzner[1], Tomasz Zok[3], Fabio D. Steffen[4], Marta Szachniuk[2,3], and Richard Börner[1] — [1]Laserinstitut Hochschule Mittweida, University of Applied Sciences Mittweida, Mittweida, Germany — [2]Institute of Bioorganic Chemistry, Polish Academy of Sciences, Poznan, Poland — [3]Institute of Computing Science, Poznan University of Technology, Poznan, Poland — [4]Department of Oncology, University of Zurich, Zurich, Switzerland

Integrative RNA modeling requires structurally validated ensembles and experimental data that reflect binding and folding behavior. However, predicting such structure collections remains challenging due to rugged energy landscapes and extensive conformational heterogeneity. We address these limitations with a FRET-guided selection strategy that identifies RNA conformational states consistent with single-molecule FRET (smFRET) data. We predicted 3D structures of a ribosomal RNA tertiary contact containing a GAAA tetraloop and a kissing loop using RNAComposer, FARFAR2, and AlphaFold3, and validated them based on Watson-Crick base pairing and an eRMSD threshold. For all retained models, we computed accessible contact volumes of the sCy3/sCy5 dye pair using FRETraj and derived FRET distributions, which were weighted against experimental smFRET data. Our results demonstrate that in silico predicted structures can reproduce the experimental transfer efficiencies, and that our selection reliably identifies RNA conformations consistent with the smFRET data.

BP 14.55 Tue 18:00 P2

Intrinsically disordered regulators of endocytosis - an integrated NMR/single molecule fluorescence approach — •Sigrid Milles — Leibniz-Forschungsinstitut für Molekulare Pharmakologie (FMP), Berlin, Germany

Intrinsically disordered proteins (IDPs) lack clearly defined structure and are therefore highly flexible and easily adaptable to different binding partners. This makes them important players in many biological processes, often with vital regulatory functions. Their dynamic features and broad range of interaction modes, however, render them difficult to study and analyzing their complexes often requires integrated approaches. Integrating complementary parameters from of nuclear magnetic resonance (NMR) and single molecule fluorescence approaches allowed us to describe the conformational landscape of IDPs at molecular resolution and promises to shed new light onto various biological processes. Among those counts clathrin mediated endocytosis. The early phases of clathrin mediated endocytosis are organized through a highly complex interaction network mediated by clathrin associated sorting proteins (CLASPs) that comprise long intrinsically disordered regions (IDRs). We characterize the IDRs of those CLASPs in their entirety and at molecular resolution, uncovering a plethora of interactions of various strengths and dynamic features with their endocytic interaction partners, proposing a rationale for how first interactions and dynamic rearrangement of partners take place during the uptake of a coated vesicle.

BP 14.56 Tue 18:00 P2

Adaptive NK cell analysis by t-SNE — •Andrea Schneider[1], Wiebke Moskorz[2], Jörg Timm[2], and Thomas Heinzel[1] — [1]Heinrich-Heine University Duesseldorf — [2]University Hospital od Duesseldorf

High-dimensional flow cytometry data from Natural Killer (NK) cells, collected using a comprehensive panel of typical and adaptive NK cell markers, poses a challenge for the characterization of complex cell subsets. To visualize the complete receptor expression profile in a two-dimensional cellular plot, we applied t-distributed Stochastic Neighbor Embedding (t-SNE) to the multi-parameter dataset. The resulting t-SNE projection successfully resolved distinct immune subpopulations regarding NK cell development and adaptive NK cells. Crucially, the map enabled the simultaneous visualization and comparison of different definitions of adaptive NK cells (including NKG2C+ and FceRIg- subsets within mature NK cells), visually confirming their close relatedness. Furthermore, while CD95 is known to be increased in adaptive NK cells, the t-SNE visualization clearly confirmed that this high expression level is consistently shared across all defined adaptive cell clusters, which were tightly localized within the embedding. This methodology demonstrates the power of non-linear embedding techniques for validating complex immunological phenotypes. Moreover, it establishes a visual framework for comparative studies of NK cells across different patient groups, including Hepatitis C Virus (HCV) seronegative, chronically HCV infected, and HCV resolved donors, with each cohort further stratified by Cytomegalovirus serostatus.

BP 14.57 Tue 18:00 P2

Exploring coarse graining RNA force fields via Machine Learning — •Anton Emil Dorn[1], Emile de Bruyn[1], Fabrice von der Lehr[3], Stefan Kesselheim[1,4], Philipp Knechtges[3], and Alexander Schug[2] — [1]Forschungszentrum Jülich — [2]KIT — [3]DLR Köln — [4]Universität zu Köln

In Protein structure prediction there have been massive improvements

recently with the help of machine learning. In RNA structure prediction however the situation is less ideal due too much sparser experimental data. Here we attempt to solve a modified version of the problem by determining a coarse-grained RNA force field for Molecular Dynamics simulations. The data sparsity can here be alleviated by atomistic RNA simulations using proven and established force fields. In a first step we show the viability of this approach with a limited scenario of only small RNA molecules. We also explore different bead numbers for the coarse graining to determine the best approximation.

BP 14.58 Tue 18:00 P2

Segmentation and classification of retinal pigment organelles in fluorescence lifetime imaging microscopy (FLIM) data — •Maryam Ali[1,2], Hala Alhaj Ahmed[3,4], Martin Hammer[4], Rainer Heintzmann[1,2,5], and Ondrej Stranik[1,2] — [1]Leibniz Institute of Photonic Technology, Jena, Germany — [2]Friedrich Schiller University, Jena, Germany — [3]Ernst-Abbe University of Applied Sciences, Jena, Germany — [4]Jena University Hospital, Jena, Germany — [5]Abbe Centre of Photonics, Jena, Germany

Retinal Pigment Epithelium (RPE) granules can be categorized based on their autofluorescence and morphology like Lipofuscin (L), Melanolipofuscin (ML), and Melanin(M)[1]. Fluorescence lifetime measurements reveal another discriminative feature; however, identifying individual granules remain challenging by human eye. Here, we present a computational analysis pipeline for segmenting and classifying RPE granules from fluorescence lifetime imaging microscopy (FLIM) data. The analysis was implemented in a custom Python script employing seeded watershed segmentation to isolate individual granules and discriminate hyperfluorescent lipofuscins, characterized by longer lifetimes. Granules with shorter lifetimes were further analyzed by examining their lifetime distribution across their surfaces, allowing MLs to be distinguished from other melanin-rich granules. The proposed approach achieved high performance, with mean sensitivity 87% and mean specificity 98% compared to manually classified ground truth data. [1] K. Bermond et al., IOVS 2020, 61, 35

BP 14.59 Tue 18:00 P2

Modeling the Clustering of Pma1 in the Yeast Plasma Membrane under Starvation — •Annemarie Quas[1], Roland Wedlich-Söldner[2], and Andreas Heuer[1] — [1]Institut für Physikalische Chemie, Universität Münster — [2]Institut für Zelldynamik und Bildgebung, Universität Münster

Starvation of yeast cells leads to the internalization of most plasma membrane (PM) proteins via endocytosis, strongly reducing the overall protein content of the PM. However, the level of the H^+-ATPase Pma1 is hardly affected by starvation. Instead, clustering of Pma1 is observed under these conditions. FF-EM images reveal 2D crystals composed of hexagonal units corresponding to Pma1 hexamers. Interestingly, deletion of Mrh1 blocks the clustering of Pma1. An interplay between the positively charged C-terminus of Mrh1 and the negatively charged phosphatidylserine (PS) is proposed, as Mrh1 is not required for clustering in the absence of PS. Because experimental insight into the mechanism of cluster formation is limited, we employ a coarse-grained Monte-Carlo model to investigate how interactions between Pma1 hexamers can drive large-scale organization. In our 2D model, Pma1 is represented as hexamers with attractive corner-to-corner interactions. By systematically varying particle density and interaction strength, we explore the system's phase behavior and identify conditions under which extended cluster formation emerges. We analyze cluster sizes, time-dependent growth, and characteristic cluster shapes to gain mechanistic insight into how molecular interactions could stabilize the observed protein crystals.

BP 14.60 Tue 18:00 P2

Refining Coarse-Grained Models for Accurate Protein Folding and Mechanics — •Yi-Chen Tsai and Chi-cheng Chiu — National Cheng Kung University, Tainan, Taiwan

Accurately modeling protein folding and mechanical behavior in coarse-grained (CG) simulations requires balancing structural fidelity with physical realism. We develop a mesoscale modeling framework that advances CG protein simulations by integrating refined structure-based and hybrid physics-based approaches. The Gō-type structure-based model is refined by incorporating overlaid native-specific potentials, backbone dihedrals, improper torsions, and sidechain interactions. These additions improve folding accuracy, suppress chiral inversion, and yield more realistic mechanical responses across diverse proteins[1]. Building on this, a hybrid CG approach denoted as GōSPICA is developed by combining native-contact potentials with the physics-based SPICA CG force field. The hybrid model enables spontaneous folding, reproduces native fluctuation patterns and force-extension behavior, and remains fully compatible with membrane environments without relying on elastic network restraints. Together, these developments establish a versatile CG modeling framework for simulating protein behavior in biologically relevant environments.

[1] Y. Tsai *et al.*, Phys. Chem. Chem. Phys., Advance Article (2025).

BP 14.61 Tue 18:00 P2

PINNs based inference in reaction-diffusion systems — •Lukas Pöschl[1,2] and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander Universität Erlangen-Nürnberg — [2]Max Planck Zentrum für Physik und Medizin

Physics-informed neural networks (PINNs) promise to serve as universal function approximators that embed governing equations and biophysical constraints to operate under noisy, low data conditions. However, PINNs exhibit various training pathologies that limit broad practical application beyond simple benchmarking problems. We identify situations in biophysical models where PINNs fail, including stiff kinetics, sharp gradients and chaotic dynamics and map these to corresponding failure modes in the standard PINN formulation, together with the respective mitigations. We assess this improved formulation on four problems with synthetically generated experimental data. These tasks include the classical forward and inverse problems for parameter estimation and inference of experimentally inacessible species. Furthermore, we address the issue of discovering chaotic and pattern forming dynamics and thus the optimization of experimental parameters to explore these biophysically relevant regimes. Across selected problems, the modified PINNs suggest promising performance in handling the tested systems and the ability to operate with sparse measurements and noisy data.

BP 14.62 Tue 18:00 P2

Self-assembly of sarcomeres by pairwise interactions in muscle fibers — •Amirali Zandieh, Abhinav Kumar, Francine Kolley-Köchel, and Benjamin M. Friedrich — Cluster of Excellence "Physics of Life", Dresden University of Technology

Walking, flying, and heartbeat are powered by the contraction of sarcomeres, the elementary contractile units of striated muscle, which are arranged in series into periodic myofibrils extending across the length of a muscle cell [1]. While the physical principles underlying sarcomere self-assembly remain unclear, recent work on Drosophila indirect flight muscle revealed that myosin motor filaments, Z-disk proteins, and titin/Sallimus form an initial periodic pattern, with actin filaments becoming polarity-sorted only later, motivating 1D minimal models [2].

To develop more realistic 3D descriptions of myofibrillogenesis and capture their cross-sectional organization, we employ ESPResSo [3] for agent-based simulations. With only pairwise interactions, sarcomere-like periodic patterns emerge and become registered in-phase along the transverse direction, as quantified by Kuramoto order parameters. Additionally, the catch-bond behavior of actin crosslinkers enhances and stabilizes this order. Together, these results show that pairwise interactions between sarcomeric components are sufficient to drive the emergence of order, marking a key step toward understanding the physical basis of sarcomere self-assembly.

[1] F. Kolley, et al. PRX Life (2024) [2] F. Kolley-Köchel, et al. Biophysical Reviews, in press [3] Weik, Florian, et al. The European Physical Journal (2019)

BP 14.63 Tue 18:00 P2

Assessing the performance of quantum-mechanical descriptorsin physicochemical and biological property prediction — •Alejandra Hinostroza Caldas[1], Artem Kokorin[2], Alexandre Tkatchenko[2], and Leonardo Medrano Sandonas[1] — [1]TUD Dresden University of Technology, 01069 Dresden, Germany — [2]University of Luxembourg, L-1511 Luxembourg City, Luxembourg

Understanding how molecular structure relates to physicochemical and biological properties is essential for computer-aided drug design. A major challenge in applying machine learning (ML) to this problem is defining numerical representations that capture both geometric and electronic information. We introduce the QUantum Electronic Descriptor (QUED) framework [ChemRxiv, doi:10.26434/chemrxiv-2025-hj4dc], which integrates geometric descriptors (BOB, SLATM) with a quantum-mechanical descriptor (D_{QM}) that encodes global and local electronic properties computed efficiently with the DFTB method. We

validate QUED on the QM7-X dataset of small drug-like molecules and show that incorporating electronic structure information substantially improves ML predictions of physicochemical properties. For biological endpoints, QUED also demonstrates predictive value for acute toxicity (LD50) in TDCommons-LD50 and for lipophilicity in the MoleculeNet benchmark. Our findings underscore the benefits of integrating electronic structure information with geometric descriptors and highlight the role of conformational diversity in improving the robustness of molecular property prediction.

BP 14.64 Tue 18:00 P2

Modelling neuron growth dynamics and role of extra-cellular matrix — •Mathar Kravikass, Federica Furlanetto, Lars Bischof, Pritha Dolay, Ben Fabry, Sven Falk, Marisa Karow, and Vasily Zaburdaev — Friedrich-Alexander-Universität (FAU)

Biological tissues are composed of cells embedded in extracellular matrix (ECM) and extracellular fluid. We study the role of cell-matrix interactions in the context of brain tissues and the mechanism of neurite growth through this matrix. We consider two modes for the neurite growth: linear growth by tip extension and growth by the traction force at the tip of the neurite with the modeled ECM particles. In a liquid-like ECM model, we demonstrate how growth is influenced by the ECM interactions when the matrix is freely deformable. These growth patterns were also shown to fit to a run-and-tumble process, which describes how the interaction parameters relate to the persistence and speed of the growth. Additionally, solid-like ECMs were considered in which the ECM particles are connected by springs, thus forming a lattice. In this scheme, we were able to study more closely how lattice stiffness affects neurite growth patterns. These simulations recapitulated growth patterns of neurites in organoids models of neurodevelopmental disease and neurite growth in artificial ECMs with controlled properties. Finally, we present how this model could be used in the future to describe more complex systems, such as neuronal network formation.

BP 14.65 Tue 18:00 P2

Motion or Player? Identifying Structural Drivers of Rare Transitions — •Ali Sharifian and Alexander Schug — Scientific Computing Centre, Karlsruhe Institute of Technology, Karlsruhe, Germany

Rare transitions in complex molecular and soft-matter systems are often described by low-dimensional collective variables (CVs) that track progress between long-lived states. Here we distinguish between the motion -pathway in high-dimensional space- and the players -specific atoms, residues, or coarse-grained units- that most strongly drive that motion. With accurate structure prediction now routine for many proteins, the central challenge is to move from static models to a mechanistic view of functional dynamics based on full ensembles. We present an ensemble-based framework that takes high-dimensional structural data from simulations or experiments and, for any chosen CVs, identifies these structural players. From a structural ensemble and user-defined CVs, we construct the free-energy landscape, determine a minimum-barrier path between metastable states, and define a transition tube that isolates barrier-crossing configurations. Within this tube, a path-conditioned principal component analysis captures transition-specific fluctuations, while time-lagged independent component analysis resolves the associated slow modes. Combining each feature's contribution to variance and slowness into a single importance score yields a ranked map of transition hotspots. These hotspots can guide mutations, targeted coarse-graining, and allosteric drug design across biomolecular and synthetic systems.

BP 14.66 Tue 18:00 P2

Electronic and structural properties of (doped) bilayer systems of graphene and molybdenene — •Sabrina Smid — RWTH Aachen, Worringer Weg 3, 52074 Aachen

Two-dimensional (2D) materials have attracted intense interest since the discovery of semi-metallic graphene in 2004. Owing to its exceptional electronic, thermal, and mechanical properties, graphene has become a key platform for exploring van der Waals (vdW) heterostructures. Stacking different 2D crystals enables emergent phenomena absent in the isolated layers, as exemplified by graphene encapsulated in hexagonal boron nitride, where interfacial screening enhances carrier mobility. The introduction of twist angles in such heterostructures has further unlocked new electronic behavior, including flat-band correlated states in twisted bilayer graphene.

Recently, the emergence of metallic molybdenene, synthesized via microwave-assisted exfoliation of MoS_2, has further expanded the 2D materials landscape. Its intrinsic metallic character and tunable properties in vdW architectures suggest promising opportunities for heterostructure engineering. Motivated by this, we additionally perform density-functional theory calculations on a vdW bilayer composed of semi-metallic graphene and metallic molybdenene, examining how twist angle and carrier doping modify its structural and electronic properties.

BP 14.67 Tue 18:00 P2

Dynamic Generation of Rigidity and Curvature during Clathrin-mediated Endocytosis — •Johannes Dreckhoff, Leon Lettermann, and Ulrich Schwarz — University of Heidelberg, Germany

Clathrin-mediated endocytosis is a main transport pathway across cell membranes, yet the physical mechanisms by which the clathrin coat assembles to drive generation of membrane curvature are not understood well. In particular, it has been argued that bending would not be possible if the coat attained its high stiffness already at the initial stages. Here we address this crucial issue using agent-based kinetic Monte Carlo simulations for coat assembly in spherical geometries with variable curvature. By formulating a microscopic Hamiltonian governing individual clathrin legs, we elucidate the interplay between lattice growth, topological defects, effective membrane stiffness and macroscopic curvature generation. Our simulations reveal that the effective bending rigidity of the coat increases by approximately two orders of magnitude during assembly, driving the curvature generation. We also observed the growth curvature imprinting itself onto the system, resulting in a "curvature memory" effect. Crucially, our simulations capture the distinct dynamical regimes observed in experiments: we successfully reproduce the flat-to-curved transition, while also predicting stalled, flat growth events, potentially driven by premature lattice stiffening. This unifying description demonstrates that clathrin-mediated endocytosis is a multi-facetted process during which rigidity and curvature are generated in a cooperative manner.

BP 14.68 Tue 18:00 P2

Revealing Temporal Hierachy in Larval Zebrafish Behaviour and Its Neuronal Representation — •Leonard Constien[1], Gautam Sridhar[2], Joao C. Marques[3], Drew N. Robson[3], Jennifer M. Li[3], Antonio C. Costa[1], and Claire Wyart[1] — [1]Paris Brain Institute (Institut du Cerveau), Sorbonne University, INSERM U1127, CNRS UMR 7225, Paris, France — [2]Okinawa Institute of Science and Technology 1919-1 Tancha, Onna-son, Kunigami-gun Okinawa, Japan 904-0495 — [3]Max-Planck-Institut für biologische Kybernetik, Tubingen, Germany.

On a given timescale, animal behaviour can be structured into behavioural states, each defined by a similarity of kinematics, immediate goals and physiological states. Further, coarse behavioural state divide into substates, unfolding on faster timescales. How are these states represented in the brain and which structures control their dynamics across timescales? To address these questions, we apply a Markov chain analysis framework to a dataset of larval zebrafish behaviour with parallel recording of whole-brain activity at cellular resolution. The approach identifies behavioural states in a principled and unbiased manner and reveals a hierarchical organization of hunting behaviour from the seconds to minutes timescale. Further, by applying the framework independently on neuronal activity, we reveal a similar structure of the dynamics, identify representing brain regions and investigate the links to behaviour. This work will motivate further studies to determine the circuits and mechanisms behind the regulation of behavioural dynamics.

BP 14.69 Tue 18:00 P2

Dynamic Health Monitoring: Predicting COVID-19 with Wearable Sensor Data and catch22 Features — •Paul Buttkus and Dirk Brockmann — Technical University Dresden (SynoSys), Dresden, Germany

In the initial stages of a pandemic, when intervention leverage is highest, controlling infectious-disease spread hinges on timely detection of emerging cases. The rapid, global transmission of COVID-19 highlighted the need for scalable sensing tools that can pick up early physiological signatures of infection. Using data from the Corona Data Donation Project, which provides resting heart rate, step count, and sleep duration time series from over 120,000 voluntary participants in uncontrolled, real-world settings, we trained regression models to classify COVID-19 test results. Based solely on daily aggregated features,

this model achieved an above random guessing success rate, revealing a non-trivial signal despite coarse temporal resolution and strong noise. To better highlight the underlying dynamics, we employ the catch22 (22 CAnonical Time-series Characteristics) feature set to map raw sensor data to a compact set of interpretable descriptors, and additionally extend our framework to higher-temporal-resolution data to incorporate periodicity metrics (e.g., circadian modulation of heart rate and activity) that are lost under daily aggregation. We show which dynamical features are most informative for distinguishing COVID-19-positive from negative individuals and discuss how this framework could turn large-scale wearable data into a real-time surveillance tool for public health.

BP 14.70 Tue 18:00 P2

A Computational Approach to Drug Screening for the Sphingosine-1-Phosphate Receptor Family for Therapeutic Use against Autoimmune Diseases — •Janos Hintze, Tim Bennet Hausmann, Jonathan Hungerland, and Ilia Solov'yov — Institute of Physics, Carl von Ossietzky Universität, Carl-von-Ossietzky-Str. 9-11, 26129 Oldenburg, Germany

Current drugs used in the treatment of multiple sclerosis (MS) often lead to a variety of unwanted side effects. Some of the target proteins in MS treatment are sphingosine-1-phosphate receptors (S1PRs), which form a family of five structurally similar G protein-coupled receptors (GPCRs) that are found in various tissues throughout the human body. In this work, a generative diffusion model was used to design a broad spectrum of novel ligand candidates. To account for receptor flexibility, molecular docking was performed on different protein conformations obtained through molecular dynamics (MD) simulations. Analysis of the generated ligand candidates showed a consistently low similarity to existing S1PR-targeting drugs. Approximately 2000 candidates show a favorable binding affinity and subtype-specific selectivity based on their docking scores. This dataset can be further investigated based on other criteria such as toxicity, synthesizability, and stability, aiming to identify selective ligands for S1PRs, relevant for MS therapy.

BP 14.71 Tue 18:00 P2

Applying a topology sensitive metric for RNA contact prediction — •Christian Faber[1], Utkarsh Upadhyay[1], Oskar Taubert[2], and Alexander Schug[1,2] — [1]Jülich Supercomputing Centre, Forschungszentrum Jülich, 52428, Jülich, — [2]Scientific Computing Centre, Karlsruhe Institute of Technology, 76344, Eggenstein-Leopoldshafen

Predicting the spatial structure of non-coding RNA (*ncRNA*) is an important task for understanding fundamental processes in living nature. Physical force fields are used to infer the structure from a sequence using simulations on high-performance computers. However, the best results are obtained by incorporating probable contacts as additional restraints. These can be derived from evolutionary data using statistical methods or from more recent artificial intelligence (AI) algorithms.

In the past, the focus was on achieving the highest possible proportion of correctly predicted contacts, while the distribution of these contacts on the contact map was overlooked. We have demonstrated the importance of this distribution for structure prediction and have therefore introduced a measure of it.

In our current work, we apply our new metric to a state-of-the-art algorithm *Barnacle*. To achieve this, the algorithms must undergo complete retraining and a new dataset must be generated that avoids data leakage. While our results demonstrate the practical application of such a procedure, they also underscore the challenges posed by the limited availability of data for RNA molecules, a problem which becomes particularly apparent when modelling AI networks.

BP 14.72 Tue 18:00 P2

Structure and Dynamics of Network-Forming Protein Solutions using SAXS and megahertz XPCS — •Adrian Maximilian Roda Lentz[1], Michael Paulus[1], Michelle Dargasz[2], Florian Wieland[3], and Christian Gutt[2] — [1]Department Physics/DELTA, TU Dortmund, Dortmund, Germany — [2]Department of Physics, University of Siegen, Siegen, Germany — [3]Institute of Metallic Biomaterials, Helmholtz-Zentrum Hereon, Geesthacht, Germany

This study explores the structure of networks formed by the biopolymer hyaluronic acid, together with the dynamics of embedded proteins, in this framework ferritin and apoferritin. Hyaluronic acid is a major constituent of synovial fluid and a key component in tissue dynamics and repair; therefore, characterization is essential for advancing biomedical applications. Static Small-Angle X-ray Scattering (SAXS) conducted at P10 (DESY) and BL2 (DELTA) was employed for structural characterization, complemented by megahertz Xray Photon Correlation Spectroscopy (XPCS) at MID (EuXFEL) to quantify the dynamics. First results indicate a pronounced impact of hyaluronic acid on the collective diffusion behavior of proteins.

BP 14.73 Tue 18:00 P2

Quantum mechanical/molecular mechanics (QM/MM) calculations for absorption spectra of photoactive proteins, including many-body screening contributions — •Jelena Schmitz[1,2], Maximilian Graml[1,2], Till Rudack[1,3], and Jan Wilhelm[1,2] — [1]Regensburg Center for Ultrafast Nanoscopy (RUN), University of Regensburg, Germany — [2]Institute of Theoretical Physics, University of Regensburg, Germany — [3]Structural Bioinformatics, Regensburg Center for Biochemistry, University of Regensburg, Germany

The GW method and the Bethe-Salpeter equation (BSE) capture many-body screening effects, important for the full quantum mechanical description of excitations in large biological structures. Spectral shifts in photoactive proteins resulting from conformational changes can be described using a hybrid quantum mechanics/molecular mechanics (QM/MM) framework [1]. Our work investigates the impact of incorporating GW+BSE in QM/MM calculations, and examines how larger QM regions influence the accuracy of predicted shifts. We aim to compare to experimental results and QM/MM calculations using different ab initio approaches [1]. In order to perform calculations on larger, non-periodic systems, we are implementing RI-DFT as a precalculation method within the CP2K software package, prior to GW. This could provide us with access significantly larger system sizes, even full electrostatic protein surroundings, and therefore even higher accuracies.

[1] ChemBioChem 20, 1766 (2019)

BP 14.74 Tue 18:00 P2

Investigating molecular mechanisms of signaling in the multistep phosphorelay system of Magnaporthe oryzae via All-Atom Molecular Dynamics Simulations — •Jonas Paulus[1], Dennis Martin[1], Antonia Preuss[1], Milena Runge[2], Stefan Jacob[2], and Lukas Stelzl[1] — [1]Institut für molekulare Physiologie, Mainz, Germany — [2]Institut für Biotechnologie und Wirkstoff-Forschung, Mainz, Germany

Pathogenic fungi cause an annual loss of 15% of the world's major crops and the phenylpyrrole class of fungicides are upon the most successful to combat these pathogens, precisely because of their specificity and outstanding resistance management. The mode of action (MoA) takes place in a multistep phosphorelay system (MSP) thereby hyperactivating the high osmolarity glycerol (HOG) signaling pathway, but has not yet been clarified in detail on molecular level. Using all-atom molecular dynamics (MD) simulations, we investigate the structural and functional mechanisms of the cytosolic osmosensor MoHik1, its phosphotransfer signaling cascade, and nuclear import of downstream effectors. With this, we aim to design a multidimensional model of signal encryption and fungicide action in fungal MSP systems which will provide both, fundamental insights into fungal signal transduction and the chance to shed light on MSP systems as target for antifungal strategies.

BP 14.75 Tue 18:00 P2

Cryogenic Structural Stability of Human Serum Albumin in Aqueous Solution Studied by SAXS/WAXS — •Lukas Tepper, Michael Paulus, Jaqueline Savelkouls, and Metin Tolan — TU Dortmund, Maria-Goeppert-Mayer-Straße 2, 44227 Dortmund

The behavior of proteins during extreme temperature changes plays a crucial role in the development of stable biopharmaceutical formulations. Freezing and thawing processes are widely used in the production, processing, and long-term storage of protein-based drugs, but they can cause denaturation, aggregation, or loss of biological activity.

Cryoprotectants such as glycerol or other polyols are commonly used to mitigate these effects. They can stabilize proteins and prevent aggregation, among other things by changing the water structure and the hydration shell.

For structural characterization of these processes, Small- and Wide-Angle X-ray Scattering offer direct access to protein conformation, intermolecular distances, and mesoscale ordering phenomena, enabling analysis of proteins in solution without crystallization.

In this work, we use SAXS/WAXS at beamlines BL2 and BL9 at DELTA to study human serum albumin in aqueous and cryoprotective

environments during cooling down to −100 °C and subsequent thawing. This allows us to analyze structural changes, stability, and possible reorganization processes across the entire cryogenic temperature range.

BP 14.76 Tue 18:00 P2

Coarse grained simulations for the peptide lge1 1-80 — Agaya Johnson[1], Anton Polyansky[2], Terpsichori Alexiou[1], Bojan Zagrovic[2], and •Sofia Kantorovich[1] — [1]Computational and Soft Matter Physics, University of Vienna, Kollingasse 14-16, 1090 Vienna — [2]Department of Structural and Computational Biology, Campus-Vienna-Bio Centre 5, 1030, Vienna

Due to the structural heterogeneity and fast dynamics of the bimolecular condensates, capturing their organization requires a coarse-grained modeling approach that bridges atomistic details with mesoscale properties. In this work, we develop a coarse-grained model based on atomistic potentials to study the formation of condensates of Lge1, a protein of interest in biomolecular phase separation. We implemented nonbonded interactions for these peptides derived from iterative Boltzmann inversion, with Martini force field parameters and votca tool kit into the espresso simulation package. We employ cluster analysis as a criterion to ensure that all these CG models retain key features of the self-assembly and phase separation comparatively, as it is observed in atomistic simulations. By leveraging CG modeling, we extend simulations to longer timescales and larger system sizes, enabling us to explore whether biomolecular condensates form through phase separation, self-assembly, or aggregation. Our approach provides insights into the structural transitions of Lge1 within condensates and the fundamental mechanisms governing these transitions. This work contributes to the development of predictive models for biomolecular organization in crowded cellular environments.

BP 14.77 Tue 18:00 P2

Investigating the binding of clients to small heat shock protein 16.5 using electrospray ion bean deposition and cryogenic electron microscopy — •Manami Imada, Noor Naseeb, and Stephan Rauschenbach — University of Oxford, Oxford, UK

Small heat shock proteins (sHSP) act as the first line of defence, preventing protein aggregation. sHSP do this by binding to the protein under stress to form a stable complex. We explore how these sHSPs bind to clients such as lysozymes using cryogenic electron microscopy (cryo-EM). However, sHSP are hard to image due to their dynamic nature and potential to form different oligomers.

Electrospray ion bean deposition (ES-IBD) is used to deposit the sample onto the cryo-EM grids. ES-IBD utilises native mass spectrometry (nMS), which transfers the complexes into the gas phase intactly and allows for mass filtration of the ion beam by a quadrupole. This allows specific complexes and binding stoichiometries to be deposited selectively onto the cryo-EM grids to be imaged.

BP 14.78 Tue 18:00 P2

Sparse sampling in single molecule spectroscopy — •Sebastian Stadler and Markus Lippitz — Universitätsstraße 30, 95447 Bayreuth

Single-molecule spectroscopy (SMS) is fundamentally limited by photobleaching, leaving only a short time window to record spectra from individual emitters. These constraints motivate measurement strategies that extract maximal information from minimal data. Sparse sampling provides a compelling alternative to traditional Fourier spectroscopy, which requires dense, uniformly spaced measurements to satisfy the Nyquist condition. In contrast to traditional Fourier spectroscopy, sparse or sub-Nyquist sampling enables accurate spectral reconstruction from substantially reduced datasets.

In this theoretical study, we explore optimized sparse sampling strategies using simulated single-molecule spectra. By systematically varying sampling patterns, we identify regimes and procedures in which sparse acquisition offers significant gains in efficiency without compromising spectral fidelity. As a conceptual example of such optimized strategies, we discuss the pathway toward sampling optimization based on ensemble spectra and adaptive sampling approaches that iteratively adjust measurement points based on previously obtained information.

Our results outline design principles for efficient measurement protocols and highlight the potential of sparse acquisition to push SMS beyond traditional limits imposed by photobleaching and limited interrogation time.

BP 14.79 Tue 18:00 P2

Single-molecule PIE-FRET and nsFCS Studies of Metal Ion-dependent Folding of an rRNA Tertiary Contact — •Mara Henschel[1], Vanessa Schumann[1], Andreas Hartmann[2], Michael Schlierf[2], and Richard Börner[1] — [1]Laserinstitut Hochschule Mittweida, Mittweida, Germany — [2]Technische Universität Dresden, Dresden, Germany

Tertiary interactions in ribosomal RNA are crucial for shaping the folding landscape. However, the dynamics of these interactions across different timescales are not well understood. We investigate the tertiary contact of a double fluorescent-labelled ribosomal RNA from Saccharomyces cerevisiae at the single-molecule level in vitro. We quantify metal-ion-dependent folding and dynamics during K(I) and Mg(II) titrations using single-molecule PIE-FRET as a nanometre-distance readout combined with nanosecond fluorescence correlation spectroscopy (nsFCS). FRET-histograms reveals ion-dependent broadening beyond shot noise, indicating structural dynamics on the microsecond to millisecond timescale. Furthermore, nsFCS measurements show fast domain motions ranging from nanoseconds to microseconds. By employing two complementary labeling schemes, we distinguish local folding of the kissing loop from formation of the long-range tertiary contact, resolving distinct folding trajectories within the same RNA construct. Our results provide a dynamic insight of rRNA tertiary-contact formation and lay the foundation for a quantitative, mechanistic model of metal-ion-regulated folding of ribosomal RNA.

BP 14.80 Tue 18:00 P2

Multiplexed magnetic tweezers for high-throughput measurements — •Leonhard Schatt, Stefanie D. Pritzl, Alptuğ Ulugöl, and Jan Lipfert — University of Augsburg, Augsburg, Germany

Single-molecule techniques, such as magnetic tweezers, are powerful tools for studying forces and torques on the nanoscale. However, throughput in single-molecule measurements can still be limiting. To solve this problem, we present a multiplexed magnetic tweezer setup that can perform real-time high-throughput force and torque measurements. In addition, our setup enables controlled excitation in the UV and visible range, to study the response to photo-triggers and photo-excitation.

BP 14.81 Tue 18:00 P2

Pulling Geometry as a Design Parameter for Coiled Coil-Based Molecular Force Sensors — •Laura M. Wolfthaler[1], Zeynep Atris[2], Angelo Valleriani[2], Russell J. Wilson[1,2], and Kerstin G. Blank[1,2] — [1]Johannes Kepler Universität, Linz, Austria — [2]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Molecular force sensors (MFSs) measure piconewton-scale forces central to cell adhesion, migration and differentiation. While DNA-based MFSs are well established, their functionalization requires multistep chemistry. We introduce a protein-based MFS building block derived from heterodimeric coiled coils (CCs). Building on our prior work showing how CC length, helix stability and core packing shape mechanics, we now identify pulling geometry as a powerful and versatile parameter for tuning CC mechanical stability without altering thermodynamic or kinetic properties. Using atomic force microscope-based single-molecule force spectroscopy, we applied force parallel and perpendicular to the CC superhelix and observed strongly geometry-dependent rupture forces, including distinct responses for the two shear modes of a 4-heptad heterodimer. These results highlight how local helix stability and structural anisotropy determine CC mechanical behavior. This work establishes a foundation for using MFSs across a wide range of cell culture applications. Their ability to report forces at molecular scales could transform how mechanical signaling is studied at cell-material interfaces.

BP 14.82 Tue 18:00 P2

Thermal noise particle tracking and interaction measurements at interfaces under minimal external force — •Nils le Coutre and Alexander Rohrbach — Bio- and Nano-Photonics, IMTEK, University of Freiburg, Germany

Forces play a vital role in experimental biophysics. From receptor-binding studies to flow-drag analysis, understanding the magnitude, direction, and origin of these forces is essential for uncovering underlying mechanisms. Optical tweezers are widely used in this context because they not only enable the measurement of biophysical interactions, but also deliberately manipulate a biological system to trigger

and observe otherwise highly unlikely yet relevant interactions between the system's individuals.

To leverage this advantage for studying specific interaction processes, a robust understanding of the probe position distributions, defined by both the trapping and the surface potential and the interferometric tracking response is required, especially near interfaces and surfaces such as cell membranes. We discuss the question how far an optical trap has to approach an interface such that a natural interaction process between two binding partners is enabled (e.g. receptor on surface and ligand in optical trap).

In this presentation, I expound experiments by exploring the underlying theory and by conducting benchmark measurements in electrolyte-controlled systems, characterizing the behavior of trapped probes as their microscopic environment is altered.

BP 14.83 Tue 18:00 P2

Plasma elastic properties in cross microchannels — •Michelle Kron, Joséphine Van Hulle, and Christian Wagner — Experimental Physics Saarland University

Cross-slot microfluidic geometries produce planar extensional flows and are used to investigate flow instabilities in Newtonian and complex fluids. In Newtonian liquids, an inertial instability produces a steady vortex beyond a critical Reynolds number. In viscoelastic polymer solutions, elastic stresses near the stagnation point lower this threshold. Here we investigate human plasma, which is weakly elastic under extensional flow. Using cross-slot experiments, we quantify how plasma elasticity shifts the Reynolds number threshold for vortex onset and compare the impact of common anticoagulants on this response. We show that plasma reduces the Reynolds-number threshold for vortex onset, underscoring the importance of considering its weak elasticity for physiological studies.

BP 14.84 Tue 18:00 P2

Effective binary models of multicomponent phase separation — •Henri Schmidt and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Biological cells rely on biomolecular condensates for spatiotemporal organization. Condensates consist of many differently interacting biomolecules, which leads to a rich and complex configuration space.

Yet, only a few types of molecules can be measured in experiments, and the resulting phase behavior is typically explained using low-dimensional models. To understand the conditions under which such dimensionality reduction is feasible, we numerically explore multicomponent phase separation and ask when the behavior of a particular component can be explained by simple binary phase separation. This is surprisingly often the case, even when the unobserved components undergo phase separation on their own. However, the predicted interaction parameters and molecular volumes typically deviate from their true values, indicating that the reduction introduced systematic measurement errors.

Understanding the details of the dimensionality reduction will allow us to better probe multicomponent phase separation by observing a few components in the future.

BP 14.85 Tue 18:00 P2

Dynamics of tissue sampling of resident tissue macrophages — •Miriam Schnitzerlein[1,2], Eric Greto[3,4], Stefan Uderhardt[3,4], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Erlangen — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen — [3]FAU und Universitätsklinikum Erlangen — [4]Optical Imaging Competence Center Erlangen, FAU

Resident tissue macrophages (RTMs) are a type of immune cell present in essentially every tissue in the human body. One of their main functions is to keep the tissue in homeostasis by resolving lesions or removing dead cells, thereby preventing unnecessary inflammation and avoiding collateral damage to the tissue. To find such incidents, RTMs show continuous sampling behaviour by extending and retracting cell protrusions. This sampling behaviour needs to be tightly regulated - due to finite amounts of available cell cytoplasm and membrane - while still guarding the entirety of the tissue.

In this project, we have employed a high-resolution, intravital imaging protocol to generate dynamic data of murine RTMs in vivo in the peritoneum. Next we have built a custom image processing pipeline to segment RTM protrusions and their dynamic behaviour. We could then analyse the sampling range of protrusions and found correlations between outgrowth and shrinking of protrusions. Furthermore, the data hints at a division of labour approach protrusions employ when scanning the tissue.

BP 14.86 Tue 18:00 P2

Bottom-up emergence of a primitive replicator — •Magdalena Häupl, Ivar Haugerud, and Christoph Weber — Faculty of Mathematics, Natural Sciences, and Materials Engineering: Institute of Physics, University of Augsburg, Universitätsstraße 1, 86159 Augsburg, Germany

Non-equilibrium selection pressures were proposed as a mechanism of forming oligonucleotides whose sequences encode rich functionalities, including catalysis. Since phase separation was shown to direct various chemical processes, we ask whether condensed phases can provide mechanisms for sequence selection.

To answer this question, we develop a non-equilibrium thermodynamic theory to describe oligomerization, templated ligation, and sequence fragmentation away from equilibrium and under non-dilute conditions prone to phase separation.

We show the emergence of a strong selection mechanism. Most strikingly, a primitive replicator arises that is solely based on the inter-sequence interactions that drive sequence condensation. These results highlight that out-of-equilibrium condensed phases may provide versatile hubs for Darwinian-like evolution toward functional sequences, both relevant for the molecular origin of life and de novo life.

BP 14.87 Tue 18:00 P2

Wetting of Chemically Active Condensates on Membranes — •Mengmeng Wu and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany

Droplets undergo partial spreading, division, merging, engulfment, and exocytosis in cellular environments. When these droplets are chemically active, as is common for many condensates in cells, the resulting long-range fluxes further enrich and modify these behaviors. To analyze the interplay between chemically active droplets and membranes, we develop a coarse-grained molecular dynamics model together with a continuum theory based on Cahn-Hilliard reaction-diffusion dynamics coupled to membrane curvature elasticity. Our approach demonstrates how chemical reactions and the resulting fluxes control both droplet morphology and membrane deformation, providing physical insight for cellular condensates as well as for the design of synthetic responsive membrane-droplet systems.

BP 14.88 Tue 18:00 P2

staged self-organized attack mechanisms of camponotus japonicus against intruders — •yifan zhang and zhangang han — School of Systems Science, Beijing Normal University, Beijing, China

Social insect colonies display complex collective behaviors that emerge from local interactions, enabling decentralized strategies to counter external threats. Although ant collective activities such as foraging and nest construction are well studied, the self-organized attack mechanisms ants employ against specific intruders remain poorly understood. Using the camponotus japonicus and earwigs as research subjects, we show that ants exhibit a staged escalation pattern when confronting an invader: from individual probing, to small-group containment, and ultimately large-scale coordinated assaults. Building on a master-equation framework, we establish continuous-space dynamical equations and propose an ant attack behavior model to characterize these processes. Notably, the collective attack displays strong nonlinear synergy*six ants generate an attack intensity far exceeding a simple tripling of that from two ants. These findings highlight the adaptive advantages of coordinated aggression, demonstrating how cooperative interactions among individuals greatly amplify group-level defensive efficiency. Our study offers new insights into how decentralized biological systems achieve swarm intelligence and produce emergent combat behavior, and clarifies the role of self-organization in shaping effective group decision-making.

BP 14.89 Tue 18:00 P2

Protein self-assembly, infinitely complex yet simple? — •Lukas Kalvoda[1] and Martin Lenz[1,2] — [1]LPTMS, CNRS, Université Paris-Saclay — [2]PMMH, CNRS, ESPCI Paris, PSL University

Cells rely on protein self-assembly to form functional complexes, but a lack of regulation gives rise to pathological fibers in diseases like Alzheimer's and sickle cell anemia. Why proteins robustly form these

well-defined morphologies is largely unknown.

Beyond the molecular details, the complexity of proteins in shape and interactions suggests that their self-assembly may be governed by the laws of statistical physics. We introduce an analytical lattice model of anisotropic self-assembling particles to study what we term the "infinite complexity limit". Therein the number of distinct interactions grows to infinity. Strikingly, in this limit, the "molecular" details of the interactions do not matter anymore. Instead their distribution and extreme value statistics determine the self-assembly outcome.

BP 14.90 Tue 18:00 P2

From Individuals to Waves: Mechanisms Shaping Collective Responses in Sulphur Mollies — •Bianca Pacini[1], Yunus Sevinchan[1,3], David Bierbach[2,3], Korbinian Pacher[2,3], Jens Krause[2,3], and Pawel Romanczuk[1,3] — [1]Institute for Theoretical Biology, HU Berlin, Berlin, Germany — [2]Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Berlin, Germany — [3]Science of Intelligence, TU Berlin, Berlin, Germany

Collective biological systems, from neuronal networks to animal groups, exhibit the remarkable ability to rapidly modify their collective behaviour in response to changing environmental cues. By integrating local interactions with external information, they achieve flexible and coordinated group-level responses.

We investigated large fish shoals of sulphur mollies (*Poecilia sulphuraria*) in Southern Mexico, which perform collective diving cascades as a response to predation, producing wave-like patterns on the water surface. Interestingly, as a form of collective perception, we found that the group responds as a unified entity, showing a gradual stimulus-response pattern in their initial reaction.

Informed by empirical patterns extracted from a large video dataset of surface waves triggered by synthetic stimuli or bird attacks, we developed an agent-based model which captures the system's essential features. Systematic exploration of the model identifies the key individual-level mechanisms driving collective dynamics and shows how changes in local behaviour can drive collective adaptations across ecological contexts.

BP 14.91 Tue 18:00 P2

Confirmation of Jarzynski's equality based on single molecular and macroscopic interaction force measurements — •Iago Peters, Laura Mears, Stefan Szokoll, and Markus Valtiner — TU Wien, Wien, Austria

Knowledge about the free energy landscape of biomolecular reactions is necessary to understand how life works on the smallest scale. Unfortunately, obtaining experimental values of the free energy difference between two states like an unbound and a bound state of two molecules is rather difficult. Jarzynski proposed an equality that connects the free energy difference between two states with the irreversible work that leads from one state to the other. Precisely, an average of all possible realizations of a process that moves the system from an equilibrium state to another state in equilibrium. Here, we test this hypothesis with experimental values. Using a simple model system, the different nucleobase-pair interactions are measured using three different techniques that are able to measure the interaction forces between two single molecules and up to several million interactions in a single experiment run. Using the Atomic Force Microscope (AFM), Optical Tweezers and the Surface Force Apparatus allows us to additionally investigate the scaling of biological single molecule interactions. Together with molecular dynamics simulations a strong foundation is laid to confirm Jarzynskis equality and investigate the scaling of single-molecule interactions.

BP 14.92 Tue 18:00 P2

Phase separation in chemically reacting systems controls cross-phase pH difference — •Linge Li, Omar Adame-Arana, and Frank Jülicher — Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187, Dresden

Biomolecular condensates are increasingly recognized as dynamic chemical environments whose properties are strongly modulated by their pH environment. Recent experiments have focused on the pH differences between the coexisting liquid phases, but a minimal theoretical framework that can account for these observations and elucidating their physical principles is still lacking. Here, we develop a minimal thermodynamic model that integrates charge-regulated macromolecules and their counterions. By identifying the conjugate thermodynamic variables constrained by chemical equilibrium and charge neutrality, we construct the thermodynamics at equilibrium and uncover a variety of phase behaviors. We show that asymmetric partitioning of ions in phase separated compartments naturally generates electric potential and pH differences, with the dense-phase pH consistently buffered toward the macromolecular isoelectric point. We further demonstrate that these pH differences are governed by macromolecular interactions and molecular properties. Together, our results suggest that phase separation provides a robust mechanism for buffering dilute-phase pH variations and enabling controlled modulation of pH in the presence of condensates. The framework uncovers general physical principles of how pH regulation can be achieved phase-separated environments.

BP 14.93 Tue 18:00 P2

Phase separation in chemically reacting systems controls cross-phase pH difference — Linge Li, •Omar Adame-Arana, and Frank Jülicher — Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187, Dresden

Biomolecular condensates are increasingly recognized as dynamic chemical environments whose properties are strongly modulated by their pH environment. Recent experiments have focused on the pH differences between the coexisting liquid phases, but a minimal theoretical framework that can account for these observations and elucidating their physical principles is still lacking. Here, we develop a minimal thermodynamic model that integrates charge-regulated macromolecules and their counterions. By identifying the conjugate thermodynamic variables constrained by chemical equilibrium and charge neutrality, we construct the thermodynamics at equilibrium and uncover a variety of phase behaviors. We show that asymmetric partitioning of ions in phase separated compartments naturally generates electric potential and pH differences, with the dense-phase pH consistently buffered toward the macromolecular isoelectric point. We further demonstrate that these pH differences are governed by macromolecular interactions and molecular properties. Together, our results suggest that phase separation provides a robust mechanism for buffering dilute-phase pH variations and enabling controlled modulation of pH in the presence of condensates. The framework uncovers general physical principles of how pH regulation can be achieved phase-separated environments.

BP 14.94 Tue 18:00 P2

Statistical mechanics of disordered buckling instabilities — •Tangdi Luan[1,2,3] and Pierre A. Haas[1,2,3] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute of Molecular Cell Biology and Genetics — [3]Center for Systems Biology Dresden

Buckling instabilities drive the emergence of biological shape during morphogenesis, but the effect of the large variability of these systems at the microscopic cell scale on these instabilities at the macroscopic scale of tissues is largely unknown. The buckling of a rod with disordered growth [1] is perhaps the simplest setup of this problem. Numerical simulations [1] reveal that even in this minimal setup, the distribution of growth disorder has complex effects on the buckling threshold.

Here, we provide the theoretical underpinnings for these observations: we develop the statistical theory that explains how the spatial distributions of disorder of growth and material properties conspire to determine the threshold for the instability. Our results thus indicate how correlations and hence feedbacks between stress and growth can control mechanical instabilities and, by extension, the emergence of biological shape in development.

[1] Ramachandran *et al.*, Phys. Rev. E **110** (2024)

BP 14.95 Tue 18:00 P2

Exchange controls coarsening of surface condensates — •Riccardo Rossetto[1,2], Marcel Ernst[1,2], Gerrit Wellecke[1,2], and David Zwicker[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany — [2]University of Göttingen, Institute for the Dynamics of Complex Systems, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Biological membranes often exhibit heterogeneous protein patterns, which cells control. Strong patterns, like the polarity spot in budding yeast, can be described as surface condensates formed by physical interactions between constituents. However, it is unclear how these interactions affect the material exchange with the bulk. To study this, we analyze a thermodynamically consistent model which reveals that passive exchange leads to new equilibrium phenomena, such as re-

entrant phase transitions, and generally accelerates the coarsening of surface condensates. Active exchange can further accelerate coarsening, although it can also fully arrest it and induce complex patterns involving various length scales. We reveal how these behaviors are related to non-local transport via diffusion through the bulk, rationalizing the various scaling laws we observe and allowing us to interpret biologically relevant scenarios.

BP 14.96 Tue 18:00 P2

Noisy mixtures at the mesoscale: Vacuoles dancing in chemically active droplets — •Estéban Araspin, Leonardo Silva Dias, and Christoph A. Weber — Faculty of Mathematics, Natural Sciences, and Materials Engineering: Institute of Physics, University of Augsburg, Universitätsstrasse 1, 86159 Augsburg, Germany.

Understanding biological mixtures at the mesoscale calls for models that connect microscopic reactions with emergent continuum behavior in a thermodynamically consistent way. At such coarse-grained scales, noise, generally of multiplicative nature, is essential to capture phenomena like nucleation or stochastic switching between non-equilibrium steady states.

We developed a theoretical framework based on effective mesoscopic reaction-diffusion master equations that is applicable to both passive systems and non-equilibrium scenarios in which chemostatted fluxes make the mixture active. The framework connects to the macroscopic limit, recovering reactive Cahn-Hilliard-Cook dynamics.

As an application, we explore chemically active droplets in which a chemostatted ATP concentration leads to striking morphological dynamics. We find dilute-phase vacuoles that form and dissolve, reminiscent of bubbly phase separation in Model B+. We observe growth of small vacuoles at the expense of larger ones, dynamics that can be considered an inverse-ripening process.

Our results highlight the value of mesoscopic stochastic frameworks for understanding active phase separation and other soft-matter systems maintained away from equilibrium.

BP 15: Computational Biophysics III

Time: Wednesday 9:30–12:45 Location: BAR/SCHÖ

BP 15.1 Wed 9:30 BAR/SCHÖ

Local chain stiffening regulates non-equilibrium maturation and clustering in biomolecular condensates — •Subhadip Biswas[1] and Davit A Potoyan[2] — [1]Iowa State University, Ames, Iowa, USA — [2]Iowa State University, Ames, Iowa, USA

Biomolecular condensates formed through liquid-liquid phase separation display complex structural and dynamical features that are essential for cellular organization, signaling, and aging. Using coarse-grained molecular dynamics simulations based on a polymer model with tunable local semiflexibility and sticker stickiness, we systematically examine how angular rigidity modulates aging and clustering within condensates. We investigate four regimes involving coupled variations of sticker/spacer stiffness and interaction strength. By quantifying structural heterogeneity, orientational ordering, and rheological responses, including oscillatory shear, Green-Kubo viscosity, and uniaxial deformation, we uncover distinct non-equilibrium behaviors and maturation pathways that emerge from local chain stiffening. These results highlight angular rigidity as a key regulator of condensate stability and internal organization, with implications for understanding condensate aging in cells and for designing programmable biomaterials.

BP 15.2 Wed 9:45 BAR/SCHÖ

Uncovering the thermodynamic principles of enzymatic regulation in biomolecular condensates with reactive simulations — •Enrico Lavagna[1], Francesco Delfino[1], Georgii Koniukov[1], Matteo Paloni[1,2], Luca Ciandrini[1,3], and Alessandro Barducci[1] — [1]Centre de Biologie Structurale (CBS), Montpellier, France — [2]Department of Chemical Engineering, Thomas Young Centre, University College London, London WC1E 7JE, United Kingdom — [3]Institut Universitaire de France (IUF)

Biomolecular condensates are dynamic cellular assemblies often regulated by energy-consuming processes such as post-translational modifications (PTMs). Nevertheless, the coupling between reaction dynamics and cellular spatial organization remains poorly understood at the molecular scale. Using a minimal, particle-based model, we investigate how phosphorylation controls condensate steady-state behavior. We find that condensate formation is regulated by the steady-state fraction of phosphorylated scaffold proteins, which increases with enzyme activity. This chemical regulation exhibits a non-linear, non-trivial dependence on the phosphorylation strength. Furthermore, reaction fluxes are spatially heterogeneous, with phosphorylation activity sharply peaking at the condensate interface. Our findings highlight novel, general features of chemically active biomolecular condensates. Moreover, we observe that incorporating local detailed balance is essential for understanding how energy-consuming reactions shape the steady-state properties of phase-separated systems.

BP 15.3 Wed 10:00 BAR/SCHÖ

Multiscale Simulation of Phosphofructokinase-1 Assemblies: From Transient Interactions to Large-Scale Assembly Formation — Mehrnoosh Khodam Hazrati, Tom Miclot, and •Stepan Timr — J. Heyrovsky Institute of Physical Chemistry, Czech Academy of Sciences, Prague, Czech Republic

Human phosphofructokinase-1 (PFK1)—a key glycolytic enzyme—forms filaments and localizes into large-scale assemblies that are thought to play a major role in the regulation of glycolysis. However, the molecular interactions driving this assembly and the precise mechanisms by which it regulates the pathway remain poorly understood. In this work, we combine three levels of description—atomistic, residue-level coarse-grained, and highly coarse-grained—to characterize interactions between PFK1 tetramers and to elucidate factors governing PFK1 assembly formation. Atomistic molecular dynamics simulations of PFK1 filament interfaces reveal specific side-chain interactions that are critical for filament stability. These insights enable us to improve the description of filament formation in residue-level coarse-grained models. Using the Martini 3 and OPEPv7 coarse-grained models, we further identify key regions mediating transient PFK1–PFK1 interactions and show that these include filament-forming interfaces. Finally, we construct a highly coarse-grained model that integrates information from the more detailed simulations. Using this model, we investigate the role of membranes in PFK1 filament formation and describe how filaments may affect the recruitment of other constituents into large-scale glycolytic assemblies.

BP 15.4 Wed 10:15 BAR/SCHÖ

Multiscale Approaches to Phase Behaviour and Mechanical Properties of Synthetic DNA Networks — •Aaron Gadzekpo[1], Xenia Schneider[1], and Lennart Hilbert[1,2] — [1]Karlsruhe Institute of Technology, Institute of Biological and Chemical Systems — [2]Karlsruhe Institute of Technology, Zoological Institute

DNA can be used as a programmable material whose sequence-level design governs emergent properties. However, approaches that link sequences to the macroscopic behaviours needed in biotechnology remain limited. Here, we integrate coarse-grained simulations, Bayesian optimisation, and graph-based rheology to connect sequence-encoded, molecular-scale parameters to network-level properties. We apply our methods to DNA nanomotifs, which are nanometre-sized, multi-armed molecules assembled from single strands. Network formation among nanomotifs via sticky-end overhangs enables phase separation into liquid-like condensates or the assembly of viscoelastic hydrogels. Our multiscale approaches reveal how nanomotif flexibility, affinity, and concentration govern network formation, phase behaviour, and viscoelasticity. By combining our approaches, we propose inverse design strategies to select sequences that yield targeted emergent properties.

BP 15.5 Wed 10:30 BAR/SCHÖ

Self-Assembly of KAHRP Spirals in Malaria-Infected Red Blood Cells — Devika Magan[1], Michael Lanzer[2], and •Ulrich S. Schwarz[1] — [1]Institute for Theoretical Physics, Heidelberg University — [2]Center for Infectious Diseases, University Hospital Heidelberg

Malaria infections alter the mechanical and adhesive properties of red blood cells (RBCs). To avoid clearance by the spleen, infected RBCs develop thousands of nanoscale protrusions called knobs, which stiffen the RBC and mediate cytoadhesion to the endothelium. A central

player in this process is the exported parasite protein KAHRP. The parasite sends KAHRP to the RBC membrane skeleton, where it interacts with spectrin and actin to reorganize the local architecture. Strikingly, KAHRP also forms prominently sized spirals underneath the knobs, yet the physical principles governing their formation and how such structures might influence membrane mechanics are still not understood. In this talk, I present a coarse-grained, patchy-particle framework designed to explore how simple interaction rules can give rise to spiral formation. By tuning local binding geometry and torsional preferences, the model produces a rich variety of self-organized states, ranging from compact rings to extended curved chains. These simulations provide a starting point for connecting protein-level organization to cell-level mechanics. I will outline how this approach can be extended toward membrane-associated scenarios to investigate whether KAHRP assemblies can generate spontaneous curvature or store elastic energy - providing a path toward understanding their potential function during parasite cytoadhesion and egress.

30 min. break

BP 15.6 Wed 11:15 BAR/SCHÖ

From Data to Discovery: Machine Learning Force Fields for Fast and Accurate Ligand-Protein Screening — •Sergio Suárez-Dou[1], Miguel Gallegos[1], Hamza Ibrahim[2], Joshua T. Berryman[1], Andrea Volkamer[2], and Alexandre Tkatchenko[1] — [1]Department of Physics and Materials Science, University of Luxembourg, Luxembourg — [2]Data Driven Drug Design, Center for Bioinformatics, Saarland University, Germany

Pretrained Machine Learning Force Fields (MLFF) are transforming computational chemistry by combining speed and accuracy. In drug discovery, predicting binding energies and affinities is key to identifying viable candidates. Among MLFFs, SO3LR excels in both performance and efficiency, enabling accurate ligand binding predictions at low computational cost, surpassing semiempirical methods.

However, data coverage remains a challenge. While datasets like OMol25 and QCell offer broad molecular diversity, drug-like chemical space requires more targeted representation. To address this, we are developing a dataset optimised for docking evaluations, covering key regions of drug-like space. Our goal is a pretrained model capable of predicting drug-ligand affinities with PBE0+MBD DFT-level accuracy, bridging quantum precision with high-throughput screening and accelerating drug discovery.

BP 15.7 Wed 11:30 BAR/SCHÖ

Modelling Protein Dynamics with Machine Learned Coarse-Grained Models — •Klara Bonneau — Freie Universität Berlin, Germany

The most popular and universally predictive protein simulation models employ all-atom molecular dynamics (MD). However, understanding dynamical processes like protein folding, interactions, and aggregation requires accessing timescales beyond conventional MD capabilities. Coarse-graining (CG) accelerates simulations by focusing on essential degrees of freedom, but a universally predictive CG model for proteins remains elusive. Our work introduces the first thermodynamically consistent CG model that extrapolates to unseen protein sequences. By leveraging state-of-the-art machine learning techniques, we simulate the folding of unknown proteins, protein-protein interactions, intrinsically disordered proteins, and mutation effects. Current extensions include larger proteins and protein-ion/small molecule interactions, surpassing conventional MD timescale limitations. Additionally, explainable AI techniques enable us to interpret results and demonstrate that deep learning models capture physically consistent interactions.

BP 15.8 Wed 11:45 BAR/SCHÖ

Gradient-Estimating Gillespie Simulators for Parameter Inference in Stochastic Models — •Ludwig Burger[1], Annalena Kofler[2], Lukas Heinrich[3], and Ulrich Gerland[1] — [1]Physics of Complex Biosystems, School of Natural Sciences, Technical University Munich — [2]Max Planck Institute for Intelligent Systems, Tübingen — [3]Data Science in Physics, School of Natural Sciences, Technical University Munich

Stochastic models are ubiquitous in (biological) physics, yet fitting such parameterized models to experimental data remains challenging. While gradients in deterministic systems can be obtained efficiently through numerical or automatic differentiation, these tools cannot be directly applied to stochastic simulation algorithms such as the Gillespie algorithm, where sampling from a discrete set of reactions introduces non-differentiable operations. In this work, we adapt three gradient estimators from machine learning for use in Gillespie simulations: the Gumbel-Softmax Straight-Through estimator, the Score Function estimator, and the Alternative Path estimator. We extend all three estimators to address the specific requirements of gradient estimation in Gillespie simulations. We analyze the statistical properties of the estimators and highlight practical advantages and limitations in two representative systems: a minimal bimolecular association-dissociation model and the repressilator. Our results demonstrate that gradient estimators can be effectively integrated into the Gillespie algorithm, providing a systematic approach for gradient-based parameter inference in stochastic models.

BP 15.9 Wed 12:00 BAR/SCHÖ

Deep-Pose-Tracker: a unified model for behavioural analysis of *Caenorhabditis elegans* — •Debasish Saha[1], Shivam Chaudhary[1], Dhyey Vyas[2], Anindya Ghosh Roy[2], and Rati Sharma[1] — [1]Indian Institute of Science Education and Research Bhopal, Bhopal, India — [2]BRIC-National Brain Research Centre, Gurugram, India

The ability to respond to environmental stimuli by living organisms is essential for survival and adaptation. Locomotion and posture-based analyses of animals are commonly performed; however, manually performing these tasks is effort-intensive, time-consuming, and error-prone. Automation of this process is therefore crucial for accurate and fast detection. To this end, in this work, we report the development of Deep Pose Tracker (DPT), an end-to-end deep learning model to automate the study of posture dynamics and locomotion behaviour of *C. elegans*, a model organism useful to study neuroscience, genetics, drug design, *etc.* The DPT model enables automatic detection and tracking of these animals while measuring essential behavioural features like locomotion speed, orientation, forward or reverse locomotion, complex body bends as omega turns, and eigenworms (representing the overall posture dynamics in a low-dimensional space). Our DPT model can generate highly accurate data, with very high inference speed, while being user-friendly and robust to experimental variabilities. DPT, therefore, can be a valuable toolkit for researchers studying behaviour under different environmental stimuli.

BP 15.10 Wed 12:15 BAR/SCHÖ

Adaptive Determination of Cluster Number in Single-Cell RNA-seq — •Cornelius Miller, Felix Wehrenberg, Dominik Egger, and Sophia Rudorf — Institute of Cell Biology and Biophysics, Leibniz University Hannover, Hannover, Germany

Single-cell RNA sequencing (scRNA-seq) has transformed transcriptomic research by enabling gene expression profiling at the resolution of individual cells. The complexity and high dimensionality of scRNA-seq data pose substantial challenges for effective data interpretation. Current analysis pipelines often struggle with computational scalability and the subjective nature of parameter selection. Here, we introduce a comprehensive Python-based framework that automates key analytical stages while maintaining user flexibility. A critical innovation of this framework is the implementation of an adaptive clustering algorithm designed to estimate cluster count without prior knowledge. This method was specifically developed to define the number of distinct subpopulations in Mesenchymal Stem Cell (MSC) datasets, where cellular heterogeneity is often ambiguous. Furthermore, by leveraging parallelization, the proposed architecture handles high-dimensional datasets with improved latency compared to sequential execution. This approach resolves common ambiguities in defining cell types, offering a robust tool for unbiased exploratory data analysis.

BP 15.11 Wed 12:30 BAR/SCHÖ

AI-Guided Transition Path Sampling of Lipid Flip-Flop and Membrane Nanoporation — •Matthias Post and Gerhard Hummer — Max Planck Institute of Biophysics, Frankfurt, Germany

We studied lipid translocation (or *"flip-flop"*) between leaflets of a bio-membrane and the possible involvement of water nanopores via molecular dynamics simulation.[1] We used transition path sampling[2] within the AIMMD[3] framework to efficiently sample unbiased lipid flip-flops and pore formation. A neuronal network model was trained to predict the *"committor"*, that is the probability of a successful transition from a given microscopic conformational state. While coarse-grained DMPC lipids flip via tunneling through the intact membrane, atomistic (CHARMM36) simulations reveal that flip-flop requires the

formation of metastable water pores. DSPC bilayers and plasma membrane mimetics[4] facilitate flip-flop via transient water threads or nanodroplets to cross a locally thinned membrane. Deep neural networks map the transition mechanism from a high-dimensional (660d) feature space to a nearly linear committor model, consistent with Cover's theorem[5] and the concept of dominant reaction tubes.[6]

[1] Post, Hummer, *arXiv.*2502.11894 (2025) [2] Bolhuis et al., *Annu. Rev. Phys. Chem.* **53**, 291-318 (2002) [3] Jung et al., *Nat. Comput. Sci.* **3**, 334-345 (2023) [4] Pogozheva et al., *J. Chem. Inf. Model.* **62**, 1036-1051 (2022) [5] Cover, *IEEE Trans.Electron. Comput.* **EC-14**, 326-334 (1965) [6] E, Vanden-Eijnden, *J. Stat. Phys.* **123**, 503-523 (2006).

BP 16: Membranes, Vesicles and Synthetic Life-like Systems II

Time: Wednesday 9:30–12:45 Location: BAR/0205

Invited Talk BP 16.1 Wed 9:30 BAR/0205

Illuminating mitochondrial permeabilisation in apoptosis — •Ana J. Garcia Saez — Max Planck Institute of Biophysics, Frankfurt am Main, Germany

Mitochondrial permeabilization is a key step in the signaling pathway of apoptosis and in the cell*s commitment to death. It affects the outer and subsequently the inner mitochondrial membranes through the opening of membrane pores via mechanisms that are not fully clear. This releases cytochrome c and SMAC into the cytosol, leading to the activation of caspases, a set of proteases that accelerate cell death and that block inflammation by inactivating intracellular innate immunity effectors. Mitochondrial inner membrane permeabilization additionally releases mtDNA into the cytosol, which in turn activates intracellular innate immunity pathways unless counterbalanced by caspases. Here, I will discuss our work using advanced microscopy methods to advance our understanding of the molecular mechanisms of mitochondrial pores in apoptosis and how they function in the regulation of cell death and of inflammatory signaling outcomes.

BP 16.2 Wed 10:00 BAR/0205

Phase separation driven by membrane binding of receptor proteins of different size — •Samuel S. Gomez[1], Lennart Kleinschmidt[2], Daxiao Sun[2], Alf Honigmann[2], and Christoph Weber[1] — [1]Faculty of Mathematics, Natural Sciences, and Materials Engineering, Institute of Physics, University of Augsburg, Augsburg, Germany — [2]Technische Universität Dresden, Biotechnologisches Zentrum, Center for Molecular and Cellular Bioengineering (CMCB), Dresden, Germany

We aim to understand the physical mechanisms governing the spatial organisation and assembly of adherens junctions (AJs). A key open question is how size differences in the extracellular domains of AJ receptor proteins contribute to their segregation during junction formation. To address this, we develop a theoretical model of receptor-mediated adhesion between a GUV and a SLB, using both simulations and an experimental in-vitro setup to test and refine our model. Our model suggests that differences in receptor length are sufficient to drive spatial segregation, even in the absence of cis-interactions with similar adhesion affinities. We extend our model to understand the link between spatial organisation at the mesoscopic level of receptor segregation at membrane adhesion contact sites to the macroscopic heterogenous organisation of receptor proteins on the GUV. Our model aims to provide new insights into the physical principles underlying AJ assembly, in particular spatial organisation of receptor proteins on the mesoscopic and macroscopic level of the membrane within the AJ complex.

BP 16.3 Wed 10:15 BAR/0205

Selective information processing by particle distributions at living interfaces — •Jenna Elliott[1,2] and Anna Erzberger[1,2] — [1]European Molecular Biology Laboratory (EMBL), Heidelberg, Germany — [2]University of Heidelberg, Heidelberg, Germany

Living cells are capable of responding to environmental cues under noisy conditions, even in the absence of a centralised control unit or brain. Such systems therefore provide an ideal platform for uncovering the physical principles behind robust, decentralised information processing in soft materials. Motivated by the role interfaces play in relaying signals across cell boundaries, we investigate how spatially-varying particle distributions on interfaces facilitate information transmission in living cells. Starting from a statistical description of particle dynamics, we show that these distributions act as signal filters that nonlinearly amplify heterogeneities in their environment. This mechanism permits a form of pattern recognition, with inter-particle interactions tuning the response function of the filter. We explicitly identify both thresholding and edge-detecting regimes and, accounting for thermal noise in the filters, quantify the flow of information across the interface. We find that, when suitably tuned, the noisy filters selectively compress input signals, resulting in the efficient encoding of information relevant to downstream tasks. Overall, our results indicate that the noisy patterning of membranes may be used to selectively sense environmental cues in biologically inspired systems, suggesting exciting implications for how physical interactions may encode computational logic in soft materials.

BP 16.4 Wed 10:30 BAR/0205

Synthetic cell-based artificial tissues to study T cell activation — Anna Burgstaller[1] and •Oskar Staufer[1,2,3] — [1]INM - Leibniz Institute for New Materials, Saarbrücken, Germany — [2]Campus D2 2 — [3]Max Planck Bristol Center for Minimal Biology, Bristol, United Kingdom

T cells integrate biochemical and biophysical cues within lymph nodes, collectively determining activation of adaptive immunity. Quantitatively understanding how mechanical and biochemical signals converge at the single-cell and tissue level requires new model systems. To address this, we developed millimeter-sized artificial lymph nodes assembled from synthetic cells. The mechanical properties of the synthetic cells, specifically their Young*s modulus, can be precisely tuned, while their surfaces can be functionalized with biochemical stimuli. This allows to independently tune their biomechanics and biochemistry. The resulting tissue architecture, including its anisotropy and stiffness, can be engineered to probe emergent, tissue-scale phenomena. Performing live cell microscopy of migrating T-cells within synthetic lymph nodes, we validate that they reproduce in vivo T-cell motility. Statistical modeling of migration trajectories reveals that tissues must support search strategies for effective signal integration and that confinement degree promotes regulatory phenotypes of the T cells. Our synthetic cell-based tissues recapitulate architectural features of lymphatic organs, providing a platform to dissect how mechano-signaling interacts with biochemical cues to shape T-cell immunity

BP 16.5 Wed 10:45 BAR/0205

Excitable lipid nanotubes as a model system of neuron signaling and for neuromorphic systems — •Jan Steinkühler — CAU Kiel University, Germany

Voltage-sensitive ion channels stand at the centre in the study of cellular excitability in neuronal networks. However, the spatial propagation of electrical waves along nerve fibres is not a property inherent to an individual ion channel but rather emerges from the arrangement of ion channels along a tubular lipid membrane. While the *in vitro* study of functional ion channels in model membranes is well established, the propagation of an action potential along a lipid-bilayer nanotube has not yet been investigated. Here we present our experimental work examining these phenomena with electro-optical measurements on force-induced lipid nanotubes and demonstrate the cable-like properties of such nanotubes. Furthermore, we study memory effects arising from the interplay between electrical-field-induced lipid migration and ionic nanofluidic conductance. Finally, we show our lab's efforts toward automated cell-free expression of ion channels and data-driven modeling of membrane excitability. More broadly, our results help establish the interplay between membrane phase, shape, and electrical properties in a controlled experimental setup.

15 min. break

BP 16.6 Wed 11:15 BAR/0205

Membrane reshaping across the tree of life — •Felix Frey — Institute of Science and Technology Austria, Klosterneuburg, Austria — Eindhoven University of Technology, Eindhoven, The Netherlands

Across the tree of life, different designs of cellular membranes have evolved that are both stable and flexible. In bacteria and eukaryotes single-headed lipids self-assemble into flexible bilayer membranes. By contrast, archaea have distinct membranes that typically contain mixtures of single-headed bilayer lipids and double-headed bolalipids. While this composition is believed to enable extremophile archaea to survive harsh environments, the physical mechanisms underlying the reshaping of archaeal membranes are often unknown. Here, through the development of coarse-grained molecular dynamics simulations, we systematically compare the different membrane designs [1]. We explore the physical properties of archaeal membranes and explain how their stability and response to reshaping depends on the flexibility of single bolalipids and the amount of bilayer lipids they contain.

[1] M. Amaral*, F. Frey*, X. Jiang, B. Baum, A. Šarić (2025) Balancing stability and flexibility when reshaping archaeal membranes, eLife 14:RP105432, *Equal contributions.

BP 16.7 Wed 11:30 BAR/0205

Fluctuating triply periodic membranes: a phase-field study of diffusion in dynamic, confining environments — •Jakob Mihatsch and Andreas M. Menzel — Institut für Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany

Understanding how individual entities move through interconnected structures is crucial for applications in biology and technology. A key example is the diffusive motion of molecules in porous networks. This porous environment is usually not static, but subject to thermal fluctuations and interactions with the object that is transported through it. Focusing on the situation of a spherical diffusive particle confined by fluctuating triply periodic membrane structures, we investigate numerically the effect of such a dynamic environment on the motion of a confined object [1]. We employ a phase-field approach to model the membrane surface, which allows us to apply dynamic perturbations to the shape of the membrane, without having to track its location explicitly. Triply periodic membranes can form channels with narrow pores, which lead to transient trapping. We find that thermal fluctuations can widen these pores, which speeds up diffusive transport and allows larger particles to pass through the pores than one would expect for an unperturbed membrane. Our work also shows that deformation of the membrane induced by the particle plays an important role in enhancing diffusion. Our results should be directly observable, for example, during protein diffusion through biological environments.

[1] J. Mihatsch, A. M. Menzel, arXiv:2511.23192 (2025).

BP 16.8 Wed 11:45 BAR/0205

Optimizing Dynamin for Membrane Fission — •Russell Spencer and Marcus Muller — Georg-August University Göttingen, Göttingen, Germany

Membrane tube fission is a fundamental cellular process, facilitated by the dynamin protein family. The primary energetic barrier to fission arises from the (constriction-catalyzed) collapse of the tube into a hemifused intermediate. We previously developed a self-consistent field theory (SCFT) framework to systematically study this process, and validated it against experiments. The precise mechanisms by which dynamin promotes this transition, however, remain unclear. We now model membrane tubes in the presence of dynamin-like proteins, incorporating both steric constriction and surface interactions. We explore the effect of different protein-membrane coupling mechanisms on the fission barrier, including excluded volume, head-group adhesion, and leaflet splay. While membrane attraction is necessary for protein assembly and induces curvature, it also opposes local constriction, inhibiting tube collapse. In contrast, insertion of the PH domain into the head groups leads to their splaying and produces a localized chevron-shaped membrane deformation. This facilitates tube collapse without opposing local constriction, thus promoting fission.

BP 16.9 Wed 12:00 BAR/0205

Interferometric and Fluorescence Nanoparticle Tracking for Analysis of Extracellular Vesicles — •Shuhan Jiang[1,2], Anna Kashkanova[4], Morgan Miller[1,2], Hannarae Lee[1,2,3], Hamed Qazvini[1,2], and Vahid Sandoghdar[1,2,3] — [1]Max Planck Institute for the Science of Light, Erlangen, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [3]Department of Physics, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — [4]AE Eindhoven, Groene Loper 19, Flux, Netherlands

Extracellular vesicles (EVs) are considered to be important disease markers. However, their inherent heterogeneity poses a major challenge for the characterization of their physical properties and biochemical content. We combine interferometric nanoparticle tracking analysis (iNTA) with fluorescence detection to measure particle size, refractive index, and fluorescence intensity with single-molecule sensitivity. We verify that the fluorescence signal increases with particle size for dye-labeled liposomes, and that count rates shift as one changes the labeling density. In an exemplary case study applied to HEK293-derived EVs, we show that the method resolves CD9/CD81-positive subpopulations, while marker-negative particles appear more heterogeneous, suggesting contaminants or altered composition. We discuss the potential of this multimodal approach for precise differentiation of heterogeneous nanoparticles and quantitative biomarker analysis.

BP 16.10 Wed 12:15 BAR/0205

Active and Brownian Colloids interacting with Lipid Vesicles — •Antonio Stocco, Clément Marque, and Florent Fessler — Institut Charles Sadron, CNRS, Strasbourg, France

Motion of active and passive Brownian particles is strongly affected by confinement effects, which impact the persistence of the ballistic dynamics and can guide transitions and instabilities when dealing with deformable interfaces. Here, I will present some experimental results describing the dynamics of active and passive colloids interacting with soft fluctuating membranes. Our experimental systems are composed of Giant unilamellar vesicles (GUVs) with tunable membrane tension and bare or Janus self-propelled colloids showing different hydrodynamic and particle-membrane interactions. We were able to observe emerging dynamics such as autonomous particle engulfment by the vesicle membrane, hysteresis of the particle wrapping dynamics and membrane tension dependent particle drag [1,2,3]. References: [1] F Fessler, M Wittmann, J Simmchen, A Stocco. Dynamics of Active Colloid Engulfment by Giant Lipid Vesicles, Soft Matter 2024, 20, 5904. [2] F Fessler, P Muller, A Stocco, Energetics and dynamics of membrane necks in particle wrapping, Journal of Colloid and Interface Science 2025, 700, 138524 [3] C Marque, G d'Avino, D Larobina, A Michel, A Abou-Hassan, A Stocco Diffusion of a single colloid on the surface of a giant vesicle and a droplet Physical Review E2025, 111 (2), 025411

BP 16.11 Wed 12:30 BAR/0205

pH Dependence of the Structure of Drug-Free Lipid Nanoparticle Dispersions — •Marta Gallo[1], Klaus Götz[1], Bishoy Hakim[1], Carola Vogel[1], Christian Bär[1], Lionel Porcar[2], and Tobias Unruh[1] — [1]Institute for Crystallography and Structural Physics, Friedrich Alexander University Erlangen Nürnberg — [2]Institut Laue-Langevin, 71 Avenue des Martyrs, Grenoble 38042, France

Lipid nanoparticle (LNP) dispersions are promising drug-delivery systems due to their ability to encapsulate diverse therapeutics and release them in controlled ways. A key advantage of many LNPs is their sensitivity to environmental pH, enabling drug release in acidic endosomal conditions through lipid conformational changes that destabilize the particles. To clarify these mechanisms, we synthesized drug-free LNPs mimicking the Comirnaty formulation and examined how pH affects their structure. Using simultaneous small angle X-ray and neutron scattering (SAXS/SANS) at the ILL D22 instrument, we monitored particle swelling and ordered-structure formation across different pH levels. Dialysis experiments, transitioning samples between pH 3.3 and 7, demonstrated fully reversible structural changes, as confirmed by cryo-TEM. Coupling SAXS/SANS with photon correlation spectroscopy (PCS) revealed a complex particle size distribution and deeper insight into LNP dynamics under different contrasts and pH conditions. The results clarify how pH-triggered structural transitions govern LNP behavior, supporting the design of next-generation delivery systems with enhanced release control and targeting.

BP 17: Statistical Physics of Biological Systems I (joint session DY/BP)

Time: Wednesday 9:30–12:45 Location: ZEU/0114

BP 17.1 Wed 9:30 ZEU/0114

Metastability in the mixing/demixing of two species with reciprocally concentration-dependent diffusivity — •Benjamin Lindner[1,2], Alexander B. Neiman[3,4], and Xiaochen Dong[2] — [1]Department of Physics, Humboldt University Berlin, Berlin, Germany — [2]Bernstein Center for Computational Neuroscience Berlin — [3]Department of Physics and Astronomy, Ohio University, Athens, OH, United States — [4]Neuroscience Program, Ohio University, Athens, OH, United States

It is known that two species of diffusing particles can separate from each other by a reciprocally concentration-dependent diffusivity: the presence of one species at a certain location amplifies the diffusion coefficient of the respective other one in this location, causing the two densities of particles to separate spontaneously. In a minimal model, Schimansky-Geier et al. (2021) observed this with a quadratic dependence of the diffusion coefficient on the density of the other species. Here, we consider a sigmoidal dependence in the form of a logistic function on the other particle's density averaged over a finite sensing radius. The sigmoidal dependence leads to a new regime in which a homogeneous disordered (well-mixed) state and a spontaneously separated ordered (demixed) state coexist, forming two long-lived metastable configurations. In systems with a finite number of particles, random fluctuations induce repeated transitions between these two states. By tracking an order parameter that distinguishes mixed from demixed phases, we measure the corresponding mean residence in each state.

BP 17.2 Wed 9:45 ZEU/0114

Phase separation in a mixture of proliferating and motile active matter — Lukas Hupe[1], Joanna M. Materska[2], David Zwicker[1], Ramin Golestanian[1,3], Bartlomiej Waclaw[2,4], and •Philip Bittihn[1] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Dioscuri Centre for Physics and Chemistry of Bacteria, Institute of Physical Chemistry, Warsaw, Poland — [3]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, United Kingdom — [4]School of Physics and Astronomy, The University of Edinburgh, United Kingdom

Proliferation and motility are ubiquitous drivers of activity in biological systems. Here, we study a dense binary mixture of motile and proliferating particles with exclusively repulsive interactions, where homeostasis in the proliferating subpopulation is maintained by pressure-induced removal. Using large-scale simulations, we show that this heterogeneous active matter undergoes spontaneous phase separation at high density and weak enough self-propulsion. We recapitulate this behavior using an effective Active Brownian Particle model that incorporates the emergent effects of the proliferating matrix on motile particles: enhanced diffusion, renormalized self-propulsion, reduced persistence, and an effective attraction between motile particles. Our results establish a new type of phase transition and reveal how mechanical activity from growth can mediate non-equilibrium interactions and fluctuations. This mechanism provides a conceptual framework to reinterpret the physics of dense pattern-forming cellular populations, such as bacterial colonies or tumors, as systems of mixed active matter.

BP 17.3 Wed 10:00 ZEU/0114

Reentrant phase separation and critical behaviour in cellular aggregates — •Subhadip Chakraborti[1,2] and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

We study pili-mediated bacterial colonies as a paradigm for attractive cellular aggregates. The interplay between inherent motility and intercellular attraction leads to a reentrant phase separation between attraction-induced and motility-induced phase separation separated by a homogenous state. Using finite-size scaling of the largest cluster we characterise these two transitions and thereby determine the associated critical lines in terms of the control parameters - density, pili lifetime and attraction strength. We further evaluate critical exponents corresponding to two transitions in the parameter space and from their relations determine the respective universality classes.

BP 17.4 Wed 10:15 ZEU/0114

Phase separation with non-local interactions — Filipe C. Thewes, Yicheng Qiang, Oliver W. Paulin, and •David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Phase separation takes place in many complex systems, notably biological cells. While simple theories predict coarsening until only macroscopically large phases remain, concrete models often exhibit patterns with finite length scales, e.g., caused by chemical reactions, elasticity, membrane interactions, or charge. To unify such models, we here propose a field theory that combines phase separation with non-local interactions. If these interactions are long-ranged, they generally suppress coarsening, whereas systems with non-local short-range interactions additionally exhibit a continuous phase transition to patterned phases. Only the latter system allows for the coexistence of homogeneous and patterned phases, which we explain by mapping to the conserved Swift–Hohenberg model. Taken together, our generic model provides a framework that unifies similar phenomena observed in many complex phase-separating systems.

BP 17.5 Wed 10:30 ZEU/0114

Motile response of bacterial swimmers towards competing chemical signals — •Agniva Datta[1], Robert Grossmann[1], and Carsten Beta[1,2] — [1]Institute of Physics and Astronomy, University of Potsdam, Germany — [2]Nano Life Science Institute (WPI-NanoLSI), Kanazawa University, Kakuma-machi, Kanazawa 920-1192, Japan

Understanding how bacteria navigate in bulk fluid has gained significant interest in the field of active matter and random transport processes in the last few decades. We use the soil bacterium *Pseudomonas putida* as our model organism, the motility pattern of which is characterized by persistent runs, interrupted by random reorientation events (turns). In addition to this, bacteria sense chemical signals and adapt their motility pattern accordingly. Recent experiments show that bacteria can change the frequency of turns (duration of runs) depending on the concentration of nutrients as well as auto-inducer molecules that they themselves produce in the medium. This complex interplay of the dynamics of nutrients, auto-inducers and bacterial density may lead to dynamic instabilities. Combining experiments and theory, we are elucidating the dynamics of bacteria in the presence of these two competing signaling factors.

BP 17.6 Wed 10:45 ZEU/0114

Anisotropic hierarchy decides the fate of an amorphous droplet — •Andrey Zelenskiy, Pietro Caracciolo di Torella, and Martin Lenz — LPTMS, CNRS, Orsay, France

The classical description of ordering, from theories of phase transitions to classical nucleation, typically emphasizes a direct transition from disorder to order. Yet, the majority of systems in nature deviate from this simple description, and often choose indirect pathways to ordering. In particular, complex structures often form via disordered or partially ordered intermediates – the amorphous precursors.

We present a model of self-assembling patchy particles, where the interactions are characterized by a hierarchy of geometric competitions. By tuning the anisotropy, we can stabilize a variety of aggregate morphologies, including crystals, gels, lamellar sheets, and fibers. However, due to geometric frustration, self-assembly proceeds via a dense amorphous intermediate, where the anisotropic interactions are largely averaged out. Our simple framework based on an anisotropic hierarchy sheds light on this non-classical mechanism of particle assembly, and provides a platform for new experimental principles of complex structure design.

15 min. break

BP 17.7 Wed 11:15 ZEU/0114

Improving neuronal information transmission with pathway splitting — •Kolja Klett[1,2] and Benjamin Lindner[1,2] — [1]Humboldt University, Berlin — [2]Bernstein Center for Computational Neuroscience, Berlin

In many organisms sensory information can take different neuronal paths from sensory cells to destinations in the brain. These paths can be made up of neurons serving distinct functions. Often, pathways consisting of neurons coding the increase (ON) or decrease (OFF) of a signal are observed which have been found to improve the transmission

static signals. Here, we consider a simple network of spiking ON and OFF neurons to study the effects of pathway splitting on the transmission of dynamic signals. To that end, we use the coherence function as a frequency-resolved measure of informations transmission. We relate the information transmission of the whole network to that of the constituting neurons by employing response theory leading to approximate relations for the coherence function. For a simple white noise driven integrate-and-fire model of spiking neurons, we find an optimal mixture of ON and OFF neurons which maximizes the coherence function over a broad frequency range. The effect can be attributed to the nonlinear response of the neurons that only becomes relevant for sufficiently strong stimuli.

BP 17.8 Wed 11:30 ZEU/0114

Population sparseness in recurrent spiking neural networks — •Jakob Stubenrauch[1,2], Naomi Auer[3], Richard Kempter[2,3,4], and Benjamin Lindner[1,2] — [1]Physics Department HU Berlin — [2]Bernstein Center for Computational Neuroscience Berlin — [3]Institute for Theoretical Biology HU Berlin — [4]Einstein Center for Neurosciences Berlin

It is long known that in association tasks for neural networks, the fraction of active neurons in patterns to be associated plays an important role. Specifically, the number of patterns that can be simultaneously remembered grows when the information content per pattern is decreased. In binary networks, this content can be constrained by the population sparseness (one minus fraction of active neurons). For neurons with graded activity, population sparseness can be quantified by the Treves-Rolls measure or by the Gini coefficient. Here, we present results on the spontaneous and evoked population sparseness in different variants of recurrent neural networks of integrate-and-fire neurons. We find that the type of competition between neurons plays an important role and discuss that neurons in fully disordered networks can, in a mean field limit, only compete across a low-dimensional effective inhibition hub. We showcase the relevance of our findings for association tasks in spiking neural networks.

BP 17.9 Wed 11:45 ZEU/0114

Minority-triggered reorientation yields macrocscopic cascades and maximal responsiveness in a Vicsek swarm — •Simon Syga[1], Chandraniva Guha Ray[2,3,4], Josué Manik Nava Sedeño[5], Fernando Peruani[6], and Andreas Deutsch[1] — [1]Technische Universität Dresden, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [4]Center for Systems Biology Dresden, Germany — [5]Universidad Nacional Autónoma de México, Mexico City, Mexico — [6]CY Cergy Paris Université, Paris, France

Collective motion in animals and cells often exhibits bursty reorientations and scale-free velocity correlations associated with criticality. This ensures that information, like the presence of predators, quickly spreads through a group, ensuring an adequate response. To explain this phenomenon, we introduce a simple, biologically plausible mechanism, a minority-triggered reorientation rule: when local order is high, agents sometimes follow a strongly deviating neighbor instead of the majority. This generates heavy-tailed cascades of reorientations and macroscopic spatial correlations over broad parameter ranges, without fine-tuning. Our mechanism preserves cohesion while markedly enhancing collective responsiveness: localized directional cues elicit amplified, group-level reorientation. Our results provide a parsimonious, biologically interpretable route to critical-like fluctuations and high susceptibility in collective motion.

BP 17.10 Wed 12:00 ZEU/0114

Noise structure shapes transitions in cell differentiation processes — •Sara Oliver-Bonafoux[1], Javier Aguilar[1,2], Tobias Galla[1], and Raúl Toral[1] — [1]Institute for Cross-Disciplinary Physics and Complex Systems IFISC (CSIC-UIB), Campus UIB, Palma de Mallorca, Spain — [2]Laboratory of Interdisciplinary Physics, Department of Physics and Astronomy "G. Galilei", University of Padova, Padova, Italy

Stochastic differential equations provide a natural framework to describe dynamical systems influenced by random fluctuations, but they require specifying the structure of the noise term (e.g., additive, demographic, or environmental). In biological systems, the choice of an appropriate noise description remains a matter of debate. Understanding how stochastic fluctuations shape biological dynamics is a central challenge in biophysics and systems biology.

We address this question in the context of a model of cell differentiation, the process by which an unspecialised cell commits to a specialised cell type with a specific structure and function. Both the undifferentiated state and differentiated states are stable, and transitions between them are induced by noise. A recent study has provided theoretical evidence that different noise structures can give rise to substantially distinct differentiation paths. Here, we use stochastic bridges to sample differentiation paths under different types of noise and for varying noise intensity.

BP 17.11 Wed 12:15 ZEU/0114

Darwin's paradox of the peacock tail: a stochastic perspective on sexual selection — •Ian Magalhaes Braga — CASUS, Gorlitz, Germany

Many species show male traits that are extravagant, costly, and seemingly disadvantageous, yet they evolve and persist. Classical explanations especially deterministic versions of Fisher's runaway struggle to fully account for this pattern, mostly because they ignore the inherent randomness of evolutionary processes. In this work, I propose that stochasticity is not a secondary detail but the key element that reshapes the dynamics of trait preference coevolution. Treating sexual selection at the microscopic, probabilistic level reveals a simple but unexpected idea: in finite populations, a costly trait can actually support the evolution of female preference. I refer to this effect as the cost advantage. The basic picture is that stochastic fluctuations change the timing of fixation events, creating conditions under which preference benefits from the very cost that penalizes the trait. Using large-scale simulations across multiple evolutionary architectures, I show that this behavior is general and does not depend on specific modelling choices. The results suggest that costly ornaments are not paradoxical after all they may simply reflect the true stochastic nature of evolutionary change.

BP 17.12 Wed 12:30 ZEU/0114

Local equations for the generalized Lotka-Volterra model on sparse asymmetric graphs — •David Machado Pérez[1,2,3], Pietro Valigi[1], Tommaso Tonolo[4,5], and Maria Chiara Angelini[6] — [1]Physics Department, Sapienza University of Rome, Rome I-00185, Italy — [2]Department of Theoretical Physics, Physics Faculty, University of Havana. CP10400, Havana, Cuba — [3]CNR-NANOTEC, Rome Unit, Rome I-00185, Italy — [4]Gran Sasso Science Institute, 67100 L'Aquila, Italy — [5]INFN-Laboratori Nazionali del Gran Sasso, 67100 Assergi (AQ), Italy — [6]INFN, Sezione di Roma I, 00185 Rome, Italy

Real ecosystems are characterized by sparse and asymmetric interactions, posing a major challenge to theoretical analysis. We introduce a new method to study the generalized Lotka-Volterra model with stochastic dynamics on sparse graphs. By deriving local Fokker-Planck equations and employing a mean-field closure, we can efficiently compute stationary states for both symmetric and asymmetric interactions. We validate our approach by comparing the results with the direct integration of the dynamical equations and by reproducing known results and, for the first time, we map the phase diagram for sparse asymmetric networks. Our framework provides a versatile tool for exploring stability in realistic ecological communities and can be generalized to applications in different contexts, such as economics and evolutionary game theory.

BP 18: Focus session: Integrative Structural Modeling

Modern biological questions - and the growing recognition that biomolecular dynamics are central to molecular function - demand increasingly integrated technological strategies to probe the structure and behavior of biomolecules. Yet bringing insights from diverse experimental techniques together in a rigorous, quantitative way remains a formidable challenge, requiring deep expertise across methods as well as sophisticated modeling approaches. This focus session aims to ignite collaboration at this interface. By gathering experimentalists with complementary skill sets and researchers specializing in computational and theoretical modeling, we will create a space for vibrant exchange, cross-disciplinary learning, to lead to the development of well-informed, predictive models of complex biological systems.

Organized by Richard Börner (HS Mittweida) and Sigrid Milles (FMP Berlin)

Time: Wednesday 10:30–12:45 Location: BAR/0106

Invited Talk BP 18.1 Wed 10:30 BAR/0106

Protein complex structure prediction, state-of-the-art and challenges — •Ezgi Karaca — Izmir Biomedicine and Genome Center — Dokuz Eylul University, Izmir, TR

The advent of artificial intelligence has reshaped structural biology, enabling unprecedented accuracy in protein modeling. As the assessor for CASP14 and CASP15, I witnessed remarkable progress facilitated by AlphaFold. While CASP14 participants struggled with intersubunit contacts, CASP15 saw prediction success rates rise from 31-percent to 90-percent by incorporating AlphaFold2 (AF2) into customized pipelines. This improvement was driven by curated multiple sequence alignments (MSAs), though complexes with shallow MSAs remained challenging. Addressing this, we developed MinnieFold, an efficient protocol achieving a 50-fold reduction in GPU usage while maintaining accuracy in antibody-antigen complexes. Further investigating AF's performance, we analyzed 276 human-parasite interactions across 15 species. Comparing AF2 and AlphaFold3 (AF3), we observed striking differences in predicted structures. This presentation highlights these advances, challenges, and our contributions to AI-driven structural biology.

BP 18.2 Wed 11:00 BAR/0106

Extending the Fluorophore Dye Library for FRET-guided Modeling — •Isolde Kirk[1], Felix Erichson[1], Josephine Meitzner[1], Patrick K. Quoika[2], and Richard Börner[1] — [1]Laserinstitut Hochschule Mittweida, Mittweida, Germany — [2]Technische Universität München, Munich, Germany

Integrative structural modeling combines experimental observables with computational methods to obtain realistic descriptions of biomolecular structures and their dynamics. One such approach integrates Förster Resonance Energy Transfer (FRET) and dynamic fluorescence anisotropy with molecular dynamics (MD) simulations. Ensuring comparability between experiment and simulation requires realistic modeling of fluorescent dyes in silico. In practice, existing dye libraries do not cover the full range of available fluorophores, including phosphate-backbone-linked carbocyanine (Cy) dyes. We therefore modeled and parametrized a FRET dye pair of Cy3 and 5 with a backbone-linked Cy3 fragment for MD simulations. We used Gaussian to assign partial charges with the restrained electrostatic potential method, as implemented in Antechamber, yielding several parametrization variants. The dye fragments were then incorporated into a DNA hairpin model and characterized using MD simulations with GROMACS. Depending on the parametrization, the DNA hairpin showed different structural responses, ranging from stable dye intercalation to partial helix destabilization. One parametrization showed agreement with the experimental data and therefore provides a validated extension for future FRET-guided modeling.

BP 18.3 Wed 11:15 BAR/0106

Structural dynamics and long-range interactions controlling timing of the Neurospora circadian clock — •Muriel Hartsch[1], Ida Marie Vedel[1], Kathrin Motzny[1], Michael Brunner[2], and Sigrid Milles[1] — [1]Leibniz-FMP Berlin, Robert-Roessle-Str. 10, 13125 Berlin — [2]Heidelberg University, Biochemistry Center (BZH), Im Neuenheimer Feld 328, 69120 Heidelberg

The function and maintenance of the circadian clock in Neurospora crassa are governed by a feedback loop involving both negative and positive regulatory elements, which together drive the oscillating circadian rhythm with a period of approximately 24 hours. The dimeric, intrinsically disordered protein FREQUENCY (FRQ) is a key component of the negative feedback complex and subject to post-transcriptional hyperphosphorylation by casein kinase 1a (CK1a). Phosphorylation of clock proteins is highly conserved across species, from fungi to mammals, with the human PERIOD (PER) protein being a notable example. However, the precise functions associated with hyperphosphorylation remain poorly understood. We hypothesize that time-dependent hyperphosphorylation of FRQ at multiple sites facilitates a transition from closed to open conformation, regulating interactions with its partners. Using nuclear magnetic resonance (NMR) and single-molecule fluorescence resonance energy transfer (smFRET), we investigate the conformational dynamics going along with FRQ phosphorylation by recombinant CK1a. This will allow, combined with structural modeling of the intrinsically disordered protein, to understand how phosphorylation alters the conformation and triggers a switch in FRQ.

15 min. break

Invited Talk BP 18.4 Wed 11:45 BAR/0106

From Sparse Restraints to All-Atom Models: Integrative Reconstruction of Hidden GPCR Conformations — •Matthias Elgeti — Institute for Drug Discovery, Leipzig University Medical School, Leipzig, Germany

Transmembrane proteins such as G protein coupled receptors (GPCRs) play central roles in cellular signal transduction and constitute major targets for therapeutic intervention. Their intrinsic conformational flexibility, however, leads to the coexistence of multiple interconverting states, which complicates structural characterization by high-resolution methods. Site-directed spin labeling (SDSL) EPR spectroscopy is uniquely suited to probe such flexible systems independent of molecular size, but it provides only sparse structural restraints. To bridge this gap, we integrate SDSL-EPR distance data with deep-learning-based structure prediction and molecular dynamics simulations. Using the angiotensin receptor (AT1R), a key regulator of cardiovascular function, we demonstrate how this integrative approach reveals a ligand-stabilized conformational state with distinct functional properties. We further present a computational pipeline that reconstructs corresponding all-atom models from sparse spectroscopic restraints and enables systematic exploration of hidden conformational states, providing a general framework for structure-guided analysis of signaling mechanisms and future drug discovery.

BP 18.5 Wed 12:15 BAR/0106

RNA 3D Folding Using Diffusion Models and Agentic Tree Search — •Arunodhayan Sampathkumar and Danny Kowerko — Professorship of Media Informatics, Technische Universität Chemnitz

Accurate prediction of RNA three-dimensional structure is essential for understanding RNA function and guiding RNA-based therapeutics. However, RNA folding remains challenging due to complex tertiary interactions, context-dependent base pairing and limited structural data, especially for short sequences with fewer than 80 nucleotides. To address this, we introduce a multi-model RNA structure prediction framework that combines an RNA-adapted Protenix model, a Boltz diffusion sampler and a template-based modeling (TBM) baseline together with GAN-augmented training for underrepresented short RNAs. Protenix offers accurate local geometry, Boltz supplies diverse global conformations and TBM contributes strong constraints when templates exist. All models are evaluated on the Kaggle RNA 3D public and private test sets. Protenix reaches TM-scores of 0.48/0.46, Boltz 0.41/0.40 and TBM 0.61/0.57. We further introduce an agentic tree-search ensemble that selects and refines conformations using con-

sensus scoring and RMSD-based diversity. This ensemble significantly improves performance, achieving TM-scores of 0.68 (public) and 0.63 (private). Our results demonstrate that integrating generative models, template signals and agentic search yields more accurate RNA structures and improves robustness for novel RNA families.

BP 18.6 Wed 12:30 BAR/0106

RNA adsorption in confinement, from electrostatic properties to spatial organization — •Horacio V. Guzman, Willy Menacho, and Ian Addison-Smith — Biophysics & Intelligent Matter Lab, Material Science Institute of Barcelona, CSIC, 08193 Barcelona, Spain

Electrostatic interactions are the main driving force of the RNA-protein association during viral assembly and disassembly processes. However, the properties of confined single stranded ss-RNA inside diverse proteinaceous viral geometries remain largely unexplored due to challenges associated with their high-resolution characterization. Electrostatics and mechanical properties at the RNA-proteins interface are also the origin of ss-RNA stability in confinement. Combining archetypical RNA fragments and diverse confined symmetries, we present multiple-solvent molecular models to explore the most favorable initial spatial organization as a function of the type of confinement. Our method shows that electrostatic interactions drive the 3D RNA structure path towards possible initial conformations. In particular for small RNAs, which are frequently interacting with the proteinaceous subunits during the virus assembly process, also known as packaging signals. We compared our results to X-ray structures of small plant viruses validating the most favorable initial conformations with our method and the virus folding symmetry. Our findings start a quantitative route to elucidate the electrostatic character of RNA-protein interfaces, and a complementary understanding to RNA packaging, assembly and disassembly processes.

BP 19: Round Table Discussion: The Future of Neutrons in France and Germany (joint session CPP/BP)

Organized by Benoit Coasne and Christine M. Papadakis.

Time: Wednesday 11:45–12:45 Location: ZEU/LICH

Discussion BP 19.1 Wed 11:45 ZEU/LICH

Round Table: Novel Opportunities for France/Germany Cooperation in Neutron Science — •Julian Oberdisse[1], •Frank Schreiber[2], •Arnaud Desmedt[3], •Stephan Förster[4], •Jacques Jestin[5], •Pascale Launois[6], •Christian Pfleiderer[7], and •Sabrina Disch[8] — [1]Laboratoire Charles Coulomb, U Montpellier, France — [2]Institut für Angewandte Physik, Universität Tübingen, Germany — [3]Laboratoire Léon Brillouin (LLB), Gif-sur-Yvette, France, — [4]Jülich Centre for Neutron Science (JCNS), FZ Jülich, Germany — [5]Institut Laue-Langevin (ILL), Grenoble — [6]Laboratoire de Physique des Solides d'Orsay, France — [7]Heinz Maier-Leibnitz Zentrum (MLZ), Garching, German — [8]University of Duisburg-Essen, Germany

With current and upcoming major changes in European neutron science and facilities, Germany and France are expected to play a strong role. This emerging new landscape for neutron science offers opportunities to reshape and reinvent the traditionally strong bonds between our two countries – both in terms of science cooperation and technical collaboration. The hosts Julian Oberdisse and Frank Schreiber look forward to a diverse panel discussion with the directors of the French and German neutron facilities as well as the chairs of the French and German neutron associations.

BP 20: Protein Structure and Dynamics

Time: Wednesday 15:00–17:45 Location: BAR/0106

BP 20.1 Wed 15:00 BAR/0106

Enhanced Conformational Dynamics of Biomolecules with Quantum-Accurate Machine Learning Force Fields — •Naziha Tarannam — University of Luxembourg, Luxembourg

Machine Learning Force Fields (MLFFs) address a long-standing challenge in computational biophysics: lifting quantum accuracy in the treatment of biomolecules to the large scales, above nanometres and nanoseconds, normally available only to classical-like molecular mechanics force fields (MMFFs). Our recently developed SO3LR model was trained on a diverse set of over four million configurations and achieves ab initio-level accuracy while remaining computationally efficient for large systems in explicit solvent. We explore the dynamics of several globular proteins in aqueous systems comprising up to 35,000 atoms using SO3LR, and compare its performance against a set of widely used MMFFs. While SO3LR faithfully reproduces the static structural properties of proteins, it exhibits enhanced exploration of conformational space during molecular dynamics simulations compared to MMFFs, showing qualitatively different properties of sampling and convergence. This stems from its relatively accurate treatment of quantum many-body forces. Notably, SO3LR enables proteins to explore a broader spectrum of dihedral angles (ψ/ϕ distributions) that are inaccessible to conventional force fields, leading to higher configurational entropy over comparable simulation timescales. These results imply that classical treatments of biomolecules, even if they reach an adequate thermodynamic accuracy, may often do so for the wrong reasons.

BP 20.2 Wed 15:15 BAR/0106

Molecular dynamics simulations of native state collagen fibrils — Konstantinos Steiakakis[1], Alan Pichard[2], and •Maxime Vassaux[2] — [1]Processing and Performance of Materials, Department of Mechanical Engineering, Eindhoven University of Technology, Eindhoven, 5600 MB, The Netherlands — [2]Univ. Rennes, CNRS, IPR - UMR 6251, Rennes, 35000, France

Collagen fibrils are the building block of many biological tissues, which viability depend on the fibrils properties. Altered properties of collagen fibrils are central to the appearance of many diseases, and physiological or native properties must be reproduced for tissue engineering. Yet, the self-assembly, the structure, and therefore the properties of collagen fibrils remain elusive. One main reason is the extreme sensitivity of the fibrils to their environmental conditions, and in particular hydration which is only loosely bound by experimental measurements. Furthermore, mechanics are an integral part of the self-assembly process and may result in internal stresses in collagen fibrils in native conditions. Here, we investigate hydradtion, structure and internal stresses in collagen fibrils by means of molecular dynamics simulations of the collagen microfibril model. Overall, our findings provide insights into the native properties of collagen fibrils such as longitudinal prestrain and water content. More than ever, collagen fibrils appear to be assembled via an out-of-equilibrium process key for the synthesis of viable tissues.

BP 20.3 Wed 15:30 BAR/0106

Atomic-Level Insights into Amyloid Resistance Gained from Molecular Dynamics Simulations — •Adrian Felix Schnell[1], Tim Moderer[2], Marcus Fändrich[2], and Nadine Schwierz[1] — [1]Institute of Physics, Computational Biology, University of Augsburg, Universitätsstraße 1b, 86159 Augsburg, Germany — [2]Institute of Protein Biochemistry, Ulm University, 89081 Ulm, Germany

Systemic AA amyloidosis arises from the misfolding and aggregation of normally soluble serum amyloid A1 (SAA1) protein into pathogenic fibrils. Despite extensive experimental efforts, the molecular driving forces that govern fibril formation and resistance remain only partly understood.

Using atomistic molecular dynamics (MD) simulations of experimentally resolved structures in both the fibrillar and native states, we investigated sequence-specific features that modulate amyloid stability and resistance. Simulations of wild-type SAA1 and two naturally occurring variants known to display amyloid resistance reveal how single-point mutations can markedly influence fibril stability and impede fibril growth. Specifically, the atomistic MD trajectories show that the resistant variants fail to stably adopt the pathogenic fibril conformation, pointing to distinct structural and dynamical mechanisms underlying their protective effect.

Invited Talk BP 20.4 Wed 15:45 BAR/0106

Solution scattering and MD simulation as quantitative probes of protein-specific and temperature-dependent hydration — •Jochen S Hub — Saarland University, Saarbrücken, Germany

The hydration shell is an integral part of proteins since it plays key roles for confor- mational transitions, molecular recognition, and enzymatic activity. While the dynam- ics of the hydration shell have been described in detail by spectroscopic techniques, the structure of the hydration shell remain less understood due to the lack of hydration shell-sensitive structural probes with high spatial resolution. Whether MD simulations correctly reproduce the hydration shell structure is not known. Small-angle scattering (SAS) with X-rays or neutrons (SAXS/SANS) is sensitive to the hydration shell; however, the hydration shell effects on SAS data has traditionally been considered as a problem, which had to be absorbed into free fitting parameters, rather than a chance to learn the hydration shell structure. We combine SAS data with MD simulations and explicit-solvent SAS predictions to reveal how factors such as surface properties, temperature, and force fields influence protein hydration. We find that (i) MD simulations with certain (but not all) force fields yield excellent agreement with the SAS data; (ii) chemical characteristics of surface-exposed moieties strongly modulate the hydration shell contrast and structure; (iii) temprature-ramp SAXS and MD show consistently that the protein hydration shell is remarkably temperature-sensitive. Our studies demonstrate the combination of SAS and explicit-solvent MD simulations as quantitative structural probes of protein hydation.

15 min. break

BP 20.5 Wed 16:30 BAR/0106

Microscopic Insights into the Solvation of Stapled Peptides A Case Study of p53-MDM2 — Vikram Gaikwad, •Asha Rani Choudhury, and Rajarshi Chakrabarti — Indian Institute of Technology Bombay, Mumbai, India

Water often termed the universal solvent, plays a vital role in numerous biomolecular processes, including protein-protein interactions. One such critical complex is p53-MDM2, which is central to cellular regulation. Inhibiting the p53-MDM2 interaction remains a therapeutic challenge, and stapled peptides have emerged as promising candidates in this context.The stapled peptides are peptidomimetics in which the side chains of two suitably positioned amino acids are covalently linked using an appropriate chemical moiety. In this study, we investigate the role of water in the binding of stapled p53 peptides to MDM2 using molecular dynamics simulations. Our aim is to understand how variations in the chemical nature and stapling position of the hydrocarbon cross-linker influence the behavior of water molecules surrounding the p53 peptide. Using rigorous entropy calculations, we rationalize the enhanced binding affinity of stapled p53 peptides compared to that of their unstapled counterparts from a solvent-centric perspective. Specifically, the entropy gain of water molecules around the stapled peptides, combined with the conformational entropy loss of the peptide, contributes favorably to binding. These findings offer valuable insights into the rational design of stapled peptides and support the development of improved therapeutic inhibitors targeting the p53-MDM2 interaction.

BP 20.6 Wed 16:45 BAR/0106

What is the structure of biomolecular condensates? — •Charlotta Lorenz[1,2], Nathaniel Hess[3], Sully Bailey-Darland[1], Teagan Bate[1], Takumi Matsuzawa[1], Tong Wang[1], Kaarthik Varma[1], Dana Matthias[1], Harsha Koganti[1], Lois Pollack[1], Benjamin Schuler[2], Jerelle Joseph[3], and Eric Dufresne[1] — [1]Cornell University, Ithaca, NY, USA — [2]University of Zurich, Zurich, Switzerland — [3]Princeton University, Princeton, NJ, USA

Biomolecular condensates are important for a variety of cellular functions, such as biochemical regulation, structural organization, and RNA metabolism. While the properties and physiology of these condensates depend on their structure, this important aspect has received little experimental consideration. We expect a structure-function relationship determined by protein-protein interactions. Recent simulations of disordered proteins with interactions based on the sticker-and-spacer suggest fascinating structures in the bulk and surface of condensates. We reveal the structure of biomolecular condensates using small-angle X-ray scattering. We show that condensates made from a simple model system of bovine serum albumin (BSA) and polyethylene glycol (PEG) behave like a classical liquid. We extend our approach to the structure of condensates made of disordered proteins such as fused in sarcoma (FUS) and we find that FUS inside condensates structurally behaves like a gas. Our approach is applicable to a variety of different condensates and shows that diverse condensates have diverse structures.

BP 20.7 Wed 17:00 BAR/0106

Dynamics and (self-)interactions of the endocytic protein Eps15 — •Andromachi Papagiannoula, Ida M Vedel, Arbesa Saiti, Kathrin Motzny, and Sigrid Milles — Leibniz-Forschungsinstitut für Molekulare Pharmakologie im Forschungsverbund, Berlin

Eps15 is one of the earliest initiators of clathrin-mediated endocytosis (CME). The dimeric protein carries three EH domains per monomer, which are known to recognize Asn-Pro-Phe (NPF) motifs in intrinsically disordered regions (IDRs). Using nuclear magnetic resonance (NMR) spectroscopy, we examined interactions between EH domains and the IDR of the endocytic partner Dab2. In addition to canonical NPF recognition, we detect a high level of binding promiscuity leading to interaction with other phenylalanine-rich regions. This behavior enables EH domains to also engage with Eps15's own IDR, creating partial competition with Dab2. Nevertheless, Dab2 and the Eps15 IDR can bind EH domains simultaneously, leading to recruitment of Dab2 into Eps15 condensates. When EH domains are expressed in row, as they naturally occur in the wild type full length protein, EH2 and EH3 tumble together as one entity, while EH1 moves independently. Using single molecule Forster resonance energy transfer (smFRET), we assess the three dimensional organization of the three EH domains with respect to each other and assess binding with both Dab2 and Eps15 IDRs.

BP 20.8 Wed 17:15 BAR/0106

ASAXS Based Absolute Intra-Molecular Distance Measurements for Proteins — •Samuel Stubhan[1], Anna Baptist[1], Caroline Körösy[1], Alessandra Narducci[2], Gustavo Gabriel Moya Munoz[2], Nicolas Wendler[2], Aidin Lak[1], Michael Sztucki[3], Thorben Cordes[2], and Jan Lipfert[1] — [1]Department of Physics and Center for NanoScience, LMU Munich, Amalienstr. 54, 80799 Munich, Germany — [2]Physical and Synthetic Biology, Faculty of Biology, LMU Munich, Großhadernerstr. 2-4, 82152 Planegg-Martinsried, Germany — [3]ESRF, 71 Avenue des Martyrs, 38043 Grenoble, France

Intramolecular distance measurements are key to understanding macromolecular structure and dynamics. Anomalous Small-Angle X-ray Scattering (ASAXS) interferometry enables such measurements by attaching small (˜1 nm) gold nanoparticles to target molecules and using X-ray scattering to extract distance distributions. ASAXS provides absolute distances over >10 nm, full ensemble distributions, and minimal sensitivity to label orientation, offering advantages over FRET and NMR.

We demonstrate ASAXS on proteins for the first time using two cysteine variants of maltose binding protein in apo and holo states, directly revealing ligand-induced conformational changes. The resulting distance distributions agree with single-molecule FRET measurements. Requiring only a double-labeled sample and accommodating diverse solution conditions, ASAXS offers a robust, broadly applicable tool for probing protein conformational ensembles.

BP 20.9 Wed 17:30 BAR/0106

Probing membrane protein dynamics on lipid-functionalized graphene transistors through low-frequency noise — •Florian Steinbach[1], Mykola Fomin[1], Eduard Haar[2], Svetlana Vitusevich[3], Mykhaylo Petrychuk[3], Christian Ungermann[2], and Carola Meyer[1] — [1]Institute of Physics, University of Osnabrück — [2]Department of Biology/Chemistry and Center for Cellular Nanoanalytics, University of Osnabrück — [3]Institute of Biological In-

formation Processing (IBI-3), Forschungszentrum Jülich

Graphene field-effect transistors (GFETs) functionalized with lipid monolayers provide a controlled and label-free platform for studying membrane-associated proteins [1]. Here, we present electronic transport experiments where the Rab7-like GTPase Ypt7 is immobilized within a lipid monolayer. While there is not electrostatic gating effect observed, the addition of the protein causes a pronounced increase in low-frequency 1/f noise. This noise signal is diminished upon binding of the membrane tethering HOPS complex [2]. The persistence of distinct noise signatures despite strong screening indicates a transduction mechanism that may circumvent the screening within the Debye length.

[1] M. Fomin, L. Jorde, F. Steinbach, C. You, C. Meyer, Phys. Status Solidi B 2300324 (2023).

[2] M. Fomin et al, accepted for publication in Fluctuation and Noise Letters (2025).

BP 21: Focus Session: Sequence Spaces, Populations and Evolution

Evolutionary processes are central in the living world: they leave patterns in sequence databases and underlie phenomena such as cancer progression and antibiotic resistance. Achieving a quantitative understanding of evolution relies on two key components: variation and selection. The first component - variation - arises from random mutations in genotypic sequences that lead to selectable changes in phenotype and fitness. Thus, variation depends on how phenotype and fitness are distributed in biological sequence spaces. The second component - selection * shapes the composition of future generations and thus acts at the population level. Since these components jointly shape evolutionary processes, this focus session will encompass both: variation in sequence spaces and selection on the population level.

Organized by Nora Martin (Centre for Genomic Regulation, Barcelona) and Paula Garcia Galindo (University of Cambridge)

Time: Wednesday 15:00–17:30 Location: HÜL/S386

Invited Talk BP 21.1 Wed 15:00 HÜL/S386

Microbial Behavior in Context — •Fernanda Pinheiro — Human Technopole, Milan, Italy

Predicting microbial responses to antibiotics, nutrient shifts, or invading species requires models linked to metabolic pathways and cellular functions. In this talk, I present quantitative approaches for characterizing microbial behavior, from growth kinetics to coarse-grained models of cell metabolism and empirical growth laws. I will connect growth parameters to resource allocation and physiological constraints, and I will show how growth perturbations reveal layers of organization, from cellular physiology to ecological interactions and evolutionary change. In a broader context, I will discuss how metabolic models linking systems biology, ecology, and evolution can become tools for prediction.

BP 21.2 Wed 15:30 HÜL/S386

Insertions and Deletions make important contributions to the arrival of phenotypic variation — •Manuela Giraud[1,2] and Nora Martin[1] — [1]CRG (Barcelona Collaboratorium for Modelling and Predictive Biology), Dr. Aiguader 88, Barcelona 08003, Spain — [2]Universitat Pompeu Fabra (UPF), Barcelona, Spain.

In evolution, phenotypic variation is a prerequisite for selection and arises from random genotypic mutations. An extensive mapping of genotypes to their corresponding phenotype (GP map) provides us with a quantitative model for variation, thus informing evolutionary predictions. The features of GP maps and their relevance for evolutionary processes have been analyzed for different model systems, but these analyses have largely been limited to short substitutions. Insertions and deletions (InDels) of different lengths have been neglected despite their presence in natural sequence families. In this study, we analyze InDels in computational GP maps modelling RNA secondary structure, enzyme functionality, and a toy-model for protein quaternary structure self-assembly. We find that InDels are more likely to preserve the phenotype than expected from null models. These phenotype-conserving indels imply large sequence changes, affecting the effect of subsequent mutations: after a phenotype-conserving InDel, the distribution of accessible phenotypes shifts increasingly with the mutation size. Evolutionary simulations indicate that such phenotype-conserving indels can fix and strongly affect the number of encountered phenotypes. These results imply that InDels, even if rare, can make an important contribution to the arrival of phenotypic variation.

BP 21.3 Wed 15:45 HÜL/S386

Bias toward simplicity and symmetry in protein self-assembly — •Prarthana Agrawal — University of Oxford

Symmetry is ubiquitous in protein complexes and other biological assemblies and is often attributed to natural selection. Algorithmic information theory offers an alternative explanation: when structures are generated by simple local rules, outcomes that require less information to specify are intrinsically more likely [1]. Because symmetry enables reuse of the same assembly instructions, symmetric structures typically have low algorithmic (Kolmogorov) complexity and are therefore strongly favored.

We test this idea using a three-dimensional polycube self-assembly model as an abstract representation of protein quaternary structure. By sampling interaction rule spaces, we find a strong bias toward low-complexity assemblies, with symmetric structures occurring far more frequently than asymmetric ones. We further show that not all symmetries are equally accessible: some symmetry operations reduce assembly complexity more effectively than others and are therefore disproportionately likely.

These results indicate that biases toward simple and symmetric structures in self-assembly arise from intrinsic generative constraints rather than natural selection alone, suggesting that evolutionary outcomes are shaped not only by selection but also by how phenotypic variation is generated.

[1] Johnston et al., Proc. Natl. Acad. Sci. U.S.A. 119, e2113883119 (2022)

15 min. break

Invited Talk BP 21.4 Wed 16:15 HÜL/S386

The navigability of fitness landscapes shaped by global and universal epistasis — •Joachim Krug — Institute for Biological Physics, University of Cologne, Germany

Epistasis is the dependence of the effect of a mutation on the genetic context in which it occurs. Epistatic interactions shape the topography of the fitness landscape, the mapping from genotype to reproductive success. Global epistasis refers to interactions that arise when a nonlinear phenotype-fitness map acts on a lower-dimensional set of non-epistatic phenotypes, and has been argued to be a common occurrence at different scales of biological organization. It is therefore of interest to ask what features characterize fitness landscapes when epistasis is purely global. Here I show that, under certain conditions, global epistasis implies universal negative epistasis [1], an order relation on sequence space that is closely related to submodularity of set functions [2]. Universal epistasis makes fitness landscapes easily navigable, because any fitness peak is accessible through combinatorially many fitness-increasing mutational paths. I will discuss the theoretical results within the context of recent studies of large-scale empirical fitness landscapes that have found that rugged landscapes may also be highly navigable.

[1] Krug, J. & Oros, D.: Evolutionary accessibility of random and structured fitness landscapes. J. Stat. Mech. 034003:2024

[2] Pahujani, S. & Krug, J.: Complexity and accessibility of random landscapes. arXiv:2502.05896

BP 21.5 Wed 16:45 HÜL/S386

Adaptive Response of Quantitative Traits to a Moving Fitness Landscape — •Sakshi Pahujani, Yuna Zhang, Markus G. Stetter, and Joachim Krug — University of Cologne, Cologne, Germany

Phenotypic adaptation to long term persistent changes in the environment is typically studied using moving optimum models which consider a fitness landscape traversing the phenotypic space over time. Invoking the strong-selection-weak-mutation regime, we study adaptation as a walk towards the moving fitness optimum described by a continuous-state-discrete-time stochastic process. In this framework, at a critical speed of the optimum, we elucidate a transition, from a regime where the phenotypic gap of the adapting population from the optimum attains a stationary mean value to one where it increases indefinitely. Through a special case of the problem, we provide an alternative description of this transition in terms of a force that drives the adaptive process and a corresponding potential that switches from being confining to non-confining at the critical speed. Further analysis of this case suggests that adaptation is rather successfully carried out, until the population becomes limited by the maximum rate at which it can adapt. Remarkably, despite the simplicity of this special case, its predictions align well with observations from the original, more complex model [1].

[1] Sakshi Pahujani, Yuna Zhang, Markus G. Stetter, Joachim Krug, Adaptive Dynamics of Quantitative Traits in a Steadily Changing Environment, bioRxiv 2025.09.28.679017

BP 21.6 Wed 17:00 HÜL/S386

A simplified Rough Mount Fuji model clarifies how local adaptive walks can reach the highest peaks in rugged fitness landscapes — •Kye E Hunter[1,2] and Nora Martin[1] — [1]CRG (Barcelona Collaboratorium for Modelling and Predictive Biology) — [2]Facultat de Física, Universitat de Barcelona (UB)

Adaptive evolution selects random genotypic mutations according to their fitness. This can be modeled using a fitness landscape, a network of possible genotypes with a fitness value associated to each sequence. In the simplest models of adaptive evolution, populations move through this network in fitness-increasing steps until reaching a genotype whose fitness exceeds that of all its neighbors—a fitness peak. In evolutionary simulations on their empirical folA landscape, Papkou et al. (Science 2023) found that such fitness-increasing walks are likely to reach the globally-highest-ranked peaks among a large number of peaks, despite only being based on local rules. Similar results were found in a mathematical model of fitness landscapes, the Rough Mount Fuji model (Li & Zhang MBE 2025).

We use a simplified Rough Mount Fuji model to find simple analytical explanations for how a landscape can have both a large number of peaks and populations that reach the highest-ranked peaks. Our explanation proceeds by dividing the landscape into different regions, and considering the number of peaks relative to the total number of genotypes in each region. We then identify the degree to which those same arguments apply in the empirical folA landscape.

BP 21.7 Wed 17:15 HÜL/S386

Mean adaptive basin size for fitness peaks in the House of Cards landscape — •Daniel Oros and Joachim Krug — Institute for Biological Physics - University of Cologne

Fitness landscapes have been studied extensively in evolutionary theory. In a simple form, the fitness landscape maps the genotype of an organism to its reproductive success, denoted by fitness. While being a drastic simplification of biology, the concept is useful for understanding how evolution navigates such a landscape. When the time between mutations is much larger than the fixation time, one can think of a genetically homogeneous population moving one mutation at a time. The fitness value increases at each step and the population eventually reaches a fitness peak, a genotype having larger fitness than all its single mutant neighbors. The adaptive basin of a peak is composed of all genotypes which have a monotonically increasing fitness path to it.
Large scale fitness landscape measurements show that the basins of high fitness peaks contain a large fraction of all genotypes, a finding that has been argued to be inconsistent with existing fitness landscape models [1]. In House of Cards (HoC) landscapes fitness values are assigned independently at random, resulting in a maximally rugged landscape. Building on previous work on accessibility percolation [2] we show that typical peak adaptive basins in the HoC landscape contain a positive fraction of all genotypes, and derive an explicit expression for the mean basin size.

[1] Papkou A et al. 2023 *Science* **382** eadh3860
[2] Schmiegelt B and Krug J 2023 *J. Math. Biol.* **86** 46

BP 22: Statistical Physics of Biological Systems II (joint session DY/BP)

Time: Wednesday 15:00–16:30 Location: ZEU/0114

Invited Talk BP 22.1 Wed 15:00 ZEU/0114

Learning the statistical folding of bacterial chromosomes — •Chase Broedersz — Vrije Universiteit, Amsterdam, Nertherlands

The physical organization of bacterial chromosomes is inherently variable, with large conformational fluctuations both from cell to cell and over time. Yet, chromosomes must also be structured to facilitate processes such as transcription, replication, and segregation. A physical description of this dynamic statistical folding of bacterial chromosomes remains largely elusive. Hi-C experiments probe chromosome organization by measuring average contact frequencies of chromosomal loci pairs. I will present a principled approach to infer and analyze the dynamic and statistical organization of chromosomes. In particular, we developed a rigorous and fully data-driven 4D Maximum Entropy approach to extract a generative model for the dynamic organization of a replicating bacterial chromosome directly from time-course Hi-C and microscopy data. This data-driven approach aims to unravel the dynamic statistical folding of chromosomes - and its impact on functional processes - in growing and replicating bacteria. Finally, I will discuss how these data-driven inferences can be used to develop mechanistic insights into the contributions of various chromosome segregation mechanisms, including ParABS and loop-extruding SMC complexes. Together, our results illustrate how changes in the geometry and topology of the polymer, induced by DNA-replication and loop-extrusion, impact the organization and segregation of bacterial chromosomes.

BP 22.2 Wed 15:30 ZEU/0114

A freely jointed chain with two-state hinges — •Minsu Yi and Panayotis Benetatos — Department of Physics, Kyungpook National University, Daegu, South Korea

We discuss aspects of the stretching and bending elasticity of a freely jointed chain, where the hinges can be open or closed in a random fashion. This two-state-hinge model captures a specific degree of freedom associated with the local bending stiffness of the polymer, and its variation can be due to internal changes or to the attachment of ligands from the environment. In this presentation, we focus on comparing the effects of two different types of disorder on the hinges: annealed (reversible Freely Jointed Chain, rFJC) or quenched (quenched Freely Jointed Chain, qFJC). It turns out that, as expected, those different types of disorder yield qualitatively different behaviors. For finite-size systems, we obtain a recurrence relation, which allows us to calculate the exact force-extension relation numerically for an arbitrary size of the system for both systems. In the thermodynamic limit, when the contour length is much larger than the persistence length, we obtain an exact expression for the force-extension relation. The difference between the two systems still exists in the thermodynamic limit.

[1] M. Yi, D. Lee and P. Benetatos, J. Chem. Phys. 161 (23): 234908 (2024)
[2] M. Yi and P. Benetatos, J. Stat. Mech. 073501 (2025)

BP 22.3 Wed 15:45 ZEU/0114

Impact of cytosine methylation on the diffusion of charges along DNA: a quantum perspective — •Mirko Rossini, Dennis Herb, Paul Raschke, and Joachim Ankerhold — Institute for Complex Quantum Systems, University of Ulm, Ulm, Germany

We develop a coarse-grained tight-binding (TB) framework that treats electrons and holes on equal footing. TB parameters, required to characterize the model, are derived from an ab-initio molecular scheme (linear-combination-of-atomicorbitals (LCAO)) that includes all valence orbitals. Simulations address unmethylated vs. methylated CpG-

rich and regulatory sequences sensible to DNA methylation, enabling us to investigate the impact methylation has on the charge diffusion along models of critical relevance in epigenetics and shedding new light on possible undiscovered mechanisms for epigenetic regulation in cells.

Methylation substantially lowers cytosine charge energies (¯150 meV) while leaving the opposite guanine nearly unchanged (<20 meV), thereby introducing site-selective energetic shifts that redesign diffusion pathways. Statistical investigations, such as time-averaged populations and Inverse Partecipation Ratio (IPR) analyses, show enhanced electron localization at methylated cytosines, contrasted by increased hole delocalization: these dual trends suppress electron-hole co-localization (localization at same sites) and reduce recombination probability, leading to higher trapping times of excess charges along the DNA. Consistently, modelled excitations lifetimes increase upon cytosine methylation.

BP 22.4 Wed 16:00 ZEU/0114

Efficient control of F_1 molecular motor — •Deepak Gupta — Institut für Physik und Astronomie, Technische Universität Berlin, Germany

Designing low-dissipation control driving protocols for small-scale systems is an active field of research. In this talk, I will specifically discuss designing efficient driving procedures for a biomolecular motor-the F_1ATPase. In general, designing such protocols is challenging due to the spatial nonlinearity of the systems and the presence of environmental thermal fluctuations. Nonetheless, a near-equilibrium (linear response) framework is found to apply to a broad class of small-scale systems. We follow this framework to design non-trivial protocols to drive the F_1's γ-shaft to synthesize ATP at low-dissipation cost. Our analysis reveals that the designed protocols, based on the linear response approach, dissipate lower energy as compared to the constant velocity driving protocol for a wide range of protocol durations[1]. In the second part of my talk, I will show our recent experimental results on the F_1 ATPase motor, where we compared the dissipation of driving this motor using two experimentally viable protocols: angle clamp and torque clamp. Our experimental results (supported by analytical findings) suggest that angle clamp driving requires less work than that of the torque clamp[2].

[1] J. Phys. Chem. Lett. 13 (51), 11844-11849 (2022). [2] Phys. Rev. Lett. 135 (14), 148402 (2025).

BP 22.5 Wed 16:15 ZEU/0114

Elementary spectrum for the dissonance curve: from biophysics to number theory of musical harmony — •Alexandre Guillet — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Musical harmony, as the ancient problem of finding tunings and scales based on the commensurability of sound waves, has been approached by Helmholtz in terms of a dissonance curve in the frequency domain. This model is here recast in an elementary form related to number theory and a thermodynamical formalism for musical intervals and frequency ratios. The idea of the pioneer of biophysics connects with Riemann's zeta function along the critical line, and Minkowski's question mark measure. The former models rational relationships resulting from the acoustics of a harmonic timbre, while the latter models the probability distribution of the neurocognitive effort to assess the commensurability of frequency pairs. The spectrum of the resulting fractal curve predicts the quasi-periods of widely used musical scales, from the pentatonic division of the octave to microtonal ones, thus constituting a biophysical and mathemusical common ground to harmony across musical genres and cultures.

BP 23: Biopolymers, Biomaterials and Bioinspired Functional Materials I (joint session CPP/BP)

Time: Wednesday 15:00–16:45 Location: ZEU/0255

Invited Talk BP 23.1 Wed 15:00 ZEU/0255

Engineering, processing and application of recombinant spider silk proteins — •Thomas Scheibel — Universität Bayreuth, Lehrstuhl Biomaterialien, Prof.-Rüdiger-Bormann-Str. 1, 95440 Bayreuth

Proteins reflect one fascinating class of natural polymers with huge potential for technical as well as biomedical applications. One well-known example is spider silk, a protein fiber with excellent mechanical properties such as strength and toughness. We have developed biotechnological methods using bacteria as production hosts which produce structural proteins mimicking the natural ones. We employ silk proteins in application forms such as fibers, hydrogels, particles or films with tailored properties, which can be employed especially for biomaterials applications. In case of implants or catheters cell adhesion plays a crucial role for the overall function of the to-be-used material. To change the properties of in-use polymers and to adopt their biocompatibility, we established coatings based on engineered spider silk proteins. Spider silk hydrogels can be employed as new bioinks for biofabrication. Their elastic behavior dominates over the viscous behavior over the whole angular frequency range with a low viscosity flow behavior and good form stability. Cell-loaded spider silk constructs can be easily printed without the need of additional cross-linkers or thickeners for mechanical stabilization. Our bio-inspired approach serves as a basis for new materials in a variety of medical, biological, or technical applications.

BP 23.2 Wed 15:30 ZEU/0255

Inferring Structure-Property Relationships with Artificial Intelligence: A Lignin Case Study — •Matthias Stosiek and Patrick Rinke — Department of Physics, Atomistic Modelling Center, Munich Data Science Institute, Technical University of Munich

The potential of lignin as an abundant, underutilized biopolymer is increasingly being realized. A key challenge for the targeted production of lignins remains the poorly understood relation between lignin properties and its complex structure. Artificial intelligence (AI) methods could reveal such structure-function relationships but remain elusive in biomaterials research.

95 structurally diverse lignins are extracted from birch wood combining the Aqua Solv Omni (AqSO) biorefinery process and AI-guided data acquisition [1, 2]. Each lignin sample is characterized with 2D NMR spectroscopy and complemented with measurements of key lignin properties such as antioxidant activity.

To establish structure-function relationships, we correlate regions of the NMR spectra with corresponding property measurements. With a feature importance analysis, we identify structural relevant features for each property and provide a chemical interpretation. For instance, we find that more β-O-4 bonds lead to lower surface tension in water indicating a more linear lignin structure. Our structure-inference approach is designed to be general and applicable to a wide range of materials and characterization data.

[1] D. Diment et al., ChemSusChem, e202401711 (2024). [2] M. Alopaeus, M. Stosiek et al., Sci Data 12, 996 (2025).

BP 23.3 Wed 15:45 ZEU/0255

A minimalist view on biopolymer phase separation and aging — •Jasper Michels — Max Planck Institute for Polymer Research, Mainz, Germany

Phase separation of proteins is a ubiquitous process by which cells regulate biological processes. In aberrant cases, such as encountered in neurodegeneration, initially liquid condensates age to become more solid-like. Understanding the interplay between phase separation and aging seems essential in the development of new therapeutic strategies. We apply minimal models that aim to capture the essence of biological transitions in terms of driving forces and thermodynamics. Models discriminating between mono- and multivalent directed association on the one hand and non-specific interactions on the other appear surprisingly versatile in reproducing and predicting biopolymer phase behavior, while at the same time providing essential mechanistic insight. We will review our efforts, combining theory with experiments and demonstrating how relatively simple descriptions can (re)produce complex multi-component phase behavior. We will also present a dynamic version of the model, which provides for a thermodynamically fully consistent and intuitive description of the experimentally observed changes in viscoelasticity during aging. Our calculations explain how the stick-

iness of the proteins changes with time and concentration and how the coupling between association and solvation determines condensate viscoelasticity.

BP 23.4 Wed 16:00 ZEU/0255

Cellulose-colloid hybrid materials for refractive index tuning — •Stephan V. Roth — Deutsches Elektronen-Synchrotron DESY, Hamburg, Sweden — KTH Royal Institute of Technology, Stockholm, Sweden

Cellulose nanofibrils (CNF) with tailored (negative) surface charge are ideal for stable, nanoporous, structure-guiding network for thin film composite materials. Colloid materials offer the possibility for tunable structural colors, templates for metamaterials, and refractive index tuning. Here, core-shell-colloids with a hydrophobic core and positively charged, hydrophilic shell are used as additive in CNF thin films to tune their refractive index. The imbibition and self-assembly of the colloids as a function of colloid diameter in the CNF network was quantified, with colloids smaller than the pores in the CNF network penetrating into the thin film. Subsequent heat treatment allows for nanoscale composite formation on the level of the ~ 10 nm sized CNF bundles, while humidity treatment homogenizes the colloid distribution. Furthermore, the influence of the colloid size on the CNF structure inside the thin film was investigated and related to the mechanical properties of the colloid-CNF composite.

BP 23.5 Wed 16:15 ZEU/0255

A universal material basis for biocompatible printed electrolytes in Organic Electrochemical Transistors (OECTs) — •Moritz Flemming, Paul Zechel, Rakesh Nair, Laura Teuerle, Hans Kleemann, and Karl Leo — Institute of Applied Physics, Technische Universität Dresden

Organic Electrochemical Transistors (OECTs) stand out for their interplay between ionic and electronic conduction, making them ideal analogues to biological synapses for neuromorphic computing or biosensors. Furthermore, they can be printed into integrated circuits on flexible substrates, allowing for low-cost and high throughput fabrication of full electronic systems. However, most OECT electrolytes for integrated circuits still lack biocompatibility and suffer from rheology-related printing challenges. This talk presents a novel material basis that can be combined with an ionic liquid to fabricate a biocompatible electrolyte for OECTs. It allows rheological adjustments to enable the use of electrolyte in both inkjet and screen printing. Furthermore, the electrolyte is UV-curable, enabling it to transition into solid-state structures after printing. Extended ink and device lifetimes for screen-printed structures enable the fabrication of state-of-the-art OECTs that can operate in ambient air more than 30 days after fabrication. Ultimately, a fully biocompatible and screen-printed OECT on a leaf substrate is demonstrated.

BP 23.6 Wed 16:30 ZEU/0255

Nonequilibrium dynamics of the helix-coil transition in polyalanine — •Maximilian Conradi[1], Fabio Müller[1], Suman Majumder[2], and Wolfhard Janke[1] — [1]Institut für Theoretische Physik, Universität Leipzig, IPF 231101, 04081 Leipzig, Germany — [2]Amity Institute of Applied Sciences, Amity University Uttar Pradesh, Noida 201313, India

As a continuation of our previous work, the nonequilibrium pathways of the collapse of the helix-forming biopolymer polyalanine are investigated in an explicit solvent. To this end, the full time evolution of the helix-coil transition is simulated using molecular dynamics simulations. We compare the phenomenology of the transition between the two studies and investigate the dynamics.

BP 24: Biopolymers, Biomaterials and Bioinspired Functional Materials II (joint session CPP/BP)

Time: Wednesday 17:00–18:45 Location: ZEU/0255

BP 24.1 Wed 17:00 ZEU/0255

Coarse-grained simulations of network-forming DNA nanostructures — •Takahiro Yokoyama[1,2] and Arash Nikoubashman[1,2] — [1]Leibniz-Institut für Polymerforschung Dresden, Dresden, Germany — [2]Technische Universität Dresden, Dresden, Germany

DNA nanotechnology offers exceptional nanoscale designability through precise control of DNA sequences. These individual DNA strands can form predetermined building blocks, which then hierarchically assemble into super-structures such as nanotubes, nanocapsules, or nanostars. The latter can assemble further into (percolated) networks, where sequence-level design enables systematic control of the rheological and mechanical network properties. This multi-scale self-assembly can lead to cascading effects, where even a single unpaired nucleotide on the building block level can act as a highly flexible hinge that dramatically alters the network mechanics. To understand how such variations on the nucleotide-scale affect the network properties, we designed a series of DNA networks by systematically altering the arm number and junction flexibility of the star-shaped building blocks using coarse-grained molecular simulations of the oxDNA model. Our study revealed that the bulk modulus of the network decreased with increasing number of DNA arms; this counter-intuitive behavior stems from the addition of flexible junctions on the single-star level, which preferentially absorb deformation and soften the overall network. This result highlights the importance of precise nanoscopic design on the order of one nucleotide to obtain optimal network properties.

BP 24.2 Wed 17:15 ZEU/0255

Characterizing interactions between glycoproteins and RNA at the lipid membrane interface — •Horacio V. Guzman[1] and Viviana Monje[2] — [1]Biophysics & Intelligent Matter Lab, Material Science Institute of Barcelona, CSIC, Spain — [2]Department of Chemical and Biological Engineering, State University of New York at Buffalo, 308 Furnas Hall, Buffalo, USA

Biological membrane interfaces interacting with proteins, nucleic acids, and glycans are integral to many cellular processes. The interplay between membrane lipids and biopolymers is highly sensitive to their flexibility grade, secondary structure, and electrostatics. Consequently, the cell membrane interface experiences changes in local lipid distribution and fluctuation in local properties. Projecting biophysical and structural membrane and biopolymer properties onto a two-dimensional plane simplifies the quantification of molecular signatures by reducing the dimensional space and identifying relevant entropic and short-range interactions at the interface of interest, as well as, characterizing interaction patterns and spatial correlations of complex lipid bilayers as they interact with biopolymers. We compare lipid-lipid interaction patterns in membrane-only systems to the corresponding systems containing small proteins and RNA fragments, respectively. These analyses quantify the effect of peripheral biopolymers on local lipid composition, structure, packing, deformation ratio of the biopolymer, and surface topology of the membrane upon adsorption. Such characterization is crucial for starting with the next-generation rational design of lipid vesicles and lipid-coated RNA drug delivery systems.

BP 24.3 Wed 17:30 ZEU/0255

Nanoscale characterization of piezoelectric nanofibers blended with Salmon Gelatin — •Martín Chavarría-Vidal[1], Dragica Bezjak[2], María Saavedra-Fredes[1], Benjamín Schleyer-Thiers[1], Ilka Hermes[3], and Tomás P. Corrales[1] — [1]Universidad Técnica Federico Santa María, Valparaíso, Chile — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]Leibniz Institute of Polymer Research, Dresden, Germany

We electrospin salmon gelatin (SG) mixed in a polyvinyl alcohol (PVA) matrix containing chitosan (Ch). Furthermore, we used a coaxial electrospinning approach to blend these nanofibers together with polyvinylidene fluoride (PVDF). Such biomaterials could lead to the potential development of biocompatible and piezoelectric heart patches. After electrospinning our polymers, we observe by SEM two size distributions. Mechanical characterization of the large nanofibers obtained by AFM reveals two Youngs moduli peaks, centered at 1.77 GPa and 209 MPa. Small nanofibers also show a two component mechanical moduli distribution with peaks at 565 MPa and 1.33 GPa (10.1016/j.bbadva.2025.100168). EDS shows that both distributions

contain Fluor. However, complimentary PFM measurements indicate that large nanofibers have a piezoelectric response comparable to pure electrospun PVDF, while the small ones do not exhibit such response. These measurements lead us to believe that the large nanofibers are mainly β-phase PVDF, while the smaller ones are composed of PVA/SG/Ch with α-phase PVDF (10.1177/15589250221125437).

BP 24.4 Wed 17:45 ZEU/0255

Structural investigations using in situ SAXS on flexible bio-based vitrimeric carbon nanocomposites — •Sarathlal Koyiloth Vayalil[1,2], Vaishnav B[2], Viranchika Bijalwan[2], Sravendra Rana[2], and Ajay Gupta[2] — [1]Deutsches Elektronen Synchrotron DESY, Hamburg, Germany — [2]Applied Science Cluster, UPES, Dehradun, India

In this work, in situ small- and ultra-small-angle X-ray scattering has been employed to investigate the real-time structural evolution of 3D-printed vitrimeric thiol-acrylate photopolymers and their carbon-based nanocomposites designed for healable strain-sensing and soft-robotic applications. Flexible bio-acrylate based vitrimers reinforced with graphene/CNT fillers at varying concentrations are examined to elucidate temperature-dependent phase segregation and enable direct visualization of nano- and microscale filler morphologies, their spatial distribution, and their evolution across key thermal transitions (Tg and Tv of the polymer matrix). The effects of the stress/strain and cyclic-thermal cycles on the filler aggregates affecting the composites conductivity in carbon-filled samples are also evaluated. These insights into nano- and microscale morphology, reinforcement, and conductive behavior help us understand the dynamic structure-property relationships governing vitrimer-based conductive networks

BP 24.5 Wed 18:00 ZEU/0255

Nanomechanical testing of suspended single nanofibers and humidity-induced glass transition — •Benjamin Schleyer-Thiers[1], Diego Benavente[2], Yusser Olguin[2,3], and Tomas P. Corrales[1,3] — [1]Physics department of Universidad Tecnica Federico Santa Maria, Valparaiso, Chile — [2]Technological and Scientific Center (CCTVal), Valparaiso, Chile — [3]Biotechnology Center Daniel Alkalay Lowitt

In this work we will study the interaction of water molecules with polymeric nanofibers made from hygroscopic biopolymers and contrast them in environments with variable relative humidity. For this, we will suspend single nanofibers over micropatterns etched on silicon. In this suspended configuration, we shall perform three-point bending tests utilizing the environmental Atomic Force Microscope (AFM) and detect bending forces of the nanofiber, at different relative humidities. As bending tests are performed over the suspended nanofiber, the position-dependent stiffness can be plotted to find its mechanical modulus through bending models. The stiffness of single nanofibers drops with the increase in relative humidity, hinting a glass transition induced by this environmental condition. To test this behavior, we attempt to perform fracture experiments on a micro structured grid made by photolithography.

BP 24.6 Wed 18:15 ZEU/0255

Probing light-induced drug release to lipid monolayers — •Ipsita Pani, Michael Hardt, and Björn Braunschweig — Institute of Physical Chemistry, University of Münster, Corrensstraße 28-30, Münster 48149, Germany

Light-induced drug release using photoresponsive nanocarriers is increasingly explored for targeted therapeutic applications. While most studies characterize release in bulk aqueous environments, drug release across aqueous-organic interfaces is equally important, as these interfaces represent the entry point into cells. We recently demonstrated light-induced drug release to air-water interface.[1] In cancer therapeutics, passive diffusion of anticancer drugs across lipid membranes is a key transport mechanism, yet direct quantitative data on drug-lipid interactions and their effect on release remain limited. Here, using arylazopyrazole photosurfactant nanocarriers and doxorubicin as a representative anticancer drug, we investigate how interfacial lipid composition governs light-induced drug release. By combining Langmuir monolayers with interface-specific vibrational sum frequency generation (SFG) spectroscopy, we quantitatively estimate drug release at lipid-adsorbed interfaces as a model membrane. To systematically probe headgroup effects, we employ four dimyristoyl lipids- DMPC, DMPG, DMPS, and DMPE which share identical acyl chains but differ in charge and polarity. These results elucidate how lipid-drug interactions modulate release efficiencies at membrane-like interfaces, providing insights key to the design of photoresponsive nanocarriers for targeted drug delivery. [1] Pani et al. Chem. Sci., 2024, 15, 18865-18871.

BP 24.7 Wed 18:30 ZEU/0255

Hetero-aggregation of microplastic particles — Thomas Witzmann[1], Anja F. R. M. Ramsperger[2], Hao Liu[2], Yifan Lu[3], Holger Schmalz[2], Lucas Kurzweg[4], Tom C. D. Börner[4], Kathrin Harre[4], Andreas Greiner[2], Christian Laforsch[2], Holger Kress[2], Christina Bogner[3], Stephan Geckle[2], Andreas Fery[1], and •Günter K. Auernhammer[1] — [1]Leibniz-Institut für Polymerforschung Dresden, Germany — [2]Universität Bayreuth, Germany — [3]Universität zu Köln, Germany — [4]Hochschule für Technik und Wirtschaft Dresden, Dresden

Microplastic particles (MPP) in the environment are surrounded by a layer known as an 'eco-corona'. This is made up of natural organic matter (NOM), such as biomolecules, humic substances, and other natural molecules. NOM substantially alters the surface properties of MP particles, thereby influencing their interaction with other surfaces in an aqueous environment and their aggregation behaviour. We studied the interactions of eco-corona-covered MP particles on the nanoscale using colloidal probe-AFM. Measurements were performed at different ionic concentrations to mimic changing environmental conditions. We found that the eco-corona can pull on the silica colloidal probe via polymer bridging. This mechanism leads to aggregation and, consequently, sedimentation in the environment. By comparing our AFM results with experiments and simulations at different length scales, we consistently found that this type of heteroaggregation is conducive to stable aggregate formation and retains MPPs in sediments.

BP 25: Members' Assembly

Time: Wednesday 18:30–20:00 Location: BAR/0205

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

BP 26: Biomaterials and Biopolymers (joint session BP/CPP)

Time: Thursday 9:30–12:45 Location: BAR/SCHÖ

BP 26.1 Thu 9:30 BAR/SCHÖ

Characterization and Application of Honey-PVA Electrospun Scaffolds in Tissue Engineering — •Catalina Navarrete-Vera[1], Karen Yáñez[2], Cristian Acevedo[2], and Tomas Corrales[1,2] — [1]Departamento de Física, Universidad Técnica Federico Santa María, Valparaíso, Chile — [2]Centro de Biotecnología Daniel Alkalay Lowitt, Universidad Técnica Federico Santa María, Chile

Tissue engineering seeks to develop functional biomaterials that integrate seamlessly with biological systems. Electrospinning with static collectors enables the production of nanostructured scaffolds suitable for cell regeneration (10.1021/acsomega.3c06436). Incorporating natural components, such as honey, valued for its regenerative, anti-inflammatory, and antimicrobial properties, offers a route to bioactive wound-dressing alternatives (10.1016/j.carbpol.2019.05.004).

In this study, Manuka and Ulmo honeys were each combined with PVA to generate nanofibers and scaffolds via electrospinning. AFM force spectroscopy was used to assess individual fiber mechanics, and SEM and cell-culture assays were employed to evaluate morphology and biocompatibility. Both formulations produced fibers of similar diameter (100-300 nm) and nanomechanical stiffness (˜200 MPa), while honey-containing scaffolds improved cell growth over controls. These results indicate that Ulmo honey is a promising alternative to Manuka honey for tissue-engineering applications.

BP 26.2 Thu 9:45 BAR/SCHÖ

Additive Manufacturing in Wound Care Innovation from Sugarcane Bagasse — •Ahmed El-Hussein Elnewishy[1], Muhammad Mounir[1], Mona Tarek[1], and Ita Junkar[2] — [1]Biotechnology Program, Faculty of Science, Galala University — [2]Department of Surface Engineering, Jožef Stephan Institute, Ljubljana, Slovenia

Three-dimensional (3D) printing technology is capable of creating highly complex, customizable objects, offering unique advantages for various biomedical applications through methods such as inkjet-based, extrusion-based, and light-assisted techniques. This study focuses on using direct ink writing for additive manufacturing to print antibacterial wound dressings, addressing a critical gap in the current wound care market. The management of chronic and acute wounds presents significant challenges facing human health and overall wellness. Current wound dressing fails to meet patients needs in terms of high adhesion, poor gas exchange, low moisture retention, and the use of systemic and synthetic antibiotics. Additionally, the presence of unused agricultural waste and weak waste management increase greenhouse gas emissions, thus contributing to global warming. To address these issues, we utilized agricultural waste, specifically sugarcane bagasse, to create biopolymer 3D printing ink for wound dressings. We extracted cellulose from sugarcane bagasse and antibacterial bioactive compounds from plant extracts. The synthesized ink was then printed and post treated to enhance mechanical properties. We evaluated the cytotoxicity, antibacterial activity, and morphological structure of the patches using scanning electron microscopy.

BP 26.3 Thu 10:00 BAR/SCHÖ

FCS-Based RNA Payload Quantification and FLIM Analysis of pH-Dependent Lipid Phase Transitions in Lipid Nanoparticless — •Bernhard Kirchmair[1], Judith Müller[1], Thomas Kellerer[2], Ekaterina Kostyurina[1], and Joachim Rädler[1] — [1]Ludwig-Maximilians-Universität München, Germany — [2]Max Planck-Institut für Biochemie, Martinsried, Germany

Lipid nanoparticles (LNPs) emerged as one of the most promising delivery systems for transfecting mammalian cells with synthetic messenger RNA (mRNA). However, LNPs show a substantial heterogeneity both in shape and cargo and the precise mRNA payload and stoichiometric ratios in multi-component nucleic acid delivery remain poorly quantified. In this project we investigate how mRNA payload depends on LNP size and surface composition using fluorescence correlation spectroscopy (FCS) supported by dynamic light scattering, enabling estimation of particle concentration and RNA copies per LNP. Fluorescence cross-correlation spectroscopy further allows measurement of siRNA/mRNA ratios in mixed cargos. To link payload properties to endosomal escape rates and hence delivery efficiency, we probed pH-dependent lipid phase transitions using fluorescence lifetime imaging (FLIM) and fluorescence anisotropy, capturing changes both in bulk lipid phases and in intact LNPs. These measurements build a framework to monitor structural changes relevant to endosomal escape and can be applied to other LNP formulations and cargo types. Quantitative knowledge about content and ratios will ultimately support the delivery of genetic programs for regulated gene expression.

BP 26.4 Thu 10:15 BAR/SCHÖ

pH-dependent phase transitions in ionizable lipid mesophases — •Ekaterina Kostyurina[1], Susanne Liese[2], Akhil Sudarsan[2], Julian Philipp[1], and Joachim Rädler[1] — [1]Faculty of Physics, Ludwig-Maximilians University, 80539 Munich, Germany — [2]Faculty of Mathematics, Natural Science, and Materials Engineering, Institute of Physics, University of Augsburg, 86159 Augsburg, Germany

Lipid Nanoparticles (LNPs) have proven valuable in modern medicine as a medium for RNA delivery. Nanoparticles containing cationic ionizable lipid (CIL), cholesterol and structural lipids complex with nucleic acids into size-controlled particles that transport nucleic acid molecules across cell membranes via the endocytic uptake pathway. The delivery efficiency of a drug or vaccine is directly related to the efficiency of the endosomal release. Here, we study pH-dependent structural transitions of the CIL core phase which are believed to play an essential role in this process. We use bulk phases of ionizable lipid/cholesterol as a model system of the LNP core which allows us to study the structure of the lipid phases with high precision using X-ray diffraction. We show that the commonly used ionizable lipids overcome the inverted micellar-inverted hexagonal phase transition within the pH range typical for endosomal life cycle, and connect structural properties of the phases with LNP efficacy. Furthermore, we are aiming to understand the thermodynamics of these phase transitions by combining experimental measurements with theoretical modeling. This will help to better understand the structure-activity relation of LNPs and to increase the delivery efficiency in clinically relevant LNP delivery systems.

BP 26.5 Thu 10:30 BAR/SCHÖ

To gel or not to gel? Assembly phase changes of engineered spidroin proteins induced by temperature and time — •Isabell Tunn[1,2,3], Dmitry Tolmachev[2,4], Adam L. Harmat[2,4], Nea B. Möttönen[1,2], Alberto Scacchi[2,4,5], Maria Sammalkorpi[2,4], and Markus B. Linder[1,4] — [1]Department of Bioproducts and Biosystems, Aalto University, Finland — [2]Academy of Finland Center of Excellence in Life-Inspired Hybrid Materials (LIBER), Aalto University, Finland — [3]Fraunhofer Institute for Applied Polymer Research (IAP), Germany — [4]Department of Chemistry and Materials Science, Aalto University, Finland — [5]Department of Mechanical and Materials Engineering, University of Turku, Finland

Bioinspired silk-like proteins offer exciting possibilities for developing the next generation of advanced materials - from medicine to food packaging. Here, we investigate the temperature- and time-dependent assembly behaviour of engineered silk-like proteins into hydrogels conducting experiments and molecular dynamics simulations.* Phase transitions are controlled by entropic changes in flexible glycine-rich regions and hydrophobic interactions of alanine-rich α-helical regions. High-temperature gelation proceeds through interactions between alanine-rich domains, leading to β-sheet formation while time-induced gelation occurs via protein percolation mainly driven by dimerization of terminal domains. These findings provide guidelines for engineering protein-based materials with tailored assembly properties and gel characteristics, advancing the rational design of biomimetic soft materials. *https://doi.org/10.1016/j.ijbiomac.2025.147712

BP 26.6 Thu 10:45 BAR/SCHÖ

Power-Law Analysis of Force Relaxation and Creep Compliance in Nanoindentation of Glassy Gelatin in Humid Air — Paul Zech, Martin Dehnert, Mario Zerson, and •Robert Magerle — Fakultät für Naturwissenschaften, TU Chemnitz

Gelatin-based materials are widely used in food technology, drug delivery systems, and tissue engineering. Water acts as a plasticizer, softening gelatin and reducing its glass transition temperature. Using AFM-based nanoindentation experiments, we examined the mechanical response of a gelatin film to nanoindentations under constant strain (force relaxation) or constant stress (creep compliance) at a wide range

of tip approach velocities and relative humidity levels. Scaling analysis using a fractional rheology model reveals that force relaxation and creep compliance exhibit universal power-law behavior. Temporal evolution depends only on the tip indentation time, which defines the externally imposed timescale of the process, and the power-law exponent α, which characterizes the degree of viscoelasticity. At relative humidity $> 85\%$, the α values differ between the force relaxation and creep compliance data. This indicates differences in the underlying molecular processes.

15 min. break

Invited Talk BP 26.7 Thu 11:15 BAR/SCHÖ

Directed evolution of material-producing bacteria — •André Studart — Complex Materials, Department of Materials, ETH Zürich

Engineers often use high temperatures, pressures and polluting chemicals to make synthetic materials. By contrast, biology produces remarkable materials like wood and bone using widely available chemicals in water and at ambient temperature. The ability of organisms to create materials under mild conditions relies on the intricate biological machinery of living cells. Notably, natural selection processes have evolved such machinery for hundreds of millions of years to fulfill the demands of biological environments. Can we harness the machinery and evolutionary processes of biology to create materials more sustainably while still meeting engineering needs ? To explore this question, we utilized a microfluidic platform to evolve material-forming microorganisms towards cell mutants that meet the high productivity needed in industrial processes. Using cellulose-producing bacteria as an example, we show that this directed evolution approach enabled the isolation of a bacterial mutant that produces up to 70% more cellulose than its native counterpart. The overproducing bacterial strain offers an attractive alternative to wood to meet the growing demand for cellulose in the textile, medical and packaging industries. Beyond cellulose, the proposed technology offers a compelling approach to isolate bacteria for the bio-fabrication of other sustainable materials, such as silk, polyesters and clay-based bricks.

BP 26.8 Thu 11:45 BAR/SCHÖ

Controlling Axonal Outgrowth of Organoids by 3D Nanoprinted Scaffolds — •Tobias Müller[1], Malte Siegmund[1], Emma Wollesen[1], Kim Krieg[2], Ole Pless[2], Jan Hahn[3], Robert Zierold[1], and Robert Blick[1] — [1]Center for Hybrid Nanostructures, University of Hamburg, 22761 Germany — [2]Fraunhofer ITMP, Discovery Research Screening Port, 22525 Germany — [3]Section Facility Mass Spectrometry and Proteomics, University Medical Center Hamburg-Eppendorf, 20246 Germany

Cortical organoids are promising models for neurodegenerative disease research, yet their integration into defined neural networks remains challenging. We use two-photon polymerization (2PP) to fabricate three-dimensional scaffolds that direct axonal outgrowth and support organoid integration into engineered circuits.

Scaling structures from single neurons to millimeter-scale organoids introduces adhesion and imaging challenges. We address this by combining tailored scaffold geometries with a polydimethylsiloxane (PDMS)-based anchoring strategy, critical-point drying and quantitative analysis of electron microscopy images. Walls, stairs and microwires enhance organoid-scaffold interactions, promoting axonal outgrowth along intended paths and reducing extension into non-target regions.

These results demonstrate that 2PP-fabricated microarchitectures can guide axon growth and stabilize organoid-substrate contact, enabling more controlled organoid-based neuronal networks and advancing brain-on-a-chip approaches.

BP 26.9 Thu 12:00 BAR/SCHÖ

Stimulus-induced biomechanical perturbations via smart hydrogel microstructures — •Katja Zieske — Max Planck Institute for the Science of Light, Erlangen, Germany

Cells reside within complex three-dimensional extracellular matrices, where mechanical interactions play essential roles in tissue development, and disease progression. To mimic these interactions, we developed a lab-on-a-chip platform that applies spatially and temporally controlled mechanical perturbations using intelligent hydrogel microstructures.

First, we optimized material composition and photopolymerization parameters and demonstrated reliable, stimulus-dependent expansion and contraction of the hydrogel microstructures within microfluidic chambers. Using these microstructures, we then applied compressive forces to Matrigel and collagen networks. Finally, we applied mechanical perturbations to cellular systems.

By mimicking cellular pushing forces with hydrogel microstructures, this lab-on-a-chip system provides a versatile tool for studying mechanical remodeling of biopolymers and cellular systems.

BP 26.10 Thu 12:15 BAR/SCHÖ

Functionally Connecting High- and Low-Density Neuronal Networks Using 3D-Nanoprinted Structures — •Emma Wollesen, Malte Siegmund, Tobias Müller, Josephine Hoppe, Robert Zierold, and Robert Blick — Center for Hybrid Nanostructures, University of Hamburg, 22761 Hamburg, Germany

Tracing the propagation of interneural communication from high- to low-density networks is essential for exploiting information processing at the single-cell level. Given the multitude of synaptic connections, high-density networks of hiPSC-derived neurons may generate bursts of action potentials, a key communication mode that can be analyzed at the single-cell level in receiving low-density networks. Here, we move toward such a cultivation platform by evaluating 3D nanoprinted (3DN) structures fabricated by two-photon polymerization for their efficiency in facilitating connected high- and low-density networks. We demonstrate the prerequisite formation of hiPSC-derived low-density neuronal networks in tower-shaped 3DN structures. For augmentation with high-density networks, a stomach-shaped structure and connecting elements were fabricated. A minimum structure height of 30 micrometers proved critical for clear network demarcation. For future region-specific chemical stimulation, millimeter-scale structures for media reservoir separation were conceptualized, and fabrication feasibility was confirmed, requiring a 10 micrometer overlap and a suitable shear angle at structure interfaces. These results extend established 3DN platforms for low-density networks and support the integration of neural networks into Brain-on-a-Chip applications.

BP 26.11 Thu 12:30 BAR/SCHÖ

Multiplex sensing of respiratory viruses using surface plasmon resonance spectroscopy — •Ghazaleh Eshaghi[1], David Kaiser[1], Hamid Reza Rasouli[1], Dominik Gary[2], Tobias Fischer[2], Katrin Frankenfeld[2], Abhishek Sharma[3], and Andrey Turchanin[1] — [1]Institute of Physical Chemistry, Friedrich Schiller University Jena, 07743 Jena — [2]Forschungszentrum für Medizintechnik und Biotechnologie (fzmb) GmbH, 99947 Bad Langensalza, Germany — [3]BioNavis Ltd., Hermiankatu 6-8H, 33720 Tampere, Finland

We present label-free and real-time biosensing of three major respiratory viruses using the Multi-Parametric Surface Plasmon Resonance (MP-SPR) technique. In this approach, MP-SPR SPR Au sensors are functionalized with ultrathin (˜1 nm) azide-terminated carbon nanomembranes (N3-CNMs), enabling covalent attachment of virus-specific antibodies and thereby providing selective immobilization of target antigens on the sensor surface. We demonstrate specific detection of SARS-CoV-2, Influenza A, and Respiratory Syncytial Virus (RSV) antigens with negligible cross-reactivity and high reproducibility in both PBS-P buffer (physiological pH) and clinically relevant nasopharyngeal swab matrices. For SARS-CoV-2, Influenza A, and RSV antigens, we determine dissociation constants (KD) of 7.0 * 0.5 nM, 86 * 4 pM, and 3.0 * 0.2 pM, respectively, with corresponding limits of detection (LOD) of ˜65 pM, ˜80 pM, and ˜2 pM.

BP 27: Cell Mechanics I

Time: Thursday 9:30–12:45 Location: BAR/0205

Invited Talk BP 27.1 Thu 9:30 BAR/0205

Tissue interplay and the coordination of morphogenesis — •Elias Barriga — Physics of Life (PoL), Dresden, Germany

How tissues achieve robust morphogenesis in development and regeneration is the driving question in our research. In my talk I will share our results arising from a combination of mechanical and electrical measurements and perturbations in living tissues; and will discuss how our work support the exciting idea that biophysical properties emerging from tissue interplay coordinate morphogenesis in time and space.

BP 27.2 Thu 10:00 BAR/0205

Mechanical polarity in cell migration — •Steffen Grosser[1], Leone Rossetti[2], Isabela Corina Fortunato[3], Ricard Alert[4,5], and Xavier Trepat[1,5,6,7] — [1]Institute for Bioengineering of Catalonia (IBEC), Barcelona — [2]Faculty of Dentistry, Oral & Craniofacial Sciences, King's College, London — [3]Institut d'Investigació Sanitària Illes Balears (IdISBa), Palma — [4]MPI für Physik komplexer Systeme (MPI-PKS), Dresden — [5]University of Barcelona, Barcelona — [6]ICREA, Barcelona — [7]CIBER-BBN, Barcelona

Cells migrate on substrates in the absence of any net force, which poses a fundamental challenge in cell dynamics. All forces transmitted from the cells to the substrate cancel out. Neither force magnitude nor force dipole are related to neither cell speed nor direction.

We have recently found, however, that a higher moment of the cell traction distribution, the quadrupole, is in fact closely related to cell velocity - to both speed and direction. The quadrupole characterizes the asymmetry of the traction distribution, even when the total net force cancels out. It can be thought of as a mechanical cell polarity readout. Experimentally, the relation between force asymmetry and velocity holds for single cells and for short multicellular trains, and even for cells moving along gradients of adhesion.

To interpret this traction asymmetry, we propose to decompose the force into an active, unbalanced part that drives cell motion, and a frictional component. This leads to a novel, actual force-velocity relation for cell dynamics.

BP 27.3 Thu 10:15 BAR/0205

Mechanics of "apical bulkheads" in the bile canaliculi of the liver — •Matthew J. Bovyn[1,2,3], Maarten P. Bebelman[2], Yannis Kalaidzidis[2], Marino Zerial[2,4], and Pierre A. Haas[1,2,3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden — [3]Center for Systems Biology Dresden — [4]Human Technopole, Milan

In the liver, bile is transported through the network of bile canaliculi. They are bicellular tubes ("lumina"), in which the apical cortices of apposed cells bear bile pressure. When bile canaliculi must hold high pressures, either in development or disease, they generate folds protruding into the tubes, termed "apical bulkheads". These structures are under tension and contribute significantly to the ability of the bile canaliculus as a whole to bear pressure [1]. Here, we use lightsheet microscopy to discover that bulkheads are also dynamic, forming and retracting on a timescale of 20 min. We investigate the mechanical origins of this process by constructing a mechanical model balancing pressure and anisotropic surface tensions and spontaneous curvature of the apical cortices. We discuss the cell biological origins of these mechanical ingredients, the experimental evidence for them, and their role in bulkhead formation.

[1] Bebelman, M. P., Bovyn, M. J., *et al.* Hepatocyte apical bulkheads provide a mechanical means to oppose bile pressure. J. Cell Biol. **222**, e202208002 (2023).

BP 27.4 Thu 10:30 BAR/0205

Blebbing under confinement functions as a pressure-relief mechanism following cortical contraction — •Fatemeh Abbasi[1,2], Timo Betz[2], and Eva Kiermaier[1,3,4] — [1]Life and Medical Sciences (LIMES) Institute, Immune and Tumor Biology, University of Bonn, Bonn, Germany. — [2]Third Institute of Physics-Biophysics, Georg August University Göttingen, Göttingen, Germany. — [3]Department of Medicine, Friedrich-Alexander University Erlangen-Nürnberg (FAU), Erlangen, Germany. — [4]Deutsches Zentrum Immuntherapie (DZI), Universitätsklinikum Erlangen, Erlangen, Germany.

Cells migrating through tissues experience mechanical confinement that reshapes their morphology and internal stress. Using Confinement Force Microscopy (CFM), we dynamically controlled vertical confinement during live imaging and quantified 3D stress responses. A single confinement step triggered a biphasic response: an immediate passive stress spike from nuclear compression followed by a slower, actomyosin-driven buildup linked to bleb formation. Both blebbistatin and Y-27632 reduced traction stresses; notably, Y-27632 fully blocked blebbing, while blebbistatin allowed it only under strong compression, indicating partial decoupling between contractility and morphology. Blebbistatin also lowered cellular stiffness and viscosity, promoting rapid stress relaxation. These results suggest that blebbing functions as a pressure-relief mechanism allowing cells to maintain mechanical balance under confinement.

BP 27.5 Thu 10:45 BAR/0205

Moving without motors: Amoeboid cell migration and shape dynamics driven by actin polymerization — •Winfried Schmidt, Alexander Farutin, and Chaouqi Misbah — Univ. Grenoble Alpes, CNRS, LIPhy, F-38000 Grenoble, France

Mammalian cell migration is essential for many physiological and pathological processes, such as embryonic development, wound healing, and cancer metastasis. Cells have developed the amoeboid migration mode, which is characterized by large, dynamic shape deformations. This strategy allows cells to move rapidly and in the absence of strong adhesion across a variety of different environments, including two-dimensional confinement, three-dimensional matrix, and bulk fluids. Molecular motors, such as myosin, are traditionally considered essential for cell polarization or motility. Here, a model of an amoeboid cell is analyzed both analytically and numerically. It is shown that actin polymerization alone is sufficient to trigger both cell polarity and motility, in line with recent experiments on T-lymphocytes showing that inhibition of molecular motors does not significantly affect motility. Depending on parameter values, the cells exhibit straight, circular, or even chaotic trajectories. A similar variety of motion is observed in experiments across multiple motile cells. These findings open up a new perspective on amoeboid motility, providing a scenario for the onset of polarity, migration, and dynamical cell shape changes without contractile activity.

15 min. break

BP 27.6 Thu 11:15 BAR/0205

Living Cells Respond to the Surface Tension of Soft Solids — •Johannes Rheinlaender, Leah Gumbsch, Hendrik von Eysmondt, and Tilman E. Schäffer — Institute of Applied Physics, University Tübingen, Germany

It is widely known that living cells respond to the stiffness of their environment in terms of spreading area as well as other properties such as the cytoskeletal structure, migration, or gene expression. These effects are usually investigated by seeding cells on elastic substrates with varying bulk stiffness, either hydrogels or soft elastomers. However, cellular behavior differs on hydrogels and elastomers, which has been attributed to various material properties like surface roughness or porosity. Using scanning ion conductance microscopy (SICM), we show that elastomers routinely used in mechanobiology studies exhibit a significant surface tension on the order of several tens of mN/m, independent of their bulk stiffness. We thereby demonstrate that living cells mostly respond to the surface tension rather than the bulk stiffness of the substrate on soft elastomers with Young's moduli below approximately 10 kPa and introduce possible solutions to address this problem. To conclude, the influence of surface tension is an important yet underestimated aspect in cellular mechanobiology.

BP 27.7 Thu 11:30 BAR/0205

Complex Rheology in Single Cells: Compression Stiffening but Shear Softening — •James P. Conboy[1], Luis Alonso[2], Haiqian Yang[2], Nicole van Vliet[1], Pouyan E. Boukany[1], Fred C. MacKintosh[3], and Gijsje H. Koenderink[1] — [1]TU Delft, NL — [2]MIT, USA — [3]Rice University, USA

In multicellular organisms, cells are constantly subjected to physical

forces. Cells in the heart, lungs and skin experience primarily compression and stretching, whereas shear forces are dominant in the brain and in blood vessels. The mechanical resilience to compression and shear forces is essential for preventing cell damage or even rupture. Our aim is to understand the response of cells to external mechanical cues. For this purpose, we have developed a novel single cell rheology setup that allows us for the first time to make direct comparisons between a living mammalian cell's response to compression and shear strain. In this work, we have identified the relative contribution of actin and vimentin intermediate filaments in uniaxial compression experiments on single fibroblasts. Our findings reveal that individual fibroblasts undergo stiffening under physiologically relevant compressive strains, but the removal of vimentin reduces this stiffening effect. Furthermore, we present, to our knowledge, the pioneering example of single-cell shear rheology experiments, where we discovered that cells soften when sheared, in stark contrast to their stiffening behaviour under compression. Finally, we propose a minimal model to elucidate these phenomena and compare our results to semiflexible polymer models used to explain the mechanics of reconstituted cytoskeletal systems.

BP 27.8 Thu 11:45 BAR/0205

Intracellular ROS generation under ultra-high dose rate electron irradiation at FLASHlab@PITZ — •Y. Komar[1,2,3], E. Fujan[2], C Richard[1], X. Li[1], N. Aftab[1], A. Aksoy[1], Z. Amirkhanyan[1], A. Chiravuri[1,2], J. Good[1], M. Gross[1], F. Hausmann[3], S. Khammee[1], M. Krasilnikov[1], B. Li[1], Z. Lotfi[1], G. Montoya-Soto[1], F. Müller[1], A. Oppelt[1], F. Riemer[1], K. Suzart[1], E. Tarakci[1,2,3], I. Tinhofer[3], D. Villani[1], S. Worm[1], D. Xu[1], S. Zeeshan[1], M. Frohme[2], F. Stephan[1], S. Aminzadeh[1,2], and A. Grebinyk[1,2] — [1]Deutsches Elektronen-Synchrotron, Zeuthen, Germany — [2]Technical University of Applied Sciences Wildau, Wildau, Germany — [3]Charité University Medicine Berlin, Corporate Member of Freie Universität Berlin and Humboldt-Universität zu Berlin, Berlin, Germany

The new FLASHlab@PITZ beamline commissioning started in August 2025 for radiobiological studies at the Photo-Injector Test Facility at DESY in Zeuthen (PITZ). It enables irradiation with dose rates ranging from conventional (CDR, 0.05Gy/s) up to ultra-high (UHDR, 10^14Gy/s). The in vitro effects of UHDR versus CDR irradiation were examined using human lung cancer A549 and healthy HEL299 cells exposed to CDR (0.05Gy/s) and UHDR (7.8*10^5Gy/s). Reactive oxygen species production assessment showed 84% decrease in HEL299 cells and no difference in A549 at ~7.5Gy under UHDR compared with CDR. That indicates UHDR irradiation having a milder impact on healthy than on cancer cells, highlighting the potential of FLASHlab@PITZ for future in vivo studies.

BP 27.9 Thu 12:00 BAR/0205

Probing the influence of mechano-chemical cues on the size of nuclei — •Pooja Yadav, Florian Rehfeldt, and Matthias Weiss — University of Bayreuth, Experimental Physics I,95447,Bayreuth

The size of nuclei in eukaryotes is frequently observed to scale with the size of the cell that harbours them. Yet, our understanding of how cells can measure and regulate nuclear size is still fragmentary. A recently developed model suggests nuclear size to be determined by a dynamically maintained but limited amount of membrane material that needs to be distributed between organelles and the plasma membrane. Given that membrane homeostasis and cell morphology can be altered biochemically and mechanically, we have used drug treatments and polyacrylamide (PA) hydrogels of varying stiffness as a substrate for cells. As a result, we have found that softening the substrate alters the shape and size of cells and nuclei, but maintains the ratio of their projected areas. Similarly, affecting the actomyosin cortex had little effect on this ratio. However, when enforcing changes in membrane homeostasis by pharmaceuticals, the ratio of cellular and nuclear cross-sectional areas was markedly altered. Altogether, our data suggest that dynamically maintaining and limiting membrane material is a core mechanism of how cells determine the size of their nuclei.

BP 27.10 Thu 12:15 BAR/0205

Nuclear downsizing: Dynamic volume and cell-cycle control in emerging tumour spheroids — •Vaibhav Mahajan[1], Keshav Gajendra Babu[1], Markus Mukenhirn[1], Antje Garside[1], Timon Beck[1,2], Byung Ho Lee[3], Kyoohyun Kim[2], Carsten Werner[4], Alf Honigmann[1], Sebastian Aland[5], Raimund Schlüssler[1], and Anna Taubenberger[1,4] — [1]Dresden University of Technology, Dresden, Germany — [2]Max Planck Institute for the Science of Light, Erlangen — [3]MPI-CBG, Dresden — [4]Leibniz Institute of Polymer Research Dresden — [5]Hochschule für Technik und Wirtschaft Dresden

Tumour development involves biophysical changes across scales, yet how cancer cells regulate properties such as volume and mechanics within dense multicellular environments remains unclear. Using tuneable biohybrid hydrogels, we quantified cell and nuclear volumes as single cancer cells formed multicellular tumour spheroids. We found that transition to multicellularity led to strong reductions in cellular and nuclear volumes, delayed cell-cycle progression, and altered mechanics, with these changes tightly coupled. Nuclear volume dropped by up to 60%, not primarily due to confinement but due to cell-cycle adaptations, namely accumulation of smaller-sized G1 cells-an effect reversed by CDK1 inhibition. Additional nuclear volume decreases within clusters were associated with increased mass density and cell stiffness, both reversible upon cell release. Conversely, cells invading out of spheroids increased nuclear volumes and softened. These findings reveal how cancer cells dynamically adjust volume, cell-cycle state, and mechanics in the multicellular context.

BP 27.11 Thu 12:30 BAR/0205

A protein-DNA surface hydrogel mechanically reinforces the cell nucleus — •Yahor Savich[1,2,3], Ramesh Adakkattil[1], Pranay Mandal[1,2,3], Valentin Ruffine[4], Mareike Jordan[1], Henrik Dahl Pinholt[5], Elisabeth Fischer Friedrich[4], Frank Jülicher[2,3,4], Stephan Grill[1,3,4], and Alexander von Appen[1,4] — [1]MPI-CBG, Dresden — [2]MPI-PKS, Dresden — [3]Center for Systems Biology Dresden — [4]TUD, Dresden — [5]MIT, Cambridge

Cells safeguard their genome while nuclei are deformed. The nuclear envelope is known to protect DNA from such mechanical stress, but how forces are buffered across the scales from individual DNA strands to the nucleus remains unknown. We show that the nuclear envelope protein LEM2 and the DNA-binding protein BAF, together with DNA, form an unconventional stiffening system. When DNA is held at a given force in optical tweezers, the addition of these proteins causes a force increase proportional to the initial force. This behaviour can be captured by an effective spring model that emerges from multivalent protein-protein and protein-DNA interactions. At the nuclear surface, the same components form an elastic surface hydrogel in which the multivalent interactions contract the surface hydrogel relative to its relaxed state, introducing a pre-stress. Using parameters obtained at the molecular scale, a continuum model of this surface hydrogel yields free-energy-minimizing nuclear shapes and an area stiffness that are in agreement with measurements in control and LEM2 knockdown cells. These results identify a load-bearing, mesoscale protein-DNA surface hydrogel that mechanically reinforces the nucleus.

BP 28: Active Matter V (joint session DY/BP)

Time: Thursday 9:30–12:45 Location: ZEU/0160

Invited Talk BP 28.1 Thu 9:30 ZEU/0160

Active memory and non-reciprocity as pathways to pattern formation in conserved scalar fields — •Suropriya Saha and Vaishnavi Gajendragad — Max Planck Institute for Dynamics and Self-organisation

Active phase separation has emerged as a field within active matter that investigates pattern formation in number-conserving scalar fields. The field has also gained momentum from developments in biological systems, where phase separation has been implicated in the formation of biological condensates. In this talk, I will explore two different paths to non-Hermiticity in number-conserving scalar fields. Non-Hermiticity, or the emergence of complex eigenvalues in the linear dynamics of scalar densities, is associated with traveling patterns that break time-reversal symmetry and parity.

The first pathway I will discuss is a feedback mechanism in which particles store and use information about their past trajectories to influence their time evolution. I will present a model in which the particle velocity acquires an active contribution that depends on its past trajectory, weighted by a memory kernel. This memory kernel is independent of the thermal noise acting on the particle, implying a microscopic violation of detailed balance. The number density of these particles is described by a modified Cahn*Hilliard equation that incorporates this non-equilibrium effect. The second pathway involves non-reciprocal interactions between two or more species. I will describe the phenomenology observed in both cases, focusing on the role of fluctuations, nonlinearities, and the stability of the resulting patterns.

BP 28.2 Thu 10:00 ZEU/0160

Self-propulsion via non-transitive phase coexistence in chemically active mixtures — •Yicheng Qiang, Chengjie Luo, and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany

Chemical activity is common in many active matter systems. For example, active reactions can lead to the self-propulsion of particles, which can finally give rise to rich collective dynamics, including phase separation, even in the absence of attractive interactions. With interactions that already favor phase separation, chemical activity and multiple coexisting phases will further intertwine. To unveil the basic effect of active reactions on coexistence, we study mixtures where solvent species interconvert while solutes segregate. We demonstrate that active reactions alter the chemical potential balance between the coexisting phases and defy the construction of pseudo-pressure balance. As a result, the transitivity of phase coexistence is broken, and the bulk compositions depend on the contact topology among all the coexisting phases. With cyclic topologies, the pressure imbalance leads to self-propelled phases and other complex dynamics such as budding and engulfment.

BP 28.3 Thu 10:15 ZEU/0160

Contraction waves in pulsating active liquids: from pacemaker to aster dynamics — Tirthankar Banerjee[1], Thibault Desaleux[1], Jonas Ranft[2], and •Etienne Fodor[1] — [1]Department of Physics and Materials Science, University of Luxembourg, L-1511 Luxembourg City, Luxembourg — [2]Institut de Biologie de l'ENS, Ecole Normale Supérieure, CNRS, Inserm, Université PSL, 46 rue d*Ulm, 75005 Paris, France

We propose a hydrodynamic theory to examine the emergence of contraction waves in dense active liquids composed of pulsating deformable particles. Our theory couples the liquid density with a chemical phase that determines the periodic deformation of the particles. This mechanochemical coupling regulates the interplay between the flow induced by local deformation, and the resistance to pulsation stemming from steric interaction. We show that this interplay leads the emergent contraction waves to spontaneously organize into a packing of pacemakers. We reveal that the dynamics of these pacemakers is governed by a complex feedback between slow and fast topological defects that form asters in velocity flows. In fact, our defect analysis is a versatile platform for investigating the self-organization of waves in a wide range of contractile systems. Our results shed light on the key mechanisms that control the rich phenomenology of pulsating liquids, with relevance for biological systems such as tissues made of confluent pulsating cells. Refs: arXiv:2509.19024, arXiv:2407.19955

BP 28.4 Thu 10:30 ZEU/0160

Topology of pulsating active matter: Defect asymmetry controls emergent motility — •Luca Casagrande[1], Alessandro Manacorda[2], and Étienne Fodor[1] — [1]Department of Physics and Materials Science, University of Luxembourg, Luxembourg City, Luxembourg — [2]CNR Institute of Complex Systems, Uos Sapienza, Rome, Italy

When heartbeats become irregular, spiral waves and motile defects emerge at the surface of cardiac tissues [1]. Capturing the emergence of defect motility despite the absence of any cellular flows is a theoretical challenge which has recently been tackled by models of actively deforming particles [2-4]. The interplay between individual pulsation of particles sizes, synchronization, and repulsion yields deformation waves resembling those of cardiac tissues. Combining particle-based and hydrodynamic approaches, we examine the statistics of defects in the collective deformation of particles. We rationalize defect motility as stemming from the breakdown of time-reversal and spatial symmetries, and provide predictions for the deformation profile near the defect core to quantify motility. [1] A. Karma, Annu. Rev. Condens. Matter Phys., 4, 313-337 (2013) [2] Y. Zhang, É. Fodor, Phys. Rev. Lett., 131, 238302 (2023) [3] A. Manacorda, É. Fodor, Phys. Rev. E, 111, L053401 (2025) [4] W. Piñeros, É. Fodor, Phys. Rev. Lett., 134, 038301 (2025)

BP 28.5 Thu 10:45 ZEU/0160

Avalanche statistics in dense active matter — •Vinay Vaibhav[1] and Peter Sollich[1,2] — [1]Institut für Theoretische Physik, University of Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [2]Department of Mathematics, King's College London, The Strand, London, UK

Reorganization processes in dense active matter remain a central open question in non-equilibrium physics. In particular, how persistent self-propulsion drives local rearrangements and triggers collective failure events is not well understood. Here, we investigate such activity-induced rearrangements, that sometimes rapidly cascade to avalanches, in a dense assembly of self-propelled particles with extremely persistent activity. These systems evolve through abrupt transitions between mechanically stable configurations, giving rise to rich intermittent behavior. Using large-scale simulations, we systematically characterize avalanche statistics across a range of system sizes and activity protocols. We quantify the scaling properties of avalanche-size distributions for two widely studied active matter models: active Brownian particles and active Ornstein-Uhlenbeck particles. By comparing these classes of dynamics, we identify how the nature of the propulsion mechanism influences the exponents associated with the avalanche size distribution. In addition, we report the frequency and temporal organization of avalanches. Our results provide a unified picture of how persistent activity drives rearrangements in dense active systems and highlight the connections between active intermittency, mechanical stability, and avalanche dynamics.

15 min. break

BP 28.6 Thu 11:15 ZEU/0160

Coupling intracellular processes and extracellular environment in a Cellular Potts model — •Cornelis Mense[1,2], Falko Ziebert[1,2], and Ulrich Schwarz[1,2] — [1]ITP, Heidelberg — [2]BioQuant, Heidelberg

The Cellular Potts Model (CPM) is a computationally very efficient framework to study cell dynamics, wherein cells are simulated through Hamiltonian based update rules on a discretised lattice. The model has traditionally been used to predict cell migration and shape in scenarios such as immune response, morphogenesis, cancer, and wound healing. In contrast to e.g. active gel models, however, the CPM usually does not represent subcellular processes. Here, we propose an extension to the CPM by which cells can contract their bulk to both actively transport material and strain their substrate. This model allows us to represent feedback loops between intracellular processes, cell shape and the mechanical and geometrical properties of the extracellular environment. Migration can emerge both as internal symmetry break or as response to an external gradient. We apply it to some standard situations of experimental interest, in particular 3D-printed scaffolds

for cell adhesion and migration.

BP 28.7 Thu 11:30 ZEU/0160

Exact Stationary State of a d-dimensional Run-and-Tumble Particle in a Harmonic Potential — •Mathis Guéneau[1], Grégory Schehr[2], and Satya N. Majumdar[3] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Germany — [2]Sorbonne Université, Laboratoire de Physique Théorique et Hautes Energies, CNRS UMR 7589, 4 Place Jussieu, 75252 Paris Cedex 05, France — [3]LPTMS, CNRS, Univ. Paris-Sud, Université Paris-Saclay, 91405 Orsay, France

We study the stationary state of a run-and-tumble particle (RTP) confined in a harmonic potential in arbitrary dimension d. Owing to isotropy, all statistical properties of the steady state are fully encoded in the distribution of a single coordinate. This coordinate follows an effective one-dimensional dynamics with a piecewise-constant self-propulsion velocity drawn from a prescribed distribution. We obtain the exact stationary distribution by identifying a stick-breaking process and a Dirichlet process in the dynamics, and by using known results for these processes. This framework allows us to compute exactly the full radial distribution, the joint law of the coordinates, and their moments, and to extend these results to include thermal noise. We further characterize the shape transition of the stationary state, from active-like to passive-like behavior, and show that it can be analyzed for arbitrary external potentials.

BP 28.8 Thu 11:45 ZEU/0160

Jerky active particles — •Hartmut Löwen and Stephy Jose — Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine Universität Düsseldorf, Universitätsstraße 1, 40225 Düsseldorf

We introduce jerky active particles, a generalization of inertial active Brownian particles subjected to jerk, the time derivative of acceleration. These particles can be realized by feedback in active macroscopic granules or in mesoscopic colloids moving in a viscoelastic background with memory. We analytically derive their mean squared displacement (MSD) and show that there is a gigantic dynamical spreading with extremely high scaling exponent of the MSD as a function of time [1]. We also generalize jerky dynamics to a chiral active particle and demonstrate that the mean displacement shows damped and exploding Lissajous-like patterns alongside the well-known classical spira mirabilis [2]. Our work on jerky chiral active particles opens a new route to explore rich dynamical effects in active matter.

[1] H. Löwen, Physical Review E 112, 045412 (2025)
[2] S. Jose, H. Löwen, Chiral jerky active particles, New Journal of Physics (in press), see also arXiv:2508.18180

BP 28.9 Thu 12:00 ZEU/0160

Diffusion of active particles on curved manifolds — •Maxim Root[1], Lorenzo Caprini[2], and Hartmut Löwen[1] — [1]Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, 40225 Düsseldorf, Germany — [2]Physics Department, Sapienza University of Rome, 00185 Rome, Italy

Active Matter rarely exists in isolated idealized systems. In nature, it is rather typical that active particles are surrounded by complex environments and experience external forces. So far, passive Brownian motion constrained to curved surfaces [1,2] was studied extensively and similar work was done on clusters of active particles [3]. In this talk we explore the emergent effects of active particles constrained to two-dimensional curved surfaces and in presence of an external homogeneous force field, e.g., gravity. This is done for an overdamped active particle that exhibits persistent motion on a short time scale and diffusion in the long-time limit. The lateral long-time diffusion coefficient is computed for different scenarios and criteria for localization are derived.

[1] T. Ohta and S. Komura, *Lateral diffusion on a frozen random surface*, EPL **132**, 50007 (2020)
[2] A. Naji and F. L. H. Brown, *Diffusion on ruffled membrane surfaces*, J. Chem. Phys. **126**, 235103 (2007)
[3] E. D. Mackay et al., *Emergent Dynamics of Active Systems on Curved Environments*, arXiv:2505.24730 (2025)

BP 28.10 Thu 12:15 ZEU/0160

Modeling dissipation in quantum active matter — Alexander P. Antonov[1], Sangyun Lee[2], Benno Liebchen[3], Hartmut Löwen[1], Jannis Melles[1], Giovanna Morigi[4], Yehor Tuchkov[2], and •Michael te Vrugt[2] — [1]Institut für Theoretische Physik II, Weiche Materie, Heinrich-Heine-Universität Düsseldorf — [2]Institut für Physik, Johannes Gutenberg-Universität Mainz — [3]Institut für Physik der kondensierten Materie, Technische Universität Darmstadt — [4]Theoretische Physik, Universität des Saarlandes

In classical active matter systems, dissipation plays a major role. Currently, there is an increased focus in exploring quantum mechanical active matter systems, for which the question of how to model dissipation is far from obvious. In fact, for open quantum systems, a variety of quantum heat bath models have been proposed that are valid in different physical situations. Here, we compare the effects of different quantum heat baths based on a recently proposed quantum active matter model [Phys. Rev. Res. **7**, 033008 (2025)]. We find that the choice of the quantum heat bath strongly influences the dynamics at short timescales, which is the regime in which quantum effects are most relevant.

BP 28.11 Thu 12:30 ZEU/0160

Active Magnetic Particles in Magnetic Gradient Fields — •Laris Berekovic, Margaret Rosenberg, and Hartmut Löwen — Heinrich-Heine University Düsseldorf, Universitätsstraße 1, 40225 Düsseldorf

Active particles are common in nature, underlying many complex phenomena. Since the motion of active particles has no intrinsic directionality, steering the particles' motion requires an additional control parameter, such as a magnetic interaction. In this contribution, we present an analysis of the effect of magnetic vortex fields created by a current carrying wire on the ground states and motion of active Brownian particles (ABP) carrying a fixed magnetic dipole moment. We present an analytical solution for the single-particle case, compute the ground state for multiple particles via simulated annealing in the passive case and explore the activity-induced phase transition created by increasing the self-propulsion. We find new forms in the ground state, as well as a rich variety of activity-induced structures. These results can be applied to ferrofluid systems, biophysical systems of magnetotactic bacteria or form the basis of more complex industrial applications.

BP 29: Focus Session: Theoretical Modeling and Simulation of Biomolecular Condensates I (joint session CPP/BP)

Biomolecular condensates play a central role in many cellular processes and provide a fascinating example of self-organized, highly dynamic systems. Physical methods, particularly from statistical physics and soft matter, have emerged as valuable tools for understanding and predicting their fundamental properties. Conversely, the complexity and diversity of biological systems open new perspectives and challenges for physical modeling. This focus session will highlight current research at the interface of physics and biology, with an emphasis on theoretical modeling and simulation of the physics of biomolecular condensates.

Organized by Arash Nikoubashman, Tyler Harmon and Lukas Stelzl.

Time: Thursday 9:30–11:15 Location: ZEU/0260

Topical Talk BP 29.1 Thu 9:30 ZEU/0260

Wetting transitions in biomolecular coacervates — •Susanne Liese[1], Tiemei Lu[2], Evan Spruijt[3], and Christoph Weber[1] — [1]University of Augsburg — [2]University of Oxford — [3]Radboud University

Biomolecular coacervates are liquid-like droplets that can interact with membranes and self-organize into complex structures. Understanding the principles governing their shapes and higher-order assemblies is crucial for controlling compartmentalization in biological and synthetic systems.

We present a theoretical framework describing the shape and organization of biomolecular coacervates interacting with membranes and each other. Large coacervate droplets adopt morphologies determined by the balance of surface tensions, from partial adhesion to full engulfment. Scaled membrane tension and droplet-membrane interactions predict transitions between spherical, lens-shaped, partially wrapped, and endocytosed droplets, with composition-dependent contact angles linking molecular properties to macroscopic shapes.

For multiphase coacervates, we model the impact of interfacial species on droplet organization. Enrichment of an interfacial component at phase boundaries drives partial wetting between droplets, promoting the formation of dimers and extended chains. Numerical simulations show that surface tension minimizes the contact area, straightening droplet arrangements and generating polymer-like behavior with bending stiffness and segment-length constraints.

BP 29.2 Thu 10:00 ZEU/0260

Elastic regulation of biomolecular condensates — •Oliver Paulin and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany

In recent years, biomolecular condensates have emerged as a vital component of sub-cellular organisation. Here, we discuss the role that elastic interactions can play in regulating condensate size, count, and mechanical properties. First, we focus on the impact of 'external' elasticity that arises from a confining mesh such as the cytoskeleton. We find that the additional energetic cost of network deformations induced by condensate growth limits condensate size, and can even suppress condensate formation entirely. Additionally, when condensate size is comparable to characteristic heterogeneities of the network, non-local interactions may arrest thermodynamic coarsening and drive the formation of stable patterned states with an energetically selected length scale. Second, we study how 'internal' elasticity, resulting from the intrinsic viscoelasticity of condensate material, can inhibit condensate growth, but also impart condensates with mechanical strength. For the case in which condensate growth is driven by active incorporation of new material, we demonstrate how a delicate balance of material properties provides condensates with solid-like mechanical strength, without compromising their liquid-like ability to form and grow rapidly. For both examples, we construct dynamic continuum models that couple phase separation with elastic deformation, analysing the key parameters that control condensate form, and identifying how cells can use elasticity to fine-tune condensate behaviour to fulfil a specific function.

BP 29.3 Thu 10:15 ZEU/0260

Phase Separation of a Nucleator in a Self Straining Active Filament Network — •Jakob Schindelwig[1], Quentin Bodini-Lefranc[1,2], and Sebastian Fürthauer[1] — [1]Institute of Applied Physics, TU Wien, Lehargasse 6, 1060 Vienna, Austria — [2]Ecole polytechnique, Institut Polytechnique de Paris, Route de Saclay, 91120 Palaiseau, France

Many membraneless compartments of cells, such as stress-granules, form via liquid-liquid phase separation. In cells many compartments of the same type and similar sizes can coexist. Since this is inconsistent with equilibrium phase separation physics, we ask if active mechanics could explain this observation. We develop a model coupling dynamics of the droplet material to an active self-straining filament network. This model shows (i) arrested coarsening , (ii) oscillations, (iii) scale selection. We establish that our model is physiologically plausible by comparing to recent work on a phase separating nucleator of actin.

BP 29.4 Thu 10:30 ZEU/0260

Active Transport as a Mechanism of Microphase Selection in Biomolecular Condensates — •Le Qiao, Peter Gispert, and Friederike Schmid — Institut für Physik, Johannes Gutenberg-Universität Mainz, D55099 Mainz, Germany

Cells control the size and organization of biomolecular condensates formed by liquid-liquid phase separation (LLPS), yet the underlying physical principles remain incompletely understood. We propose a transport-driven mechanism in which undirected motor-mediated motion along cytoskeletal filaments redistributes phase-separating components, generating an effective non-equilibrium long-range repulsion that arrests coarsening. This is explored using a minimal reaction-diffusion-transport model that captures the interplay between binding-release kinetics, diffusion, and active transport. A linear stability analysis and three-dimensional simulations reveal a transition from macroscopic to microphase separation at remarkably low binding/release fractions, corresponding to minute fractions of motor-bound proteins. Tuning motor binding rates b or transport velocities enables sublinear control of condensate dimensions ($L \sim b^{1/4}$) from nanometers to micrometers. This mechanism provides a simple physical route for spatially programmable condensate organization in living cells and active materials.

BP 29.5 Thu 10:45 ZEU/0260

Positive feedback in chemically active droplets — •Xi Chen[1], Jens-Uwe Sommer[1,2], and Tyler Harmon[1] — [1]Leibniz Institute of Polymer Research, Dresden, Germany — [2]Dresden University of Technology

Biomolecular condensates are dynamic compartments that can be maintained far from equilibrium by active chemical reactions. Active condensates can be driven by phase-dependent reaction fluxes, for example via localized enzymatic activity, and thereby exhibit emergent behaviors that cannot be realized in equilibrium condensates. We analyzed condensates with positive feedback between phase separation and reactions: droplets enhance reactions, and the resulting products stabilize the droplets. We show that this feedback produces pronounced hysteresis, making droplets resilient to cellular fluctuations. We show the hysteresis persists across a broad range of reaction schemes and parameter choices, indicating that it is a robust feature of droplets with positive feedback. Condensates that form to satisfy transient cellular needs may benefit from such hysteresis, because it ensures that they persist long enough to carry out their functions despite fluctuating conditions.

BP 29.6 Thu 11:00 ZEU/0260

Chemically driven simulations of enzymatic phosphorylation in protein condensates — •Emanuele Zippo[1], Dorothee Dormann[1,2], Thomas Speck[3], and Lukas Stelzl[1,2] — [1]Johannes Gutenberg University Mainz, Mainz, Germany — [2]Institute of Molecular Biology (IMB), Mainz, Germany — [3]University of Stuttgart,

Stuttgart, Germany

The condensation and aggregation of intrinsically disordered proteins (IDPs) in cells are governed by enzyme-driven, non-equilibrium processes. Kinases such as Casein kinase 1 delta (CK1d) phosphorylate proteins using ATP as chemical fuel, tuning intermolecular interactions and modulating condensate assembly. The neurodegeneration-linked protein TDP-43 undergoes CK1d-mediated hyperphosphorylation, proposed as a cytoprotective mechanism through condensate dissolution, yet the mechanisms underlying kinase-condensate interactions remain unclear. Using coarse-grained molecular dynamics simulations, we investigate how CK1d phosphorylates TDP-43 and how this reaction drives the structural reorganization and dissolution of its condensates. To ensure thermodynamic consistency in such fuel-driven simulations, we employ an automatic, generally applicable Markov state modeling framework. Post-translational modifications (PTMs), such as phosphorylation, can actively regulate condensate stability and suppress Ostwald ripening, offering a mechanism to control mesoscale structure in soft materials. Understanding such reaction-structure coupling in non-equilibrium environments is key to explaining cellular self-organization and designing biomimetic systems.

BP 30: Focus Session: Controlling Microparticles and Biological Cells by Ultrasound (joint session BP/CPP/DY)

Recently ultrasound has emerged as a very promising physical modality to control the behavior of microparticles and even of biological cells, which can be moved and stimulated by sound waves. For biological cells, one can further control the effect of sound through gene expression (sonogenetics), similar to the control by light (optogenetics). However, because the wavelength of sound is much larger than the one of light, one of the challenges is to localize the effect of sound waves, e.g. by using gas bubbles. Here, we bring together experimental and theoretical researchers who currently explore the potential of ultrasound to control active and passive microsystems and to develop new applications ranging from biomedicine to soft robotics.

Organized by Peer Fischer and Ulrich S. Schwarz (Heidelberg)

Time: Thursday 10:15–12:45 Location: BAR/0106

Invited Talk BP 30.1 Thu 10:15 BAR/0106

Mechanogenetics for Cell ImmunoTherapy — •Yingxiao Wang — 1002 childs way, Los Angeles, CA 90089

Cell-based cancer immunotherapy is a promising therapeutic intervention for cancer treatment. However, non-specific toxicity against healthy tissues (e.g. off-tumor toxicity) is a major hurdle for solid tumor treatment. We have developed controllable on-switch gene cassettes in which a specific antigen production on the target cancer cell can be remotely and mechanically induced by an external focused ultrasound (FUS). FUS was applied to stimulate the production of the synthetic and clinically validated antigen on tumor cell surface orthogonal to the endogenous proteins. SynNotch was further engineered into primary human T cells (SynNotch-CAR T) to recognize the synthetic antigen expressed on the ultrasound-induced tumor cells and activate the production of CAR, which can lead to the recognition of a native tumor specific antigen (TSA) universally expressed on the whole population of tumor cells for immunotherapy. We applied this system to treat prostate cancer cells whose locally metastasized tumors are confined in space but intermingled with vessels and nerves. Our results showed that FUS can mechanically induce the synthetic antigen production in prostate cancer cells, which results in the engagement and activation of SynNotch CAR T cells for the tumor eradication. This local activation of engineered tumor cells by FUS should allow a high precision and safety in eradicating tumors. Hence, this approach for immunotherapy should open new opportunities to integrate engineering mechanics with genetic medicine for successful translation.

BP 30.2 Thu 10:45 BAR/0106

Shaping sound to tickle cells — •Dimitris Missirlis[1,2], Athanasios Athanassiadis[1,2], Rom Lerner[1,2], and Peer Fischer[1,2] — [1]Institute for Molecular Systems Engineering and Advanced Materials, Im Neuenheimer Feld 225, 69120 Heidelberg, Germany — [2]Max Planck Institute for Medical Research, Jahnstr. 29, 69120, Heidelberg, Germany

The ability to shape ultrasonic waves precisely is finding growing relevance in biomedical applications, where ultrasound is increasingly used to noninvasively stimulate biological tissues for therapeutic purposes. However, it remains an unsolved question how high-frequency ultrasound can interact with cells to excite biological responses. Our recent work on shaping and controlling ultrasound waves has provided us with a new tool to address the fundamental question how ultrasound interacts with and influences cells. To this end we have developed adaptable setups where we can control relevant ultrasound parameters in vitro as well as in vivo. By systematically examining the critical parameters, we discuss the role of different ultrasonic effects, including thermal effects, radiation forces, and sound-induced shear flows. Further, we discuss both physical and sonogenetic methods that can be used to enhance the coupling of ultrasound to cells.

BP 30.3 Thu 11:00 BAR/0106

A Theoretical Model for Ultrasound-Induced Intracellular Streaming — •Niels Gieseler[1,2,3], Falko Ziebert[1,2], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, Philosophenweg 19, Heidelberg 69120 Germany — [2]BioQuant, Heidelberg University, im Neuenheimer Feld 267, Heidelberg 69120 Germany — [3]Max Planck Institute for Medical Research, Jahnstrasse 29, Heidelberg 69120, Germany

Ultrasound is not only the basis of an essential imaging method for biomedicine, recently it has also become a promising avenue to control biological systems, for example, in sonogenetics or ultrasound neuromodulation. However, the underlying physical effects are not well understood, and a complete theoretical description is missing. In fact, many different physical effects compete, including radiation forces, streaming, cavitation, and local heating. Here, we focus on intracellular streaming, which might induce organelle movement or alter gene expression, as the steady second-order rotational flow generated by an acoustic source. As a model for the viscoelastic nature of cells and their surroundings, we use Oldroyd-B fluids. Building on existing work, we calculate the streaming flows inside and outside of a sphere sonicated with a plane wave. The streaming is treated as a second-order perturbation expansion of the Navier-Stokes equations, which is solved separately for both media and combined using suitable boundary conditions. Our work shows under which conditions intracellular streaming can be induced in biological cells.

15 min. break

Invited Talk BP 30.4 Thu 11:30 BAR/0106

Recent theoretical progress on sound-propelled microsystems — •Raphael Wittkowski — Department of Physics, RWTH Aachen University, 52074 Aachen, Germany — DWI – Leibniz Institute for Interactive Materials, 52074 Aachen, Germany

The research area of sound-propelled microsystems is growing fast and has a great potential for various future applications in engineering, medicine, and other fields. The progress in this area is accelerated by theoretical methods, as analytical modeling and computer simulations can provide new insights that cannot be obtained by experiments.

In this talk, I will address the theoretical investigation of sound-propelled microsystems and present examples from the recent research progress in this area. The talk will cover different types of sound-propelled microsystems including microrobots, micromachines, artifi-

cial muscles, and soft robots.
Funded by the Deutsche Forschungsgemeinschaft (DFG) – 535275785.

BP 30.5 Thu 12:00 BAR/0106

Rarefaction wave amplification from non-resonant deforming bubbles — Yuzhe Fan, Saber Izak Ghasemian, and •Claus-Dieter Ohl — Otto-von-Guericke University, Magdeburg, Germany

Gas bubbles in liquids or soft matter exposed to acoustic waves behave as oscillators, with maximum response at their resonance frequency. When driven below resonance at sufficient pressure amplitudes, bubbles can collapse with strong energy focusing and even emit light; when driven near resonance, surface instabilities and fast jet flow develop during oscillation. Like other oscillators, bubbles cease to respond when driven far above resonance. Although their oscillations are minimal, bubbles in this regime act as pressure-release interfaces, can reflect high peak pressure shock into rarefaction wave, and may therefore seed cavitation when interacting with high-power therapeutic ultrasound. Yet, here we show that even diagnostic ultrasound with peak positive pressures as low as ∼10 MPa can nucleate cavitation in microseconds. This is caused through the non-resonant deformation of the bubble into a concave shape that refocuses scattered waves, amplifying the tension leading to microcavitation. Our findings reveal that cavitation can be triggered by high-frequency positive pressure over a much wider amplitude range than previously recognized, offering a new perspective for current safety guidelines for ultrasound bioeffects and applications in medical ultrasound.

BP 30.6 Thu 12:15 BAR/0106

Optimizing acoustically propelled microrobots using genetic algorithms — •Lennart Gevers[1,2,3] and Raphael Wittkowski[1,2,3] — [1]Department of Physics, RWTH Aachen University, Aachen, Germany — [2]DWI – Leibniz Institute for Interactive Materials, Aachen, Germany — [3]Institute of Theoretical Physics, Center for Soft Nanoscience, University of Münster, Münster, Germany

The promising potential applications of acoustically propelled microparticles demand methods to create particle designs that allow for targeted autonomous motion. Current methods remain largely based on experiments due to the intricate nature of the underlying dynamics. Large-scale computational studies, specifically when combined with optimization algorithms, are impeded by the cost of traditional acoustofluidic simulations.

In this talk, we present the implementation of an analytical framework describing non-Brownian motion of colloidal molecules driven by acoustic streaming. The analytical framework is combined with vectorized, GPU-accelerated, and distributed computation. This enables fast, large-scale simulations, where 10^5 trajectories over 10 s real time can be simulated on a normal personal computer within one minute. Coupling this approach with genetic algorithms reveals particle geometries, control parameters, and underlying principles for acoustically propelled particles that exhibit controllable and stable behavior over long times.
Funded by the Deutsche Forschungsgemeinschaft (DFG) – 535275785.

BP 30.7 Thu 12:30 BAR/0106

Equations of motion for arbitrarily shaped acoustically propelled rigid microparticles — •Justus Schnermann[1,2,3] and Raphael Wittkowski[1,2,3] — [1]Department of Physics, RWTH Aachen University, Aachen, Germany — [2]DWI – Leibniz Institute for Interactive Materials, Aachen, Germany — [3]Institute of Theoretical Physics, Center for Soft Nanoscience, University of Münster, Münster, Germany

Much experimental research concerns the acoustic propulsion of microparticles, but theoretically, only axisymmetric particles with a stable orientation have been studied thus far. In this talk, we present an analytical derivation of the ordinary differential equation of motion for an arbitrarily shaped acoustically propelled rigid microparticle. This equation governs the time evolution of the orientation and position of the particle. Its parameters depend only on the particle's leading-order oscillation velocity field. Based on this equation, we classify qualitatively the possible long-term trajectories of arbitrary particles in unidirectional ultrasound.
Funded by the Deutsche Forschungsgemeinschaft (DFG) – 535275785.

BP 31: Focus Session: Theoretical Modeling and Simulation of Biomolecular Condensates II (joint session CPP/BP)

Time: Thursday 11:30–12:45 Location: ZEU/0260

BP 31.1 Thu 11:30 ZEU/0260

Exponential Size Control in Biomolecular Condensates via Universal Scaling of Power-Law Distributions — •Yifan Huang[1], Chuan Tang[1], Haoyu Song[2], Bing Miao[3], and Qiyun Tang[1,4] — [1]Key Laboratory of Quantum Materials and Devices of Ministry of Education, School of Physics, Southeast University, Nanjng 211189, China — [2]School of Physics, Zhejiang University, Hangzhou 310058, China — [3]Center of Materials Science and Optoelectronics Engineering, College of Materials Science and Opto-Electronic Technology, University of Chinese Academy of Sciences, Beijing 100049, China — [4]Jiangsu Physical Science Research Center, Nanjing 210093, China

Power-law distributions are ubiquitous phenomena in diverse systems, whereas concomitant scale invariance hinders the exploration of precise size control for biocondensates in recent experiments. Using massive computer simulations and the kinetic theory of coalescence, we demonstrate that the cutoff volume can collapse all power-law distributions of biocondensates in different parameters onto one master curve. Remarkably, the cutoff size can increase exponentially by increasing monomer concentrations $R \sim e^{\phi}$, of which nanometer condensates in simulations can be extrapolated to micrometer droplets in experiments. The findings provide a new mechanism to rapidly tailor the biocondensates to appropriate sizes through power-law distributions, which can stimulate explorations in biological and other nonequilibrium systems

BP 31.2 Thu 11:45 ZEU/0260

Droplet-assisted folding of long regulatory RNAs — Simon Doll[1], Lukas Pekarek[1], Fathima Ferosh[1], Jovana Vasiljević[1], Marcus Jahnel[1], and •Tyler Harmon[2] — [1]BIOTEC, Dresden, Germany — [2]IPF, Dresden Germany

Long regulatory RNA regions orchestrate complex cellular processes, including gene expression and epigenetic modifications. How these RNAs dynamically fold and refold in response to cellular signals remains poorly understood. Given that RNAs interact with ubiquitous RNA-binding proteins (RBPs) prone to form biomolecular condensates, we explore how protein droplets interacting along an RNA impact its folding process. Attached droplets prevent premature folding by competing with RNA:RNA interactions. When droplets dissolve due to cellular signals, capillary effects cause the RNA to collapse while refolding. We test this process of condensate-guided RNA folding by adapting established RNA secondary structure predictors to mimic various folding pathways and supplement this with coarse-grained simulations. We find that interactions with transient droplets robustly leads to the formation of long-range RNA contacts, which are otherwise hard to achieve. Our results compare favorably with available experimental data. We propose that this strategy, which we call droplet-assisted RNA folding, represents a previously unexplored mechanism for shaping RNA structures. Given the widespread propensity of RBPs to form condensates, this process could play a fundamental role in the structural organization, conditional reshaping, and functional regulation of long regulatory RNAs.

BP 31.3 Thu 12:00 ZEU/0260

Simulation Insights into the Assembly of Polyplexes for RNA Delivery — •Jonas Hans Lehnen[1], Jorge Moreno Herrero[3], Heinrich Haas[3], Friederike Schmid[1], and Giovanni Settanni[1,2] — [1]Department of Physics, Johannes-Gutenberg University Mainz — [2]Faculty of Physics and Astronomy, Ruhr University Bochum — [3]BioNTech SE, Mainz

RNA-based pharmaceuticals proved successful with the COVID-19 vaccines and are now undergoing clinical trials for a broad range of therapeutic indications. Lipid-based nanoparticles (LNPs) have been used so far as delivery systems, although alternatives are still needed to meet efficacy and safety requirements across a broader range of

applications. Polyplexes, formed by the self-assembly of cationic polymers with the anionic nucleic acids, constitute a valuable substitute, especially if precise control of the number and shape of the encapsulated RNA chains is possible. Here[1], we use molecular dynamics simulations of a coarse-grained polyplex model to show that the most important factors controlling it are the charge ratio between polyelectrolytes and RNA and their concentration during assembly. Close to the isoelectric point, the polyplexes are large, whereas in large excess of cationic polymer, their size decreases, allowing one RNA copy per nanoparticle. Our results are consistent with recent experimental work on polyethylenimine polyplexes.

[1] Simulation Insights into the Assembly of Polyplexes for RNA Delivery, Lehnen et al., Biomacromolecules (2025), DOI: 10.1021/acs.biomac.5c01219

BP 31.4 Thu 12:15 ZEU/0260

Polymer-assisted condensation as key to chromatin localization — •Arghya Majee[1] and Jens-Uwe Sommer[1,2,3] — [1]Leibniz Institute of Polymer Research Dresden, Germany — [2]Institute for Theoretical Physics, TU Dresden, Germany — [3]Cluster of Excellence Physics of Life, TU Dresden, Germany

We put forward a novel mechanism [1] to account for the experimentally observed [2] positional shifts of chromosomes within the cell nucleus, which appear to be driven by compositional alterations in the nuclear lamina. By considering chromatin as a biomolecular condensate we demonstrate that the adsorption of the chromatin-binding proteins at the lamina leads to a wetting of the condensate while spreading of the chromatin on the lamina is avoided. This leads to the non-monotonous density profile of the polymer with respect to the surface which can be explained by the competition between the tendency of the protein component to wet the surface and the conformational restrictions of the polymer near the impenetrable surface. A change in the composition of the the lamina can lead to repositioning of chromatin towards the center of the nucleus. Our theory not only offers an explanation for specific chromatin conformation experiments, but also contributes to the broader understanding of wetting onto responsive surfaces in multi-component systems.

References:

[1] A. Majee and J.-U. Sommer, bioRxiv 2025.06.11.658974 (submitted).

[2] Amiad-Pavlov *et al.*, Sci. Adv. **7**, eabf6251 (2021).

BP 31.5 Thu 12:30 ZEU/0260

Bridging Scales to Understand the Role of Ubiquitylation and Sumoylation in Protein Phase Separation — •Supriyo Naskar, Kurt Kremer, and Oleksandra Kukharenko — Max Planck Institute for Polymer Research, Ackermannweg 10, 55128 Mainz, Germany

The post-translational modifiers, such as mono- and poly-ubiquitins and SUMOs, are known for their ability to modulate protein-protein interactions by becoming covalently attached to other target proteins. Despite the high similarity in the tertiary structure and sequence, they differentially influence the target protein properties. In this work, we employed a multiscale simulation approach that encompasses atomistic to different levels of coarse-grained modeling techniques, combined with data-driven methods, to explore the structural differences and multidimensional energy landscapes of ubiquitin, SUMO, and their conjugates. We finally investigate the influence of distinct features of the targets and modifiers on protein phase separation and aggregation, providing molecular-level insight into the corresponding in vitro measurements and informing further experiments through the adjustment of relevant parameters.

BP 32: Statistical Physics of Biological Systems III (joint session BP/DY)

Time: Thursday 15:00–18:15 Location: BAR/SCHÖ

BP 32.1 Thu 15:00 BAR/SCHÖ

Efficiency of Droplet Formation and Dissolution by Chemical Reactions — •Gerrit Wellecke[1,2], Riccardo Rossetto[1,2], Jan Kirschbaum[1], and David Zwicker[1] — [1]Theory of Biological Fluids, Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany — [2]University of Göttingen, Institute for the Dynamics of Complex Systems, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Droplets formed by phase separation are vital for intracellular organization, and cells often control the formation and dissolution of these droplets through chemical reactions. To understand how cells can influence droplets in space and time, we consider a ternary system that exhibits a bistability between homogeneous and phase-separated states. We use a thermodynamically consistent approach to describe the diffusive and reactive dynamics, which allows us to quantify the energy dissipation and entropy production during transitions between these states. We find that reaction-controlled droplet formation and dissolution in the bistable regime are fundamentally different processes. While droplet formation is generally aided by relaxation to equilibrium, we find that a droplet's size determines whether it is best dissolved internally or externally. Further, our model identifies plausible mechanisms by which cells may regulate their intracellular droplets, providing insights that could guide the development of synthetic soft matter systems with tunable droplet behaviour.

BP 32.2 Thu 15:15 BAR/SCHÖ

Size control and fluctuations of chemically active droplets — •Guido Kusters and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Biological cells use liquid-liquid phase separation to dynamically compartmentalize their environment for various applications, many of which require size control. This process is challenging because (i) large droplets tend to grow at the expense of smaller ones, and (ii) thermal fluctuations can disturb droplets since cells are typically small and soft. Chemical reactions can, in principle, control droplet sizes, but there are no clear guidelines on how to robustly achieve size control. To provide guidelines, we consider a binary fluid model driven out of equilibrium by chemical reactions. We reveal two different classes of size-controlled droplets, depending on the ratio of droplet radius to the reaction-diffusion length. Moreover, we determine parameter regimes in which droplets become small. To study fluctuations in this case, we use fluctuation-dissipation arguments to predict the size fluctuations of size-controlled droplets, consistent with our numerical simulations. Taken together, our theory allows us to predict the chemical reactions necessary for maintaining small droplets, e.g., in biological cells or synthetic applications.

BP 32.3 Thu 15:30 BAR/SCHÖ

Anomalous diffusion and directed coalescence of condensates out of equilibrium — •Andriy Goychuk — Helmholtz Centre for Infection Research, Braunschweig, Germany — Lower Saxony Center for Artificial Intelligence and Causal Methods in Medicine, Hannover, Germany

Phase separation is ubiquitous in engineered and in biological systems. For example, biomolecular condensates contribute to the organization of the cytoplasm and nucleoplasm in cells. Here, I will first extend our understanding of textbook phase separation models by showing how condensates consisting of nonpolar molecules can effectively polarize and undergo coarsening by directed coalescence when subjected to a global drift, for example due to electrostatic potential gradients, chemical concentration gradients, or gravitation. Next, to better model the intracellular solution, I will incorporate viscoelastic stress propagation and nonequilibrium fluctuations. In this context, the Brownian motion of condensates has been barely explored despite being a cornerstone of statistical and colloidal Physics. If the active stresses, for example generated by molecular motors, have a different correlation time than the viscoelastic relaxation time of the solution, then the fluctuation-dissipation theorem is broken and the mixture is driven out of equilibrium. In this case, the size-dependence of the center-of-mass diffusion coefficient of the condensates can be either suppressed or enhanced, and the droplet can show superdiffusive motion. Together, these findings improve our understanding of the dynamics of domains in viscoelastic media and conserved order parameters in general.

BP 32.4 Thu 15:45 BAR/SCHÖ

A Minimal Theoretical Framework Linking Translation Activity to Stress-Induced Condensates — •Pascal S. Rogalla[1],

Alessandro Barducci[1], and Luca Ciandrini[1,2] — [1]Centre de Biologie Structurale, Université de Montpellier, CNRS, INSERM, Montpellier, France. — [2]Institut Universitaire de France

The formation of intracellular membraneless organelles, such as stress-granule-like condensates formed via liquid-liquid phase separation (LLPS), is a common response to cellular stress. RNA, including mRNA, promotes the assembly of many of these condensates, while the resulting aggregation of mRNAs reduces their availability for translation and thereby modulates ribosome loading. This establishes a feedback loop between condensate formation and translational activity. Here we develop a minimal physical model that makes this coupling explicit by combining Flory-Huggins theory for LLPS with the Totally Asymmetric Simple Exclusion Process (TASEP) for ribosomal traffic on mRNAs. This hybrid framework provides a proof-of-principle description of how LLPS and translation dynamically influence one another. Our analysis reveals that the phase behaviour of both subsystems becomes mutually dependent: a low-occupancy ribosomal phase promotes mRNA aggregation, whereas a high-occupancy phase suppresses condensate formation. These results suggest that cells may regulate condensate formation through translation modulation and, conversely, that LLPS can reshape the translatome. This provides a first proof-of-principle framework for quantifying stress-induced reorganisation of the translational landscape.

BP 32.5 Thu 16:00 BAR/SCHÖ

Optimal sensing through phase separation — •Henry Alston[1], Mason Rouches[2], Arvind Murugan[2], Aleksandra Walczak[1], and Thierry Mora[1] — [1]Laboratoire de Physique, Ecole Normale Superieure — [2]The James Franck Institute & Department of Physics, The University of Chicago

Cells are constantly tasked with making accurate measurements of their surroundings. A paradigmatic example is the sensing of signalling molecule concentrations: the work of Berg and Purcell derived limits for the precision and speed of this sensing through ligand-receptor binding. However, recent experimental work has identified the formation of condensates (liquid droplets coexisting with the cell cytoplasm through phase separation) as a potential mechanism for selectively initiating downstream processes by effectively amplifying small concentration differences between competing signalling molecules. Using a minimal model for droplet nucleation and growth in a fluid mixture, we observe that phase separation can distinguish concentration differences of 1% in minutes, a significant improvement upon well-established pathways for precise concentration sensing.

BP 32.6 Thu 16:15 BAR/SCHÖ

Thermodynamics of DNA sequence recognition by a transcription factor — •Jonas Neipel[1,2,3], Anne Schwager[1], Yahor Savich[1,2,3], Douglas Diehl[1], Anthony A. Hyman[1], Frank Jülicher[2,3], and Stephan W. Grill[1,3] — [1]Max Planck Institute for Molecular Cell Biology and Genetics, Dresden Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden Germany — [3]Center for Systems Biology Dresden, Dresden, Germany

Transcription factors (TFs) are proteins that regulate the transcription of genes by binding to specific genomic positions defined by the DNA sequence. The sequence of preference of a TF is typically characterized by a single sequence motif that maximizes binding affinity. However, eukaryotic TFs bind to a spectrum of low affinity binding sites that vastly outnumber canonical motif sequences in the genome. Here, we develop an Ising model of DNA sequence recognition that yields quantitative prediction of TF binding energies across sequence space for the human TF KLF-4. The model is parametrized by in vitro experiments, where we quantify relative binding energies for various sequences in a competitive assay using fluorescence anisotropy. Strikingly, we find that the thus fully parametrized thermodynamic model quantitatively predicts KLF-4 occupancy across the human genome. Finally, we discuss how this genomic energy landscape guides the formation of TF condensates.

15 min. break

BP 32.7 Thu 16:45 BAR/SCHÖ

Kinetic inference of entropy production — •Ivan Di Trelizzi — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Nonequilibrium steady states, from planetary dynamics to biological processes, constantly dissipate energy to their environment, producing entropy at a constant rate. Quantifying this dissipation is key to understanding how far systems operate from equilibrium but remains experimentally challenging. I will present a new approach to infer entropy production directly from trajectory data, using measurable kinetic quantities known as traffic and inflow rate, without requiring knowledge of microscopic forces or fluxes. The method remains effective even under partial observation, providing a practical framework to quantify nonequilibrium behaviour in complex physical and biological systems.

BP 32.8 Thu 17:00 BAR/SCHÖ

Frequency-space trajectory Fisher Information to quantify sensitivity in complex living systems — •Zhiheng Wu[1] and Isabella Graf[1,2] — [1]European Molecular Biology Laboratory, Heidelberg, Germany — [2]Department of Physics and Astronomy, Heidelberg University, Heidelberg, Germany

Living systems sense their environment by stochastically mapping external signals onto internal states. For example, several animals including fruit flies and pit vipers encode small changes in the ambient temperature in terms of changes in the interspike time of neurons. The sensitivity of these measurements can be evaluated by the so-called Fisher information (rate). While living systems constantly adapt to changing environments, calculations of Fisher information have so far mostly focused on static signals and internal states. To evaluate measurement sensitivity in the non-static case, we evaluate the trajectory Fisher information and show that, under common assumptions, it can be expressed as an integral over frequency space involving the power spectral density. This expression provides a tractable way to quantify information in adaptive and complex biological systems and we discuss some interesting applications.

BP 32.9 Thu 17:15 BAR/SCHÖ

Ergodicity shapes inference in biological reactions driven by a latent trajectory — •Ricardo Martinez-Garcia[1], Benjamin Garcia de Figueiredo[2], Justin Calabrese[1], and William Fagan[3] — [1]CASUS-HZDR, Görlitz, Germany. — [2]Princeton University, Princeton NJ, USA. — [3]University of Maryland, College Park MD, USA.

Many natural phenomena, from intracellular reactions to predator-prey encounters, can be described as counts of events triggered at random intervals when an underlying dynamical system enters reactive regions of its phase space. These reactions control biological functions across scales, from cellular processes to ecosystem services and stability. We compute the exact distribution of inter-count times under the only assumption that the latent dynamical system is Markovian and ergodic, recovering widely used Poisson statistics as a limiting case. These results limit what information about the latent process can be inferred from a local detector, which we explore in two biophysical scenarios. First, in estimating an animal's activity from detector crossings, we show that mean counts may fail to capture movement parameters, encoded in higher-order moments. Second, we show that the variance of inter-reaction times imposes a fundamental limit on how precisely detector measurements can infer the size of an ensemble of trajectories, generalizing the Berg-Purcell limit for chemosensation. Overall, we develop a flexible framework for quantifying inter-event time distributions in reaction-diffusion systems that shows which properties of latent processes are inferable from observed reactions.

BP 32.10 Thu 17:30 BAR/SCHÖ

Information Bottleneck in Gene Regulation — •Marianne Bauer — TU Delft

Biological systems need to process information in order to perform specific functions. In the context of gene regulation, regulatory regions process transcription factor signals in order for cells to differentiate towards correct fates. Previously, we have shown that the information bottleneck (IB) framework provides a useful framework for understanding regulatory binding site regions. Here, I will discuss two recent collaborative advances to provide an improved biological understanding from IB based predictions. First, using two complementary models for clustering transcription factors at binding site sensors, we can study information transfer during early fly embryo development with local transcription factor clustering. We find that weak cooperativity or clustering can allow for maximal information transfer, especially about the relevant variable, and that weak clustering also allows the binding site sensors to achieve optimality consistent with the IB bound. Second, we investigate how optimal activation changes when multiple binding site elements can process information, and find that activation

profiles consistent with IB optimality resemble gene expression profiles in the early fly embryo.

BP 32.11 Thu 17:45 BAR/SCHÖ

Binary karyotypes are universally selected for across cancers — •Lucija Tomašić[1], Shane A. Fiorenza[1], Hajime Okada[2], Thomas W. van Ravesteyn[3], Uri Ben-David[2], Geert J.P.L. Kops[3], and Nenad Pavin[1] — [1]Univ. of Zagreb, Zagreb, Croatia — [2]Tel Aviv University, Tel Aviv, Israel — [3]Hubrecht Institute, Utrecht, the Netherlands

Aneuploidy, an abnormal chromosome number, is a defining feature of most cancers, yet its vast diversity has made it difficult to identify universal evolutionary rules. By analyzing over 90,000 patient-derived cancer karyotypes using a new visualization approach and mathematical modeling, we uncover a simple organizing principle. Across cancer types, and even in yeast, aneuploid genomes overwhelmingly assemble into "binary karyotypes" composed of only two chromosome copy numbers. Despite the enormous space of theoretically possible chromosome configurations, these states dominate patient data, comprising more than three-quarters of observed karyotypes. Our model shows that this pattern arises from a modest but consistent fitness advantage of binary karyotypes over more complex configurations. This principle also provides insight into how aneuploid cells withstand stress responses, as binary karyotypes exhibit lower rates of tumor suppressor gene inactivation. Together, our results identify binary karyotypes as a conserved evolutionary class of aneuploidy, governed by global organizational rules that may reveal shared vulnerabilities across cancers.

BP 32.12 Thu 18:00 BAR/SCHÖ

Inertial instability of blood in cross microchannels — •Joséphine Van Hulle and Christian Wagner — Experimental Physics, Saarland University, Germany

A localized reduction of vessel diameter (stenosis) increases the local blood flow speed and can trigger downstream recirculation which promotes conditions for the vessel blockage (thrombosis). The role of fluid elasticity in these flows remains underexplored. We isolate the extensional effects using cross-slot microfluidics, which creates an elongation plane with a well-defined inertial instability. By varying the hematocrit and plasma composition, we show that red blood cell deformability and plasma viscoelasticity lower the critical Reynolds number for the onset of vortex formation. These results highlight that even weak elastic stresses of blood can favor recirculation, a characteristic rarely modeled but necessary for physiologically realistic arterial simulations.

BP 33: Bioimaging

Time: Thursday 15:00–18:30 Location: BAR/0205

Invited Talk BP 33.1 Thu 15:00 BAR/0205

Expanding the Bag of Optical Tricks for (Neuro)Biology — •Fabian F. Voigt — Department for Molecular and Cellular Biology, Harvard University, Cambridge, USA — Max Planck Institute for the Science of Light, Erlangen, Germany — Max Planck Center for Physics and Medicine, Erlangen, Germany

Seeing is believing and thus, optical imaging techniques are extremely useful to study brain structure and function. I will present several projects aimed at providing the neuroscience community with better instrumentation: These range from open-source light-sheet microscopes for imaging cleared tissue (https://mesospim.org/) to novel multi-immersion microscope objectives that take inspiration from scallops and astronomical telescopes as well as utilizing metasurfaces for improving light collection efficiency in light-sheet microscopy.

BP 33.2 Thu 15:30 BAR/0205

Using Rotating Coherent Scattering (ROCS) Microscopy for Binding and Uptake Analysis of Virus-Mimicking Particles — •Dominik Huber and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, University of Freiburg, Germany

The investigation of viruses with their host cell is an important topic in medical research, yet direct observation of these nanoscale dynamics remains challenging, since conventional fluorescence microscopy is limited by photobleaching and labelling constraints. To address these limitations, we employ label-free Rotating Coherent Scattering (ROCS) microscopy, an imaging approach that enables high-speed, high-resolution visualization of virus-mimicking particle behaviour at the cell.

ROCS microscopy uses backscattering of oblique illumination of a rotating laser beam to achieve around 160 nm spatial resolution at imaging rates up to around 200 Hz. By combining several illumination wavelengths and illumination angles, ROCS microscopy can be used in brightfield and darkfield as well as in total internal reflection mode. Leveraging this flexibility in imaging, allows us to capture the binding dynamics of particles to cells and to investigate them from their first attachment up to the investigation of single particle uptake events.

The analysis of particle fluctuation widths and mean square displacements enabled us to detect differences in binding characteristics of two different types of virus-mimicking particles, thus demonstrating that ROCS microscopy provides a powerful tool for investigation of particle-cell interactions at the single-particle level.

BP 33.3 Thu 15:45 BAR/0205

Pharmacological modulation of intrinsic tissue transparency for enhanced microscopy — •Adrián Puerta, Susan Wagner, and Moritz Kreysing — Institute of Biological and Chemical Systems, Karlsruhe Institute of Technology, 76344 Eggenstein Leopoldshafen, Germany

Light microscopy remains as one of the primary methods for data acquisition in biological research, yet its performance is frequently limited by the strong scattering properties of experimental tissues. Hence, the use of clearing agents that are incompatible with living samples is often required (1). To overcome these limitations, we aim to modulate the intrinsic transparency of biological samples, enabling more effective live-cell imaging.

Conventional clearing strategies rely on chemicals that modify the refractive index of aqueous or lipid-rich tissue components (2). In contrast, our approach involves screening small molecules with pharmacological properties that may enhance transparency in mammalian cells. To investigate this, we have developed a high-throughput screening system based on flow cytometry that will allow us to identify potential changes at a single-cell scale.

(1) Yu, T. et al. Physical and chemical mechanisms of tissue optical clearing. iScience 24, 102178 (2021).

(2) Ou, Z. et al. Achieving optical transparency in live animals with absorbing molecules. Science 385, eadm6869 (2024).

BP 33.4 Thu 16:00 BAR/0205

Imaging viral infection in live cells with confocal interferometric scattering microscopy (iSCAT) — •Anirudh Khemani[1], David Albrecht[1], Jan Renger[1], Marco Heisig[1], Kiarash Kasaian[1], and Vahid Sandoghdar[1,2] — [1]Max Planck Institute for the Science of Light, 91058 Erlangen, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, 91054 Erlangen, Germany.

Fluorescence-based microscopy can suffer from observational bias, functional perturbation, phototoxicity, or insufficient signal. Confocal interferometric scattering microscopy [1] provides quantitative, label-free imaging of nanoscale dynamics in live-cell processes. iSCAT is a shot-noise-limited homodyne interferometric technique. By rejecting out-of-focus light, confocal iSCAT yields high structural contrast of nano-bioparticles, like vesicles and viruses, and we validate structural assignments with fluorescence. We apply this platform to study rare, dynamic events in the vaccinia virus life cycle. To improve experimental control and statistics, we developed a microfluidic system to deliver individual virions with defined timing and position. Furthermore, we combine confocal SCAT with concomitant wide-field iSCAT [2] to span a large range of spatial and temporal resolutions. We report on complex processes such as virus-induced nucleation of actin tails and high-speed tracking of single virions at cell-cell junctions and on membranes. [1] Küppers, M., Albrecht, D., *et al. Nat. Commun.* **14**, 1962 (2023). [2] Mazaheri, M., Kasaian, K., *et al. Optica* **11**, 1030 (2024).

BP 33.5 Thu 16:15 BAR/0205

Image segmentation of treated and untreated tumor spheroids by fully convolutional networks — Matthias Streller[1], Soňa Michlíková[2], Katharina Lönnecke[1], Leoni A. Kunz-Schughart[2], Anja Voss-Böhme[1], and •Steffen Lange[1,2] — [1]HTW Dresden — [2]OncoRay, TU Dresden, HZDR, Germany

Multicellular 3D tumor spheroids (MCTS) are advanced preclinical cell culture systems for assessing the impact of combinatorial radio(chemo)therapy as they exhibit therapeutically relevant in vivo-like characteristics. State-of-the-art assays quantify long-term curative endpoints based on collected brightfield image time series from large treated spheroid populations, which requires laborious spheroid segmentation of up to 100,000 images per treatment arm. While several image analysis algorithms are available for spheroid segmentation, they all focus on compact MCTS with a clearly distinguishable outer rim throughout growth and often fail for the common case of treated MCTS, which may partly be detached and destroyed and are usually obscured by dead cell debris. To address these issues, we successfully train 2 fully convolutional networks, UNet and HRNet, and optimize their hyperparameters to develop an automatic segmentation for both untreated and treated MCTS[1]. We extensively test the automatic segmentation on larger, independent datasets and observe high accuracy for most images with Jaccard indices around 90%, with deviations consistent to inter-observer variability. We also successfully test against previously published datasets and spheroid segmentations.

[1] Streller et.al, GigaScience 2025, doi.org/10.1093/gigascience/giaf027

BP 33.6 Thu 16:30 BAR/0205

Predicting treatment response of tumor spheroids from radiomics analysis of post-treatment dynamics — Pejman Shojaee[1,2], Tom Bischopink[1], Daria Bolotova[1], Sona Michlikova[2], Leoni A. Kunz-Schughart[2], Steffen Lange[1,2], and •Anja Voss-Böhme[1] — [1]DataMedAssist Group, Faculty of Informatics/Mathematics, HTW Dresden — [2]OncoRay - National Center for Radiation Research in Oncology Dresden

Radiomics has significantly advanced radiation oncology by providing quantitative, objective metrics to predict therapeutic efficacy. However, these methods have not been applied to three-dimensional, multicellular tumor spheroids yet, which are the preferred in vitro model for pre-animal, pre-clinical selection of novel, future-oriented treatment modalities. We present an AI-driven predictive modeling workflow to predict long-term tumor spheroid relapse using radiomics data from early post-treatment imaging of spheroids of two human cancer cell lines subjected to radiation therapy and hyperthermia. Our approach integrates multiple feature selection methods and machine learning algorithms for optimal classification performance. A detailed evaluation of the model performance reveals a time gain by early prediction of 2-14 days, while cases of late relapse remain challenging. The presented radiomics-based approach reduces the resource-intensive demands associated with prolonged experimental monitoring and allows accurate prediction for up to three days beyond the observation horizon.

15 min. break

BP 33.7 Thu 17:00 BAR/0205

Photothermal chemical imaging of nano-structured cells and cell organelles with less than 5 nm resolution — Maryam Ali[1,2], Christin David[1,3], and •Daniela Täuber[1,2] — [1]Friedrich Schiller University Jena — [2]Leibniz Institute of Photonic Technology, Jena — [3]University of Applied Sciences Landshut, Germany

Mid-infrared photoinduced force microscopy (PiF-IR) is a new imaging technique that enables the chemical characterization of surfaces with an unprecedented spatial and high spectral resolution. PiF-IR bridges the gap between high-resolution structure elucidation using electron microscopy, fluorescence microscopy and conventional infrared spectroscopy. It is complementary to tip-enhanced Raman spectroscopy (TERS). PiF-IR was successfully applied to map the local chemistry and structure of the antibiotic interaction on the surface of individual bacterial cells with a resolution of a few nanometers using the model system Bacillus subtilis and vancomycin [Ali et al., Anal. Chem., 2025, 97, 23914] and to map the surface of retina pigment organelles. Frequently observed anisotropic signal distributions on soft nanostructures in tip-enhanced photothermal imaging methods could be attributed to hybrid field coupling in a study combining modeling and experiment [Anindo et al., J. Phys. Chem. C, 2025, 129, 4517].

BP 33.8 Thu 17:15 BAR/0205

Phase Analysis of Photothermal Signal Enables Sub-Cellular Chemical Mapping of Complex Biological Systems — •Felix Hermann Patzschke and Frank Cichos — Molecular Nanophotonics Group, Peter Debye Institute for Soft Matter Physics, Leipzig University, Linnéstraße 5, 04103 Leipzig

Optically probed Photothermal Infrared (O-PTIR) microscopy is a powerful technique for label-free chemical imaging at sub-micron resolution, promising for cell and tissue analysis. However, the mechanism of signal generation is complex, suffering from the dynamic crosstalk between background and target heating. This lack of a rigorous, quantitative understanding of these dynamics currently forces users to sacrifice either chemical specificity or spatial resolution.

We conducted systematic experiments on defined nanoscale structures to motivate and validate a quantitative theoretical model based on the transient heat equation. This model reveals that the phase of the photothermal signal, a dynamic quantity often neglected, contains essential, localized information.

This phase directly encodes the time delay associated with thermal wave propagation, allowing for precise quantification of sub-cellular structural detail through effective thermal distance, even when the amplitude signal is insufficient to resolve closely-spaced features. By leveraging the full phase and amplitude response, we overcome existing spatial resolution limits, achieving enhanced, label-free chemical mapping for next-generation bioimaging, using existing hardware.

BP 33.9 Thu 17:30 BAR/0205

Effects of Optical Stimulation on the Adhesion of Human Osteoblasts — •Franziska Dorn[1], Wiebke Wollenberg[2], Meike Bielfeldt[3], Regina Lange[1], Susanne Stählke[3], Ingo Barke[1], Henrike Rebl[3], Berit Zeller-Pulmhoff[2], and Sylvia Speller[1] — [1]Physics of Surfaces and Interfaces, University Rostock — [2]Data-Driven Analysis and Design of Materials, University of Rostock — [3]Institute of Cell Biology, University Medical Center Rostock

Accelerated growth of autologous bone tissue is a promising strategy in regenerative medicine. In this study, we investigated how optical stimulation influences cell adhesion. We cultured the osteoblast-like (MG-63) cells in fetal bovine serum-free physiologic medium. As substrates, we used plain glass and glass surfaces with structured gold nanotriangular islands fabricated by nanosphere lithography. After cell seeding, the samples were illuminated with green light, inducing a spatially varying light intensity due to reflection and plasmons. Afterwards, we examined the cells using scanning electron microscopy and applied machine-learning-based/random-forest-based segmentation to extract morphological features. We found that opto-stimulated cells form more concave borders than unstimulated controls, suggesting that the cytoskeleton and the focal adhesions develop at non-uniform speed. Additionally, the adhesion area of illuminated cells is substantially larger than that of control cells on glass surfaces. However, when cells are seeded on surfaces with gold nanotriangular islands, this effect is absent. In a next step the peripheral region of the cells, in terms of lamellipodia and filopodia is addressed. (SFB 1270-299150580)

BP 33.10 Thu 17:45 BAR/0205

Imaging biomolecules for improving single-molecule diffraction — •Stefanie Lenzen[1,2], Lukas V. Haas[1,2], Kevin Janson[1], Amit K. Samanta[1,2], and Jochen Küpper[1,2] — [1]Center for Free-Electron Laser Science (CFEL), Deutsches Elektronen-Synchrotron DESY, Hamburg — [2]Department of Physics & Department of Chemistry & Center for Ultrafast Imaging, Universität Hamburg

Determining the structure and dynamics of single native biomolecules is still a challenge. In protein-crystallography and cryo-EM the molecule needs to be fixed, which might lead to structural disentegration, and the temporal resolution of these methods are limited. X-ray free-electron lasers (XFELs) provide ultrashort pulses, enabling diffraction before destruction, and a large number of photons, promising the observation of diffraction patterns *off* single nanoparticles [1]. Aerodynamic-lens stacks were used to deliver focused dense particle beams for such experiments on large nanoparticles [2]. Localization microscopy (LM), based on Mie-scattering is used to study and optimize these beams, an important step in improving single particle imaging. Due to the limitation in particle size [3], small biomolecules do not provide sufficient intensity for being detected with LM. We optimized the optical and analysis system and developed a promising method for the detection of smaller biomolecules, based on fluorescence.

[1] Poudyal, Schmidt, Schwander, *Struct. Dyn.* **7**, 024102 (2020);

[2] Ayyer, et int (39 authors), Chapman, *Optica* **8**, 15-23 (2021);
[3] Worbs, et int (2 authors), Maia, *Commun Phys* **8**, 155 (2025)

BP 33.11 Thu 18:00 BAR/0205

Optically addressable spins in proteins — •Dominik Bucher — Technical University of Munich, TUM School of Natural Sciences, Chemistry Department

Optically addressable spins have attracted significant interest for their potential in quantum sensing technologies. The current workhorses rely on spin defects in solids (such as the nitrogen-vacancy center in diamond), which lack the possibility for precise synthetic control over their properties. In my talk I will highlight our latest research on optically addressable spins in proteins, specifically flavin-based proteins. Upon excitation, these proteins generate radical pairs that can be detected optically via their flourescence and manipulated through radio wave-controlled spin chemistry. We further show that this optical spin interface is tunable by the protein structure. I will explain how these systems differ from the well-established NV center and discuss their potential as genetically encoded quantum sensors for future applications.

K. Meng et al. Optically detected and radio wave-controlled spin chemistry in cryptochrome, BioRxiv https://doi.org/10.1101/2025.04.16.649006 (2025)

BP 33.12 Thu 18:15 BAR/0205

Beyond Molecular Sensitizers: Illuminating the Role of Nanomaterials in Singlet Oxygen Photochemistry — •Zahid Ullah Khan[1], Latif Ullah Khan[2], Hermi Felinto Brito[1], and Paolo Mascio[1] — [1]Institute of Chemistry, University of São Paulo (USP), 05508-000, São Paulo-SP, Brazil — [2]Synchrotron-light for Experimental Science and Applications in the Middle East (SESAME) P.O. Box 7, Allan 19252, Jordan

Singlet molecular oxygen (1O2) plays a crucial role in various fields, including optoelectronics, photooxygenation reactions, and biomedical therapies, particularly as a major contributor to the success of photodynamic therapy (PDT). Since direct excitation of oxygen from the triplet ground state (3O2) to the singlet-excited state is spin-forbidden, thus, making the design of heterogeneous sensitizers crucial for efficient 1O2 production. For this purpose, nanomaterials, such as quantum dots (QDs) and rare earth fluoride nanoparticles (NPs), have emerged as versatile sensitizers for 1O2 generation, either individually or in combination with other inorganic or organic materials. Hence, conjoining the photophysical properties of QDs and rare earth NPs with other materials, e.g., coupling/combining with other inorganic materials, doping with the transition metal ions or lanthanide ions, and conjugation with a molecular sensitizer provide the opportunity to achieve high-efficiency quantum yields of 1O2 which is not possible with either component separately. Hence, the current work focuses the development of semiconductor QDs and rare earth-based nanosensitizer for efficient production of 1O2.

BP 34: Focus Session: Emergent Transport in Active Systems (joint session DY/BP)

Collective motion and directed transport are hallmark phenomena of active matter, arising from the interplay of self-propulsion, interactions, and nonequilibrium fluctuations. Even in the absence of global biases, assemblies of active particles can exhibit spontaneous currents, self-organized chemotaxis, and rectified transport due to broken symmetries or nonlinear feedbacks. Directed transport often emerges in inhomogeneous environments, where variations in particle activity or interaction strength can bias motion and organization. Activity gradients represent a particularly relevant example, providing a tunable mechanism to steer collective motion and pattern formation. These processes link microscopic activity to macroscopic material behavior and transport. This focus session aims to bring together theorists and experimentalists working on the fundamental mechanisms and control of emergent transport in active systems.

Organized by Abhinav Sharma (Augsburg) and Jens-Uwe Sommer (Dresden)

Time: Thursday 15:00–18:00 Location: ZEU/0160

Invited Talk BP 34.1 Thu 15:00 ZEU/0160

Out-of-equlibrium synthetic cells: the future of active matter — •Laura Alvarez — Univ. Bordeaux, CNRS, CRPP, UMR 5031

Colloidal active swimmers are broadly used as model systems to design microswimmers, yet their rigid and solid architecture limits their adaptability and functionality. A promising alternative is using bioinspired soft compartments for the design of cell-mimetic functional architectures while avoiding the complexity of living cells.

Here, I will showcase our latest results on driving giant unilamellar vesicles (GUVs) out of equilibrium via controlled external actuation to mimic and study life-like processes. We fabricate phase-separated Janus lipid vesicles, harnessing membrane fluidity to obtain reconfigurable motion. Under external electric fields, these asymmetric compartments self-propel and display transient run-and-tumble-like dynamics arising from the coupling between mobile membrane domains and the field. By tuning lipid composition and using temperature as an external trigger, we modulate membrane fluidity and phase separation, enabling in situ control over the frequency of tumble events. Beyond motility, we exploit electric fields to induce controlled shape transformations and vesicle division events, showing that the same actuating scheme can access higher-order cell-like functions. In parallel, we use light to drive strong, localized membrane fluctuations, providing a route to study active, non-thermal shape dynamics in soft compartments. These results highlight synthetic cell membranes as versatile platforms in which different functions can be triggered using simple external fields.

BP 34.2 Thu 15:30 ZEU/0160

Biohybrid active matter: active cargo transport by motile cells — Jan Albrecht[1], Lara S. Dautzenberg[1], Manfred Opper[2], Carsten Beta[1], and •Robert Grossmann[1] — [1]University of Potsdam, Potsdam, Germany — [2]Technical University Berlin, Berlin, Germany

We describe the transport of polystyrene beads whose motion is actively driven by cells via direct mechanical contact. We will first discuss the stochastic dynamics of a single cell-cargo pair, focusing on the existence of an optimal cargo size that enhances the diffusion of the load-carrying cells, and estimate the active forces exerted by cells to move colloids. Furthermore, we present the collective transport of these micron-sized particles on a monolayer of motile cells. The colloids' mean-square displacement shows a crossover from superdiffusive to normal-diffusive dynamics. The particle displacement distribution is, however, distinctly non-Gaussian even at macroscopic timescales exceeding the measurement time. We attribute the non-Gaussian statistics to heterogeneity and non-stationarity of the dynamics, and particularly apply a likelihood-based inference framework to estimate the heterogeneity of the bead dynamics from their discretely sampled trajectories. We showcase how this approach can deal with information-scarce situations and provides natural uncertainty bounds for heterogeneity estimates. Similar transport properties are expected for many composite active matter systems. These results thus provide the basis for the future design of cellular microcarriers and for more advanced transport tasks in complex, disordered environments, e.g. tissues.

Invited Talk BP 34.3 Thu 15:45 ZEU/0160

Chemotactic like behavior in by active Brownian particles: from single particles to to polymers — •Hidde Vuijk — University of Augsburg, Universitätsstraße 1, 86159, Augsburg, Germanz

Active Brownian particles can be used as simplified models for mi-

croscopic, motile organisms. This research investigates the behavior of such self-propelled objects in spatial gradients of activity, where their self-propulsion speed varies with position. A single active particle tends to accumulate in low-activity regions. When activity is assumed to be proportional to fuel, this corresponds to antichemotactic like behavior. We demonstrate how this behavior can be reversed by structuring particles into simple complexes. For example, by connecting active particles to passive cargo or linking them into chains, we predict a crossover from accumulation in low-activity regions to accumulation in high-activity regions, that is chemotaxic like behavior. These active dimers and polymers can autonomously move up an activity gradient, accumulating where the fuel concentration is highest. This emergent gradient-sensing arises from the physical interactions, offering a novel mechanism for the design of active matter and providing insight into how primitive life forms without complex information processing might have located nutrients.

BP 34.4 Thu 16:15 ZEU/0160

Fluctuation-induced transition in transport of active colloidal cells — •Shashank Ravichandir[1,2], Jens-Uwe Sommer[1,2], and Abhinav Sharma[1,3] — [1]Leibniz Institute of Polymer Research, Dresden, Germany — [2]Technical University Dresden, Dresden, Germany — [3]University of Augsburg, Augsburg, Germany

The transport of active-passive assemblies and their self-localization behavior have been studied in some detail in recent years [1,2]. The "chemotactic" property these exhibit has been attributed to the separation of time scales, i.e between the persistence time of the active particle and the characteristic time scale associated with the interaction between the particles (ex - harmonic springs). We consider a gas of active particles enclosed in a circular vesicle and observe that the transport behavior of the vesicle depends on the density of the enclosed gas or the number of active particles. This is a new mechanism for achieving desired transport of active colloidal cells as no new timescales are introduced by changing the number of active particles. This transition in transport behavior of these vesicles seems to be driven by fluctuations. The proposed model is also experimentally reproducible, contrary to the active-passive assemblies that have been studied so far.

References: [1] H. D. Vuijk et al., Phys. Rev. Lett., 126(20), 2021. [2] P. L. Muzzeddu et al., Phys. Rev. Lett., 133(11), 2024.

15 min. break

Invited Talk BP 34.5 Thu 16:45 ZEU/0160

From non-reciprocal torques towards shape-flexible and responsive prototypic worms — •Holger Stark and Jeanine Shea — Institute of Physics and Astronomy, Theoretical Physics, Technische Universität Berlin, Hardenbergstr. 36, 10623 Berlin, Germany

Non-reciprocal interactions as seen in active matter allow the formation of novel collective states that are only observable in the non-equilibrium. They may serve as prototypes for mimicking what is observed in the real world or for guiding robotic applications.

We start from non-reciprocal orientational interactions, where an active Brownian particle turns away from its neighbors [1]. By varying range and strength of the torque, we discover novel states such as travelling bands or dynamic flocking. Reversing the sign, makes the orientational interaction cohesive. We combine it with aligning torques and again for varying range and torque strength observe multiple, rotary, and persistent worms as well as an aster state [2]. In particular, the persistent worm represents a prototype for a flock of active constituents, either natural or robotic, which shows a remarkable flexibility and integrity when performing shape changes. This becomes obvious when hunting a prey, which leaders inside the worm sense via some chemotactic mechanism. In contrast to the macroscopic world, here without inertia, moving on a straight line seems the best strategy to escape. We also observe that the worm stays intact, even when squeezing through a narrow, long pore.

[1] M. Knezevic, T. Welker & H. Stark, Sci. Rep. 12, 19437 (2022).
[2] Jeanine Shea & Holger Stark, EPJE 48, 22 (2025).

BP 34.6 Thu 17:15 ZEU/0160

Directed motion of active collectives in activity gradients — •Hossein Vahid[1], Jens-Uwe Sommer[1,2], and Abhinav Sharma[1,3] — [1]Leibniz-Institut für Polymerforschung Dresden, 01069 Dresden, Germany — [2]Technische Universität Dresden, 01069 Dresden, Germany — [3]Institute of Physics, University of Augsburg, Universitätsstraße 1, 86159 Augsburg, Germany

Directed motion appears across all scales of active matter, from biomolecular condensates inside cells to large assemblies of migrating filaments. By simulating active particles and polymers, we identified the mechanisms that enable activity gradients to steer these collectives and control their assembly [1,2]. In cohesive mixtures, droplets climb activity gradients, fragment when the activity becomes too intense, and reassemble in low activity regions. This creates a robust cycle of positioning without needing any biochemical feedback. Similarly, in assemblies of active polar polymers, spatial gradients in activity, combined with temporally stochastic propulsion, generate net body forces on dimers, asters, and multiarm structures. This biases their motion toward high-activity regions and stabilizes long-lived entangled clusters even at low concentrations.

[1] H. Vahid, J.-U. Sommer, A. Sharma, Self-Organization and Cyclic Positioning of Active Condensates, arXiv preprint arXiv:2510.15771 (2025). [2] H. Vahid, J.-U. Sommer, A. Sharma, Collective dynamics in active polar polymer assemblies, Phys. Rev. Res. 7, L042031 (2025).

BP 34.7 Thu 17:30 ZEU/0160

Activity hallmarks in kinetic theory: Exceptional Points, Disorder Regularization, Non-Reciprocal Orientation-Displacement Coupling — •Horst-Holger Boltz and Thomas Ihle — University Greifswald, Institute for Physics, Greifswald

The dynamics of active systems are not subject to the same constraints as that of passive classical systems. This is particularly true for self-propelled particles with alignment interactions that have orientation-displacement coupling, i.e. the alignment is dependent on the relative position of the interacting particles to each other. We present recent work within first-principle kinetic theory that highlights key hallmarks of these more generalized dynamics. In particular, we discuss the effect of a cascade of exceptional points in the relevant dynamical operators under finite noise and also how to generally include noise in collision-based kinetic theory beyond mean-field. This allows us to provide analytical insights into the numerically established scaling relations (Kürsten, 2025) underlying the critical exponents in flocking transitions. Also, we are going to explain how to derive a systematic mesoscopic description for aligning self-propelled particles with orientation-displacement coupling and will present results showing a flocking transition in a system of a single species with purely anti-aligning torques and without any forces, simplifying an earlier reported flocking by turning-away mechanism (Das et al, 2024).

References: Boltz, Ihle, in preparation; Kürsten, arXiv:2402.18711 (2025); Das et al, Phys. Rev. X 14, 031008 (2024); Boltz et al, Entropy, 26(12), 1054 (2024); Ihle et al, arXiv:2303.03357 (2023)

BP 34.8 Thu 17:45 ZEU/0160

Rouse Polymers in Time-dependent Nonequilibrium Baths — •Bhavesh Valecha[1] and Abhinav Sharma[1,2] — [1]Mathematisch-Naturwissenschaftlich-Technische Fakultät, Institut für Physik, Universität Augsbur, Augsburg, Germany — [2]Leibniz-Institut für Polymerforschung Dresden, Institut Theory der Polymere, Dresden, Germany

Directed transport is a characteristic feature of numerous biological systems in response to nutrient and chemical gradients. These signals are often time-dependent owing to the high complexity of interactions in these systems. In this study, we focus on the steady-state behavior of polymeric systems responding to such time varying signals. We model them as ideal Rouse chains submerged in a time-dependent and inhomogeneous nonequilibrium bath, which is described by a spatially and temporally varying self-propulsion wave field experienced by the monomer units. Through a coarse-graining analysis, we show that these chains display rich emergent response to the temporal stimuli as a function of their length and topology. In particular, for slow moving waves, short chains composed of up to 3 monomers drift against self-propulsion wave, whereas, longer chains drift in the direction of the wave. In contrast, for fast moving waves, all chains drift along the wave regardless of their length. Moreover, we find that the star topology displays the highest drift for both slow and fast moving waves. We confirm these analytical predictions with robust numerical simulations, showing that response of polymeric systems to temporal stimuli can be controlled by the topology or the length of the polymer.

BP 35: Focus Session: 75 Years Division Polymer Physics: From Curiosity to Smart Materials (joint session CPP/BP)

Polymer materials are ubiquitous in modern society. In recent years, the focus has been on the development of functional, tunable or responsive materials, oftentimes inspired by biological materials. At this, a number of fundamental problems arise, e.g. regarding the interaction of polymers with water, biomolecules or inorganic nanoparticles and the resulting self-assembled morphologies as well as the underlying dynamics and the kinetics of morphological changes upon a stimulus. These problems are nowadays addressed in an interdisciplinary way by experimental methods, computer simulations and theory, often in close collaboration with polymer chemists. In five talks by renowned speakers, the focus session aims at highlighting few of these aspects that are currently under investigation worldwide. The fact that the Polymer Physics Division of the German Physical Society was founded in 1951 and hence, 2026 is the 75th anniversary, seems to be a good occasion to bring modern polymer physics into the focus.

Organized by Christine M. Papadakis, Christian Holm, Tayebeh Ameri and Kristian Franze.

Time: Thursday 15:15–17:45 Location: ZEU/LICH

Topical Talk BP 35.1 Thu 15:15 ZEU/LICH
The Loops of Life — Brian Chan and •Michael Rubinstein — Duke University, Durham, NC, USA

In mammalian cells, the cohesin protein complex is believed to regulate chromatin during interphase through active loop extrusion, in which dynamic loops are formed by cohesin translocating along chromatin. We developed a theoretical model that quantifies how key parameters, including cohesin residence time on chromatin, extrusion velocity, and the number density of chromatin-bound cohesins, regulate genomic contacts. The model describes chromatin contact probabilities and predicts that loop formation probability is a nonmonotonic function of loop length. Our theory demonstrates that active loop extrusion causes the apparent fractal dimension of chromatin to cross over between two and four at contour lengths on the order of 30 kilobase pairs. This work provides a theoretical basis for the compact organization of interphase chromatin, explaining the physical reason for the segregation of topologically associated domains and suppression of chromatin entanglements by up to a factor of 50, which contributes to efficient gene regulation by distal elements such as enhancers or silencers.

Topical Talk BP 35.2 Thu 15:45 ZEU/LICH
Polyelectrolytes and Biological Systems: A Charged Relationship — •Matthias Ballauff — Chemie und Biochemie, Freie Universitaet Berlin

If charges are appended to linear or crosslinked polymers, a polyelectrolyte results. Polyelectrolytes are ubiquitous and play a major role in biophysics. Important natural polyelectrolytes as e.g. DNA or Heparin are central in biology, and a thorough understanding of these systems and of charge-charge interaction is one of the main tasks of biophysics. In my lecture, I will discuss our recent research done on -Interaction of linear polyelectrolytes with proteins. This problem is also relevant for the formation of biocondensates by the interaction of cationic and anionic proteins; -Charged polymer networks and their interaction with proteins; -Role of polyelectrolytes in virus infections. In all cases, a quantitative understanding of the systems in terms of analytical models can be achieved, which may pave the way for future pharmaceutical applications.

Topical Talk BP 35.3 Thu 16:15 ZEU/LICH
From block copolymer morphologies to functional polymer membranes — •Volker Abetz — Helmholtz-Zentrum Hereon, Institute of Membrane Research, Max-Planck-Str. 1, 21502 Geesthacht, Germany — University of Hamburg, Institute of Physical Chemistry, Martin-Luther-King-Platz 6, 20146 Hamburg, Germany

Depending on solvent selectivity and the time of evaporation different structures can be obtained in cast block copolymers, showing that there is an interplay between kinetics and thermodynamic driving forces during the self-assembly before the sample is dry. When preparing membranes from block copolymer solutions, besides molecular weight, composition of the block copolymer and its concentration, also the choice of solvent, and the casting conditions play an important influence on the obtained morphology of the finally obtained membrane. This is especially important when membranes are prepared via the so-called non-solvent induced phase separation process after initial self-assembly by partial evaporation of solvent. The obtained membranes, when prepared successfully, display a rather isoporous top layer and can be subsequently post functionalized, in order to tune pore size and pore surface property. Different examples of the separation properties will be shown and also the potential use as a membrane reactor will be discussed.

Topical Talk BP 35.4 Thu 16:45 ZEU/LICH
Molecular electronic materials and devices for solar energy conversion — •Jenny Nelson — Imperial College London

To maximize the potential of solar power, new materials will be needed to harvest and convert solar energy alongside existing photovoltaic technologies. Molecular electronic materials, such as conjugated polymers and molecules, can achieve photovoltaic conversion through a process of photon absorption, charge separation at a heterojunction, and charge collection. Through a remarkable series of advances in materials design, the efficiency of photovoltaic energy conversion in molecular materials has risen from 1% to over 20% within two decades. We will discuss the factors that control the function of molecular solar cells including the nature of the charge separating heterojunction, and the impact of chemical and physical structure on phase behaviour, energy and charge transport, light harvesting, and loss pathways, comparing experimental measurements with a computational model of the generation and evolution of excited states and charges in such systems. We identify key molecular parameters that are likely to assist charge generation and consider the extent to which these parameters are optimised in the best performing materials. Finally, we will address the limits to conversion efficiency in such systems.

Topical Talk BP 35.5 Thu 17:15 ZEU/LICH
Control of cell and tissue stiffness by biopolymer networks and particle inclusions — •Paul Janmey — University of Pennsylvania, Philadelphia, PA, USA

Filamentous networks of semiflexible polymers are ubiquitous in biology. Collagen fibers form much of the extracellular matrix, the cytoskeleton controls cell mechanics, and chromatin fibers span the volume of the nucleus. The mechanical properties of the biopolymer fibers, the way in which the fibers link into networks, and the types of cells within the network all affect the way in which tissues respond to mechanical stress.

BP 36: Statistical Physics of Biological Systems IV (joint session BP/DY)

Time: Friday 9:30–12:45 Location: BAR/SCHÖ

Invited Talk BP 36.1 Fri 9:30 BAR/SCHÖ

Swimming in complex environments — •Christina Kurzthaler — Max Planck Institute for the Physics of Complex Systems

Microorganisms are omnipresent in the ocean, the human body, and our soils and therefore play an important role for various geological, biological, and medical processes. To optimize their survival and perform biological functions many microorganisms convert chemical energy into directed motion. In this talk, I will illustrate the underlying physical concepts and show concrete examples of our research, focusing on the interactions of microorganisms with their complex habitats. I will first discuss the motion of sperm in complex fluids and address their emergent dynamics in the presence of a hyperactivation agonist, modifying the sperm beating pattern. Second, I will focus on the first-passage-time statistics of active agents moving towards a target boundary. Our results highlight how swim gait impacts spreading and search efficiency in active systems with potential consequences for sperm motion in the reproductive tract and the accumulation of microbial communities.

BP 36.2 Fri 10:00 BAR/SCHÖ

Motor shot noise explains active fluctuations in a single cilium — •Maximilian Kotz[1], Veikko F. Geyer[2], and Benjamin M. Friedrich[1] — [1]Cluster of Excellence Physics of Life, TU Dresden, Dresden, Germany — [2]B CUBE, TU Dresden, Dresden, Germany

Molecular motors drive seemingly regular motion, making living matter move - yet also cause non-equilibrium fluctuations that can serve as a probe of internal motor dynamics. Here, we use motile cilia as a model system to investigate how small-number fluctuations shape collective dynamics. Motile cilia exhibit regular bending waves; this motion is driven by the self-coordinated activity of thousands of molecular motors inside the cilia's cytoskeletal core. By developing, to the best of our knowledge, the first stochastic model of cilia beating, we show that the finite number of motors leads to active fluctuations on the mesoscale, sufficient to explain frequency jitter in beating cilia observed in experimental data. We rigorously compare observables of this model, including the quality factor of the oscillation, to experimental data in which motors have been partially extracted from cilia. This is a strong test of this stochastic model. The model also reproduces other phenomena of experimental data, like correlation lengths of intra-cilium synchronization and noise-induced phase slips. We propose that active fluctuations are important new observables, which can guide theoretical models of motor dynamics in beating cilia and other motor systems.

BP 36.3 Fri 10:15 BAR/SCHÖ

Theory of Forces Between Crosslinked Filaments — •Cedrik Barutel and Sebastian Fürthauer — Institute of Applied Physics TU Wien Austria

The cytoskeleton drives essential cellular processes like cell division and chromosome segregation. It consists of filaments that are crosslinked by proteins, many of which are molecular scale motors that consume ATP to do work. The forces that crosslinking proteins generate between cytoskeletal filaments are the key drivers of active cellular mechanics. We derive a generic theory to describe such crosslinking forces.

We construct a theory to describe and predict the forces generated collectively by crosslinking proteins between biofilaments using symmetries, conservation laws, and out-of equilibrium thermodynamic principles. Our approach identifies the full set of phenomenological coefficients governing entropic, active, and frictional crosslinking forces, which allows a quantitative comparison between the effects of different crosslinker mixtures between two filaments. We demonstrate the power and validity of this framework by quantitatively explaining a set of different experimental setups, which combine the effects of passive and active crosslinks

BP 36.4 Fri 10:30 BAR/SCHÖ

Modeling Cooperative Remodeling and Energy Landscapes in the Bacterial Flagellar Motor — •Nils-Ole Walliser — Laboratoire Charles Coulomb, University of Montpellier, Montpellier, France

Bacteria use the flagellar motor to adapt their motility to changing mechanical conditions. This rotary motor tunes its torque by recruiting and releasing torque-generating stator units. I will present statistical-physics-based models that use single-motor measurements to infer interaction potentials and energy landscapes in the bacterial flagellar motor. First, using single-motor bead assays that resolve stepwise changes in rotation speed and thus stator occupancy, we model stator recruitment as a finite-size lattice gas and infer stator-stator cooperativity from occupancy fluctuations. This reveals moderate attractive interactions and shows that the motor operates in a regime that balances responsiveness to load changes with noise in stator number. Second, I will discuss experiments where the motor load is actively perturbed, uncovering a strong asymmetry in the relaxation to the steady state when starting from higher versus lower stator occupancy. A two-state catch-bond model quantitatively explains this stoichiometry-dependent asymmetry and captures the mechanosensitive nature of stator anchoring to the cell wall. Finally, I will show how high-temporal-resolution rotation traces can be used to reconstruct, in a model-independent way, the tilted periodic energy landscape of the rotor/LP ring within a Smoluchowski framework, yielding barrier heights, torque and internal friction.

BP 36.5 Fri 10:45 BAR/SCHÖ

Anisotropic (sub)diffusion of organelles in living cells — •Aranyak Sarkar, Pooja Yadav, and Matthias Weiss — Experimental Physics I, University of Bayreuth, Universitätsstraße 30, 95447 Bayreuth

Eukaryotic cells are neatly organized into distinct, membrane-enclosed compartments ('organelles') with specific duties. A prominent example are peroxisomes, which feature vesicle-like shapes with radii $0.1-1\ \mu$m that are dispersed across the cytoplasm. Using time-lapse fluorescence microscopy, we have tracked the motion of individual peroxisomes over extended periods. Analysis of the experimental data revealed two distinct modes of motion: a prevailing (sub)diffusive motion and a quite rare super-diffusive characteristics that is associated with motor-driven transport along microtubules. Focussing on the seemingly unremarkable subset of (sub)diffusive trajectories, we have found a significant anisotropy in the motion that persisted even when microtubules were disrupted. In particular, diffusive steps along the cells' long axis were seen to be favored over steps in the perpendicular direction, indicating an anisotropic materials characteristic of the cytoplasm. Using a simple model, we were able to capture and explain the observed features of the anisotropic diffusion of organelles.

15 min. break

BP 36.6 Fri 11:15 BAR/SCHÖ

Understanding Influenza A Virus particles detaching from reconstructed cell surfaces — •Thomas Kolbe[1,2], Pierre Gaspard[1], and Bortolo Matteo Mognetti[1,2] — [1]CENOLI, Université Libre de Bruxelles (ULB) — [2]IB2 - Interuniversity Institute of Bioinformatics in Brussels

Influenza infection is a multistage process that involves the trafficking of viral particles across the cell membrane. Before endocytosis, virions target the membrane by binding hemagglutinin ligands to sialic acid residues on cell receptors. After budding, neuraminidase cleaves these residues, enabling virions to detach from the infected cell surface.

We examine detachment dynamics through simulations and theoretical analysis. We explain experimental findings showing that the time required for virions to detach can decrease as the single-trajectory average number of bonds increases - a counterintuitive result specific to neuraminidase activity. Furthermore, we demonstrate that the detachment time is not governed by a Poisson distribution but depends on multiple factors, including ligand-receptor reaction rates, virion size, and receptor diffusion constant. These results clarify how biochemical parameters regulate the residence time of virions at the cell surface.

BP 36.7 Fri 11:30 BAR/SCHÖ

Band pattern formation of erythrocytes in density gradients is due to competing aggregation and net buoyancy — •Felix Maurer[1], Camila Romero[1], Nikolas Lerch[1], Thomas John[1], Lars Kaestner[1,2], Christian Wagner[1,3], and Alexis Darras[1,4] — [1]Experimental Physics, Saarland University, Saarbruecken, Germany — [2]Department of Theoretical Medicine and Biosciences, Saar-

land University, Homburg, Germany — [3]Physics and Materials Science Research Unit, University of Luxembourg, Luxembourg — [4]School of Physics, University of Bristol, Bristol, United Kingdom

Centrifugation of biological matter in density gradient solutions is a standard method for separating cell types or components. It is also used to separate RBCs by age, as they lose water and become denser over their lifespan. When the density gradient is prepared with Percoll, discrete bands of RBCs are systematically observed, despite the continuous density distribution of RBCs. We developed a continuity equation incorporating cell aggregation to describe the macroscopic evolution of RBC volume fraction in a density gradient, considering a continuous RBC density distribution. Numerical solutions demonstrate that the competition between net buoyancy and aggregation is sufficient to create band patterns. Our model reproduces the temporal evolution observed in experiments, but also predicts several types of bifurcation-like behaviors for the steady-state patterns in constant gradients, depending on RBC volume fraction and aggregation energy.

BP 36.8 Fri 11:45 BAR/SCHÖ

Adaptive self-organization in excitable biological collectives — •Bianca Ariani[1,3], Yunus Sevinchan[2,3], and Pawel Romanczuk[2,3] — [1]Bernstein Center for Computational Neuroscience, Berlin — [2]Science of Intelligence, TU Berlin — [3]Institute for Theoretical Biology, HU Berlin

Biological collectives often display complex, context-dependent behavior, such as coordinated responses to predators, despite individuals following simple local rules. This class of phenomena is broadly understood as self-organization.

We examine a system showing rich spatio-temporal dynamics: Sulphur Mollies, Mexican freshwater fish whose group behavior resembles a stochastic excitable medium. To probe the mechanisms behind their collective activity, we study a bio-inspired agent-based model in which individuals estimate the shoal's mesoscale activity from the cues they perceive as they move. Each agent adjusts its sensitivity to cues through a simple homeostatic plasticity rule, allowing the group to regulate its collective state. This formulation links individual adaptation to population-level patterns.

Our results show that local adaptive regulation reproduces key qualitative features of the biological system. More generally, they illustrate how distributed plasticity mechanisms can support robust self-organization in complex biological collectives.

BP 36.9 Fri 12:00 BAR/SCHÖ

Visual-based Collective Shepherding in Swarm Robotic System — •Yating Zheng[1,2] and Pawel Romanczuk[1,2] — [1]Department of Biology, Humboldt Universität zu Berlin, Berlin, Germany — [2]Research Cluster of Excellence 'Science of Intelligence', Berlin, Germany

Collective shepherding presents a rich example of two interacting multi-agent systems coupled through non-reciprocal interactions. While most existing models assume that shepherd agents have global knowledge of the flock-an unrealistic premise for physical or biological systems-we introduce a vision-based, locally interacting model that captures the essential physics of shepherd-flock coordination. The model produces robust, self-organized behavior among shepherds without explicit communication, and we analyze how key control parameters, such as flock size and the number of shepherds, shape the resulting dynamics.

The framework also performs effectively in more challenging regimes, including the manipulation of non-cohesive agents and passive (non-self-propelled) agents, demonstrating its broad dynamical applicability. We further validate the model on a mixed-reality swarm-robotic platform, where physical robots successfully shepherd a virtual flock.

Overall, these results provide a minimal yet powerful physics-based description of multi-agent herding using only local visual information, offering insight into non-reciprocal collective behavior and enabling scalable real-world implementations in swarm robotics.

BP 36.10 Fri 12:15 BAR/SCHÖ

Polymer theory shows DNA motors extrude loops in the monomeric mode — Kirill Polovnikov[1,2] and •Dmitry Starkov[2] — [1]Institute for Physics and Astronomy, University of Potsdam, Potsdam-Golm, Germany — [2]Moscow, Russia

Cohesin-dependent loop extrusion is a key active mechanism of DNA organization, yet it remains unclear whether chromatin loops in living cells are generated primarily by individual cohesin motors or by higher-order structures. To fill this major gap, we build an analytical polymer-physics model that extracts a missing parameter - *the linear density of loops* - directly from Hi-C data. We focus on short genomic distances, where contact statistics simplify, resulting in a perturbative expression for the contact probability of a looped chain under a finite contact-detection radius. Our theory recapitulates a characteristic dip in the *logarithmic derivative* of the contact-probability that is *broadly observed in experiments*. By fitting this minimal model to a diverse range of mammalian Hi-C datasets, we infer approximately six loops per megabase. Independent imaging and mass spectrometry measurements of cohesin density are consistent with our inferred loop density, supporting the monomeric mode of DNA motors extrusion.

BP 36.11 Fri 12:30 BAR/SCHÖ

Universal loop statistics from active extrusion — •Anastasia Chervinskaya[1] and Kirill Polovnikov[1,2] — [1]Moscow, Russia — [2]Institute for Physics and Astronomy, University of Potsdam, Potsdam-Golm, Germany

Cohesin-dependent loop extrusion is a key active mechanism of genome organization, yet quantitative links between extrusion kinetics and measurable loop statistics remain incomplete. We develop an analytical model that predicts the mean loop scale, full loop-length distributions, state composition, and arm-arm correlations for one-sided versus two-sided extrusion. The theory maps the master equations onto diffusion on a state graph yielding state-resolved loop-length PDFs.

We show that one-sided extrusion yields a universal exponential loop-length distribution, whereas two-sided extrusion generates a sum of exponentials that approaches a gamma-like form at high barrier density. The model also predicts a strictly positive lower bound of $1/4$ on arm-arm correlations.

Parameterized with independent measurements for HeLa G1 (cohesin residence and spacing; barrier densities and lifetimes), our model quantitatively accounts for the observed loop size. Also, it reproduces the experimentally measured distribution of CTCF-CTCF loop lengths under the assumption of two-sided extrusion, providing additional evidence that cohesin extrusion in living cells is predominantly bidirectional. Our results provide a compact route to infer biophysical parameters of active extrusion from experimental data.

BP 37: Tissue Mechanics II

Time: Friday 9:30–12:45 Location: BAR/0106

BP 37.1 Fri 9:30 BAR/0106

Active rheology and feedback-controlled stress in a multi-purpose platform for tissue mechanics — •Anna Mukhina[1,2], Till Muenker[1], Mattias Luber[1], Polina Malova[1,2], and Timo Betz[1,2] — [1]Third Institute of Physics - Biophysics, University of Goettingen — [2]Max Planck School Matter to Life

3D tissue engineering offers unique opportunities to study simplified, but accurate models of complex biological systems, where especially force generation, mechanical properties, and active regulation can be addressed. However, most current methods to raise engineered tissues do not allow quantitative characterization of their mechanics without a strong perturbation of these delicate systems.

Here, we present a novel experimental platform to apply well-defined strain to tissues and measure the resulting forces with an optical readout. Tissues are grown between flexible posts, where one post can be actuated by a piezo bending element, and direct optical detection of both posts movement allows for precise force and strain measurement. With this setup, we avoid complex microscopy measurements, can position the system in an incubator, and the rapid readout enables a large variety of experimental protocols. The system can conduct oscillatory rheology, simulate isometric/eccentric contractions, reproduce changes in environmental stiffness during physiological and pathological processes, and adapt stress or strain to mechanical changes of the system. We demonstrate the potential of the developed setup by carrying out oscillatory rheology of engineered skeletal muscles over the course of their maturation, covering three orders of frequency magnitude.

BP 37.2 Fri 9:45 BAR/0106

demonstrating normal tissue sparing with pitz PITZ electron beams in zebrafish embryos — •E Tarakci[1,2,3], C Schulze[2], C Richard[1], M Gross[1], N Aftab[1], A Aksoy[1], Z Amirkhanyan[1], A Chiravuri[1,2], J Good[1], F Hausmann[3], S Khammee[1], Y Komar[1,2,3], M Krasilnikov[1], B Li[1], X Li[1], Z Lotfi[1], G Montoya-Soto[1], F Mueller[1], A Oppelt[1], F Riemer[1], K Suzart[1], I Tinhofer[3], D Villani[1], S Worm[1], D Xu[1], S Zeeshan[1], M Frohme[2], F Stephan[1], S Aminzadeh Gohari[1], and A Grebinyk[1] — [1]Deutsches Elektronen-Synchrotron, DESY, Zeuthen — [2]Technische Hochschule Wildau,Wildau — [3]Charité Universitätsmedizin Berlin, Berlin

Zebrafish (Danio rerio) embryos provide a sensitive model for studying normal tissue responses. This study was conducted within FLASH-lab@PITZ, where PITZ delivers electron beams from conventional to ultra-high dose rates up to 10^15 Gy/s. Wild-type AB embryos at 24 hours post fertilization (hpf) received 10 Gy via conventional X-rays (0.04 Gy/s), low dose rate electrons (LDR, 0.05 Gy/s), or ultra-high dose rate electrons (UHDR, 10^5 Gy/s). At 119 hpf, toxicity was assessed through spinal curvature, pericardial edema, eye diameter, and body length. X-rays and LDR increased toxicity (X-rays: 50% medium, 50% none*mild; LDR: 33% severe, 17% mild, 50% normal). UHDR greatly reduced effects, with no medium or severe toxicity and 42% none and 58% mild changes. These results demonstrate a marked tissue-sparing trend under UHDR conditions and provide early evidence for a FLASH-mediated normal tissue sparing effect.

BP 37.3 Fri 10:00 BAR/0106

Holographic vibration spectroscopy - extracting mechanical properties of adherent cells from their vibrational response — •Eric Schneider[1], Bob Fregin[1], Dominic Mokbel[2], Sebastian Aland[2], and Oliver Otto[1] — [1]Institute of Physics, University of Greifswald, Greifswald, Germany — [2]Institute of Numerical Mathematics and Optimization, TU Bergakademie Freiberg, Freiberg, Germany

The mechanical properties of biological cells are closely linked to their pathophysiological state, and high-throughput quantification is essential for using them as biomarkers in basic and translational research. While microfluidic technologies can characterize suspended cells at rates above 1,000 cells per second, no comparable method exists for adherent cells or tissues. Here, based on preliminary experiments with holographic vibration spectroscopy (HVS), developed in our group, we present a theoretical framework to address this gap. In HVS, adherent cells are harmonically oscillated at defined frequencies and amplitudes, and their deformation and phase shift encode their mechanical properties. To validate this concept, we developed a finite-element simulation framework using the open-source library AMDIS, capable of modeling cellular vibration across a broad parameter space. From these simulations, we derive a protocol to solve the inverse problem and show that viscoelastic properties can be uniquely determined using only the amplitude response at two vibration frequencies. Combined with HVS, this framework will next be used to rapidly and non-invasively quantify the viscoelastic properties of adherent cells and tissues.

BP 37.4 Fri 10:15 BAR/0106

Investigating the dynamics of cellular rearrangements in minimal four-cell clusters — •Agathe Jouneau, Tianyi Cao, and Joachim Rädler — Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität, Munich, Germany

Animal cells assemble into tissues that exhibit diverse mechanical responses, from solid-like to liquid-like states. In solid-like states, tissues can withstand mechanical stress, whereas in liquid-like states, they release stress through cellular rearrangements. Recent evidence suggests that the transition between solid and liquid-like states is central to biological processes such as embryogenesis, wound healing and cancer metastasis. However, the way in which local interactions between the constituent cells control the tissue fluidity remains unclear. The process by which cells exchange neighbors is known as a cell intercalation, or a T1 transition in foam physics terminology. Theoretical models have shown that the height of the energy barrier associated with T1 transitions determines tissue fluidity. In our work, we study the dynamics of T1 transitions in a minimal system of four epithelial cells. We confine the cells onto adhesive micropatterns or in hydrogel microcavities, and use time-lapse microscopy to record the evolution of cell-cell junctions over time. We aim to use this platform to study how perturbations of cell-cell adhesion proteins impact cell rearrangement, as well as to experimentally test existing models for cellular dynamics.

BP 37.5 Fri 10:30 BAR/0106

Collective actuation in solid tissues: Dynamics and mechanics of an oscillating tissue shell during morphogenesis — •Zoë Lange[1], Henrik Jaeschke[1], Lea Möller[1], Mariia Golden[2], Artemiy Golden[2], Marc Pereyra[1], Frederic Strobl[2], Ernst H.K. Stelzer[2], and Franziska Matthäus[1] — [1]Frankfurt Institute for Advanced Studies — [2]Buchmann Institute for Molecular Life Sciences

Morphogenesis relies on coordinated mechanical deformations of embryonic tissues, yet the dynamic material properties that enable these shape changes remain incompletely understood. In the *Tribolium castaneum* embryo, the extraembryonic serosa tissue forms a closed and oscillating epithelial shell, providing a powerful model to study active mechanical processes in vivo. Here, we combine quantitative live imaging with particle image velocimetry, cell-boundary segmentation, cell-boundary tracking, and stress inference methods to characterize the spatiotemporal mechanics of the oscillatory contractions in the tissue shell. We show that the extraembryonic epithelium behaves as an active elastic solid whose global oscillation emerges from synchronizing cellular contraction. By integrating measured deformation with inferred force maps, we identify a cellular program of mechanosensitive remodeling. Our results provide a mechanistic link between active force production at the cellular scale and emergent morphogenetic dynamics at the tissue scale, establishing the *Tribolium* tissue shell as a model system for collective actuation in active elastic materials *in vivo*.

BP 37.6 Fri 10:45 BAR/0106

Plant movement systems enabled by plant hinges: diversity, evolution, form-structure-function relationships and their biomimetic potential — Arooj Sajjad and •Simon Poppinga — Technische Universität Darmstadt, Botanischer Garten, Schnittspahnstraße 2, 64287 Darmstadt, Germany.

Plants are often described as comparatively static systems, yet many species exhibit diverse and mechanically sophisticated forms of movement. In recent decades, such plant movement systems have gained increasing attention due to their remarkable flexibility, versatility, and structural robustness. Plants move in a variety of ways, e.g. to align themselves with sunlight or the earth's gravitational field, to catch

prey, to interact with pollinators, and to adhere to nearby structures in the environment. Plant movements are often enabled by joint-like structures, commonly referred to as plant hinges in the literature. Unlike technical hinges, which allow for rigid body movements and are maintenance-intensive and prone to failure, compliant mechanisms as found in plant movement systems fulfil roles analogous to technical joints, albeit fundamentally differing in form, kinematics, and structure. Interestingly, the hinges in most motile plant structures (e.g. motile sepals in orchids or lever mechanisms in sages) have not been investigated regarding their form-structure-function relationships. In this broad research study, we approach these compliant mechanisms in plants from an engineering perspective on kinematic pairs. Our research also aims to understand convergent mechanisms in plants. One aim is to develop future biomimetic actuator design.

15 min. break

BP 37.7 Fri 11:15 BAR/0106

Understanding tissue mechanics through tumour organoids — •Mathilde G. Lettinga[1], Vaibhav Mahajan[1], Raimund Schlüssler[1], Stefanie Hübner[2,3], Valeria Lozovanu[2,3], Franziska Baenke[2,3,4], Daniel E. Stange[2,3,4], and Anna V. Taubenberger[1] — [1]BIOTEC, CMCB, TU Dresden — [2]VTG, University Hospital Carl Gustav Carus, TU Dresden — [3]DKTK, Heidelberg — [4]NCT/UCC, Dresden

Tumours exhibit altered physical properties that manifest across spatial scales. Compared to healthy tissue, solid tumours are typically stiffer, which can partly be attributed to the extracellular matrix. However, the contributions of the epithelial cancer cells to the emergent tissue properties remain unclear.

Aiming to elucidate the role of cells in tissue mechanics, we investigated the mechanical and morphological properties of patient-derived colorectal liver metastasis organoids. Organoids from different patients varied in morphology, displaying either a large central lumen or a multitude of small lumina. We performed bulk compression with AFM and found that single-luminal organoids are stiffer and more elastic than multi-luminal organoids. Concurrently, Brillouin microscopy in situ showed a higher Brillouin frequency shift for single-luminal organoids, indicating lower compressibility. 3D segmentation revealed more elongated, ordered, homogeneous and smaller nuclei in the single-luminal organoids compared to their multi-luminal counterparts. Thus, our data suggest that the mechanical properties of organoids are coupled to the physical properties of their constituent cells.

BP 37.8 Fri 11:30 BAR/0106

A morphoelastic phase field model predicts buckling instability in tumor growth — Luise Zieger[1], Min Wu[3], John Lowengrub[4], and •Sebastian Aland[1,2] — [1]TU Freiberg — [2]HTW Dresden — [3]Worcester Polytechnic Institute, USA — [4]UC Irvine, USA

It is well known that growing tumors generate and respond to stress in their local environment. On the one hand, local cell proliferation and apoptosis lead to complex strain patterns in the tissue. On the other hand, tissue re-arrangements can relax the resulting mechanical shear stresses and make the tissue more fluid-like. To predict the outcomes of these nonlinear visco-elastic interactions, we introduce the framework of morphoelasticity to phase field modeling of a growing tumor embedded in a surrounding host tissue. Coupling this continuum system to diffusible growth-promoting nutrient, our simulations identify a symmetry-breaking instability in 2D and 3D driven by two primary mechanisms: (i) elastic buckling instability generated by tangential stresses along the tumor-host interface and (ii) instabilities generated by local imbalances between cell divisions and cell death. Further, tissue fluidity and compressibility can lead to changes in tumor topologies. Our modeling framework provides a robust methodology for investigating how tissue mechanics and growth factor signaling influence the progression and invasive potential of solid tumors.

BP 37.9 Fri 11:45 BAR/0106

Orientational lineage memory and mechanical ordering during diffusion-limited growth — •Ilias-Marios Sarris[1], Ramin Golestanian[1,2], and Philip Bittihn[1] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, United Kingdom

Growth and shape formation in crowded multicellular assemblies arise from the interplay of chemical gradients, single-cell expansion, and mechanical interactions. Using a particle-based model that resolves nutrient fields and cellular orientations with tunable lineage memory, we study how orientational order emerges in expanding fronts whose morphology is set by nutrient limitation. We find a transition in nematic order controlled by front morphology: under strong orientation inheritance, both thin active layers (fingering fronts) and thick active layers (flat fronts) produce strong alignment, while intermediate cases are less ordered. Velocity, reorientation, and stress statistics reveal a crossover from inheritance-dominated to mechanically driven alignment that progressively overrides lineage memory. As a result, orientational memory yields a fitness advantage only in the diffusion-limited, memory-dominated regime, elucidating how nutrient supply and mechanics jointly shape self-organization during growth.

BP 37.10 Fri 12:00 BAR/0106

Feedback-controlled epithelial mechanics: emergent soft elasticity and active yielding — •Fridtjof Brauns[1,2], Pengyu Yu[3,4], and M. Cristina Marchetti[3] — [1]MPI-PKS, Dresden, Germany — [2]KITP, Santa Barbara, USA — [3]University of California, Santa Barbara, USA — [4]Tsinghua University, Beijing, China

Biological tissues exhibit distinct mechanical and rheological behaviors during morphogenesis. While much is known about tissue phase transitions controlled by structural order and cell mechanics, key questions regarding how tissue-scale nematic order emerges from cell-scale processes and influences tissue rheology remain unclear. Here, we develop a minimal vertex model that incorporates a coupling between active forces generated by cytoskeletal fibers and their alignment with local elastic stress in solid epithelial tissues. We show that this feedback loop induces an isotropic–nematic transition, leading to an ordered solid state that exhibits soft elasticity. Further increasing activity drives collective self-yielding, leading to tissue flows that are correlated across the entire system. This remarkable state, that we dub plastic nematic solid, is uniquely suited to facilitate active tissue remodeling during morphogenesis. It fundamentally differs from the well-studied fluid regime where macroscopic elastic stresses vanish and the velocity correlation length remains finite, controlled by activity. Altogether, our results reveal a rich spectrum of tissue states jointly governed by activity and passive cell deformability, with important implications for understanding tissue mechanics and morphogenesis.

BP 37.11 Fri 12:15 BAR/0106

Neuromechanics of peristalsis — •Sifan Yin[1], Suraj Shankar[2], and Lakshminarayanan Mahadevan[3] — [1]MPI-PKS, Dresden, Germany — [2]University of Michigan, Ann Arbor, MI, US — [3]Harvard University, Cambridge, MA, US

The peristalsis of cylindrical-shaped organisms or organs is driven by the propagation of rhythmic waves of contraction and relaxation along the tube wall. These waves are generated by coupled interactions of neural control, mechanotransduction, and active muscular contraction. Here, we propose a minimal neuromechanical model for spontaneously coordinated peristaltic waves by locally coupling the neuro-muscular dynamics to the mechanics of an active elastic tube, such as the Nematostella body, the gastro-intestinal tract, and the ureters. We analyze our model using a combination of analytical and numerical methods to investigate the nucleation, propagation and extinction of pulse, and the transitions between disordered twitching and coordinated traveling waves. Our theory naturally elucidates how the interactions among mechanics and neural activities can give rise to coordinated peristaltic motion without any center pattern generator (CPG). This work can supplement ways to robustly design robotics with neural feedback and help to understand early peristaltic wave generation before CPG formation, especially in early embryonic development.

BP 37.12 Fri 12:30 BAR/0106

Muscle growth by sarcomere divisions — Clement Rodier[1], Ian D. Estabrook[2,3], Frank Schnorrer[1], and •Benjamin M. Friedrich[2] — [1]IBDM, Marseilles, France — [2]EXC Physics of Life, TU Dresden, Germany — [3]EMBL, Heidelberg, Germany

The sarcomere is the elementary contractile unit of muscles. Sarcomeres are organized into highly regular periodic chains termed myofibrils, which span the millimeter-length of muscle cells. During development, new sarcomeres are added to mechanically tensed myofibrils as muscle cells increase in length. Yet, how muscles add new sarcomeres to facilitate muscle growth remained elusive. Using live imaging and high-throughput image analysis of the Drosophila flight muscle, we identified a new mechanism of tension-driven sarcomere addition where individual sarcomeres divide along the myofibril tension axis into daughter sarcomeres. Thereby, new sarcomeres can be inserted

into contractile myofibrils without compromising their mechanical integrity. A similar mechanism may apply in vertebrate muscle development and regeneration.

[1] Rodier et al. Sci. Adv. 11(28), 2025

BP 38: Active Matter VI (joint session DY/BP)

Time: Friday 9:30–12:15 Location: ZEU/0160

Invited Talk BP 38.1 Fri 9:30 ZEU/0160

Morphogenesis, transport, and computation in micro-scale swarms — •Akira Kakugo — Division of Physics and Astronomy, Graduate School of Science, Kyoto University, Kyoto, Japan

Collective behavior at the microscale offers a powerful route to creating adaptive and functional materials. In this talk, I present a series of studies in which microtubule/kinesin active matter is treated as an ensemble of active agents, and swarming is engineered through DNA-mediated interactions. By introducing programmable dipole-dipole like binding via designed DNA motifs, we establish tunable microscale swarms with controllable cohesion. First, I describe how external mechanical stimuli trigger diverse modes of morphogenesis within these swarms, leading to the emergence of ordered structures and pattern transformations. Next, I introduce a DNA-programmable transport system in which a swarm of millions of active agents cooperatively captures, carries, and releases microscale cargo, enabling light-controlled, spatiotemporally precise transport. Finally, I demonstrate how such active swarms can function as a physical reservoir, where their high-dimensional, nonlinear dynamics are directly harnessed for computation within an active-matter ensemble.

BP 38.2 Fri 10:00 ZEU/0160

Learning effective hydro-phoretic interactions in active matter — •Palash Bera, Aritra K. Mukhopadhyay, and Benno Liebchen — Technische Universität Darmstadt, Darmstadt, Germany.

In the quest to understand collective behaviors in active matter systems, the complexity of hydrodynamic and phoretic interactions remains a fundamental challenge. Despite the substantial progress in identifying effective models, existing approaches often rely on minimalistic approximations, neglecting many-body interactions and the near-field contributions to the full interaction dynamics. We propose a machine learning-based framework to systematically learn hydrophoretic interactions among active colloids from first principles. By combining high-fidelity simulations with symmetry-preserving descriptors and neural network architectures, our approach captures the effective representations of both near- and far-field interactions. This framework bridges the gap between microscopic continuum models and coarse-grained active matter simulations, enabling scalable many-particle modeling without explicitly resolving the fluid flow or concentration fields. Built on two-body interactions, the coarse-grained model captures clustering phenomena consistent with those observed experimentally in active matter systems. We envision that the principles and tools developed here will have broad applicability across a wide range of active and nonequilibrium systems, including driven colloids, active gels, and field-responsive materials, providing a robust framework for modeling emergent behaviors in living and life-like systems.

BP 38.3 Fri 10:15 ZEU/0160

Interactions between Janus particles in optical tweezers — •Arnaud Compagnie[1], Abhimanyu Nowbagh[2], Ivo Buttinoni[2], and Hartmut Löwen[1] — [1]Institute for Theoretical Physics II, Heinrich Heine University Düsseldorf, 40225 Düsseldorf, Germany — [2]Institute for Experimental Physics of Condensed Matter, Heinrich Heine University Düsseldorf, 40225 Düsseldorf, Germany

Janus particles, by using their asymmetric properties to self-propel due to phoretic effects, are the most prominent artificial active colloids at the microscale. Their ability to extract energy from their surroundings and to self-assemble are used to perform specific tasks. However, due to the vast amount of types of Janus particles and the complex systems they evolve in, the way they interact with their environment remains poorly understood. Optical tweezers can be used to trap them and control their behaviour. By studying how a trapped Janus particle affects the movements of another one in a separate trap, we aim to identify the main physical phenomena - optics, hydrodynamic fluxes, and phoretic fields - that influence the interactions between them. We establish and simulate physical models in order to derive the characteristic dynamical properties of the Janus particles thanks to the comparison with experimental data.

BP 38.4 Fri 10:30 ZEU/0160

Programmable Hydrodynamic Reconfiguration of Active Particles — •Lisa Rohde, Gordei Anchutkin, and Frank Cichos — Molecular Nanophotonics Group, Peter-Debye-Institute for Soft Matter Physics, University Leipzig, Leipzig, Germany

Self-propelled microparticles generate hydrodynamic flow fields that govern their interactions with boundaries and neighbouring particles. The long-range behavior of the flow patterns classifies them as either pushers, pullers or neutral swimmers - each exhibiting fundamentally different collective behaviours. In nature, some microorganisms can adaptively switch between swimming modes in response to their environment. However, in synthetic matter, the hydrodynamic signature is fixed during fabrication constraining our ability to study how switching between modes might enable new emergent behavior. Here, we demonstrate a novel approach for real-time switching of the hydrodynamic character of the microswimmer. By illuminating the particle with a structured light field, we create tailored temperature gradients that drive controllable slip flows on the particle*s surface. This effectively allows control over the swimmer*s flow field and enables mode switching by dynamically changing the illumination pattern on demand. The ability to alter the propulsion characteristics established a versatile platform for experimentally investigating swimming efficiency, adaptivity, and collective behavior.

BP 38.5 Fri 10:45 ZEU/0160

From Passive to Active: Active Particles in Coatings Formulation and Film Formation — •Jan Cammann[1], Karnika Singh[1], Luka Burduli[1,2], Edgar Espinosa Rodriguez[3], Franck D'Agosto[3], Muriel Lansalot[3], and Ignacio Martin-Fabiani[1] — [1]Loughborough University — [2]Constructor University Bremen — [3]Universite Claude Bernard Lyon

Coatings are widely used in protective and functional applications but are fundamentally limited by the passive nature of their formulation ingredients. This leads to a critical lack of control over the spatial distribution of ingredients and prevents the optimization of key functional properties. Addressing this challenge, we propose a paradigm shift towards active coatings formulation. We introduce active Janus particles in coatings formulations and demonstrate how they overcome sedimentation and chemical gradients to accumulate at both the top and bottom coating interfaces. To achieve this programmable microstructure, we balance the timescales of active particle fuel depletion and evaporation induced assembly. We find that Janus particles at the top coating surface have an orientational bias, with the sub-equatorial orientation being the most common. This work lays the foundation for future studies developing functional coatings with programmable microstructures and dual functionalities enabled by orientation-biased active particles.

15 min. break

BP 38.6 Fri 11:15 ZEU/0160

Critical Dynamics of Active, Isotropic Systems — •Emir Sezik and Gunnar Pruessner — Imperial College London

A central result of field theory and renormalisation group (RG) is the concept of universality classes. Systems with different microscopic properties display the same physics near a continuous phase transition as they share the same symmetries. In equilibrium critical dynamics, where systems relax to a thermal steady state, Hohenberg and Halperin have provided the authoritative catalogue, which however, does not immediately extend to critical active matter systems. As they display exciting and new phases by their breaking of detailed balance, we have every reason to attempt to identify the relevant terms and to catalogue these non-equilibrium, critical systems. Motivated by this, in this work, we study an active version of Model A by including the relevant terms that are allowed by symmetry in the coarse-grained

description. We show that this universality class encompasses diverse systems including spins with vision-cone interactions and Malthusian flocks. Finally, using field-theoretic RG, we perform a 1-loop calculation, approaching the critical point from the disordered regime, and elucidate the effects of activity on the Wilson-Fisher fixed point.

BP 38.7 Fri 11:30 ZEU/0160

Conservation laws and slow dynamics determine the universality class of interfaces in active matter — •Raphael Maire[1], Andrea Plati[1], Leonardo Galliano[2,3], Frank Smallenburg[1], Ludovic Berthier[2], and Giuseppe Foffi[1] — [1]Université Paris-Saclay, Laboratoire de Physique des Solides, 91405 Orsay, France — [2]Gulliver, ESPCI Paris, PSL Research University, 75005 Paris, France — [3]Dipartimento di Fisica, Università di Trieste, Strada Costiera 11, 34151, Trieste, Italy

While equilibrium interfaces display universal large-scale statistics, interfaces in phase-separated active and driven systems are predicted to belong to distinct non-equilibrium universality classes. Yet, such behavior has proven difficult to observe, with most systems exhibiting equilibrium-like fluctuations despite their strongly non-equilibrium microscopic dynamics.

We introduce an active hard-disk model that is far from equilibrium but lacks self-propulsion. Contrary to self-propelled models, it displays clear non-equilibrium interfacial scaling and allows the first observation of the $|\boldsymbol{q}|$KPZ and wet-$|\boldsymbol{q}|$KPZ universality classes while revealing a new, previously overlooked universality class arising in systems with slow crystalline or glassy dynamics. We also show that hyperuniformity in the bulk suppresses accordingly the fluctuations of the interface. These distinct classes are selected by conservation laws and slow hydrodynamic modes.

Our model can be experimentally realized in vibrated granular systems and offers a new route to study far from equilibrium interfaces.

BP 38.8 Fri 11:45 ZEU/0160

Spontaneous emergence of solitary waves in active flow networks — Rodrigo García[1], •Gonçalo Antunes[2,3], Jens Harting[2,4], Holger Stark[3], Chantal Valeriani[1], Martin Brandenbourger[5], Juan Mazo[1], Paolo Malgaretti[2], and Miguel Ruiz-García[1] — [1]Universidad Complutense de Madrid, Madrid, Spain — [2]Helmholtz-Institut Erlangen-Nürnberg für Erneuerbare Energien (IET-2), Erlangen, Germany — [3]Technische Universität Berlin, Berlin, Germany — [4]Friedrich-Alexander-Universität Erlangen-Nürnberg, Nürnberg, Germany — [5]Aix Marseille Université, Marseille, France

Flow networks like animal/plant vasculature and power distribution grids can encode, transmit, and transform information embodied in the spatial and temporal distribution of their flows. To study these emergent dynamics, we focus on a minimal yet physically grounded system which supports information transmission. The system is composed of a one-dimensional network of active units that pump fluid via phoresis and elastic units that store volume. We coarse-grain the elastohydrodynamics to an active flow network model. We show that the pressure field can develop solitary waves, resulting in the spontaneous creation and transmission of localized packets of information stored in the physical properties of the flow. We show how the shape and speed of these waves depend on the physical parameters. When the elastic units are coupled to their neighbors, a critical size emerges, below which the solitary waves have a finite lifetime.

BP 38.9 Fri 12:00 ZEU/0160

Instabilities and turbulence in extensile swimmer suspensions — •Purnima Jain[1], Navdeep Rana[3], Roberto Benzi[4,5], and Prasad Perlekar[2] — [1]Leibniz-Institut für Polymerforschung Dresden, Germany — [2]Tata Institute of Fundamental Research, Hyderabad, India — [3]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Göttingen, Germany — [4]Hangzhou International Innovation Institute, Beihang University, Hangzhou, China — [5]Department of Physics and INFN, Tor Vergata University of Rome, Via della Ricerca Scientifica 1, Rome, Italy

Swimmers moving in the same direction form an ordered state of living matter. However, this ordered state is not always stable to ambient disturbances. This may lead to chaotic flows characterized by the presence of topological defects, a phenomenon known as active turbulence. The ordered state of microswimmers can be destroyed by an instability created by their swimming stresses. For slightly larger swimmers, where viscous and inertial forces are comparable, an instability due to the fluctuations in the concentration of swimmers destroys the order [1].

In this talk, I will discuss about the instabilities and turbulence in weakly inertial suspensions of extensile swimmers, where the defect turbulent state transitions to the concentration-wave turbulent state. These findings reveal new ways in which living matter may get organized in nature.

[1] P. Jain et. al., Phys. Rev. Lett. 133, 158302 (2024). [2] P. Jain et. al., Phys. Rev. Fluids 10, 114602 (2025).

BP 39: Focus Session: Theoretical Modeling and Simulation of Biomolecular Condensates III (joint session CPP/BP)

Time: Friday 9:30–11:15 Location: ZEU/0260

Topical Talk BP 39.1 Fri 9:30 ZEU/0260

Data-driven modelling of phase-separating intrinsically disordered regions — •Giulio Tesei[1,2], Fatima Kamal Zaidi[3], Shanlong Li[4], Julian O. Streit[1], Jianhan Chen[4], Tanja Mittag[3], and Kresten Lindorff-Larsen[1] — [1]Department of Biology, University of Copenhagen, Copenhagen, Denmark — [2]Department of Biomedical Science, Malmö University, Malmö, Sweden — [3]Department of Structural Biology, St. Jude Children's Research Hospital, Memphis, U.S.A. — [4]Department of Chemistry, University of Massachusetts, Amherst, U.S.A.

Intrinsically disordered regions (IDRs) constitute about one third of the human proteome and play important roles in biological processes. While lacking well-defined 3D structures, IDRs adopt heterogeneous ensembles influenced by multivalent interactions; these same interactions can promote phase separation and contribute to the formation of biomolecular condensates. I will first present CALVADOS, an efficient one-bead-per-residue model optimized on experimental data reporting on IDR conformational properties and extensively validated on both single-chain and phase behavior across diverse sequences. I will then describe how we used large sets of CALVADOS simulations to train machine-learning models that accurately predict single-chain compaction and homotypic phase-separation propensity directly from sequence. Finally, I will introduce a hybrid-resolution model with an atomistic backbone representation that matches the accuracy of CALVADOS for global dimensions and phase separation while also capturing local structure and backbone hydrogen bonding.

BP 39.2 Fri 10:00 ZEU/0260

Born to Condense: Polysomes Drive Co-Translational Condensation of Biomolecular Condensate Proteins — •Zhouyi He, Jens-Uwe Sommer, and Tyler Harmon — Leibniz Institute of Polymer Research, 01069, Dresden, Germany

Biomolecular condensates formed by protein LLPS are ubiquitous and crucial in cells. While the physics and functions of LLPS are well studied, its interplay with protein synthesis, translation, remains largely unexplored. Here we propose Co-Translational Condensation (CTC), a mechanism in which nascent protein chains of polysomes, multiple ribosomes on one mRNA, interact with condensates, localizing translation to condensate surfaces. Using coarse-grained simulations, we show that protein domain architecture dictates the extend of CTC, consistent with a Langmuir adsorption model. Bioinformatic analysis reveals that most condensate-associated proteins have architectures favoring CTC, with strong interaction regions of nascent chains exposed on polysomes. Dynamically, simulation and reaction-diffusion modeling reveal that CTC is kinetically feasible within typical polysome lifetimes, either through large polysomes nucleating new condensates or via diffusion to pre-existing condensates. As a case study, we demonstrate that CTC enhances post-translational modifications by minimizing unmodified intermediates. More broadly, we anticipate CTC may also influence protein folding, misfolding, and signal-integration

latency. Together, our results establish CTC as a general mechanism coupling translation with phase separation, with broad implications for protein evolution, cellular organization, and synthetic biology.

BP 39.3 Fri 10:15 ZEU/0260

Local RNA/protein stoichiometry tunes the electrostatic microenvironment inside reconstituted multicomponent condensates — •Patrick M. McCall — Leibniz Institute for Polymer Research Dresden, Dresden, DE

Biomolecular condensates are demixed phases of biopolymers and, in living cells, commonly form through the associative phase separation of strongly-charged nucleic acids together with protein polyampholytes carrying a weak net charge. While condensates are proposed to offer distinct aqueous environments for the organization of cellular biochemistry, it remains unclear which physical aspects of the microenvironment are relevant and how widely they can vary between condensates. Motivated by the large asymmetry in structural charge between typical condensate components such as RNAs and RNA-binding proteins, we explore here the implications of electroneutrality on the electrostatic environment within model multicomponent condensates. Combining classical Donnan theory with recent measurements of the macromolecular composition of condensates reconstituted from full-length FUS protein and a homopolymeric RNA [McCall et al Nat Chem 2025], we compute the partitioning of salt ions as well as the Donnan potential across the phase boundary. We find that RNA/FUS stoichiometry tunes both co-ion exclusions over a wide range and is coupled to a pH jump across droplet interface. We also find that co-ion exclusion is suppressed by counter-ion condensation and enhanced by non-ideality of un-bound ions. These results provide insight into the range of ionic conditions accessible to a prominent class of biomolecular condensate.

BP 39.4 Fri 10:30 ZEU/0260

Coarse-grained model to study the effects of electric fields on protein interactions — •Agaya Johnson[1], Debes Ray[2,4], Mahnoush Madani[3], Jan Dhont[2,3], Florian Platten[2,3], Kyongok Kang[2], and Sofia Kantorovich[1] — [1]University of Vienna, Kolingasse 14-16, 1090, Vienna, Austria. — [2]nstitute of Biological Information Processing IBI-4, Forschungszentrum Jülich, 52428 Jülich, Germany. — [3]Faculty of Mathematics and Natural Sciences, Heinrich Heine University Düsseldorf, 40225 Düsseldorf, Germany. — [4]Solid State Physics Division, Bhabha Atomic Research Centre, Trombay, Mumbai 400085, India.

Proteins can undergo transition between a wide range of organisational states, from soluble monomers to disordered phases and ordered structures. Experiments have shown that lysozyme in sodium thiocyanate solution can form homogeneous, crystalline, or liquid phases depending on the salt and protein concentrations, and that these phase boundaries can be shifted by applying an electric field. We present a coarse-grained model of lysozyme in sodium thiocyanate solution, representing the protein as an ellipsoid decorated with charged and adhesive surface patches. Counterions and monovalent salt are treated explicitly via excluded-volume repulsion and Coulombic interactions. We investigate (i) how patch size and salt*patch interactions influence ion distributions around a single protein, with and without an external electric field, and (ii) the resulting effective interactions between two proteins as functions of patch properties, salt concentration, and applied electric field.

BP 39.5 Fri 10:45 ZEU/0260

Entropic Clustering of Stickers Induces Aging in Biocondensates — •Hugo Le Roy[1] and Paolo De Los Rios[2] — [1]Department of Civil, Chemical and Environmental Engineering, University of Genoa, Genoa, Italy — [2]Institute of Physics, Ecole Polytechnique Fédérale de Lausanne

Neurodegenerative conditions, such as Parkinson's disease, results from the aggregation of synaptic proteins such as alpha-synuclein. In a healthy presynaptic neuron, effective neurotransmission relies on the spatial organization of synaptic vesicles within phase-separated droplets. These vesicles release neurotransmitters into the synaptic cleft to activate ion-gated channels on the postsynaptic neuron.

In this work, we investigate how this transmission process is impaired during neurodegeneration. Specifically, we focus on the solidification of these phase-separated droplets, a phenomenon described as aging, leading to protein aggregation and associated with the emergence of pathology. We explore the connection between the mechanical properties of the condensates and their microscopic structure using a minimal physical model that treats complex molecules as stickers and spacers. We show that entropy maximization of spacers leads to an effective attractive force between stickers. As a result, our system displays a surprisingly slow relaxation toward equilibrium, reminiscent of glassy systems and consistent with the liquid-to-solid transition observed in aging droplets. By analyzing the clustering dynamics of stickers, we successfully explain the microscopic origin of this glassy relaxation.

BP 39.6 Fri 11:00 ZEU/0260

Biomolecular condensates with a Twist: From Assembly to Arrest — •Mahesh Yadav[1,2] and Lukas Stelzl[2] — [1]Institute of Physics, Johannes Gutenberg University, Mainz — [2]Institute of Molecular Physiology, Johannes Gutenberg University, Mainz

In this work, we investigate the phase behavior of RNA-binding protein Fused in Sarcoma (FUS), whose multivalent and intrinsically disordered regions drive the formation of biomolecular condensates through liquid-liquid phase separation. FUS is a multi-domain protein with arginine-glycine-rich segments (RG-rich domains) that participate in essential cellular proceses. We examine how characteristic sequence motifs such as RGG.. mediate homotypic and nucleic acid binding, and how targeted point mutations (e.g., RtoK, RtoA) disrupt these motifs and impair condensate formation. Using the thermodynamics phase diagram as a benchmark we highlighted the shift in phase separation propensity of the FUS and its variants. Furthermore, we identify the role of key interactions such as electrostatics, π-π and cation-π in nucleic acid binding at atomistic scale. We further characterized the emergent viscoelastic behavior of FUS condensates at multiple scales. We observe that upon mutations the overall dynamics slows down which reflects the gel-like state. Within the condensate interior, protein chains exhibit sub-diffusive dynamics arising from intermittent binding and viscoelastic resistance, mobility at the interface is further suppressed due to anisotropic interactions and interfacial confinement. To quantify these behaviors across relevant scales, we employ multi-resolution simulation models.

BP 40: Cell Mechanics II / Cytoskeleton II

Time: Friday 10:00–11:15 Location: BAR/0205

BP 40.1 Fri 10:00 BAR/0205

The keratin network adapts the nucleus to cellular strain — •Ruben Haag[1], Ruth Meyer[1], Sascha Lambert[2], Hajaani Manoharan[3], Ulrike Rölleke[1], Jens Konrad[3], Bernd Hoffman[3], Rudolf Merkel[3], Stefan Klumpp[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]Institute for the Dynamics of Complex Systems, University of Göttingen, Germany — [3]Institute of Biological Information Processing, Forschungszentrum Jülich, Germany

Intermediate filaments (IFs) comprise one of the cytoskeletal network types and are cell-type specific. In epithelial cells, the keratin IF network connects the desmosomes in the cell membrane with the perinuclear keratin cage, thus forming a mechanical link from the nucleus to the cell membrane. We now ask whether this link transmits mechanical signals from outside the cell to the nucleus. To answer this question, we stretch both epithelial wild type and keratin knockout cells uniaxially and equibiaxially. During stretching, we image cell nuclei and measure their individual deformation to study the influence of the keratin IF network on them. To understand how the keratin network transmits force to the nucleus, we image the keratin network during cell stretching and create a minimal model to mimic how the keratin network deforms the nucleus. Our results suggest that stretching the keratin network is a two-step process: individual keratin bundles are initially pulled straight and are then stretched. Possibly, by this two-step process, the keratin network adapts the nucleus to cellular strain.

BP 40.2 Fri 10:15 BAR/0205

Improving T cell migration and invasion with the Microtubule destabilizing agent Pretubulysin. — •Lukas Schuster[1], Galia Montalvo[1], Reza Shaebani[1], Anna Burgstaller[2], Shweta Nandakumar[1], Rhoda Hawkins[3], Laura Schaedel[1], Bin Qu[4], and Franziska Lautenschläger[1] — [1]Saarland University, Saarbrücken, Germany — [2]Leibniz Institute for New Materials, Saarbrücken, Germany — [3]School of Mathematical and Physical Sciences, University of Sheffield, Sheffield, United Kingdom — [4]Center for Integrative Physiology and Molecular Medicine (CIPMM), Saarland University, Homburg, Germany & Department of Biomedical Sciences, Osnabrück University, Osnabrück, Germany

The immune response depends on the ability of cytotoxic T lymphocytes (CTLs) to migrate and invade into dense 3D environments, such as tumors, and to kill cancer cells. Thus, optimizing the migratory behavior of CTLs is crucial to boost immune response in the treatment against cancer. Here, we focused on the role of destabilized microtubules (MTs) in cell migration. We showed that the disruption of MTs in CTLs with the compound Pretubulysin enhances the infiltration of 3D collagen gels and the killing of target cells. In addition, we confirmed the motile phenotype in 2D and 1D migration assays. We further studied the mechanism of how MT disruption induces cell motility in a theoretical active droplet model. We found enriched actomyosin in the back of CTLs to be linked to a fast and persistent migrating cell.

BP 40.3 Fri 10:30 BAR/0205

Role of mechanics in early immune recognition — •Kheya Sengupta — CINaM, CNRS, Luminy, France.

Our immune system depends on cell scale forces, which are implicated in various phenomena ranging from migration to recognition of pathology or for potentiating diseased cells for killing. Here the focus will be on the first steps of immune recognition which hinges on formation of bonds between specialised receptors and their specific ligands called antigens, where mechanics and forces are thought to be essential to discriminate our own antigens from those indicative of pathology. Intriguingly, unlike for tissue forming cells, the response of T cells is biphasic with the stiffness of their environment when the interaction is mediated through the T-cell receptors (TCRs). However, when the adhesive ligands of integrins are additionally involved, the cellular response becomes monotonic. Based on a mesoscale model, this ligand-specific response can be attributed to molecular properties of a putative link between the ligand/receptor pair and the cytoskeleton. While the molecules linking integrins and actin are known, the equivalent molecules for TCR are yet to be identified. Our model predicts kinetic and mechanical parameters for this putative link, whose existence we prove by mechanical extraction of membrane tubes. We also measure cell scale forces and show that their spatio-temporal patterns depend on chemistry, mechanics and T cell sub-type. Overall, our findings reinforce the proposition that force application provides a general mechanism for immune cells to discriminate mechanosensitive bonds.

BP 40.4 Fri 10:45 BAR/0205

Investigating the interaction between cardiac fibroblasts using ROCS and fluorescence microscopy — •Arash Felekary and Alexander Rohrbach — IMTEK, University of Freiburg, Germany

Cell-cell interaction is essential for cardiac function. Tunneling nanotubes (TNTs), thin actin-based membrane protrusions, mediate long-range interactions by transporting organelles and signaling molecules. To study their role in cardiac fibroblast (FB) interaction, we combined Rotating Coherent Scattering (ROCS) microscopy with fluorescence imaging. ROCS provides label-free, high-contrast recordings at up to 100 Hz and resolves TNTs and lamellipodia across several micrometers above the substrate. Using this approach, we observed a linear correlation between TNT density and lamellipodia motion velocity. Collagen labeling revealed that TNTs frequently align with collagen fibers, suggesting a structural coupling between ECM-linked TNTs and actin-driven protrusions. These observations motivated a spatially resolved simulation of actin filament polymerization and branching, incorporating integrin*collagen interactions and Arp2/3 activation. The model reproduces the experimentally observed increase in lamellipodial velocity with TNT density and supports a mechanism in which TNTs locally amplify integrin-mediated actin remodeling. In this presentation, we discuss how TNTs, lamellipodia, and ECM components cooperatively guide FB interaction, offering new insight into the structural and mechanical coordination underlying cardiac tissue remodeling.

BP 40.5 Fri 11:00 BAR/0205

How to determine cell property distributions from high-throughput experiments via computer simulations — •Stephan Gekle — Biofluid Simulation and Modeling, Theoretische Physik VI, Universität Bayreuth

A central challenge in computer simulations of living cells is the accurate determination of model parameters based on experimental data. This challenge arises since cell properties such as membrane or cytoplasm viscosities are often difficult or impossible to directly measure in an experiment. The current paradigm in the field is to try to find a single "optimal" value for each such property. This approach completely disregards biological heterogeneity and cell-to-cell variability.

Here, we will present a novel inference method which starts from the assumption that *the* optimal value of a cellular property does not exist and that biological reality must rather be reflected by a *distribution* of values for each cell property. We will show how to obtain such property distributions for a realistic and technologically relevant scenario of disease detection via red blood cell membrane alterations.

For this, we will present boundary-integral simulations of red blood cells passing through a microchannel setup corresponding to real-time deformability cytometry (RT-DC) experiments. We will show how the resulting large amounts of scattered experimental data can be combined with our efficient simulations to infer distributions of cytosol and membrane viscosities in a heterogeneous cell population taking full account of cell-to-cell variability.

BP 41: Franco-German Session: Bacterial Biophysics II

Time: Friday 11:30–12:45 Location: BAR/0205

Invited Talk BP 41.1 Fri 11:30 BAR/0205

Probing spatiotemportal electrochemical dynamics on single bacterial cells — Anaïs Biquet-Bisquert[1], Baptiste Carrio[1], Nathan Meyer[1], Thales Fernandes[1], Manouk Abkarian[1], Farida Seduk[2], Axel Magalon[2], •Ashley Nord[1], and Francesco Pedaci[1] — [1]Centre de Biologie Structurale, Université de Montpellier, CNRS, INSERM. Montpellier, France. — [2]Aix Marseille Université, CNRS, Laboratoire de Chimie Bactérienne (UMR7283), IMM, IM2B, 13402 Marseille, France.

Electrochemical gradients across biological membranes are fundamental to cellular bioenergetics. In bacteria, the proton motive force (PMF) drives critical functions such as ATP synthesis and motility. Although historically regarded as temporally and spatially stable, recent studies have revealed dynamic PMF behaviors at single-cell and community levels, which are implicated in processes like intracellular communication and coordination. The bacterial flagellar motor, a rotary nanomachine directly powered by the PMF, provides a unique and sensitive tool for probing these dynamics. By employing light-activated proton pumps and monitoring changes in flagellar motor activity, we perturb and investigate the PMF at the single-cell level. This approach reveals millisecond-scale temporal fluctuations and rapid lateral homogenization of the PMF, reminiscent of the electrotonic potential spread observed in passive neurons.

BP 41.2 Fri 12:00 BAR/0205

Cable Bacteria as Conductive Interfaces: Towards Scalable, Bacteria-derived Electronics — •Hannah Ferenz[1,2], Rakesh Nair[2], and Hans Kleemann[2] — [1]Sächsisches Landesgymnasium Sankt Afra zu Meißen, 01662 Meißen, Germany — [2]Dresden Integrated Center for Applied Physics and Photonic Materials (IAPP) and Institute for Applied Physics, Technische Universität Dresden, 01187 Dresden, Germany.

Cable bacteria (Electrothecera and Electronema spp.) are multicellular filamentous bacteria that perform centimeter-scale electron transport via parallel conductive fibers embedded in their cell envelope, achieving conductivities up to 30 S cm^-1, rivaling synthetic conjugated polymers. We present a robust bioprocess using controlled oxygen-sulfide gradients in natural sediments to produce mechanically coherent, dense biofilms (>10^5 filaments cm^-2). These living conductive networks self-assemble, remain stable for months in-culture, and self-repair via continued growth after damage.

We demonstrate how these bacterial cultures can be used for the development of bio-derived electrodes based on their inherent nickel-sulfur complexes. These results establish cable bacteria as the first genetically tractable, self-growing biological conductor suitable for integration into transient and sustainable electronics, offering a path toward low-cost, environmentally benign bioelectronic interfaces for sensing, energy harvesting, and wearable devices.

BP 41.3 Fri 12:15 BAR/0205

Biophysics of bacterial survival during starvation — •Severin Schink — LMU München, Fakultät für Biologie

Most bacteria live in nutrient-limited states, yet the physical principles that set their lifespan and govern loss of viability during starvation remain poorly understood. I present a framework that links death dynamics, proteome adaptation and competition under starvation in E. coli.

Using time-lapse microscopy, we show that starving cells maintain a plasmolysed state and typically die via a rapid collapse of ion homeostasis. A coarse-grained model of ion transport maps death to a Kramers-like escape process set by nutrient recycling. The model predicts how death rates scale with permeability, ionic strength and cell geometry, and how modified media extend lifespan by lowering maintenance costs.

Proteome-wide analysis reveals that envelope proteins are key for survival: reallocating proteome into the envelope lowers ion permeability and death rate but constrains growth, generating a trade-off between proliferation and starvation survival. Co-cultures of physiologically distinct populations reveal cross-feed feedback: nutrients released by dying cells are recaptured by survivors, amplifying small differences in maintenance and uptake into large fitness advantages. Together, these results identify a minimal set of physical parameters ion gradients, permeability, recycling yield and uptake capacity that control lifespan and selection under starvation.

BP 41.4 Fri 12:30 BAR/0205

Selective inhibition of microbial methanogenesis - a shortcut toward climate change mitigation — •Benedikt Sabass — TU Dortmund — LMU München

In a world that is increasingly affected by climate change, new solutions are urgently needed to reduce greenhouse gas emissions. One of the most effective measures to limit global warming is to reduce methane emissions, a significant proportion of which is produced in the rumen of cattle. Rumen methanogenesis is a complex process that involves various biochemical pathways and cooperation among species from all three domains of life.

A reduction of methane emissions through feed additives has been shown to be feasible in principle, but effective and economical solutions are not yet available. Here, I present an overview of our research on compounds that selectively inhibit methanogenesis. I summarize existing strategies, describe our in-vitro screening assay, and present results from animal tests. Finally, I outline basic open questions regarding the molecular mechanisms of methanogenesis from a biological physics perspective.

BP 42: Closing Talk (joint session CPP/BP/DY)

Time: Friday 13:15–14:00 Location: HSZ/0002

Invited Talk BP 42.1 Fri 13:15 HSZ/0002

Biomolecular Condensates: Challenges for Polymer Physics — •Jens-Uwe Sommer — Leibniz-Insitut für Polymerforschung Dresden, Bereich Theorie der Polymere,Hohe Straße 6, 01069 Dresden, Germany — TU Dresden, Insitut für Theoretische Physik, Zellescher Weg 17, D-01069 Dresden, Germany

Biomolecular condensates (BMCs) constitute an emerging paradigm in the understanding of biological functions. They shift the focus from individual biochemical processes toward the collective behavior of biopolymers, in which phase-separation mechanisms and intrinsically disordered proteins lacking canonical enzymatic roles play central and often decisive functions. Consequently, universal principles of complex (bio)polymer solutions gain relevance, and several classical questions in the physics of living matter can now be revisited from this polymer-physics perspective. In this talk, I will discuss theoretical approaches and concepts that are based on universal principles, with a particular emphasis on current challenges in the field.