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Fachverband Biologische Physik (BP)

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Overview of Invited Talks and Sessions

(Lecture halls HÜL 386, SCH A251, and ZEU 250; Poster P2-EG, P2-1OG, P2-2OG, P2-3OG, and P2-4OG)

Invited Talks

BP 1.1	Mon	9:30–10:00	HÜL 386	**Spontaneous and driven active matter flows** — •Eric Clement
BP 4.5	Mon	10:30–11:00	ZEU 250	**How do lipids and proteins diffuse in cell membranes, and what do the diffusion experiments actually measure?** — •Ilpo Vattulainen
BP 5.1	Mon	15:00–15:30	HÜL 386	**Mirror-enhanced fluorescence for superresolution imaging and spectroscopy** — •Katrin G. Heinze, Hannah S. Heil, Benjamin Schreiber, Markus Sauer
BP 6.4	Mon	15:45–16:15	SCH A251	**Density waves, jamming and dynamic arrest in growing microbial communities** — •Oskar Hallatschek
BP 7.6	Mon	16:30–17:00	ZEU 250	**Optoregulated force application to individual cellular receptors using molecular motors** — •Aránzazu del Campo
BP 12.7	Tue	11:30–12:00	HÜL 386	**Physics of Growth: Another Form of Active Matter** — •Jens Elgeti
BP 13.1	Tue	9:30–10:00	SCH A251	**On another plane: curling and buckling in epithelia** — •Guillaume Charras, Jonathan Fouchard, Tom Wyatt, Ana Lisica, Nargess Khalilgharibi, Pierre Recho, Amsha Proag, Magali Suzanne, Buzz Baum, Alexandre Kabla
BP 14.5	Tue	10:30–11:00	ZEU 250	**Could the cytoskeleton influence liquid-liquid phase separation?** — •Eric Dufresne
BP 21.1	Wed	9:30–10:00	HÜL 386	**Cellular mechanosensing within synthetic 3D extracellular matrices** — •Britta Trappmann
BP 22.7	Wed	11:30–12:00	SCH A251	**The mechanical stability of proteins regulates their translocation rate into the cell nucleus** — •Sergi Garcia-Manyes
BP 23.4	Wed	10:30–11:00	ZEU 250	**Mechanical signalling in cell fate choice** — •Kevin Chalut
BP 26.6	Wed	16:30–17:00	SCH A251	**3 D Classification of Red Blood Cells in microchannels** — •Christian Wagner
BP 28.1	Wed	15:00–15:30	ZEU 250	**Eavesdropping on fluctuation-driven transport in living matter** — •Matthias Weiss
BP 30.1	Thu	9:30–10:00	HÜL 386	**Active behaviors of cellular monolayers.** — •Benoit Ladoux
BP 31.7	Thu	11:30–12:00	SCH A251	**Predicting Protein and RNA Structures via data inference: from Potts models to machine learning** — •Alexander Schug
BP 33.5	Thu	10:30–11:00	ZEU 250	**Atomistic ensembles of proteins and soft matter complexes from MD simulations and solution scattering data** — Milos T Ivanovic, Markus R Hermann, •Jochen S Hub
BP 35.4	Thu	15:45–16:15	HÜL 386	**Super-resolution microscopy with DNA molecules** — •Ralf Jungmann
BP 36.4	Thu	15:45–16:15	SCH A251	**Mechanical properties of intermediate filaments at high strains** — Johanna Forsting, Julia Kraxner, Charlotta Lorenz, Anna Schepers, •Sarah Köster
BP 37.1	Thu	15:00–15:30	ZEU 250	**Growth, death, and adaptation of bacterial cells: a quantitative analysis** — •Ulrich Gerland
BP 38.1	Fri	9:30–10:00	HÜL 386	**Physical phenotyping of cells in microfluidic systems** — •Jochen Guck

BP 42.1	Fri	12:30–13:15	HSZ 02	**Physics of active droplets** — •Frank Jülicher

Invited talks of the joint symposium SYSD

See SYSD for the full program of the symposium.

SYSD 1.1	Mon	9:30– 9:55	HSZ 02	**Disentangling transport in topological insulator thin films down to the nanoscale** — •Felix Lüpke
SYSD 1.2	Mon	9:55–10:20	HSZ 02	**Spintronics with Terahertz Radiation: Probing and driving spins at highest frequencies** — •Tom Sebastian Seifert, Tobias Kampfrath
SYSD 1.3	Mon	10:20–10:45	HSZ 02	**Non-radiative voltage losses in organic solar cells** — •Johannes Benduhn
SYSD 1.4	Mon	10:45–11:10	HSZ 02	**Multivalent ions for tuning the phase behaviour of protein solutions** — •Olga Matsarskaia
SYSD 1.5	Mon	11:10–11:35	HSZ 02	**Network Dynamics under Constraints** — •Malte Schröder
SYSD 1.6	Mon	11:35–12:00	HSZ 02	**Exciton spectroscopy of van der Waals heterostructures** — •Philipp Nagler

Invited talks of the joint symposium SYES

See SYES for the full program of the symposium.

SYES 1.1	Thu	9:30–10:00	HSZ 02	**Understanding the physical variables driving mechanosensing** — •Pere Roca-Cusachs
SYES 1.2	Thu	10:00–10:30	HSZ 02	**Mechanics of life: Cellular forces and mechanics far from thermodynamic equilibrium** — •Timo Betz
SYES 1.3	Thu	10:30–11:00	HSZ 02	**A hydrodynamic approach to collective cell migration in epithelial tissues** — •Jaume Casademunt
SYES 1.4	Thu	11:15–11:45	HSZ 02	**The spindle is a composite of two permeating polar gels** — David Oriola, Benjamin Dalton, Franziska Decker, Frank Julicher, •Jan Brugues
SYES 1.5	Thu	11:45–12:15	HSZ 02	**Adding magnetic properties to epitaxial graphene** — •Rodolfo Miranda
SYES 2.1	Thu	15:00–15:30	HSZ 01	**Interactions in assemblies of surface-mounted magnetic molecules** — •Wolfgang Kuch
SYES 2.2	Thu	15:30–16:00	HSZ 01	**Towards phononic circuits based o optomechanics** — •Clivia M. Sotomayor-Torres
SYES 2.3	Thu	16:00–16:30	HSZ 01	**Optical properties of 2D materials and heterostructures** — •Janina Maultzsch
SYES 2.4	Thu	16:45–17:15	HSZ 01	**Bringing nanophotonics to the atomic scale** — •Javier Aizpurua
SYES 2.5	Thu	17:15–17:45	HSZ 01	**Infrared signatures of the coupling between vibrational and plasmonic excitations** — •Annemarie Pucci

Invited talks of the joint symposium SYDW

See SYDW for the full program of the symposium.

SYDW 1.1	Thu	15:00–15:30	HSZ 02	**Statics and Dynamics of Soft Wetting** — •Bruno Andreotti
SYDW 1.2	Thu	15:30–16:00	HSZ 02	**Modelling imbibition, dynamic wetting and evaporation on structured surfaces and porous coatings** — •Tatiana Gambaryan-Roisman, Noemi Ghillani
SYDW 1.3	Thu	16:00–16:30	HSZ 02	**Droplets on shaped liquid and electrically switchable surfaces** — •Glen McHale
SYDW 1.4	Thu	16:45–17:15	HSZ 02	**Liquid-liquid Dewetting: From Spinodal Breakup to Dewetting Morphologies and Rates** — •Ralf Seemann, Stefan Bommer, Roghayeh Shiri, Sebastian Jachalski, Dirk Peschka, Barbara Wagner
SYDW 1.5	Thu	17:15–17:45	HSZ 02	**Droplet durotaxis and engulfment on yielding viscoelastic gels** — •Anne Juel

Sessions

BP 1.1–1.11	Mon	9:30–13:00	HÜL 386	**Active Matter I (joint session BP/DY/CPP)**
BP 2.1–2.10	Mon	9:30–12:45	SCH A251	**Focus: Phase Separation in Biological Systems I (joint session BP/CPP)**
BP 3.1–3.7	Mon	9:30–11:15	ZEU 114	**Biopolymers, Biomaterials and Bioinspired Functional Materials (joint session CPP/BP)**
BP 4.1–4.11	Mon	9:30–13:00	ZEU 250	**Membranes and Vesicles (joint session BP/CPP)**
BP 5.1–5.7	Mon	15:00–17:15	HÜL 386	**Bioimaging and Biospectroscopy I**
BP 6.1–6.7	Mon	15:00–17:15	SCH A251	**Statistical Physics of Biological Systems I (joint session BP/DY)**
BP 7.1–7.8	Mon	15:00–17:30	ZEU 250	**Biomaterials and Biopolymers (joint session BP/CPP)**
BP 8.1–8.20	Mon	17:30–19:30	P2/1OG	**Poster I**
BP 9.1–9.27	Mon	17:30–19:30	P2/2OG	**Poster II**
BP 10.1–10.32	Mon	17:30–19:30	P2/3OG	**Poster III**
BP 11.1–11.11	Tue	9:30–13:15	GÖR 226	**Data analytics for dynamical systems I (Focus Session joint with DY and BP) (joint session SOE/DY/CPP/BP)**
BP 12.1–12.11	Tue	9:30–13:00	HÜL 386	**Active Matter II (joint session BP/DY/CPP)**
BP 13.1–13.10	Tue	9:30–12:45	SCH A251	**Cell Mechanics I**
BP 14.1–14.10	Tue	9:30–12:45	ZEU 250	**Focus: Phase Separation in Biological Systems II (joint session BP/CPP)**
BP 15.1–15.8	Tue	14:00–16:00	ZEU 160	**Active Matter III (joint session DY/BP/CPP)**
BP 16.1–16.19	Tue	14:00–16:00	P2/EG	**Poster IV**
BP 17.1–17.31	Tue	14:00–16:00	P2/1OG	**Poster V**
BP 18.1–18.27	Tue	14:00–16:00	P2/2OG	**Poster VI**
BP 19.1–19.32	Tue	14:00–16:00	P2/3OG	**Poster VII**
BP 20.1–20.26	Tue	14:00–16:00	P2/4OG	**Poster VIII**
BP 21.1–21.11	Wed	9:30–13:00	HÜL 386	**Cell Adhesion and Migration, Multicellular Systems I**
BP 22.1–22.11	Wed	9:30–13:00	SCH A251	**Single Molecule Biophysics (joint session BP/CPP)**
BP 23.1–23.8	Wed	9:30–12:45	ZEU 250	**Focus: Physics of Stem Cells**
BP 24.1–24.9	Wed	10:00–12:30	ZEU 160	**Active Matter IV (joint session DY/CPP/BP)**
BP 25.1–25.8	Wed	15:00–17:15	HÜL 386	**Cell Mechanics II**
BP 26.1–26.8	Wed	15:00–17:30	SCH A251	**Focus: Biological Cells in Microfluidics I**
BP 27.1–27.9	Wed	15:00–17:45	ZEU 160	**Fluid Physics of Life (joint session DY/BP)**
BP 28.1–28.8	Wed	15:00–17:30	ZEU 250	**Statistical Physics of Biological Systems II (joint session BP/DY)**
BP 29	Wed	18:00–19:00	HÜL 386	**Annual General Assembly**
BP 30.1–30.11	Thu	9:30–13:00	HÜL 386	**Cell Adhesion and Migration, Multicellular Systemadhesion and Migration, Multicellular Systems II**
BP 31.1–31.11	Thu	9:30–13:00	SCH A251	**Computational Biophysics (joint session BP/CPP)**
BP 32.1–32.10	Thu	9:30–12:45	ZEU 118	**Focus Session: Nonlinear Dynamics of the Heart I (joint session DY/BP)**
BP 33.1–33.11	Thu	9:30–13:00	ZEU 250	**Protein Structure and Dynamics**
BP 34.1–34.6	Thu	14:00–15:45	ZEU 118	**Nonlinear Dynamics of the Heart II (joint session DY/BP)**
BP 35.1–35.8	Thu	15:00–17:30	HÜL 386	**Bioimaging and Biospectroscopy II**
BP 36.1–36.8	Thu	15:00–17:30	SCH A251	**Cytoskeletal Filaments I**
BP 37.1–37.8	Thu	15:00–17:30	ZEU 250	**Systems Biology, Evolution and Neural Networks I**
BP 38.1–38.7	Fri	9:30–12:00	HÜL 386	**Focus: Biological Cells in Microfluidics II**
BP 39.1–39.7	Fri	9:30–12:00	SCH A251	**Cytoskeletal Filaments II**
BP 40.1–40.8	Fri	9:30–12:00	ZEU 250	**Systems Biology, Evolution and Neural Networks II**
BP 41.1–41.6	Fri	10:00–11:30	ZEU 160	**Active Matter V (joint session DY/BP/CPP)**
BP 42.1–42.1	Fri	12:30–13:15	HSZ 02	**Closing Talk (joint session BP/DY/CPP)**

Annual General Meeting of the Biological Physics Division

Wednesday 18:00–19:00 HÜL 386

- Bericht
- Verschiedenes

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

Time: Monday 9:30–13:00 Location: HÜL 386

Invited Talk BP 1.1 Mon 9:30 HÜL 386

Spontaneous and driven active matter flows — •Eric Clement — PMMH-ESPCI-Sorbonne University, Paris, France

Understanding the individual and the macroscopic transport properties of motile micro-organisms in complex environments is a timely question, relevant to many ecological, medical and technological situations. At the fundamental level, this question is also receiving a lot of attention as fluids loaded with swimming micro-organisms has become a rich domain of applications and a conceptual playground for the statistical physics of active matter. The existence of microscopic sources of energy borne by the motile character of micro-swimmers is driving self-organization processes at the origin of original emergent phases and unconventional macroscopic properties leading to revisit many standard concepts in the physics of suspensions. In this presentation, I will report on a recent exploration on the question of collective motionspontaneous formation, in relation with the rheological response of active suspensions. I will also present new experiments showing how the motility of bacteria can be controlled such as to extract work macroscopically.

BP 1.2 Mon 10:00 HÜL 386

Light-regulated motility of microbial suspensions induces phase separation in confinement — •Alexandros Fragkopoulos[1], Jeremy Vachier[1], Johannes Frey[1], Flora-Maud Le Menn[1], Michael Wilczek[1], Marco Mazza[1,2], and Oliver Bäumchen[1] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), D-37077 Göttingen, Germany — [2]Department of Mathematical Sciences, Loughborough University, Loughborough, Leicestershire LE11 3TU, United Kingdom

A highly concentrated suspension of self-propelled particles can form large-scale concentration patterns, separating into regions of high and low particle concentrations, due to the activity of the particles and their mutual interactions. However, such a phenomenon has so far been rarely seen in biological systems. Here, we present that a sufficiently concentrated suspension of *Chlamydomonas reinhardtii* cells, a model organism of puller-type microswimmers, forms such large-scale aggregations under confinement in specific light conditions. We find that cell-cell interactions need to be dominated by collisions for the aggregation to form, resulting to a generic coupling of the cell's motility and local cell density. In addition, the cell's motility decreases with decreasing light intensity, which regulates the cell aggregation. Through active Brownian particle simulations, we show that for our system the change of the motility is sufficient to induce the aggregation. Finally, we provide evidence that the photosynthetic activity controls the cell's motility, and consequentially, the separation of the active suspension into regions of high and low cell density.

BP 1.3 Mon 10:15 HÜL 386

Motility induced transport in microbial environments — •Jayabrata Dhar, Arkajyoti Ghoshal, and Anupam Sengupta — Physics of Living Matter Group, Department of Physics and Materials Science, University of Luxembourg, 162 A, Avenue de la Faencerie, L-1511, Luxembourg City, Luxembourg

Despite their minuscule size, microbes mediate a range of processes in ecology, medicine and industry due to high local concentrations. Studies in aquatic ecosystems have demonstrated nutrient mixing via bioconvection by high concentrations of motile microbes [1] potentially impacts species distributions in natural settings. However, to date, we lack a systematic framework to capture the role of microbial traits (for instance, morphology or motility) on the onset and progression of bioconvection. Here, using different bloom-forming algal species as model organisms, we study how microbial traits underpin the onset of bioconvection and modulate mass transfer due to local density changes. Combining micro-PIV analysis of dispersed particles and auto-fluorescence imaging of algal cells, we quantify the emergent transport properties in real-time, revealing a plume-driven primary convective field. Interestingly, our results further capture relatively weak, secondary eddies that create local mixing patches with short lifetimes. Thus, bioconvection may alter the chemical environment of the microbes through distinct modes, impacting the distribution of nutrients, toxins or secondary metabolites, all of which could be vital for large-scale phenomena like harmful algal blooms.

[1] T. Sommer, et al., Geophysical Research Letters 44, 9424, 2017.

BP 1.4 Mon 10:30 HÜL 386

Reactivation of isolated axonemes by light-driven ATP regeneration system — Raheel Ahmed[1], Christin Kleinberg[2], Tanja Vidakovich-Koch[2], Kai Sundmacher[2], Eberhard Bodenschatz[1], and •Azam Gholami[1] — [1]MPI for Dynamics and Self-Organization — [2]MPI for Dynamics of Complex Technical Systems

Cilia and flagella are slender cellular appendages whose regular beating pattern pumps fluids, for example the mucus in mammalian airways, or propels unicellular organisms such as the green algae Chlamydomonas reinhardtii. Cilia and flagella have a microtubule-based structure called axoneme which performs whip-lash-like motion to provide motility. This oscillatory motion is powered by dynein molecular motors that generate active stresses for ciliary beat in the presence of ATP. In this work, we have successfully integrated light-driven energy module for continuous generation of ATP. This light-driven ATP regeneration system is built through bottom-up assembly of FOF1- ATP synthase and bacteriorhodopsin into two different types of artificial hybrid membranes based on a diblock copolymer (PBd-PEO) and a graft copolymer (PDMS- g-PEO). After illumination of the energy module with light, we mixed it with axonemes isolated from Chlamydomonas reinhardtii and observed actively beating axonemes for many hours. Interestingly, the axonemes beat even at low concentrations of ATP well below 50 μM.

BP 1.5 Mon 10:45 HÜL 386

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

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

30 min. coffee break

BP 1.6 Mon 11:30 HÜL 386

Synthetic minimal active cilia — •Isabella Guido — Max Planck Institute for Dynamics and Self-Organization, Goettigen, Germany

Cilia and flagella are microtubule based filamentous organelles that protrude into the extracellular environment from the surface of many cells for promoting fluid transport or propelling organisms in fluids by producing rhythmic bending waves. The main contribution to their beating is due to motor proteins that drive sliding of the microtubule doublets. However, the fundamental mechanism of the motor-microtubule interaction is still a puzzle. Here we present a synthetic minimal active cilium, a two-filaments system, in which the beat is initiated by a buckling instability in one of the filaments. The system presents continuous beating through association and dissociation cycles, similar to the sliding of a pair of doublet microtubules observed in a Chlamydomonas flagellum. The analysis of the conformational dynamics gives us a quantification of dynein force, motor density and bending energy. We develop a theoretical model to study the dynamics of active elastic filaments induced by internal force in which the attachment and detachment kinetics of motors play as important a role as their force generation. The active stroke of the synthetic cilium

occurs due to a buckling instability between two clamped filaments, while the recovery stroke follows a "catastrophic failure" of the bound motors.

This work is in collaboration with Prof. Ramin Golestanian and Dr. Andrej Vilfan.

BP 1.7 Mon 11:45 HÜL 386

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

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

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

BP 1.8 Mon 12:00 HÜL 386

Self-organization of active surfaces — •Alexander Mietke[1,2,3,4,7], V. Jemseena[5], K. Vijay Kumar[5], Ivo F. Sbalzarini[2,3,4,6], and Frank Jülicher[1,3,6,] — [1]MPI for the Physics of Complex Systems — [2]Faculty of Computer Science, TU Dresden — [3]Center for Systems Biology Dresden — [4]MPI of Molecular Cell Biology and Genetics — [5]ICTS-TIFR — [6]Cluster of Excellence PoL, TU Dresden — [7]Department of Mathematics, MIT, Cambridge, MA

Self-organization of morphogenetic events often arises through a feedback loop in which active forces, by inducing deformations and material flows, indirectly affect their own mechano-chemical regulation. In recent years, the existence of generic mechano-chemical patterning mechanisms in simple, fixed geometries has been demonstrated theoretically and experimentally. However, the interplay of mechano-chemical processes with the surface geometry remains to be explored. In our work, we employ the theory of active gels in complex geometries to study the properties of dynamically evolving active surfaces. Within those surfaces, diffusive and advective transport processes can redistribute molecules responsible for local stress generation. This resembles the interplay between active forces, the shape changes they imply and the effects this has on their regulation. Within our framework, a contractile ring formation, as well as the peristaltic motion of active tubular structures can be understood as natural emergent phenomena. Our approach provides novel opportunities to explore different scenarios of mechano-chemical self-organization and can help to better understand the role of shape as a regulatory element in morphogenetic processes.

BP 1.9 Mon 12:15 HÜL 386

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

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

BP 1.10 Mon 12:30 HÜL 386

Fast vs. gradual death in assemblies of immotile growing cells — •Yoav G. Pollack, Philip Bittihn, and Ramin Golestanian — Max Planck Institute for Dynamics and Self-Organization (MPI-DS), Göttingen, Germany

Cell life-cycle processes such as growth, division and death, often all happen on a similar timescale, as do the resultant mechanical and dynamical responses of the cell assembly (such as a colony, biofilm or tissue). An archetypal example is *E. Coli* where growth, division and the subsequent relative motion of the daughter cells all happen at roughly the same rate. However there are also examples of another type of system showing abrupt processes, including 'snapping' cell division in *Actinobacteria* and 'explosive' bacterial lysis.

Here we test whether going from the first type of system to the other by introducing a second *fast* timescale in one of the microscopic processes can affect the macroscopic mechano-dynamics, such as the homeostatic pressure. Specifically we simulate a closed 1D channel of cells that grow and divide to fill up the channel and are removed (via death or extrusion) when pressure builds up. We focus on varying the timescale of the cell removal process, keeping growth and division timescales fixed. We show a clear distinction in the macroscopic system properties between abrupt vs. gradual cell removal, such as a significant increase in the homeostatic pressure.

BP 1.11 Mon 12:45 HÜL 386

Simulations of an active surface immersed in viscous fluids — •Lucas D. Wittwer and Sebastian Aland — Faculty of Informatics / Mathematics, University of Applied Science Dresden, Germany

Mechanochemical processes play a crucial role during morphogenesis, the formation of complex shapes and tissues out of a single cell. On the cellular level, the actomyosin cortex governs shape and shape changes. This thin layer of active material underneath the cell surface exerts an active contractile tension, the strength of which being controlled by the concentration of force-generating molecules. Advective transport of such molecules leads to a complex interplay of hydrodynamics and molecule concentration which gives rise to pattern formation and self-organized shape dynamics.

In this talk, we present a novel numerical model to simulate an active surface immersed in viscous fluids. We show the resulting patterning and cell shape dynamics for different parameter configurations as well as the flow profiles in the surrounding fluids and compare it to results from other models.

BP 2: Focus: Phase Separation in Biological Systems I (joint session BP/CPP)

Time: Monday 9:30–12:45 Location: SCH A251

BP 2.1 Mon 9:30 SCH A251

ATP-arrested phase separation of an abundant nuclear protein — •Davide Michieletto — University of Bath

The formation and regulation of phase separated condensates is an important and ubiquitous process in biology. However, the biological functions of these condensates and how they are regulated, i.e. assembled and disassembled in vivo, are still poorly understood

I will present our recent work on an abundant nuclear protein called Scaffold Attachment Factor A, or SAF-A, that is involved in organizing the genome. It contains an intrinsically disordered RNA binding domain and an ATP-binding and hydrolysis domain. We discovered that the RGG domain of this protein undergoes phase separation in the nucleus upon transcriptional inhibition and that the size of the droplets can be controlled by tuning the amount arginine/lysine residues in the RGG domain and, more importantly, the coarsening of these droplets is arrested when the RGG domain is fused with the ATPase domain.

To explain our findings, we propose a non-equilibrium extension of the classical Model B equations in which AAA-RGG fragments can switch between binding and non-binding states.

In summary, we provide evidence that not only does SAF-A undergo phase separation but we are able to show that this behavior can be regulated using an ATP-switch linked to its functional role in the nucleus.

BP 2.2 Mon 9:45 SCH A251

Experimental measurement of the phase diagram of liquid-liquid phase separating proteins and peptides — •Emmanouela Filippidi[1,2], Anthony Hyman[1], and Frank Jülicher[2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Pfotenhauerstrasse 108

Peptides and proteins of a variety of organisms are known to undergo liquid-liquid phase separation to a dense and a dilute phase under certain conditions of temperature, pH, salt and macromolecular concentrations. Our goal is to create and study model peptide systems with sequences inspired by proteins in order to study the effect of amino acid sequence to phase separation. Herein, we will present parallel studies of both a protein, FUS, and simplified peptides of known, repetitive sequences.

As our first step, we will present quantitative measurements of both branches of the binodal curves of the phase diagrams obtained via quantitative phase imaging microscopy. We shall focus on how the multiplicity (multivalency) of pi-cation interactions at constant linear density affects their phase diagrams.

BP 2.3 Mon 10:00 SCH A251

Measuring protein concentrations in biomolecular condensates via quantitative phase microscopy — •Patrick M McCall[1,2], K Kim[3], J Wang[1], AW Fritsch[1], A Poznyakovskiy[1], B Diederich[4], M Kreysing[1], R Heintzmann[4], J Guck[3], S Alberti[3], J Brugués[1,2], and AA Hyman[1] — [1]MPI-CBG, Dresden — [2]MPI-PKS, Dresden — [3]TU Dresden — [4]Leibniz IPhT, Jena

Many compartments in eukaryotic cells are protein-rich biomolecular condensates formed via phase separation from the cyto- or nucleoplasm. Although knowledge of condensate composition is essential for a full description of condensate properties and potential functions, measurements of composition pose a number of technical challenges. To address these, we use quantitative phase microscopy and optical diffraction tomography to measure the refractive index of model condensates, from which the protein concentration may be inferred. Here, model condensates are formed by phase separation of purified protein constructs derived from the primarily disordered RNA-binding domain (RBD) of TAF15. Surprisingly, we find that phase separation of TAF15(RBD) is attenuated only weakly by salt (0.05-3 M KCl) or temperature (10-50 °C), suggesting that Coulombic and entropic interactions, respectively, play only minor roles in controlling the phase equilibria. Interestingly, we also find that partition coefficients determined by fluorescence microscopy dramatically underestimate protein concentrations in condensates. A simple model including inner filter and excited-state saturation effects suggests that the discrepancy stems primarily from reduced fluorescence quantum yields in condensates.

BP 2.4 Mon 10:15 SCH A251

Phase separation in protein solutions – a colloid physics' perspective — •Florian Platten and Stefan U. Egelhaaf — Condensed Matter Physics Laboratory, Heinrich Heine University, Düsseldorf, Germany

Protein solutions undergoing phase separation are relevant for physiological functions (e.g., intracellular compartmentalization), disease pathology (e.g., cataract and amyloid plaque formation), biopharmaceutical formulations (e.g., their solubility and aggregation stability), the tunable design of soft solids (e.g., food gels) as well as a non-classical route to crystallization. The metastable liquid-liquid phase separation of lysozyme solutions was studied in terms of their phase coexistence temperatures and static structure factors $S(Q)$. If scaled by a property of dilute solutions, namely the second virial coefficient B_2, instead of temperature, the experimental binodals fall onto a master curve, which is similar to that of an adhesive hard-sphere fluid; i.e., the extended law of corresponding states holds for protein solutions. Accordingly, $S(Q)$ of moderately concentrated solutions can be described by B_2 using Baxter's model. The interactions between protein molecules – even in test tubes – are highly complex, i.e., patchy and directional. Nevertheless, coarse-grained colloid models provide effective descriptions. These simple models facilitate further insights into the physics of protein phase separation.

BP 2.5 Mon 10:30 SCH A251

Kinetics and dynamics of LLPS in protein solutions exhibiting a LCST phase behavior probed by XPCS — •Anastasia Ragulskaya[1], Anita Girelli[1], Nafisa Begam[1], Hendrik Rahmann[2], Fabian Westermeier[3], Fajun Zhang[1], Christian Gutt[2], and Frank Schreiber[1] — [1]Universität Tübingen, Germany — [2]Universität Siegen, Germany — [3]DESY, Hamburg

Kinetics and dynamics of liquid-liquid phase separation (LLPS) are usually intimately intertwined. We investigated a model system of bovine serum albumin (BSA) with YCl_3 which shows a lower critical solution temperature (LCST) phase behavior [1]. The dynamics of spinodal decomposition after a temperature jump was studied by X–ray photon correlation spectroscopy (XPCS) and the kinetics was probed simultaneously by ultra-small angle X–ray scattering (USAXS). The analysis of two-time correlation functions obtained from XPCS shows a two-mode behavior of the dynamics. The slow mode has a relaxation rate behavior similar to the kinetic one and corresponds to the transition from a density fluctuation to a coarsening stage. The relaxation time of the fast mode has a transition from an exponential growth to a monotonic increase with a modulation as a function of time, corresponding to the further growth of domains. Results are supported by Cahn-Hilliard simulations [2]. The work demonstrates the successful use of XPCS in USAXS-mode approach to study evolution of the domains during LLPS .

[1] O.Matsarskaia et. al., Phys. Chem. B, 120 (2016), 5564.
[2] D. Sappelt, J. Jäckle, Physica A , 240 (1997) , 453.

BP 2.6 Mon 10:45 SCH A251

Quantitative droplet FRAP based on physical principles — •Lars Hubatsch[1,2], Louise Jawerth[1,2], Anthony Hyman[2], and Christoph Weber[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Fluorescence recovery after photobleaching (FRAP) is used to characterize a range of dynamic processes, for example binding kinetics and mobility of intracellular proteins, and recently liquid-liquid phase separation (LLPS) in vitro and in vivo. To gain an understanding of the relevant molecular mechanisms, data analysis must be based on the underlying physics. Strikingly, for FRAP of phase-separated droplets, no physical model from first principles has been derived, which severely restricts data interpretation. Here, we first derive a FRAP model from the physical principles underlying LLPS. Second, we use the full spatio-temporal imaging data within the droplet for fitting. This results in the following improvements: we can (i) distinguish the time scales of exchange through the droplet interface (set by bulk diffusion and boundary kinetics) from diffusion inside the droplet, (ii) quantify the impact of the interface (iii) provide improved measurements for several biologically important proteins, and (iv) use our analysis framework to explore several multi-component scenarios. Finally, we provide experimental guidelines for highly quantitative in vitro FRAP, e.g. the necessity to perform a full bleach to allow robust analysis and routines to allow spatio-temporal fitting.

30 min. coffee break

BP 2.7 Mon 11:30 SCH A251

Stress granule formation via ATP depletion-triggered phase separation — Jean David Wurtz and •Chiu Fan Lee — Imperial College, London, U.K.

Stress granules (SG) are droplets of proteins and RNA that form in the cell cytoplasm during stress conditions. We consider minimal models of stress granule formation based on the mechanism of phase separation regulated by ATP-driven chemical reactions. Motivated by experimental observations, we identify a minimal model of SG formation triggered by ATP depletion. Our analysis indicates that ATP is continuously hydrolysed to deter SG formation under normal conditions, and we provide specific predictions that can be tested experimentally.

Reference: JD Wurtz and CF Lee (2018) New Journal of Physics 20, 045008.

BP 2.8 Mon 12:00 SCH A251

Sequence dependent gelation, accumulation and sedimentation — •Alexandra Kühnlein[1], Christof Mast[1], Hannes Mutschler[2], and Dieter Braun[1] — [1]Biophysics and Center for

NanoScience, LMU Munich, Amalienstrasse 54, 80799 München — [2]Max Planck Institute of Biochemistry, Martinsried, Germany

The origins of biological information constitutes a major challenge for understanding the origins of life. Under Darwinian evolution, a localized, homogeneous sequence phenotype is selected. How could this state of matter emerge from random sequence mixtures?

To jumpstart Darwinian evolution, a random mixture of sequences have to show physical phenotypes, most likely in non-equilibrium settings. We show preliminary results that indicate a self-selection of sequences by cooperative binding.

Eight 80mer sequences, derived from tRNA to implement a hybridization-based replicator, revealed upon cooling a sharp transition to hydrogels with the size of millimeters. These agglomerates, if broken up by flow, sediment under gravity. If one of the eight sequences are missing, no significant gelation and no sedimentation is found.

Secondly, we subjected random sequences to steep thermal gradients where convection and thermophoresis lead to a size-dependent accumulation. By sequencing, we found that the initial random sequence pool accumulated end sequences with a higher affinity for binding. We speculate that in the long run, only a small number of cooperative binding sequences could remain in such a non-equilibrium setting.

BP 2.9 Mon 12:15 SCH A251

Shedding light on biomolecular condensates: optical trapping of protein & RNA liquids — •Marcus Jahnel[1,2], Titus M. Franzmann[1,2], Simon Alberti[1,2], and Stephan W. Grill[1,2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]BIOTEC / TU Dresden, Dresden, Germany

Membraneless organelles formed by liquid-liquid phase separation of proteins and RNAs influence vital aspects of cellular biology. However, the transient nature and broad chemical combinatorics of the underlying weak molecular interactions makes these materials challenging to study and reason about, requiring new approaches to make progress.

Optical tweezers use changes in light's linear momentum to measure or apply tiny molecular forces and displacements accurately. This ability has revolutionized single-molecule experiments but also bears great potential to unravel the physics of mesoscopic biomolecular assemblies.

Here, we demonstrate the use of high-resolution dual-trap optical tweezers to study various aspects of biomolecular condensation phenomena, bridging the scales from the single-molecule level to microscopic collections and multi-component mixtures of intrinsically disordered proteins and RNAs. Using this approach, we highlight the rules governing the liquid-to-solid transition in prion-like protein liquids and the influence of RNA-to-protein ratios on the material properties of compositionally complex biomolecular condensates.

BP 2.10 Mon 12:30 SCH A251

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

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

BP 3: Biopolymers, Biomaterials and Bioinspired Functional Materials (joint session CPP/BP)

Time: Monday 9:30–11:15 Location: ZEU 114

BP 3.1 Mon 9:30 ZEU 114

Dichroic FTIR spectrocopy on recombinant spider silk films at texturised silicon substrates — Mirjam Hofmaier[1,2], Birgit Urban[1], Sarah Lentz[3], Thomas Scheibel[3], Andreas Fery[1,2], and •Martin Müller[1,4] — [1]Leibniz-Institut für Polymerforschung Dresden e.V., Institute of Physical Chemistry and Polymer Physics, D-01069 Dresden — [2]Technische Universität Dresden, Chair of Physical Chemistry of Polymeric Materials, D-01062 Dresden — [3]Universität Bayreuth, Chair of Biomaterials, D-95447 Bayreuth, Germany — [4]Technische Universität Dresden, Chair of Macromolecular Chemistry, D-01062 Dresden

Films of recombinant spider silk protein eADF4 were deposited onto unidirectionally scratched silicon substrates (Si-sc) and analysed by dichroic transmission (T-) and ATR-FTIR spectroscopy addressing conformation and orientation. eADF4 films (d=0-200 nm) were casted from hexafluoroisopropanol solutions onto Si-sc. Both FTIR methods revealed low b-sheet (<10%) and high random coil content (>80%) based on Amide I band analysis. Dichroic ratios R of all Amide I components close to those of isotropic samples were found by T- and ATR-FTIR indicating no eADF4 orientation. Whereas, eADF4 films after swelling in MeOH vapor revealed higher b-sheet (>30%) and lower random coil content (<60%). By ATR-FTIR high R values for the Amide I component at 1696 cm-1 assigned to antiparallel b-sheet structure were found indicating out-of-plane orientation of b-sheets, which increased with decreasing thickness. Whereas, by T-FTIR isotropic R values indicating no in-plane orientation of b-sheets were found.

BP 3.2 Mon 9:45 ZEU 114

Keratin films from human nail and hair as artificial nail plate model — •Kim Thomann, Andreas Späth, and Rainer H. Fink — Lehrstuhl für Physikalische Chemie II, Friedrich-Alexander Universität Erlangen-Nürnberg, Erlangen, Germany

Human fingernails can be studied ex vivo only in form of clippings which offer limited insight as they do not necessarily reflect the behavior of the whole nail. Keratin films (KFs) can potentially serve as human fingernail substitute which is especially relevant for the medical and beauty sector. In order to model the nail's adhesive characteristics, films from keratin extracted from human hair and nails were produced [1]. With the fingernail serving as reference, the KFs were characterized with a number of methods, including AFM, contact angle (CA) measurements, XPS, ATR-FTIR and Raman spectroscopy. In terms of composition, KFs show a good resemblance. The topography however differs as the films are much smoother than the micro-structured nail. CA measurements revealed that the surface free energy was in the same range, but the polar component was much stronger for the KFs compared to the fingernail. KFs matching the nail's microstructure represents one approach to achieve a more satisfying model, potentially realized by micro-contact printing.

[1] Lusiana, et al., Eur. J. Pharm. Biopharm. 2011, 78, 432

BP 3.3 Mon 10:00 ZEU 114

Tracing the film formation of biotemplated titania nanostructures during spray coating with in situ GIXS techniques — •Julian E. Heger[1], Wei Chen[1], Calvin J. Brett[2,3], Wiebke Ohm[3], Stephan V. Roth[2,3], and Peter Müller-Buschbaum[1,4] — [1]Technische Universität München, Physik-Department, Lehrstuhl für Funktionelle Materialien, James-Franck-Straße 1, 85748 Garching, Germany — [2]Royal Institute of Technology KTH, Teknikringen 34-35, 100 44 Stockholm, Sweden — [3]Deutsches Elektronen-Synchrotron DESY, Notkestraße 85, 22607 Hamburg, Germany — [4]Heinz Maier-Leibnitz Zentrum (MLZ), Technische Universität München, Lichtenbergstr. 1, 85748 Garching, Germany

An interesting approach in soft matter science is to substitute synthetic polymers with biopolymers, such as proteins. Being water soluble and

non-toxic, they open a way to greener processing. We are interested in the structure directing properties of the bovine whey protein ß-lactoglobulin (ß-lg) for thin titania films. For this, denatured ß-lg is mixed with established titania precursors to form a sol-gel, which can be eventually deposited. Spray deposition is chosen as a fast technique of low material wastage and hence of industrial relevance. In situ grazing incidence X-ray scattering measurements are performed simultaneously in small- and wide-angle regime (GISAXS/GIWAXS) to reveal the morphological changes and timescales of lateral growth upon film formation. After calcination of the as-deposited samples, the remaining titania scaffolds can be backfilled with organic semiconductors in order to build e.g. hybrid photoactive layers.

BP 3.4 Mon 10:15 ZEU 114

Structural and physical properties of Cellulose/Silver nanoparticle multi-layer film by layer-by-layer deposition — Qing Chen[1], •Andrei Chumakov[1], Calvin Brett[1,2], Anton Plech[3], Peng Zhang[4], and Stephan Roth[1,2] — [1]Deutsche Synchrotron (DESY), 22607, Hamburg, Germany — [2]KTH Royal Institute of Technology, 10044, Stockholm, Sweden — [3]Karlsruhe Institut of Technology (KIT), 76021, Karlsruhe, Germany — [4]Sun Yat-sen University, 510275, Guangzhou, China

Silver nanoparticles and assembled structures thereof have attracted growing interest due to peculiar optical, electrical, catalytic and stimuli-responsive properties of these nanostructures during the past decade. We report a new strategy to fabricate multilayered cellulose/AgNP-based thin-film by layer-by-layer (LBL) coating method, and the kinetics during each layer coating cycle was monitored by using grazing incidence small-angle X-ray scattering (GISAXS). Multilayered films were prepared by spray-coating technique. Spray conditions and solvent treatment of cellulose and AgNP layer were optimized according to structural and morphological characterization for the formation of an AgNP layer and each cellulose interface. Atomic force microscopy (AFM) was performed to visualize the morphological characteristics of the film surface. Moreover, our strategy provides a platform for easy and scalable production of large-area AgNP LBL films.

BP 3.5 Mon 10:30 ZEU 114

Self-assembly of aligned cellulose nanofibrils during gel drying — •Ariane Suzzoni[1], Calvin Jay Brett[1,2,3], Susumu Yada[1], Korneliya Gordeyeva[1], Stephan Volkher Roth[1,2], and Daniel Söderberg[1,3] — [1]KTH Royal Institute of Technology, SE-11428 Stockholm, Sweden — [2]Deutsches Elektronen-Synchrotron (DESY), D-22607 Hamburg, Germany — [3]Wallenberg Wood Science Centre, SE- 11428 Stockholm, Sweden

Cellulose nano fibrils (CNF) are largely studied in order to replace synthetic materials with natural ones. These materials based on natural fibers are an alternative to materials made from fossil energies, a big challenge in today's world. High mechanical performance can be related to the nanostructure of fibrils which composed the filaments. However, the mechanism involved is still unknown. A possible hypothesis is the mesoscale structure self-assembling occurs during consolidation and drying phase. Small Angle X-Ray scattering (SAXS) is a powerful technique to investigate the system arrangement at nanoscale. A flow-focusing system has been developed in a previous project to assemble CNF fibers with a highly ordered arrangement. The suspension formed using this microfluidic device is a gel containing a low concentration of CNF. SAXS experiments have been carried out directly on the gel filament lifted up in the air. The nanostructural changes were observed by SAXS during gel drying. We will present results obtained about the structure of cellulose nanofibrils as a function of drying time. This knowledge about CNF nanostructure formation will be a key to develop new eco-friendly materials.

BP 3.6 Mon 10:45 ZEU 114

Wrinkling instability in 3D active nematics — Tobias Struebing[1], Amir Khosravanizadeh[2], Andrej Vilfan[1], Eberhard Bodenschatz[1], Ramin Golestanian[1], and •Isabella Guido[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Goettigen, Germany — [2]Institute for Advanced Studies in Basic Sciences (IASBS), Zanjan, Iran

Networks of biopolymers and motor proteins are useful model systems for the understanding of emergent behaviour of active matter. An interesting class of such systems comprises active nematics, fluids constituted by self-organising elongated particles that in-vitro assemble in dynamical structures at length scales larger than those of their components by several orders of magnitude. In the last years the active nematic behaviour of biopolymer-motor networks confined on a 2D substrate was reported. Here we present an experimental and theoretical study on 3D active nematics made of microtubules, kinesin-1 motor proteins and a depleting agent. The network is subjected to the force exerted by the motors that crosslinked the filaments and let them slide against each other. In this way the system evolves toward a flattened and contracted 2D sheet that undergoes a wrinkling instability and subsequently loses order and transitions into a 3D active turbulent state. We observe that the wrinkle wavelength is independent of the ATP concentration and our theoretical model describes its relation with the appearance time. The experimental results are compared with a numerical simulation that confirms the key role of kinesin motors in the contraction and extension of the network.

BP 3.7 Mon 11:00 ZEU 114

Viscoelastic AFM characterization of the S2 layer of wood pulp fibers — •Caterina Czibula[1,3], Christian Ganser[1,3], Tristan Seidlhofer[2,3], Ulrich Hirn[2,3], and Christian Teichert[1,3] — [1]Institute of Physics, Montanuniversitaet Leoben, Austria — [2]Institute of Paper, Pulp and Fibre Technology, TU Graz, Austria — [3]CD Laboratory for Fiber Swelling and Paper Performance, TU Graz

Wood fibers consist of several cell wall layers which differ in thickness, chemical composition, and alignment of cellulose microfibrils. The S2 layer is the thickest layer, and dominates the mechanical behavior of the fibers. Several investigations with depth-sensing methods have so far focused on the characterization of the mechanical properties of the S2 layer. However, studies on the influence of relative humidity (RH) and the viscoelastic behavior of this layer are still missing. This work focusses on the viscoelastic behavior of the S2 layer at different RH by implementing an atomic force microscopy (AFM) based method. Here, wood pulp fibers have been prepared by microtome cutting, and a possible penetration of the embedding material in the cell wall layers has been ruled out by Raman spectroscopy. The evaluation of the experimental AFM data combines contact mechanics and viscoelastic models. It will be demonstrated that the Generalized Maxwell model yields reasonable results for the S2 layer measured at different RH. With increasing RH, the S2 layer shows a decrease in elastic and viscous parameters. The effect of different load rates will be discussed, and the viscoelastic results will be compared to AFM based nanoindentation data.

BP 4: Membranes and Vesicles (joint session BP/CPP)

Time: Monday 9:30–13:00 Location: ZEU 250

BP 4.1 Mon 9:30 ZEU 250

Regulated ensembles and lipid membranes — •Martin Girard and Tristan Bereau — Max-Planck-Institut für Polymerforschung

Cellular membranes are composed of lipid bilayers, amphiphilic molecules with polar headgroups and hydrophobic tails. Their composition is highly complex, involving hundreds of different lipid types and the regulation mechanism is still the subject of intense research. A recent experiment [1] has shown that cholesterol concentration increases with temperature in zebrafishes, as well as the demixing temperature, two results which appear to be contradictory results since cholesterol promotes mixing. Here, we show that many aspects of the zebrafish experiments can be replicated if one assumes a chemical reaction network for regulation of acyl tails. Effectively, this would mean that acyl tail saturation is loosely regulated by cells and mainly directed by cholesterol fraction. This view also explains trends seen along the secretory pathway between cholesterol concentration and acyl tail saturation.[1] M. Burns, K. Wisser, J. Wu, I. Levental, S. L. Veatch, "Miscibility transition temperature scales with growth temperature in a zebrafish cell line" Biophysical Journal 113 (2017)

BP 4.2 Mon 9:45 ZEU 250

Effect of reactive oxygen species on phospholipid monolayers — •Florian Gellert, Heiko Ahrens, and Christiane A. Helm — Institute of Physics, University of Greifswald

Oxidative degeneration of lipids can lead to severe damages of the biological cell membrane. The phenomenon is initiated by reactive radicals, such as certain reactive oxygen/nitrogen species (ROS/ RNS). To investigate this behaviour, we use monolayers at the air/ water interface of unsaturated lipids as model membranes and measure isotherms. ROS induce an oxidation of the double bond. The double bond turns hydrophilic, thus increases the molecular area per lipid at the same surface pressure. This is demonstrated by using phosphocholines with the same head group, but either one or two double bonds in one alkyl chain and no double bond in the other alkyl chain. In another series of experiments, both alkyl chains contained a double bond. We conclude that the ROS/ RNS attacks mostly the unsaturated alkyl chains and has little effect on the head group of the lipid.

BP 4.3 Mon 10:00 ZEU 250

From UV to Near Infrared Optical Control of Photolipid Vesicles — •Theresa S. Kehler[1], Stefanie D. Pritzl[1], Alexander F. Richter[1], David B. Konrad[2], Dirk Trauner[2], and Theobald Lohmüller[1] — [1]Chair for Photonics and Optoelectronics, Nano-Institute Munich and Department of Physics, Ludwig-Maximilians-Universität (LMU), Königinstr. 10, 80539 Munich, Germany — [2]Department of Chemistry, New York University, Silver Center, 100 Washington Square East, New York 10003, United States

Photoswitchable azobenzene phospholipids or "photolipids" can be employed as molecular reagents in bilayer membranes to control a variety of characteristic membrane properties such as lateral fluidity, permeability or stiffness. A general drawback of the azobenzene photoswitch, however, is that illumination with UV light is required to trigger trans-to-cis isomerization, which limits the wider applicability of photolipids in biological systems.

Here, we report on the photophysical properties of a new group of halogenated azobenzene photolipids, where the wavelengths required to control photoisomerization are shifted to the visible and near-infrared range. The isomerization dynamics of red-shifted photolipid vesicles are characterized by absorption measurements, fluorescence microscopy and membrane fluctuation analysis. Notably, we observe a wavelength dependence of the switching rates, which can be harnessed to reversibly control the membrane rigidity up to a factor of two.

BP 4.4 Mon 10:15 ZEU 250

Structural and dynamical changes of biomimetic myelin membranes induced by myelin basic protein — •Benjamin Krugmann[1], Andreas Stadler[2], Aurel Radulescu[1], Alexandros Koutsioumpas[1], Marie-Sousai Appavou[1], Martin Dulle[2], Laura Stingaciu[3], and Stephan Förster[2] — [1]FZJ JCNS-1, 52428 Jülich, Germany — [2]FZJ JCNS-MLZ, 85748 Garching, Germany — [3]ORNL, Oak Ridge TN 37831, USA

A major component of the saltatory nerve signal conduction is the multilamellar myelin membrane around axons. In demyelinating diseases like multiple sclerosis, this membrane is damaged. In literature different values for the lipid composition of healthy myelin sheath and myelin with experimental autoimmune encephalomyelitis - the standard animal model for multiple sclerosis - have been found. In this work we try to elucidate the interaction mechanism of myelin basic protein - the structural protein responsible for the cohesion of the cytoplasmic leaflets of the myelin sheath - with membranes mimicking both compositions. As samples we use unilamellar vesicles and supported bilayer systems. With neutron and x-ray small angle scattering methods combined with cryo-TEM we can follow the rapid aggregation which leads to a slow process in which different structures are formed depending on the lipid composition. Those structural information can be associated with the bending rigidity of the respective membrane measured with Neutron Spin Echo. Neutron reflectometry gives insights on how the interaction mechanism between membrane and protein functions and reveals how modified membranes are destabilised by the protein.

Invited Talk BP 4.5 Mon 10:30 ZEU 250

How do lipids and proteins diffuse in cell membranes, and what do the diffusion experiments actually measure? — •Ilpo Vattulainen — Dept Physics, Univ Helsinki, Finland

There are numerous techniques able to gauge diffusion in biomembranes. For instance, quasi-elastic neutron scattering measures diffusion in a non-perturbative manner over the nanosecond time scale, yet sampling in space is in these experiments done over large distances. Meanwhile, single-particle tracking allows one to measure the dynamics of individual molecules in almost nanometer resolution, but these measurements are based on the use of markers that may interfere with the diffusion process. Here we discuss nanoscale simulation studies designed to explore the underlying molecular-scale diffusion mechanisms of lipids and membrane proteins. Also, we discuss the bases of single-particle tracking experiments by considering the effects of streptavidin-functionalized Au nanoparticle probes on the lateral diffusion. The results show that lipids diffuse in a concerted fashion as clusters of lipids whose motion is highly correlated, and membrane proteins move as dynamical complexes with tens of lipids dynamically bound to the protein. Meanwhile, lipids linked to a streptavidin-nanoparticle complex also turn out to move in a concerted manner but as a complex with the linker protein and numerous non-labeled lipids, slowing down the motion of the probe by an order of magnitude. The results highlight that prior to using any technique, it is crucial to understand the physical basis of the diffusion process that one aims to measure. Otherwise, interpretation of experimental data can be a surprisingly difficult task.

30 min. coffee break

BP 4.6 Mon 11:30 ZEU 250

Prerequisites and kinetics of lipid bilayer fusion with living cell membrane — •Justus Bednár[1,2], Anastasia Svetlova[1,2], Vanessa Maybeck[1], and Andreas Offenhäusser[1] — [1]Forschungszentrum Jülich, Institute of Complex Systems: Bioelectronic (ICS-8) — [2]Fakultät für Mathematik, Informatik und Naturwissenschaften RWTH Aachen

Fusion processes between artificial lipid vesicles and living cell membrane are studied for a variety of reasons. The delivery of anti-cancer therapeutics or the method known as lipofection are only two applications that would benefit from a detailed understanding of the prerequisites and kinetics of this fusion process.

While usually this process takes place between liposomes that have a small size relative to the cell membrane they are fusing to, an inverse approach is presented in the current work. Producing an artificial solid-supported lipid bilayer (SLB) first and letting extracts of living cell membrane fuse with it afterward allows for the application of a quartz crystal microbalance with dissipation monitoring (QCM-D). Tracking the changes in resonance frequency and energy dissipation of a quartz sensor underneath the SLB allows for real-time tracking of adhesion and fusion processes.

Using the proposed setup along with dynamic light scattering and fluorescence microscopy, the dependence of fusion efficiency and kinetics on lipid composition of the artificial lipid bilayer as well as on the concentration of cell membrane vesicles is evaluated.

BP 4.7 Mon 11:45 ZEU 250

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

Experimental setups to produce and to monitor model membranes have been successfully used for decades and brought invaluable insights into many areas of biology. However, they all have limitations that prevent the full in vitro mimicking and monitoring of most biological processes. Here, a suspended physiological bilayer-forming chip is designed from 3D-printing techniques. This chip can be simultaneously integrated to a confocal microscope and a path-clamp amplifier. The bilayer, formed by the zipping of two lipid leaflets, is free-standing, horizontal, stable, fluid, solvent-free, and flat with the 14 types of physiologically relevant lipids, and the bilayer formation process is highly reproducible. Because of the two channels, asymmetric bilayers can be formed by making the two lipid leaflets of different composition. Furthermore, proteins, such as transmembrane, peripheral, and pore-forming proteins, can be added to the bilayer in controlled orientation and keep their native mobility and activity. These features allow in vitro recapitulation of membrane process close to physiological conditions.

Small, 2019, 10.1002/smll.201900725

BP 4.8 Mon 12:00 ZEU 250

Statistics on Red Blood Cell Flow in Microchannels — •Felix Maurer, Thomas John, and Christian Wagner — Experimentalphysik Universität des Saarlandes

Half of the human blood volume consists of erythrocytes, also refered to as red blood cells. Most of the pressure induced by the heart muscle is used for microcirculation through capillary vessels. Capillary flow is strongly characterized by the soft body physics of red blood cells often described as vesicles. We established an experimental method to record individual cells during flow through straight artificial microfluidic channels. Stationary shapes could be classified. We measured the speed as a function of position at different external pressure drops and channel geometries. The velocity distributions reveal intrinsic differences between individual erythrocytes. These have been found to be the root cause of pairing in this setup. Interaction forces have no influence on the examined flow.

BP 4.9 Mon 12:15 ZEU 250

The mechanism of vesicle-vesicle detachment under shear flow — •Mehdi Abbasi, Alexander Farutin, and Chaouqi Misbah — Univ Grenoble Alpes, CNRS, LIPhy, F-38000 Grenoble, France

Red blood cells (RBCs) suspended in plasma tend to aggregate and form rouleaux, during the aggregation they start by forming doublets of RBCs. In the physiological conditions the aggregation is reversible, the RBCs aggregate and disaggregate by the shear rate. In contrast, under some pathological conditions the aggregation becomes irreversible and once the aggregates formed they can not be dispersed again. Recently, D, Flormann et al analysed the doublet shape in the absence of applied flow in vitro and in silico. They observe that contact surface of the doublet starts by flat then sigmoid shape with the increase of adhesion energy. We performed two dimensional simulations to study the doublet dynamics under shear flow in different conditions and the effect of the doublet dynamics on the doublet suspension rheology, we also invesitigate the mechanism of vesicle-vesicle detachment.

BP 4.10 Mon 12:30 ZEU 250

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

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

BP 4.11 Mon 12:45 ZEU 250

Conformal wrapping of nanoparticles — •Piermarco Fonda[1,2] and Luca Giomi[1] — [1]Lorentz Instituut, Leiden University, Leiden, The Netherlands — [2]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

It is well-known that wrapping of nanometer-sized particles by lipid membranes can happen spontaneously for sufficient adhesion energy between the particle surface and lipid molecules. In this work we show the surprising result that, even in absence of adhesion forces, there exist solutions to the shape equation that describe a stable, spontaneous wrapping of spherical particles. Mathematically, these solutions can be found analytically thanks to the scale invariant nature of the bending energy, which allows to reduce the problem to the one of finding minimal surfaces in hyperbolic and spherical spaces. From a physical standpoint, such shapes are well-behaved since, unlike for adhesive forces, they do not require any in-plane stress at the contact points, and hence they easily preserve the liquid nature of the membrane. Finally, the relevance of these solutions to experimental and biological systems will be discussed.

BP 5: Bioimaging and Biospectroscopy I

Time: Monday 15:00–17:15 Location: HÜL 386

Invited Talk BP 5.1 Mon 15:00 HÜL 386

Mirror-enhanced fluorescence for superresolution imaging and spectroscopy — •Katrin G. Heinze[1], Hannah S. Heil[1], Benjamin Schreiber[1], and Markus Sauer[2] — [1]Rudolf Virchow Center, University of Würzburg, Würzburg, Germany — [2]Biocenter of the University of Würzburg, Würzburg, Germany

The "Resolution Revolution" in fluorescence microscopy over the last decade has given rise to a variety of techniques that allow imaging with resolution up to the nanometer range. One remarkable technique is direct stochastic optical reconstruction microscopy (dSTORM), a widely-used type of single molecule localization microscopy (SMLM). The key point here is the achievable localization precision, which mainly depends on the image contrast generated by the individual fluorophore*s emission. We found that reflective metal-dielectric nanocoatings represent a tunable nano-mirror that can do both quenching and boosting fluorescence for high-contrast imaging on the nanoscale. The enhanced resolution is a near-field effect and thus restricted to surface imaging; however, most membrane fluorescence applications benefit, even if classic resolution is not the main concern: Spectroscopic methods in live-cells such as Fluorescence Correlation Spectroscopy and Fluorescence Resonance Energy Transfer also belong to the scope of application. Mirror-enhanced fluorescence is different from other surface methods based on total internal reflection microscopy or optoplasmonics. While surface-plasmon supported methods provide much higher enhancement factors, mirror-enhanced approaches are more versatile and thus highly suitable for modern bio-imaging.

BP 5.2 Mon 15:30 HÜL 386

Trans-membrane Fluorescence Enhancement by Carbon Dots: Energy Transfer, Ionic Effects and pH Dependence — •Florian H. Huber[1], Stefanie D. Pritzl[1], Santanu Bhattacharyya[1], Fernando Pschunder[2], Maria Ana Huergo[2], Theobald Lohmüller[1], and Jochen Feldmann[1] — [1]Chair for Photonics and Optoelectronics, Nano-Institute Munich and Department of Physics, Ludwig-Maximilians-Universität (LMU), Königinstr. 10, 80539 Munich, Germany — [2]INIFTA, Universidad Nacional de La Plata - CONICET, Sucursal 4 Casilla de Correo 16, 1900 La Plata, Argentina

Improved optical biosensors that are sensitive to the membrane potential of cells are highly desirable for imaging applications and microscopy studies of membrane systems. Here, we analyse how transmembrane energy transfer between fluorescent carbon dots (CDs, size ~1.0 - 1.5 nm) and fluorescein labelled phospholipid molecules across the bilayer membrane of giant phospholipid vesicles is influence by ionic interactions and the pH. A system has been designed, where positively charged CDs and negatively charged fluorescein lipids co-localize across a bilayer membrane due to electrostatic attraction [1]. By performing absorbance, photoluminescence (PL), and fluorescence life time decay measurements, we find that ionic interactions do not only facilitate energy transfer, but also result in a PL enhancement of the dye, which is further adjustable by the pH of the vesicle suspension. [1] S.D. Pritzl, F. Pschunder, F. Ehrat, S. Bhattacharyya, T. Lohmueller, M. Huergo, J. Feldmann, Nano Letters, 19 (6), 3886-3891, 2019

BP 5.3 Mon 15:45 HÜL 386

Near Infrared Imaging and Sensing with Carbon Nanotubes — •Sebastian Kruss — Universität Göttingen, Göttingen, Deutschland

Carbon nanomaterials such as semiconducting single-walled carbon nanotubes (SWCNTs) are versatile building blocks for optical biosen-

sors and labels. SWCNTs fluoresce in the near infrared (nIR, 900-1700 nm) and their optoelectronic properties are very sensitive to changes in the chemical environment but a) achieving high selectivity and sensitivity and b) targeting or delivering those sensors to specific locations in cells or organisms is still a great challenge. Therefore, we use novel chemical and physical approaches to tailor SWCNTs. In the past years we have made substantial progress in the chemical design and used it to image complex processes in biological systems. 1. We tailored the corona phase around SWCNTs to enhance selectivity and photophysics of SWCNT-based sensors for the neurotransmitters dopamine and serotonin. Such sensors were used to image release of these signaling molecules from cells (neurons, blood platelets) with unprecedented spatiotemporal resolution. 2.SWCNTs were conjugated to nanobodies that can be targeted to any Green Fluorescent Protein (GFP) moiety. These SWCNTs were used for in vivo tracking of single kinesin motors and microrheology measurements in living drosophila embryos. 3. Peptides were incorporated into the organic corona phase around SWCNTs to target cell surface receptors. This approach enabled us to label for the first time integrins on human blood platelets in the nIR.

BP 5.4 Mon 16:00 HÜL 386

Stimulated Raman scattering microscopy of biomedical systems — •Moritz Floess, Florian Werner, Tobias Steinle, and Harald Giessen — 4th Physics Institute and Research Center SCoPE, University of Stuttgart, Germany

We employ stimulated Raman scattering (SRS) microscopy as a label-free and chemically selective imaging technique to investigate a system of pectin and porcine pleura. This model system is of high interest to improve surgical treatment of lung injuries. SRS is based on addressing molecular vibrational states using two pulsed laser beams with a variable frequency detuning. Hereby, an 8-W, 1032-nm, 450-fs Yb:KGW oscillator with 41 MHz repetition rate serves as the Stokes beam and simultaneously as the pump source for an optical parametric oscillator (OPO). The frequency-doubled OPO output provides the tunable Raman pump beam. Thanks to the favorable noise properties of the solid-state laser system we can address distinctive Raman bands in the fingerprint region with a high signal-to-noise ratio.

15 min. coffee break

BP 5.5 Mon 16:30 HÜL 386

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

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

BP 5.6 Mon 16:45 HÜL 386

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

The endoplasmic reticulum (ER) is a highly dynamic organelle that pervades the entire cell and hosts a variety of vital processes. For example, the exchange of proteins with the secretory pathway occurs at specialized and long-lived membrane domains, called ER exit sites (ERES). In mammalian cells, ERES form droplet-like protein assemblies that arrange as hundreds of dispersed punctae with a quasi-crystalline ordering. Although ERES were seen to diffuse on short timescales, they appear stationary on longer periods. Notably, their dynamics is different from the cytoskeleton-dependent, shivering motion of ER tubules. To gain insights into the underlying physical mechanisms of ERES self-organization, we have studied the emerging pattern of ERES when perturbing the ER morphology in different ways. As a result, we found a significantly changed spatial arrangement of ERES components when affecting the cytoskeletons integrity or reducing the amount of curvature-inducing membrane proteins. Even more pronounced changes were observed when the ER was transformed into vesicular structures by osmotic swelling. Our findings strongly indicate that the self-organization of ERES on the ER membrane system is caused by a diffusion-driven condensation phenomenon, similar to a liquid-liquid phase separation.

BP 5.7 Mon 17:00 HÜL 386

Particle tracking via an electrically focus tunable lens (ETL) — •Oliver Köhn and Christian Wagner — Universität des Saarlandes

We describe a method for the 3D tracking of particles using an electrically focus tunable lens (ETL). Applying a current to the ETL adapts the focal plane of the lens, allowing us to track particles in three dimensions without any mechanical interactions with the sample. Based on the sharpness of the tracked particles we are able to recalculate the current z-position of the particle. This calculation can be performed during the tracking-process, enabling us to perform live-tracking of particles. We show how this tracking-method can be applied to track 1.) bacteria (Bacillus subtilis) and 2.) um-sized beads, both for several minutes.

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

Time: Monday 15:00–17:15 Location: SCH A251

BP 6.1 Mon 15:00 SCH A251

Stability and diversity in random Lotka-Volterra systems with non-linear feedback — •Laura Sidhom and Tobias Galla — The University of Manchester, Oxford Road, Manchester, M13 9Pl

Ecosystem stability is important for maintaining a healthy microbiome, so understanding the factors that contribute to stability is of great relevance. In this talk I will discuss an ecosystem of many interacting species, that evolve according to Lotka-Volterra dynamics, with interaction coefficients drawn from a random distribution. We investigate the effects of sigmoidal nonlinear feedback on the stability of the ecosystem, and on its diversity. We find that nonlinear feedback causes species growth to be bounded, increasing ecosystem stability. In the talk I will illustrate the model parameters, using examples of interactions found in nature. We also investigate how pairwise interactions, and the introduction of higher-order interactions affect ecosystem stability, and how this relates to ecosystems in nature. I will briefly discuss the generating-functional path integral approach and the linear stability analysis, and discuss these results in terms of the human microbiome and explain how attributes of the host can influence its stability.

BP 6.2 Mon 15:15 SCH A251

Towards a grammar of probabilistic models for large biological networks — •Philipp Fleig[1] and Ilya M. Nemenman[2] — [1]University of Pennsylvania, Philadelphia, USA — [2]Emory University, Atlanta, USA

Biological interaction networks such as biological neural networks, amino acid sequences in proteins, etc. are critical to the functioning of any living system. The trend of modern experiments is to record data with a rapidly increasing number of simultaneously measured network variables. Inferring models for such complex data is becoming increasingly more difficult, since one is confronted with a combinato-

rial explosion in the number of possible interactions between variables. Here we present first steps of an approach to overcome this obstacle. We investigate the question whether a small set of carefully chosen statistical models suffices to describe rich phenomenology in data of biological networks. As candidate models for this grammar we consider low-rank approximation, clustering, sparsity, etc.. We discuss the distribution of eigenvalues and pairwise correlations characteristic for each model, working under the assumption that they serve as key indicators for the phenomenology described by a model. We provide examples of modelling data of Ising spin systems and outline a vision for how combinations of models in the grammar cover a large part of model space occupied by biological networks.

BP 6.3 Mon 15:30 SCH A251

Kauffman NK models interpolated between K=2 and K=3 — James E. Sullivan, Dmitry Nerukh, and •Jens Christian Claussen — Department of Mathematics, Aston University, Birmingham B4 7ET, U.K.

The NK model was introduced by Stuart Kauffman and coworkers [1] as a model for fitness landscapes with tunable ruggedness, to understand epistasis and pleiotropy in evolutionary biology. In the original formulation, fitness is defined as a sum of fitness functions for each locus, each depending on the locus itself and K other loci. Varying K from $K = 0$ to $K = N - 1$ leads to different ruggedness of the landscape. In previous work we introduced a generalization that allows to interpolate between integer values of K by allowing K_i to assume different values for each locus. We focus on the interpolation between the most widely studied cases of $K = 2$ and $K = 3$ and characterize the landscapes by study of their local minima. Here we transfer this approach to Random Boolean Networks and investigate attractor basins and limit cycles where the average K assumes integer and noninteger values. Relaxing the assumption of degree-homogeneity is an important step towards more realistic boolean network models, relevant to a broad range of applications in the dynamics of social systems and in systems biology.

[1] Kauffman, S.; Levin, S., Journal of Theoretical Biology. 128, 11 (1987); Kauffman, S.; Weinberger, E., Journal of Theoretical Biology. 141, 211 (1989).

Invited Talk BP 6.4 Mon 15:45 SCH A251

Density waves, jamming and dynamic arrest in growing microbial communities — •Oskar Hallatschek — University of California, Berkeley, USA

Microbes often colonize spatially-constrained habitats, such as pores in the skin or crypts in the colon. The resulting micro-communities are often stable and contribute to the genetic diversity and function of our microbiomes. It is, however, unclear how spatial constraints influence microbial community assembly. By monitoring and modeling microbial populations under controlled microfluidic confinement, we find a rich spectrum of dynamical patterns that are controlled by the competition between density-dependent outflow and population growth. Our results show that density-dependent passive diffusion can drive a reproducing populations to a jamming threshold, which entails a total loss of mixing and intra-species competition.

15 min. coffee break

BP 6.5 Mon 16:30 SCH A251

Effect of alternating between sexual and asexual reproduction on the number of expected mating types in isogamous species — •Ernesto Berríos-Caro[1], George W. A. Constable[2], and Tobias Galla[1] — [1]The University of Manchester — [2]University of York

The number of mating types of sexually reproducing isogamous species can range from two to thousands. The latter case is highly unusual and contradicts the argument that new types are sexually advantaged, which would imply a consistent growth of the number of types. Recent works based on a Moran-type individual-based model seem to suggest that the rate of sexual reproduction plays a crucial role in the low number of mating types observed in nature. Motivated by species that alternate between sexual and asexual reproduction, we subject the reproduction events to a switching environment of both states. We explore how the distribution of the number of mating types is affected by different switching regimes. When the environments switch slowly, we find that the distribution of mating types can become bimodal if the population size is large enough and the time spent in both environments (on average) is similar. When the switching is fast, we find that the system behaves as if it were in an effective single-fixed environment, where the sex is facultative. Also, we investigate the transition from slow to fast switching environments by calculating the distributions of the number of types in each environment based on the Kolmogorov equations of the system.

BP 6.6 Mon 16:45 SCH A251

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

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

BP 6.7 Mon 17:00 SCH A251

Coarse graining of biochemical systems described by discrete stochastic dynamics — •David Seiferth and Stefan Klumpp — Institute for the Dynamics of Complex Systems, University of Göttingen, Friedrich Hund Platz 1, 37077 Göttingen, Germany

Many biological systems can be described by finite Markov models. A general method for simplifying master equations will be presented by merging two adjacent states. The method preserves the steady-state probability distribution and all steady-state fluxes disregarding the one between the merged states. As the order of merging states is not important, different levels of coarse-grained models of the underlying microscopic dynamics can be obtained. Different criteria for the level of coarse graining or the resolution of the process will be proposed. The application of the method will be discussed for specific biochemical examples.

BP 7: Biomaterials and Biopolymers (joint session BP/CPP)

Time: Monday 15:00–17:30 Location: ZEU 250

BP 7.1 Mon 15:00 ZEU 250

Reptation of DNA nanotube tracers in semiflexible polymer networks — •Tina Händler[1,2], Cary Tutmarc[1,2], Martin Glaser[1,2], Josef Käs[1], David Smith[2], and Jörg Schnauss[1,2] — [1]University of Leipzig, Soft Matter Physics Division — [2]Fraunhofer Institute for Cell Therapy and Immunology, DNA Nanodevices Unit, Leipzig

Over many decades, actin has been the gold standard for exploring the theories about mechanics and dynamics of semiflexible polymers. Unfortunately, naturally occurring biopolymers are limited in their properties such as stiffness and interaction strengths. Programmable polymers enable us to study parameters otherwise unavailable in nat-

ural systems and therefore expand theoretical approaches. Nanotubes formed from synthetic DNA strands are ideal model polymers: they are semiflexible and can be hybridized to have characteristics such as a persistence length which is similar to actin filaments or can be varied in a controllable way. Additionally, DNA nanotubes are extremely stable, making them both favorable for polymer physics experiments and material science applications. We visualize the dynamics of nanotube tracer filaments in entangled and crosslinked semiflexible biopolymer networks. The results can be used to measure the networks' tube width and mesh size. Scaling laws concerning the parameter persistence length that have been beyond reach before are accessible now. Furthermore, reptation analysis with our programmable filaments enables the test of latest predictions about the dynamics of single filaments inside entangled solutions vs. crosslinked networks.

BP 7.2 Mon 15:15 ZEU 250

Dynamics during thermal gelation of egg-white studied using X-ray photon correlation spectroscopy — •Nafisa Begam[1], Anita Girelli[1], Anastasia Ragulskaya[1], Hendrik Rahmann[2], Fabian Westermeier[3], Christian Gutt[2], Fajun Zhang[1], and Frank Schreiber[1] — [1]Universität Tübingen, Germany — [2]Universität Siegen, Germany — [3]DESY, Germany

Gelation of proteins is a fundamental topic in food industry as well as in condensed matter physics [1]. We report a systematic time dependent study of the dynamics of hen egg-white during its gelation at 80°C using X-ray photon correlation spectroscopy in the ultra-small angle X-ray scattering mode. Two distinct regimes of dynamics are identified. The initial growth of the aggregates, as expected for heat-induced coagulation of egg-proteins, results in an early stage non-equilibrium dynamics. Interestingly, at the later stage (after $\sim$ 30 min of heating), the system reaches an equilibrium dynamical state with an average characteristic time scale of few tens of seconds. The intermediate scattering function changes from an exponential to a compressed exponential decay, indicating gel formation. The aggregates eventually show correlated temporally heterogenous dynamics. Such dynamical fluctuations are further quantified in terms of a fourth order intensity correlation function. The monotonic increase in heterogeneity as a function of wave vector transfer observed here is similar to the behavior of strongly attractive colloidal gels [2].

[1] Croguennec et al., *J. Food. Sci.*, **67**, 2, (2002)
[2] Fluerasu et al., *Phys. Rev. E*, **76**, 010401(R), (2007)

BP 7.3 Mon 15:30 ZEU 250

Reversible Underwater Adhesion in Beetles — •Pranav Sudersan, Thomas Endlein, Michael Kappl, and Hans-Jürgen Butt — Max Planck Institute for Polymer Research, Mainz, Germany

Many animals are able to climb smooth surfaces using adhesive pads on their feet. Unlike artificial glues, animals can adhere reversibly i.e. attach and detach easily to a wide variety of surfaces. Insects such as beetles have hairy pads on their feet and also secrete an adhesive fluid resulting in capillary forces for strong attachment. In contrast to adhesion in air, reversible adhesion underwater is particularly challenging. Insects drawing their adhesive force from the capillary action of the air-fluid interface would not stick underwater as such an interface is usually abolished. Some terrestrial beetles are however able to easily adhere and walk underwater by using an entrapped air bubble around their hairy pads to de-wet the surface upon entering water. But it is unclear as to what extent the air bubble influences adhesion. In our study, we measure adhesion and friction forces in live ladybug beetles (Coccinella septempunctata) under controlled conditions. The effect of surface hydrophobicity, pad attachment/detachment speeds and de-wetted area on adhesion and friction performance is examined and compared for dry and wet surfaces. Our study aims to draw inspiration from an animal model in order to fabricate artificial adhesives which would work in a similar way.

BP 7.4 Mon 15:45 ZEU 250

Visco-elastic properties of albumin films upon periodical mechanical loading — •Lukas Böttcher[1], Sven Kraft[1], Regina Lange[1], Ingo Barke[1], Jessica Hembus[2], Carmen Zietz[2], Rainer Bader[2], and Sylvia Speller[1] — [1]Institute of Physics, University of Rostock, 18059 Rostock — [2]Biomechanics and Implant Technology Research Laboratory, University Medical Center Rostock, 18057 Rostock

The synovial fluid in human natural and endoprosthetic joints usually implies outstanding lubrication and low wear. The question is how this fluid or its components, such as albumin and hyaluronic acid, participate in this performance. The high periodic forces acting on the protein in hips and knees during walking lead to changes in protein structure and visco-elastic-plastic behavior. Therefore, we mimic the situation in the joint using a tapping nanoprobe-sample junction in a force microscope. Films from albumin and synthetic synovial fluid are prepared and maintained wet in a humidifying chamber during treatment and data acquisition. Upon applying 200000 cycles at high force of several hundred nN the albumin film has swollen by about 5 nm in height. With increasing mechanical load the film gets softer and ropier. This may be explained in terms of loosening the protein secondary structure and incorporating additional fluid in the pores.

BP 7.5 Mon 16:00 ZEU 250

Towards transparent living tissues — •Kaushikaram Subramanian[1,2,3], Heike Petzold[1], Lena Hersemann[1,2], and Moritz Kreysing[1,2,3] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Center for Systems Biology Dresden, Dresden, Germany — [3]Cluster of Excellence, Physics of Life, Technische Universität Dresden, Germany

Most biological tissues are optically opaque, largely precluding access by light microscopy. In stark contrast, some living tissues and organisms have evolved to be highly transparent. Examples include many deep-sea fish and your retina that enables you to read this text. We asked the question if directed evolution can be used to change the optical phenotype of cells. For this we used a mutation, selection, and replication scheme, in which we favoured the growth of genetic mutant cells that showed reduced light scattering. After only few rounds of selection we gained mammalian cells with upto 2-fold reduced side scattering. Further analysis revealed that the induced partial transparency goes along with last changes of the transcriptome and frequently a reduction of nuclear substructure, a phenotype similar to the photoreceptor cells in the mouse retina. Our results encourages the possibility that deep microscopy on genetically cleared living tissues might one day become reality.

15 min. coffee break

Invited Talk BP 7.6 Mon 16:30 ZEU 250

Optoregulated force application to individual cellular receptors using molecular motors — •Aránzazu del Campo — INM-Leibniz Institute for New Materials, Campus D2 2, 66123 Saarbrücken, Germany — Chemistry Department, Saarland University

Inspired by cellular mechanisms for force application, a unique molecular machine that can apply forces at cell-matrix and cell-cell junctions using light as energy source will be presented. The key actuator is a light-driven rotatory molecular motor linked to polymer chains, which is intercalated between a membrane receptor and an engineered biointerface. The light-driven actuation of the molecular motor is converted in mechanical twisting of the polymer chains, which will in turn effectively *pull* on engaged cell membrane receptors (integrins, cadherins*) within the illuminated area. Applied forces have the adequate magnitude and occur at time scales within the relevant ranges for mechanotransduction at cell-friendly exposure conditions. The presnetation will provide experimental demonstrations of force-dependent focal adhesion maturation and T cell activation in vitro using the rotary motor.

BP 7.7 Mon 17:00 ZEU 250

Experimental setups to mimic the Peritoneal Dialysis in humans — •Bernd Eberle[1,2], Christian Wagner[1], and Thomas John[1] — [1]Experimentalphysik, Universität des Saarlandes, Saarbrücken, Germany — [2]Fresenius Medical Care Deutschland GmbH, St. Wendel, Germany

Peritoneal dialysis (PD) uses the peritoneum as a semipermeable dialysis membrane to clear the patient's blood. Therefore, dialysate solution gets filled into the abdominal cavity through an implanted catheter. Due to the osmotic concentration gradient between the blood capillarys and the dialysate, excess water and uremic toxins are removed from the blood by diffusing through the pores in the peritoneum into the dialysate. In contrast to Hemodialysis, the artificial filter membrane is well characterized, properties of the peritoneum are divers and vary for each patient. Consequently, a better understanding of membrane parameters is a crucial step for optimization treatment conditions. At present, commercially available software tools are used to simulate the membrane characteristics of the peritoneum but are lacking the precision to predict the ultrafiltration behavior in vivo. Hence, we

present experiments which mimic the diffusion, convection and ultrafiltration through the peritoneum with artificial membranes allowing a patient-tailored PD-therapy with higher efficiency. Various osmotic agents and membrane compositions were investigated, and characteristic membrane parameters were extracted from the measurements.

BP 7.8 Mon 17:15 ZEU 250

Characterization of microstructures obtained by the cryo-printing method for rapid microfluidic chip fabrication — •Sebastian Ronneberger, Ales Charvat, Claudia Hackl, Christian Elsner, and Bernd Abel — Leibniz Institute of Surface Engineering (IOM), Leipzig, Germany

Cryo-printing is a non-conventional rapid prototyping method for microfluidic devices in which liquid state (aqueous) micro-droplets are deposited onto a cooled substrate surface like glass or silicon which immediately undergo transition to the frozen solid state. By a controlled motion between the substrate surface and the microdrop printing head microstructures of ice can be scribed. After coverage of the microstructures with an UV-cured polymer coating thawing releases an *inverse imprint* in the covering coating which is still bonded to the substrate forming a microfluidic device. The talk presents off-line characterization methods for the topological analysis of cryo-printed ice microstructures by using datasets obtained from a laser-scanning profilometer. The datasets were automatically analyzed applying self-coded Python3 scripts to obtain channel parameters such as channel widths and channel depths at different positions. Analysis of crafted microchannels shows that this method can be used for optimizing the printing parameters which have an influence on the shape of the created microchannel structures. Furthermore, the reproducibility of the printing process was assessed. This might enable cryo-printing of microfluidic channels with variable and customized channel parameters which could be applied in advanced cryo-printed microfluidic chips.

BP 8: Poster I

Focus: Phase Separation in Biological Systems (BP 8.1 – BP 8.12); Focus: Physics of Stem Cells (BP 8.13 – BP 8.20)

Time: Monday 17:30–19:30 Location: P2/1OG

BP 8.1 Mon 17:30 P2/1OG

Erythrocytes sedimentation rate and acanthocytosis — •Alexis Darras, Thomas John, Lars Kaestner, and Wagner Christian — Universität des Saarlandes, Experimental physics, Saarbrücken, Germany

Aggregation rate of the red blood cells (RBC), or erythrocytes, is a physical parameter of blood which is often checked in medical diagnosis. The easiest and most widespread method to assess this aggregation rate is by measuring the erythrocytes sedimentation rate (ESR). It is well known that in case of inflammation, the increase in fibrinogen and other proteins results in higher aggregation and ESR than in healthy blood. However, some rare cases also lead to a slower ESR. It is notoriously the case with acanthocytosis, where patients have deformed RBC, called acanthocytes.

In this presentation, we will report new detailed measurements of ESR from acanthocytosis' patients and discuss the origin of this slower ESR. For this, we combine macroscopic tests with microscopic data of the acanthocytes aggregation. On the basis of the dynamics of colloidal gels, we will show how the change in aggregates' morphology, due to the acanthocytes, leads to slower sedimentation rate.

BP 8.2 Mon 17:30 P2/1OG

Dynamics of pressure-induced phase transitions in concentrated lysozyme solutions — •Marc Moron[1], Clementine Lovato[2], Ahmed Al-Masoodi[2], Lisa Randolph[2], Mario Reiser[2,3], Johannes Möller[3], Fabian Westermeier[4], Göran Surmeier[1], Jennifer Bolle[1], Michael Paulus[1], Metin Tolan[1], and Christian Gutt[2] — [1]Fakultät Physik / DELTA, TU Dortmund, 44221 Dortmund, Germany — [2]Department Physik, Universität Siegen, 57072 Siegen, Germany — [3]European X-ray Free Electron Laser Facility, Holzkoppel 4, Schenefeld, Germany — [4]Deutsches Elektronen Synchrotron DESY, D-22607 Hamburg, Germany

Phase transitions in concentrated protein solutions have been in the focus of research for years. For example, many diseases can be attributed to protein aggregation or liquid-liquid phase separation in human cells. Such systems can be modeled as crowded protein solutions. Lysozyme represents a well-studied model protein. We investigated the effect of hydrostatic pressure on concentrated lysozyme solutions in different environments and were able to show that besides temperature, protein concentration, cosolvents and ionic strength also the hydrostatic pressure modulates the protein-protein interaction. However, only the static properties of the lysozyme solutions were characterized. In this work, we present first pressure dependent X-ray photon correlation spectroscopy (XPCS) measurements on concentrated lysozyme solutions to study the dynamics of pressure-induced liquid-liquid phase transitions.

BP 8.3 Mon 17:30 P2/1OG

Droplets as biochemical reactors in living cells — •Sudarshana Laha[1,2], Thomas C.T. Michaels[3], and Christoph A. Weber[1,2] — [1]Max Planck Institute for the Physics of Complex Systems,Dresden — [2]Center for Systems Biology Dresden — [3]Harvard University, Cambridge

Living cells use compartments(droplets) to spatially organise molecules that can undergo fuel-driven chemical reactions. Not much is known about the mechanisms underlying such spatial control of chemical reactions and how much the properties of chemical reactions are altered by the compartments relative to homogenous systems. Here, we derive a theoretical framework to study fuel driven chemical reactions in the presence of compartments.We study two state transitions like phosphorylation via hydrolysis of ATP and enzymatic reactions. For two state transitions, we find that the ratio of phosphorylated product can be regulated by droplets by two orders of magnitude relative to the homogenous state. In the case of enzymatic reactions, we show that the initial rate of product formation can be increased by more than ten fold. We further calculate analytically the optimal conditions of designing the system. Our studies exemplify the enormous potential of phase separated compartments as biochemical reactors in living cells and enhancing the effect of enzymes. Understanding the control of biochemical reactions via compartments is key to elucidate the functionality of stress granules for the cell and is also crucial for biochemical communication among synthetic cells and RNA catalysis in coacervate protocells.

BP 8.4 Mon 17:30 P2/1OG

Size control of Active Droplets with Non-Equilibrium Chemical Reactions — •Jan Kirschbaum and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Liquid droplets forming by phase separation play an important role in the spatiotemporal organization of material inside cells. However, in contrast to passive phase separation, e.g. oil-water emulsions, the interaction of cellular droplets with their inherently non-equilibrium environment is not well understood. Here, we investigate how ATP-driven chemical reactions, which switch a protein between a phase separating and a soluble form, influence the properties of droplets. Similar systems were already investigated using mass-action kinetics, but such descriptions are not thermodynamically consistent and are thus difficult to compare to experiments.

Here, we employ linear non-equilibrium thermodynamics to model the phase separation and the non-equilibrium reactions. We identify that droplet size and stability can be controlled when one reaction is driven and the enzymes controlling the rates are distributed heterogeneously. In this case, a non-equilibrium steady state with well-defined droplet radius can be reached, characterized by constant diffusive and reactive fluxes inside the system. Using the model, we determine the energy consumption and entropy production rate necessary to maintain droplets of certain sizes. For the biological example, we thus propose that enriching enzymes in droplets is one way to control their size by chemical reactions.

BP 8.5 Mon 17:30 P2/1OG

Unusual correlated dynamics in aqueous protein solutions due to thermal expansion induced shear flow — •Nafisa Begam[1], Anastasia Ragulskaya[1], Anita Girelli[1], Hendrik Rahmann[2], Fabian Westermeier[3], Christian Gutt[2], Fajun Zhang[1], and Frank Schreiber[1] — [1]Universität Tübingen, Germany — [2]Universität Siegen, Germany — [3]DESY, Germany

We study the dynamics of aqueous solutions of the globular protein bovine γ-globulin in the presence of polyethylene glycol, filled into quartz capillaries, during liquid-liquid phase separation using X-ray photon correlation spectroscopy (XPCS). Simultaneously, we probe the kinetics of the phase separation by USAXS. Microscopy measurements revealed that the solutions undergo a thermal expansion or contraction during the temperature change which induces a shear flow in the solution. To study the influence of such an intrinsic shear flow on the phase transition, we performed the measurements in the middle of the capillary, having a large shear flow, and rear of the capillary, having a negligible shear flow. Interestingly, the kinetics observed in these two cases are similar. However, in the middle of the capillary, the dynamics exhibits a strong heterogeneity, and in the rear of the capillary, the degree of heterogeneity is significantly smaller. Our findings could have a large impact in the field of condensed matter where XPCS is an important tool in studying bulk dynamics and the intrinsic shear flow is comparable to the time scale of the system dynamics.

[1] Busch et al., *Eur. Phys. J. E*, **26**, 55, (2008)
[2] Urbani et al., *J. Sync. Rad.*, **23**, 1401, (2016)

BP 8.6 Mon 17:30 P2/1OG

Bending rigidity of heterochromatin alone can induce segregation in model eukaryotic cell nuclei — Martin Girard[2], Kurt Kremer[2], John F. Marko[3], Monica Olvera de la Cruz[3], and •Aykut Erbas[1] — [1]Bilkent University - UNAM, Ankara 06800, Turkey — [2]Max-Planck Instutute for Polymer Science, Mainz 55128, Mainz, Germany — [3]Northwestern University, Evanston 60202, USA

One of the unresolved puzzles in biological sciences is the 3D packing of the meters-long DNA molecule into the confinement of micrometer-scale cell nucleus while regulating fundamental cellular activities, from protein transcription to replication. Although the underlying 3D conformation of the genome is a complex phenomenon resulting from the dynamic interactions between nuclear proteins and negatively charged DNA, relatively simple computational models can guide us about the large-scale and long-time behavior of the chromatin. Our extensive Molecular Dynamics simulations provide an auxiliary, possibly alternative, mechanism for heterochromatin (i.e., a histone-rich version of the chromatin) localization in the cell nucleus. We showed that coalescence of heterochromatin at the nuclear center can be mimicked even for an ideal mixture scenario throughout the suppressed bending fluctuations of the heterochromatin fiber. Further, our model system also suggests that switching of the interactions between confining nuclear shell and the heterochromatin can recover the conventional segregation regime, in which heterochromatin occupies the nuclear periphery.

BP 8.7 Mon 17:30 P2/1OG

Effective simulation of many interacting droplets — •Ajinkya Kulkarni and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

It has recently been discovered that liquid droplets play an important role in organizing material inside biological cells. However, so far it is unclear how a large number of droplets behave in the heterogeneous environment of the cell. Traditionally, liquid-liquid phase separation is numerically studied using Monte-Carlo simulations, Molecular Dynamics simulations, or by solving the Cahn-Hilliard equation on a lattice. All these methods are computationally expensive since they have to resolve spatial structures on the scale of individual particles. This severely limits the system sizes that can be studied.

We propose a novel simulation method to tackle this limitation. Our method describes droplets explicitly by a position and a radius, while the dilute phase is represented by a concentration field. Assuming that droplets are far enough away from each other, they only interact by exchanging material via the dilute phase. Since the dilute phase is sufficiently described by a coarse discretization of the diffusion equation, our method is orders of magnitude faster than the traditional ones. Consequently, our method allows simulating the dynamics of many droplets on length- and timescales relevant to biological cells.

BP 8.8 Mon 17:30 P2/1OG

Hydrodynamics of pumping cell aggregates — •Max Kerr Winter and Guillaume Salbreux — The Francis Crick Institute, London, UK

Cavitation events within tissues are ubiquitous in developmental biology. In order to study such phenomena, we derive a hydrodynamic theory of cells forming aggregates and cavities by the combined action of adhesion forces and the active, polar pumping of fluid. The theory describes a coarse grained fluid consisting of cells in a medium of solutes and water. In the limit of passive, apolar cells, we investigate the steady state phase separation behaviour of the fluid in response to the strength of cell-cell adhesions. For sufficiently strong adhesions, the system separates into two phases differing by their cell density. We also study the linear stability of active, polar cells and find the system can be driven away from a uniform state by active pumping of solutes at topological defects in the polarity field. This theory takes inspiration from recent experiments with mouse embryonic stem cells (ESCs) [Shahbazi et al., Nature, 2017], where spherical ESC aggregates form cavities by the coordination of adhesion, apicobasal polarity, and active pumping.

BP 8.9 Mon 17:30 P2/1OG

Protein-free synthetic cell division controlled by metabolic activity — •Yannik Dreher[1,2] and Kerstin Göpfrich[1,2] — [1]Biophysical Engineering Group, Max Planck Institute for Medical Research, Jahnstraße 29, 69120 Heidelberg, Germany — [2]Department of Physics and Astronomy, Heidelberg University, 69120 Heidelberg, Germany

Here, we describe the protein-free division of giant unilamellar lipid vesicles (GUVs) based on the combination of two physical principles – phase separation and osmosis. We visualize the division process with confocal fluorescence microscopy and derive a conceptual model based on the vesicle geometry. The model successfully predicts the shape transformations over time as well as the time point of the final pinching of the daughter vesicles. Remarkably, we show that two fundamentally distinct yet highly abundant processes – water evaporation and metabolic activity – can both regulate the autonomous division of GUVs. Our work may hint towards mechanisms that governed the division of protocells and adds to the strategic toolbox of bottom-up synthetic biology with its vision of bringing matter to life.

BP 8.10 Mon 17:30 P2/1OG

Designing morphology of separated phases in multicomponent liquid mixtures — Milena Chakraverti-Wuerthwein[1], Sheng Mao[1], Hunter Gaudio[2], Mikko Haataja[1], and •Andrej Kosmrlj[1] — [1]Princeton University, Princeton, NJ, USA — [2]Villanova University, Villanova, PA, USA

Morphology of multiphase membraneless organelles formed via intracellular phase separation plays an important role for their functionality. Yet, very little is known how intermolecular interactions can be tuned to achieve target microstructures of separated phases. To address this, we systematically investigate morphologies of coexisting phases obtained via phase separation in Flory-Huggins liquid mixtures with 4 or more components. We demonstrate that the topology of separated phases is completely determined by their surface tensions, while their volume fractions dictate the geometry of microstructure (e.g. droplets, percolated structure). We developed a novel method based on graphs that enabled us to enumerate all topologically distinct morphologies of separated phases. Each graph is associated with a set of inequalities for surface tensions and this enabled us to reverse engineered intermolecular interaction parameters to realize all topologically distinct morphologies for 4 coexisting phases. The developed approach is general and can be applied to design morphologies with an arbitrary number of coexisting phases.

BP 8.11 Mon 17:30 P2/1OG

Shape-instabilities in Chemically Active Multi-momponent Mixtures — •Jonathan Bauermann[1] and Frank Jülicher[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Center for Systems Biology Dresden, Dresden, Germany

Recently, it has been shown that droplets can undergo splitting events in chemically active environments (Zwicker et al., Nature Physics, 2017). The authors studied the dynamics of a binary mixture in the Cahn-Hilliard theory with an additional effective flux coming from the underlying chemical reactions. Only if the system is driven out of equilibrium, a stable droplet radius can exist. We generalize this model to more components and make the breaking of detailed balance explicit in the chemical reactions by introducing an additional energy supply.

This drives the system out of equilibrium and stable droplet radii can be found. If the external energy supply is strong enough, similar shape-instabilities of the spherical droplets can be found as described by the authors in the aforementioned paper. A framework like this allows not only for more complicated reaction schemes, but also gives insights into the energetics of chemical reactions in phase-separating systems.

BP 8.12 Mon 17:30 P2/1OG

Cross-diffusion induced patterns for a single step catalytic reaction — •Giovanni Giunta[1,2], Hamid Seyed-Allaei[1], and Ulrich Gerland[1] — [1]Physics Department, Technical University Munich (TUM), Garching, Germany — [2]Quantitative Biosciences Munich, Ludwig-Maximilians-Universität (LMU), Munich, Germany

There is mounting evidence that the motion of a given enzyme depends on the concentration of the corresponding substrate. Experiments performed in solution show that the higher the concentration of substrate, the higher the diffusion coefficient of the enzyme. Moreover experiments performed in steady gradients of substrate have also shown that cross-diffusive effects may be playing an important role. Here we analyze the different models proposed so far and we focus on the effects that the reaction has in shaping the substrate concentration, which in turns has an effect on the enzyme motion. We show that spatial patterns form when cross-diffusion and enhanced diffusion both contribute to the accumulation of enzymes in regions with low concentrations of substrate. In this scenario, the reaction causes gradients of substrate to get steeper, which in turns causes the enzyme to further accumulate where substrate is low. Experimental evidence of pattern formation could be used to discern between the different models proposed so far.

BP 8.13 Mon 17:30 P2/1OG

Embryonic lateral inhibition as optical modes — •Jose Negrete Jr and Andrew C Oates — École Polytechnique Fédérale de Lausanne

Spatial gene expression patterns define regions where specialised cells emerge within an embryo. Lateral inhibition is a common mechanism that creates fine grained patterns with a characteristic wavelength of the size of 2 cells. Here we developed a generic model for patterning with lateral inhibition, and study its characteristics by making an analogy with crystal phonons from solid state physics. The tissue is redefined in terms of a Bravais lattice where the basis of the crystal contains two to three cells. The steady states are analogous to the optical modes of phonons. The model predicts that there are two different lateral inhibition states that can coexist in a certain parameter regime. Finally, our work suggests that gene expression patterns can be thought as crystal phonons, where long wavelength (Turing like) patterns corresponds to accosting modes and lateral inhibition patterns to optical modes.

Reference: Negrete Jr J and Oates AC, Phys Rev E 99, 042417 (2019)

BP 8.14 Mon 17:30 P2/1OG

A theoretical framework to describe influence of electric field on Mesechymal cell differentiation — •Jonathan Dawson[1], Ursula van Rienen[1,2,3], and Revathi Appali[1,3] — [1]Institute of General Electrical Engineering, University of Rostock, Albert-Einstein-Str.2, 18059, Rostock — [2]Life, Light and Matter, Interdisciplinary Faculty, University of Rostock — [3]Ageing of Individuals and Society, Interdisciplinary Faculty, University of Rostock

Bone regeneration is a highly complex and tightly regulated process. Concerted and controlled action of human mesenchymal stem cell (hMSC) proliferation and differentiation into osteoblasts is pivotal in bone regeneration. Multiple biochemical and physiological factors influence the osteogenic differentiation and proliferation of hMSCs. Electromagnetic field (EMF) stimulation has been successfully used for the treatment of bone disorders. However, it is still unclear how exactly EMF influences the MSC dynamics. In close collaboration with experiments, we developed a theoretical framework to understand the effect of externally applied electric fields on hMSCs. In experiments, hMSCs were cultured in a chamber exposed to low-frequency electrical field applied via a transformer-like-coupling (TLC) [Hess et al. (2012)]. Cell differentiation was measured by cell alkaline phosphate (ALP) activity. Our mean-field theory describes the dynamics of a population of ALP stained hMSCs and takes into account cell division, cell apoptosis, cell differentiation, and intracellular ALP activity. Our model can account for the differences in the experimentally observed time course behaviour of total number of cells and the total ALP activity.

BP 8.15 Mon 17:30 P2/1OG

Arrhythmogenicity Test Based on a Human Induced Pluripotent Stem Cell (iPSC)-Derived Cardiomyocyte Layer — •Konstantin Agladze — Moscow Institute of Physics and Technology, Dolgoprudny, Russian Federation

In vitro screening for potential side-effects of drugs on human induced pluripotent stem cell-derived cardiomyocytes is cutting-edge technology in pharmaceutical industry. The using iPSC-CM is considered as a part of comprehensive battery for an accurate and complex mechanistic-based assessment of the proarrhythmic potential of drugs. Induced pluripotent stem (iPS) cells from a healthy individual were differentiated into a cardiomyocyte monolayer that was identified by immunocytochemistry and the patch-clamp technique also considering of the potential impact of the developing phenotype of the iPSC-CMs. To study the occurrence of reentry as a precursor to arrhythmias, a standard obstacle was created in the cell layer. With the aid of optical mapping, the measure of arrhythmogenicity was determined, as defined by the probability of a reentry occurrence for the particular frequency of stimulation. A change in the potassium current corresponding to LQTS type 2 at frequencies matching high heart rates was demonstrated visually and quantitatively. Also, the efficiency of this method for quantifying both the effectiveness and ineffectiveness of drugs for a particular donor and for determining the donor*s cardiovascular disease risk zone was tested.

BP 8.16 Mon 17:30 P2/1OG

The role of geometry and cell-cell communication in the migration of anterior visceral endoderm cells — Jonathan Fiorentino[1,2,3] and •Antonio Scialdone[1,2,3] — [1]IES, Helmholtz Zentrum München, Germany — [2]IFE, Helmholtz Zentrum München, Germany — [3]ICB, Helmholtz Zentrum München, Germany

The migration of Anterior Visceral Endoderm (AVE) cells during early mouse embryonic development is crucial for the establishment of an anterior-posterior axis. AVE cells might move in response to a shallow gradient of a molecular cue. Prior to migration, they form multicellular rosettes, structures in which five or more cells meet at a central point, whose functional role is still unknown.

Relying on the Local Excitation Global Inhibition model (LEGI), which considers the presence of a local and a global molecular reporter as the mechanism of gradient sensing, we explore the hypothesis that rosettes' formation enhances cell-cell communication, increasing the cells' ability to measure external signals.

We extend the LEGI model to a 2D system where all the cells or only a subset of them can exchange molecular signals. We characterize the gradient sensing ability of cells adopting different geometric configurations, which suggests that the spatial arrangements of AVE cells in the embryo likely maximize their ability to measure weak gradients of external signals. Furthermore, we identify the transcriptional differences between AVE and VE cells and the active signalling pathways through the analysis of single-cell RNA-sequencing data collected from mouse embryos at the migration stage.

BP 8.17 Mon 17:30 P2/1OG

A multidisciplinary approach to defining the identity and dynamics of adult gastric isthmus stem cells — •Seungmin Han[1,2], Juergen Fink[2], Jong Kyoung Kim[3], Benjamin Simons[1,2], and Bon-Kyoung Koo[4] — [1]WT-CRUK Gurdon Institute, Cambridge, UK — [2]WT-MRC Cambridge Stem Cell Institute, Cambridge, UK — [3]DGIST, Daegu, Republic of Korea — [4]Institute of Molecular Biotechnology of the Austrian Academy of Sciences (IMBA), Vienna, Austria

The gastric corpus epithelium is the thickest part of the gastrointestinal tract and is characterized by rapid tissue turnover. Several markers have been proposed for gastric corpus stem cells in both isthmus and base regions. However, the identity of isthmus stem cells (IsthSCs) and the interaction between distinct stem cell populations is still usnder debate. Here, based on unbiased genetic labeling and biophysical modeling, we show that corpus glands are compartmentalized into two independent zones, with actively-cycling stem cells maintaining the pit-isthmus-neck region and slow-cycling reserve stem cells maintaining the base. Independent lineage tracing based on Stmn1 and Ki67 expression confirmed that rapidly-cycling IsthSCs maintain the pit-isthmus-neck of corpus glands. Finally, single-cell RNA-seq analysis is used to define the molecular identity and lineage relationship of a single, cycling, IsthSC population. These observations define the identity and functional behavior of IsthSCs.

BP 8.18 Mon 17:30 P2/1OG

Trajectories of cell shape and state during cellular fate transitions — •Wolfram Pönisch[1,2], Agathe Chaigne[1], Irene Aspalter[1], Guillaume Salbreux[3], and Ewa Paluch[1,2] — [1]MRC Laboratory for Molecular Biology, University College London, London, UK — [2]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK — [3]Francis Crick Institute, London, UK

To form complex organisms, cells specialize to perform different tasks, a process called differentiation. The required cellular fate transitions are often accompanied by cell shape changes and there are strong indications that cell shape and state are coupled.

Here, we present a pipeline to quantify and analyze cell shapes during cellular fate changes. We will present how the high-dimensional morphometric features of cell shapes for different cellular states can be quantified and projected to a low-dimensional space with the help of dimensional reduction techniques. To identify clusters of cells and classify cells based on those clusters, we use a variety of machine learning algorithms. We can then study the trajectories of cell shape and cell state markers while cells transition between distinct states.

We use our pipeline to investigate the coupling between cell shape and fate during the exit from naïve pluripotency in mouse embryonic stem cells. We find that cells can be classified into two unambiguously distinguishable clusters, and investigate the shape and state trajectories of cells, transitioning from a spherical shape towards a spread morphology.

BP 8.19 Mon 17:30 P2/1OG

Challenging the cancer stem cell hypothesis: Markov model-based evaluation of Glioblastoma cell plasticity — Thomas Buder[1], Andreas Deutsch[2], and •Anja Voss-Böhme[1] — [1]University of Applied Sciences Dresden — [2]TU Dresden

For glioblastoma (GBM) and other cancers, intra-tumoral phenotypic heterogeneity has been proposed to rely on cancer stem cells (CSC) postulated to reside at the apex of a hierarchical organization and to sustain tumor progression and heterogeneity by generating differentiated progeny. Analyzing flow cytometry data of glioblastoma multiforme cell lines under normaxia and hypoxia with the help of stochastic Markov process models, we show that GBM phenotypic heterogeneity arises from non-hierarchical, reversible state transitions, instructed by the microenvironment and predictable by mathematical modeling. We introduce a method for automated parameter estimation and prognosis from time-course cell proportion data which supports the analysis of the hierachical pattern underlying the transition structure. This method is implemented in a freely available R package, Cell Trans.

(1) A. Dirkse, A. Golebiewska et al. Nature Comm. (2019).
(2) T. Buder et al. Front. Onc.(2019).
(3) T.Buder et al. Bioinformatics and Biology Insights (2017).

BP 8.20 Mon 17:30 P2/1OG

The morpho-rheological phenotype of hematopoietic stem cells as a novel marker for transplantation — •Angela Jacobi[1,2,3], Ahmad A Nawaz[1,2], Martin Kräter[1,2], Martin Bornhäuser[3], and Jochen Guck[1,2] — [1]MPL, Erlangen, Germany — [2]BIOTEC, TU Dresden, Dresden, Germany — [3]University Hospital Carl Gustav Carus, TU Dresden, Dresden, Germany

Hematopoietic stem cells (HSCs) are transplanted after chemotherapy to reconstitute all blood cells. Unfortunately, analysis of their surface protein expression by standard flow cytometry does not yield functional information. Morpho-rheological properties of HSCs, determined predominantly by the cells cytoskeleton, play an important role for their function and can serve as a label-free marker for their identification. Numerous methods to measure morpho-rheological properties of cells are currently available, but most of them are limited in the ability to screen large heterogeneous populations in a robust and efficient manner, a feature required for successful translational applications. With real-time deformability cytometry (RT-DC) mechanical properties of cells in suspension can be screened continuously at rates of up to 1,000 cells/s, similar to conventional flow cytometers, which makes it a suitable method for HSC screening. Based on RT-DC measurements, we establish here a specific morpho-rheological fingerprint of HSCs that allows to distinguish them from all other blood cell types. We further show that this morpho-rheological phenotype allows for sorting of HSCs from heterogeneous human bone marrow samples, which could find practical application in HSC transplantation.

BP 9: Poster II

Cytoskeletal Filaments (BP 9.1 – BP 9.14); Membranes and Vesicles (BP 9.15 – BP 9.27)

Time: Monday 17:30–19:30 Location: P2/2OG

BP 9.1 Mon 17:30 P2/2OG

Vimentin intermediate filaments stabilize dynamic microtubules — •Charlotta Lorenz, Laura Schaedel, and Sarah Köster — Institute for X-Ray Physics, Georg-August-Universität, Göttingen, Germany

Many cellular functions such as cell shape, mechanics and intracellular transport rely on the organization and interaction of actin filaments, microtubules (MTs) and intermediate filaments (IFs), which are the main constituents of the eukaryotic cytoskeleton. We study the interaction between vimentin IFs and dynamic MTs in a minimal in vitro system and show that MTs are stabilized against depolymerization by the presence of vimentin IFs. To explore the electrostatic and hydrophobic contributions to this attraction, we measure interactions between individual MTs and vimentin IFs under different buffer conditions. We theoretically model the interaction to understand the energy landscape of the attraction. Taken together, our results suggest that there is an attractive interaction between MTs and vimentin IFs that supports increased MT stability.

BP 9.2 Mon 17:30 P2/2OG

Influence of Ions on the Assembly of Vimentin Intermediate Filaments — •Manuela Denz[1], Harald Herrmann[2], and Sarah Köster[1] — [1]Institute of X-ray physics, University of Göttingen, Göttingen, Germany — [2]Institute of Neuropathology, University Hospital Erlangen, Erlangen, Germany

The cytoskeleton is mainly composed of intermediate filaments (IFs), microfilaments and microtubules. In contrast to the conserved proteins actin and tubulin, IF proteins vary between different cell types. Despite the many different types, all IF proteins share the same secondary structure of a helical rod domain and intrinsically disordered head and tail domains. The assembly of IFs follows a hierarchical pathway. The assembly of the charged monomers into filaments can be triggered by ions. Here, we focus on the assembly of the IF protein vimentin using different ions. We test the influence of several ions with varying valencies, sizes and concentrations by small angle x-ray scattering (SAXS) and fluorescence microscopy (FM). SAXS probes primarily the lateral assembly of vimentin monomers into so-called unit-length filaments, while with FM the extended filaments are directly imaged. Vimentin assembled with monovalent ions forms single filaments. On the contrary, vimentin forms networks when assembled with multivalent ions. For those ions, vimentin filaments aggregate after exceeding a threshold concentration. With increasing valency of the ion, the threshold for aggregation of vimentin filaments is lowered. However, also differences between divalent ions can be observed, which can be explained by the Hofmeister effect.

BP 9.3 Mon 17:30 P2/2OG

Comparison of mechanisms of kinetochore capture with varying number of spindle microtubules — •Indrani Nayak, Dibyendu Das, and Amitabha Nandi — Department of Physics, Indian Institute of Technology Bombay, Powai, Mumbai 400076, India

The capture of kinetochores by spindle microtubules is crucial for cell division. Earlier experimental studies have shown that dynamical instability driven search-and-capture of a kinetochore by spindle microtubules is a dominant mechanism in eukaryotes. A different mechanism has been reported in *Schizosaccharomyces pombe*, where spindle microtubules being pivoted at the spindle pole body search for the kinetochores. Our work compares these two mechanisms by studying the first passage times of kinetochore capture as a function of microtubule

number N. In addition to the *mean* times, we also estimate a more robust measure, namely the *characteristic* times associated with the rare events of capture. We find upon varying N, one mechanism may be preferred over the other. While for fewer N (as in *S. pombe*), the *characteristic* capture times due to pivoting are lesser than those for search-and-capture, the behavior reverses at larger N. Our study provides a physical basis for the selection of one mechanism over another depending upon microtubule number. The *characteristic* timescales are obtained either by computing the survival probability of a kinetochore to high precision or using the statistics of extremes.

BP 9.4 Mon 17:30 P2/2OG

Force Generation by Contractile Actomyosin in Elastic Frames — •Johannes Flommersfeld[1], David Brückner[1], Haiyang Jia[2], Petra Schwille[2], and Chase Broedersz[1] — [1]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, LMU Munich — [2]Max Planck Institute for Biochemistry, Martinsried

Contractile actomyosin gels are crucial for the mechanical properties of cells. Here, we study how the active contraction behavior of actomyosin networks responds to the elasticity of their surroundings. To this end, we design an experimental setup, which couples reconstituted actomyosin networks to 3D-printed elastic structures. Specifically, we use a micropillar array as a force and velocity sensor. These micropillar arrays can be deformed by the activity of the network, which allows for quantitative studies of the static and dynamic properties of contractile actomyosin networks. To understand the observed dynamical behavior of this contractile active gel, we introduce a phenomenological model, which highlights the role of the force-dependent myosin kinetics. Finally, we explore the potential of this setup to perform viscosity measurements of the actomyosin gel.

BP 9.5 Mon 17:30 P2/2OG

Filament Sensor - A tool for near real-time analysis of stress fiber formation in stem cells — •Lara Hauke[1], Benjamin Eltzner[2], Carina Wollnik[1], Stephan Huckemann[2], and Florian Rehfeldt[1] — [1]University of Göttingen, Third Institute of Physics - Biophysics, Germany — [2]University of Göttingen, Institute for Mathematical Stochastics, Germany

Mechanically induced differentiation of hMSC is dependent on Young's elastic modulus E of the microenvironment. While changes in lineage-specific protein expression occur over a period of days to weeks, the pattern formation of the cytoskeleton shows significant differences within the first 24 hours after seeding, therefore, quantified by an order parameter S, being an early morphological marker for mechano-induced differentiation [1]. We use a massively parallel live-cell imaging set-up to record cells under physiological conditions over a period of 24-48 hours to obtain a large, statistically sufficient data set. We aim for a full representation of filament processes over time and space. In contrast to the classification of stress fibers based on their location, we use an unbiased classification due to their temporal and spatial persistence. For this task we developed the 'Filament Sensor' [2, 3], a freely available tool for near real-time analysis of stress fibers. We present experimental data where we can distinguish the cytoskeletal structures of hMSCs on various elastic substrates with 99 % confidence. We are working on single filament tracking, 3D filament tracing, and correlation of focal adhesions and stress fibers. [1]A. Zemel, et al., Nat. Phys., 2010 [2]filament-sensor.de [3]B. Eltzner, et al., PLoS One, 2015

BP 9.6 Mon 17:30 P2/2OG

Modeling Interactions of Molecular Motors with Microtubule Lattice — •William Lecompte[1], Sarah Triclin[2], Laurent Blanchoin[2], Manuel Théry[3], and Karin John[1] — [1]Univ. Grenoble-Alpes, CNRS, Laboratoire Interdisciplinaire de Physique, 38000 Grenoble, France — [2]Univ. Grenoble-Alpes, CEA, CNRS, INRA, Biosciences & Biotechnology Institute of Grenoble, Laboiratoire de Physiologie Cellulaire & Végétale, CytoMorpho Lab, 38054 Grenoble, France — [3]Univ. Paris Diderot, INSERM, CEA, Hôpital Saint Louis, Institut Universitaire d'Hématologie, UMRS1160, CytoMorpho Lab, 75010 Paris, France

Microtubules and their associated molecular motors are ubiquitous in eukaryotic cells. On the one hand, short lived dynamic microtubules are essential for important cellular processes, such as mitotic spindle positioning during mitosis. On the other hand, long lived microtubules are important structural elements, for example as transport tracks for intracellular traffic. Over the past three decades the dynamic instability at the microtubule tip has been the subject of intensive research, however little is known about the dynamics of the microtubule shaft lattice. Recently it has been shown, that structural lattice defects or severing enzymes such as katanin or spastin may trigger a lattice turnover in the shaft. Here we explore with a kinetic Monte Carlo model the possibility, that the lattice strain induced by molecular motors, such as kinesin motors, may induce a localized lattice turnover. We compare our results with recent in vitro experimental observations on lattice turnover triggered by kinesin motors.

BP 9.7 Mon 17:30 P2/2OG

Length distributions of microtubules with a multistep catastrophe mechanism — •Felix Schwietert, Lina Heydenreich, and Jan Kierfeld — TU Dortmund University, 44221 Dortmund, Germany

Regarding the experimental observation that microtubule catastrophe can be described as a multistep process, we extend the Dogterom-Leibler model for dynamic instability in order to discuss the effect that such a multistep catastrophe mechanism has on the distribution of microtubule lengths in the two regimes of bounded and unbounded growth. We show that in the former case the steady state length distribution is non-exponential and has a lighter tail if multiple steps are required to undergo a catastrophe. If rescue events are possible, we detect a maximum in the distribution, i.e., the microtubule has a most probable length greater than zero. In the regime of unbounded growth, the length distribution converges to a Gaussian distribution whose variance decreases with the number of catastrophe steps. All results are verified by stochastic simulations.

BP 9.8 Mon 17:30 P2/2OG

Stochastic modeling of the tug-of-war between kinesin-1 and mammalian dynein motor proteins in intracellular transport — •Gina Antonieta Monzon[1], Lara Scharrel[2], Ashwin DSouza[2], Stefan Diez[2,3], and Ludger Santen[1] — [1]Center for Biophysics, Department of Physics, Saarland University, 66123 Saarbrücken, Germany — [2]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [3]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

Intracellular transport is a bidirectional, biased stochastic motion performed by teams of kinesin and dynein motors walking in opposite directions along microtubules. A tug-of-war between kinesin and dynein occurs since both motors are involved in the transport. Therfore, it is intringuingly to understand this tug-of-war in order to know how the cell manages targeted cargo transport. In our stochastic kinesin and dynein models [1] we include all known motor properties and a mechanical dynein activation. Studying bidirectional transport we see a blocked state, where forces between kinesin and dynein are balanced and the motors are strongly localized. Investigating the influence of ATP concentration, we see the blocked state remains stable as long as the forces are constant. Moreover, hindering roadblocks does not influence the blocked state neither because of the motor localization.

[1]: G.A. Monzon, L. Scharrel, L. Santen, S. Diez, Activation of mammalian cytoplasmic dynein in multi-motor motility assays, Journal of Cell Science, 2019.

BP 9.9 Mon 17:30 P2/2OG

Investigation and manipulation of the bacterial cell wall synthesis with super-resolution microscopy and optical tweezers — •Franziska Moos, Julian Roth, and Alexander Rohrbach — Department of Microsystems Engineering, Laboratory for Bio- and Nano-Photonics, University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

So far the process of the bacterial cell wall synthesis is not understood, in particular the geometric arrangement. The filamentous protein MreB, which is an actin homolog, plays an essential role in the bacterial cell wall. It is suggested that multiple cell wall synthesis motors couple to MreB filaments, which presumably synthesize the peptidoglycan (PG) strands of the cell wall. Therefore, the MreB filament traces reveal the trajectories of the motors and the position of the PG strands, which are usually invisible with existing technology.

We investigate the cell wall synthesis in Bacillus subtilis indirectly by measuring the motions of fluorescently labeled MreB proteins using total internal reflection fluorescent microscopy. Furthermore we exert mechanical pressure to the bacteria resulting in curvature changes of the cell wall to investigate the influence on the cell wall synthesis. This bending process is achieved by optical tweezers, where microbeads are pressed against the bacteria.

We show preliminary results of the effects of bending bacteria on the cell wall synthesis. The results are used to further strengthen the hypothesis that MreB is transported by several PG synthesis motors.

BP 9.10 Mon 17:30 P2/2OG

Investigation of transport behavior of multiple kinesin-3 motors coupled directly to membranous cargo — Ashwin D'souza[1], •Rahul Grover[1], and Stefan Diez[1,2] — [1]B CUBE, Center for Molecular Bioengineering, TU Dresden, Germany — [2]Cluster of Excellence Physics of Life, TU Dresden, Germany

KIF16B, a kinesin-3 family motor protein, can bind directly to phosphatidylinositols (PI3P) containing organelles such as early endosome and transport them, on microtubules, towards cell periphery. Recently, it was shown that the motor-membrane coupling can influence the transport efficiency of the cargo, dependent on the motor density and membrane fluidity. However, these studies were performed on a planar solid supported lipid bilayer, thus the influence of the cargo shape and size on the transport behavior were not determined. Here, we explore the behavior of ensembles of KIF16B motors transporting spherical liposomes of varying membrane fluidity and size, with a range of surface motor densities. We found that liposomes transported by multiple KIF16Bs have lower velocities compared to the stepping velocity of single KIF16B motors. Moreover, liposomes exhibited higher velocities at lower surface densities of KIF16B, compared to when being carried by higher motor densities. Liposomes driven by ensembles of KIF16B motors also exhibited stop-and-go motion, i.e. processive runs interrupted by pauses which could be an outcome of asynchronous stepping of individual KIF16B motors within an ensemble. This behavior appears to be an emergent property of multi-motor transport as the frequency of pauses for single KIF16B motors is much lower than the liposomes.

BP 9.11 Mon 17:30 P2/2OG

Active self-organization and division in nematic droplets — •Fabian Jan Schwarzendahl and Kinjal Dasbiswas — University of California, Merced, 5200 N. Lake Road, Merced, California 95343, USA

Self-organized droplets of biomaterial that grow and divide are potential models for cell behavior as well as novel realizations of active matter. Recent experiments which reconstitute actin filaments into elongated nematic droplets (tactoids) show that myosin motors self-organize at the tactoid center and subsequently deform and divide the tactoid. This recapitulates aspects of cell division in an in vitro model. We present a minimal continuum model that incorporates the nonequilibrium binding and sliding kinetics of myosin motors on the actin filaments that form a nematic droplet at equilibrium. Using simulations, we demonstrate how our model captures the essential dynamics and morphology observed in experiments. First a single tactoid is formed, then myosin motors bind and accumulate within the tactoid. The myosin motors organize actin filaments according to their polarity to from an aster in the tactoids center, which causes the tactoid to deform into two tactoids with myosin motors at their connecting center. We predict how the organization of filaments and timescales involved should differ from potential equilibrium mechanisms that drive myosin motor centering.

BP 9.12 Mon 17:30 P2/2OG

Functionalizing the microtubule lumen — •Foram Joshi[1], Hauke Drechsler[1], and Stefan Diez[1,2] — [1]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [2]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

Microtubules are hollow tubular protein assemblies of the cytoskeleton, which serve as tracks for motor proteins for the translocation of intracellular cargo. Motors proteins, when bound to a substrate surface in vitro, can be employed to propel reconstituted microtubules for nanodevice applications in molecular sorting, bio-diagnostics and nanometric surface imaging. Conventionally, in these assays the outer microtubule surface is used for cargo attachment via functionalization with biomolecules and/or nanoprobes. The resulting drawbacks are (i) 'roadblock effects', as the attached cargo can severely impede motor stepping, and (ii) varying distances between cargo and substrate surface, as microtubules while gliding, often rotate along their longitudinal axes. To overcome these limitations, we aim to encapsulate the cargo inside the microtubule lumen (15 nm). We will report on strategies to functionalize the lumen with gold-nanoparticles conjugated to lumen-targeting components such as (i) antibodies against acetylated alpha-tubulin, (ii) peptides derived from tau protein, and (iii) microtubule-inner proteins (FAP85). The resulting lumen-functionalized microtubules shall be applied for optimizing motility assays and for fabricating conductive nanowires by the directed growth of encapsulated inorganic nanoparticles along the microtubule lumen.

BP 9.13 Mon 17:30 P2/2OG

Profilin regulating the polymerisation velocity of Actin — •Lina Heydenreich and Jan Kierfeld — TU Dortmund

F-Actin, as a part of the cytoskeleton, drives crucial biological processes like cell motility, where the control of the polymerisation speed is essential. Experiments in [1] show a maximal polymerisation speed of F-actin at high concentrations of profilin and actin.

We present a kinetic model of F-actin growth in the presence of profilin and obtain an exact result for the mean growth velocity which is in agreement with stochastic simulations and explains the experimental data. The maximal growth speed is limited by the release rate of profilin from filamentous actin. In the limit where nearly all actin monomers are bound to profilin the polymerisation speed follows the Michaelis-Menten kinetics.

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

BP 9.14 Mon 17:30 P2/2OG

Hydrodynamics of a compressible film of active gel — •Li-Shing Lin[1] and Hsuan-Yi Chen[1,2] — [1]Department of Physics, National Central University, Zhongli, Taiwan — [2]Institute of Physics, Academia Sinica, Nankang, Taiwan

We construct the hydrodynamic equations for compressible soft active matters forming a film above a solid substrate. This serves as a generic model describing biological systems such as a growing tissue or the lamellipodium of an adherent cell. First, we characterize the hydrodynamic modes of our model and its passive counterpart. Next, we analyze the steady state and linearized dynamics close to it. The relation between the surface relaxation rates and bulk hydrodynamic modes are discussed, and crossover from bulklike (short-wavelength limit) to thin-film-like (long-wavelength limit) behavior is revealed.

BP 9.15 Mon 17:30 P2/2OG

Simultaneous measurement of surface and bilayer tension in a microfluidic chip — •Navid Khangholi, Ralf Seemann, and Jean-Baptiste Fleury — Experimental Physics and Center for Biophysics, Saarland University, 66123 Saarbrücken, Germany

Free-standing lipid bilayers are one of the most used model systems to mimic biological cell membranes. To form an unsupported bilayer, we employ two aqueous fingers in a microfluidic chip surrounded by an oily phase that contains lipids. Upon pushing two aqueous fingers forward, their interface gets decorated with a lipid monolayer and eventually zip to form a bilayer when the monolayers get in nanoscopic contact to each other. Using this straight forward approach, the easy and fast bilayer formation is facilitated by oil draining into the microfluidic device material consisting of PDMS. On the other hand, the oil drainage limits the lifetime of a bilayer to about one hour. We demonstrate that this drainage can be managed resulting in superior bilayer stability and to an increased lifetime of several hours when using a pressure controlled system. Applying different pressures to the aqueous fingers in the microfluidic chip, the formed bilayer can even be bent with a desired curvature. Extracting the contact angle and the resulting curvature of the bilayer region, for a given applied pressure difference, both the bilayer tension and the surface tension of each lipid monolayers can be derived from a single experiment using Young Laplace pressure equation.

BP 9.16 Mon 17:30 P2/2OG

Isolation of Plasma Membrane Lipids from Immobilized Trypanosomes for Model Membrane Studies — •Nicolas Hagedorn and Susanne Fenz — Department for Cell and Developmental Biology, Biocenter, University of Würzburg, Germany

The unicellular parasite Trypanosoma brucei exhibits a dense, but dynamic, homogeneous surface coat of GPI-anchored variant surface glycoproteins (VSGs). However, its plasma membrane is compartmentalized in three structural and functional distinct domains. In contrast to the homogeneous distribution of VSG, proteins with a GPI anchor have been reported to associate with membrane domains. For trypanosomes, the lipid composition of the plasma membrane is still unknown. We propose plasma membrane vesicles (PMVs) to enrich our understanding of the membrane composition and organization. PMVs

were prepared by an approach that combines hypotonic swelling followed by hypertonic cell shrinkage. The effects and mechanisms of vesiculation were studied using light-, and electron microscopy. Microscopic evidence suggests that the main vesiculation site was the flagellum. Moreover, the occurrence of VSGs in PMVs was validated by preparation from trypanosomes exhibiting a fluorescently tagged VSG coat. In the future, formation of solid supported lipid bilayers from PMVs will enable us to address the lipid organization as well as distribution and dynamics of VSGs in a model membrane with natural composition using single-molecule fluorescence microscopy.

BP 9.17 Mon 17:30 P2/2OG

Phase Separation and Mechanics of Biomimetic Membranes — •Valeska Rathe and Cornelia Monzel — Heinrich Heine University Duesseldorf, 40225 Duesseldorf, Germany

Under certain conditions, biological membranes are able to phase separate into liquid ordered and liquid disordered domains. To further understand, how this phenomenon affects cell processes, such as molecular aggregation during adhesion or signalling, it is important to examine changes in mechanical and thermodynamic properties of the membrane. Lipid phase coexistence can be induced via temperature change, osmotic shock or other influences. During this process, for example, the bending rigidity of the membrane changes. Liquid ordered domains display an increased bending rigidity compared to the liquid disordered domain and the pre-phase separation state. In this work, the membrane mechanical parameters are studied with giant unilamellar vesicles (GUVs) as they undergo phase separation. GUVs are lipid bilayer spheres, which serve as biomimetic models of the cell membrane. A ternary mixture consisting of DOPC, DPPC lipids and cholesterol is stimulated to phase separate under different conditions. Using the method of fluorescence flicker spectroscopy, changes in the membrane mechanical parameters are derived.

BP 9.18 Mon 17:30 P2/2OG

Is the swimming behavior of Paramecium controlled by the thermodynamic state of its membrane? — •Anne Paeger and Matthias Schneider — TU Dortmund, Deutschland

The transition of native lipid membranes appears to be tied to its growth conditions. How and why seems to be an open debate. Here we study the swimming velocity of Paramecium caudatum, which changes for different variables. Temperature-velocity curves are different for paramecia cultured at different temperatures, i.e. the living system adapts to its growth condition. In this project, we test the hypothesis that adaptation of the swimming behavior of the organism origins in the adaptation of the thermodynamic state of the membrane.

BP 9.19 Mon 17:30 P2/2OG

Influence of viscoelastic properties on the speed of sound in lipid membranes — Matthias F. Schneider and •Gregor Haider — Med. & Biol. Physik, TU Dortmund, Dortmund, Germany

There is an ongoing controversy on the physical origin of nerve pulse propagation. Besides the standard model of Hodgkin and Huxley a physical theory based on momentum conservation and thermodynamics in which density pulses form the basis of action potentials is proposed. In order to test the latter we study the velocity variation of density pulses both in theory and experiment. Indeed the velocity variation of action potentials by at least five orders of magnitude across different species and even up to 3 orders of magnitude within the same system represents an excellent test against theories for pulse propagation in biology and can hence presumably provide new clues to the current debate on the origin of the action potentials. We here explore the predictions of a thermodynamic theory of pulses and study the role of viscoelastic properties of the membrane as well as the surrounding medium on pulse propagation. We show experimentally that an increased shear viscosity of the subphase decreases the velocity of acoustic pulses in lipid monolayers in accordance with theoretical prediction. Finally, the influence of the 2-dimensional dilational surface viscosity on pulse propagation is investigated theoretically and experimentally.

BP 9.20 Mon 17:30 P2/2OG

Fusogenic Liposomes are Intrinsically Tensed — •Laura Schmitt, Rudolf Merkel, and Agnes Cziszár — Insitute of Complex Systems 7: Biomechanics, Forschungszentrum Jülich, Germany

Liposomes are popular carriers for drug molecules, which enter cells either by endocytosis or by fusion of membranes. The former process is slow and significant drug degradation occurs, the latter is most often mediated by fusogenic proteins and is thus costly and complex. Spurred by this dilemma, fusogenic liposomes were introduced by the last author of this contribution. These liposomes are formed from a ternary lipid mixture and fuse rapidly with cell membranes. Here, we explored basic physical properties of fusogenic membranes.

Therefore, GUVs (giant unilamellar vesicles) were prepared from the fusogenic lipid mixture. We examined their elastic properties using fluorescence microscopy and micropipet aspiration. Additionally, AFM compression was used.

Contrary to control GUVs, fusogenic GUVs showed no thermal fluctuations. Hence, we focused on tension-induced area dilation. We found that very high suction pressures are necessary to deform fusogenic GUVs, the resulting apparent area increases were exceptionally high. Furthermore, fusogenic GUVs could withstand much larger forces than control GUVs when compressed between parallel plates.

This behavior was attributed to an intrinsic membrane tension. We assume that this tension is caused by a coexistence of a non-lamellar lipid phase with the usual lipid bilayer. This non-lamellar phase presumably acts as a membrane reservoir.

BP 9.21 Mon 17:30 P2/2OG

Cooperativity among multiple types of receptor-ligand bonds in membrane adhesion — •Long Li[1,2] and Ana-Sunčana Smith[1,3] — [1]PULS Group, Institute for Theoretical Physics, FAU Erlangen-Nürnberg, Erlangen 91058, Germany — [2]Key Laboratory of Mechanics on Disaster and Environment in Western China, Ministry of Education, College of Civil Engineering and Mechanics, Lanzhou University, Lanzhou, Gansu 730000, China — [3]Division of Physical Chemistry, Ruder Bošković Institute, Bijenička 54, Zagreb 10000, Croatia

In biological system, receptor-ligand bonds rarely work alone and are often embedded into larger macromolecular structures involving more than one pair type. However, the effect of multiple types of receptor-ligand bonds on formation dynamics of adhesion domain is still elusive. We combine theoretical modelling and effective Monte Carlo simulations to investigate the nucleation dynamics of adhesion domains. Typically we find that in during pre-nucleating one or both types of bonds may transiently appear, in the bulk of the parameter space, only one bond type will appear in the stable nucleus of the adhesion domain. The other pair, on the other hand, has catalytic or anti-catalytic effects on the nucleating adhesions. These results not only shed light on the biophysical mechanism of cooperativity between multiple types of bonds in membrane adhesion and but also are interesting in the context of complex functionalisation of functional interfaces in biomedical engineering.

BP 9.22 Mon 17:30 P2/2OG

Optical characterization of thermodynamic states in biological systems — •Carina Fedosejevs and Matthias F. Schneider — Medical and Biological Physics, TU Dortmund

The biological function (permeability, fusion, fission, nerve puls propagation etc.) of membranes has often been hypothesized to be controlled by the thermodynamic state of the membrane rather than to be a sole property of the individual constituents. Phase transitions represent a highly non-linear change in state and are therefore very potent candidates for changes in function. Importantly, phase transitions have not only extensively been demonstrated in lipid membranes, but also in cells.

But how to detect phase states/transitions in biological systems? Incorporating fluorescence dyes into cell membranes as local reporters of state, by analyzing their optical properties (e.g. spectrum and lifetime) with high resolution, will allow us to create a map of the thermodynamic state of the cell. These state-maps, will be compared with biological processes observable with the system.

BP 9.23 Mon 17:30 P2/2OG

Simulation of biological vesicles using a phase-field approach — •Thomas Nevolianis[1], Erik Wittemeier[1], and Dmitry Chigrin[2] — [1]Dept. of Physics, RWTH Aachen University, Otto-Blumenthal-Strasse 18, 52074 Aachen, Germany — [2]DWI - Leibniz Institute for Interactive Materials, Forckenbeckstrasse 50, 52074 Aachen, Germany

The understanding of shape transformations and dynamic behavior of biomembrane vesicles is of fundamental importance in biological and physical sciences. In this study, the three-dimensional deformations of biological vesicles with prescribed volume and surface area, are nu-

merically investigated using a phase-field approach. Interactions of a vesicle with other vesicles, substrate, and fluid flow are incorporated into the theoretical and numerical model. The developed phase-field model is applied to systematically study constraint and unconstraint shape evolution of growing prebiotic vesicles.

BP 9.24 Mon 17:30 P2/2OG

Ellipsometric study of DPPC Supported Lipid bilayer formation evaporated by a solvent-free process on silicon substrates — Marcelo A. Cisternas[1], Francisca Palacios-Coddou[1], Sebastian Molina[1], Maria Jose Retamal[2], Nicolas Moraga[1], Hugo Zelada[1], Marco A. Soto-Arriaza[2], Tomas P. Corrales[3], and •Ulrich G. Volkmann[1] — [1]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]Department of Physics, UTFSM, Valparaiso, Chile

Recent interdisciplinary studies of biological molecules with physical techniques have opened an emerging field for applications in bionanotechnology. The new techniques of preparation and characterization of supported lipid bilayers (SLB) contribute to the creation of new silicon-based nanodevices, which are an important input to the field of bionanotechnology. In this research, we report the novel formation process of supported Dipalmitoylphosphatidylcholine (DPPC) bilayers evaporated directly on bare silicon surfaces by means of physical vapor deposition, without the use of a polymer cushions or solvents, i.e. in a completely dry process. High-resolution ellipsometry measurements in air, without further hydration, detect the characteristic phase transitions of DPPC bilayers: gel to ripple 311.5 +/- 0.9 K, ripple to liquid crystalline 323.8 +/- 2.5 K, liquid crystalline to fluid disordered 330.4 +/- 0.9 K. Acknowledgments: FONDECYT 1180939 (UGV), 1171047 (MS-A), FONDECYT postdoctoral 3160803 (MJR), FONDECYT Iniciacion 11160664 (TPC), PhD. scholarship CONICYT (MAC).

BP 9.25 Mon 17:30 P2/2OG

Verification of evaporated dry phospholipid bilayer formation with AFM — •Maria Jose Retamal[2], Marcelo A. Cisternas[1], Francisca Palacios-Coddou[1], Sebastian Molina[1], Nicolas Moraga[1], Hugo Zelada[1], Marco A. Soto-Arriaza[2], Tomas P. Corrales[3], and Ulrich G. Volkmann[1] — [1]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]Department of Physics, UTFSM, Valparaiso, Chile

Phospholipids are the main components of the cell membrane, and it is of great interest to study their behavior and phase transitions during temperature changes. In particular, we study bilayer systems on silicon surfaces covered with its native silicon oxide layer (Supported Lipid Bilayers or SLB) using Atomic Force Microscopy in air. For the first time the SLB were formed from their gas phase by a totally dry process and without further hydration. In these SLB it was possible to identify with AFM significant changes in the sample topography at the transition temperatures reported in the literature. The cantilever break through forces for single, double and triple bilayers have been measured. It was also found that the AFM tip is capable to modify at room temperature the -otherwise long time stable- SLB structures. These modifications are directly related to the force exerted by the tip on the SLB. Acknowledgments: FONDECYT 1180939 (UGV), 1171047 (MS-A), FONDECYT postdoctoral 3160803 (MJR), FONDECYT Iniciacion 11160664 (TPC), PhD. scholarship CONICYT (MAC).

BP 9.26 Mon 17:30 P2/2OG

Ordering of n-alkanes in lipid bilayers — •Anika Wurl and Tiago Mendes Ferreira — Inst. f. Physik - NMR, Martin-Luther Univ. Halle-Wittenberg, Halle (Saale), Germany

In this work we probe the organisation of n-alkanes in different phospholipid bilayers by determination of C-H order parameters. Though short n-alkanes have been shown to incorporate into lipid membranes [1], the dependency of alkane solubility on chain-length and volume fraction has not been investigated in detail.

Order parameters for both alkanes and lipid tails were measured by 2H NMR and proton-detected local field NMR [2]. Results from both methods agreed and showed increased ordering of the lipid bilayers upon addition of n-alkanes. Experimental order parameters were compared to order parameters calculated from molecular dynamics simulations. Using the CHARMM36 forcefield [3], simulations captured experimentally observed trends and suggested a preferred accumulation of n-alkanes between bilayer leaflets. Our results further showed that at constant volume fraction, n-alkane solubility and ordering decreased with increasing chain length. In addition, alkane organisation within the lipid bilayer was strongly dependent on bilayer hydration and the melting temperatures of both alkane and lipid.

[1] J.M. Pope et al., Biochim. Biophys. Acta 1989, 980, 69 [2] X. Zhao et al., Chem. Phys. Lett. 2001, 342, 353 [3] J. B. Klauda et al., J. Phys. Chem. B 2010, 114, 7830.

BP 9.27 Mon 17:30 P2/2OG

Comparison of Cholesterol and Ergosterol in Binary Bilayer Membranes: Insights from Molecular Dynamics Simulations — •Azadeh Alavizargar, Fabian Keller, Marc Lütgehermöller, and Andreas Heuer — University of Muenster

Cholesterol and Ergosterol are two dominant sterols in the membrane of eukaryotic cells and yeast cells, respectively. Although their chemical structure is very similar, with the exception of two extra double bonds and one methyl group for Ergosterol, their impact on the structure and dynamics of membranes differs. In this work, we have explored different points in the binary phase diagram of the mixtures of these sterols molecules with 1,2-Dipalnitoyl-sn- glycerol-3-phosphocholine (DPPC) lipid bilayer system, employing molecular dynamics simulations. The simulations revealed that Cholesterol has a stronger impact on ordering of the lipids chains with respect to Ergosterol, which likely arise from a more planar structure of the ring part as well as lower tilt angle of this sterol with respect to Ergosterol. Both sterols slightly decrease the order parameter of the pure bilayer system in gel phase and considerably increase it in liquid- ordered phase. From the dynamics point of view, addition of the two sterols leads to faster dynamics of lipids in gel phase with the opposite effect above phase transition temperature. Furthermore, Cholesterol apparently has a stronger influence on the dynamics than Ergosterol in accordance with available experimental data. These results may shed new lights on the impact of sterols on the binary mixtures of membranes.

BP 10: Poster III

Cell Mechanics (BP 10.1 – BP 10.25); Systems Biology, Evolution & Neural Networks (BP 10.26 – 10.32)

Time: Monday 17:30–19:30 Location: P2/3OG

BP 10.1 Mon 17:30 P2/3OG

A time resolved study of blood platelet spreading — •Anna Zelena[1], Magdalena Haaf[1], Sebastian Isbaner[2], Daja Ruhlandt[2], Anna Chizhik[2], Alexey Chizhik[2], Jörg Enderlein[2], Ulrich S. Schwarz[3], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Germany — [2]Third Institute of Physics - Biophysics, University of Göttingen, Germany — [3]Institute for Theoretical Physics, Heidelberg University, Germany

Human blood platelets are non-nucleated fragments of larger cells (*megacaryocytes*) and of high importance for blood clotting. The hemostatic function of platelets is directly linked to their mechanics and cytoskeletal morphology. However, the exact mechanism of spreading and contraction remains elusive. In our study we focus on the investigation of single blood platelets *in vitro* employing Traction Force Microscopy (TFM) and Metal-Induced Energy Transfer (MIET) imaging. By combined TFM and microscopy, we are able to correlate the force generation with the emerging actin structures in a time resolved manner. Our force maps show a hot spot distribution, typically in spindle-like, triangular or circular shape. Additionally, from fast scanning and static MIET experiments, we reconstruct the temporal evolution of the membrane-to-surface distance during adhesion and spreading with nanometer resolution. We observe in MIET three-dimensional height profiles, analogous to the TFM, hot spot distribution shapes of areas with lower membrane-to-surface distances.

BP 10.2 Mon 17:30 P2/3OG

Probing the real-time mechanical properties of cardiac fibroblasts using optical trap-based rheometry — •Heidi Somsel[1], Anna Blob[1], Wolfram-Hubertus Zimmermann[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen, Göttingen — [2]Institute of Pharmacology and Toxicology, University Medical Center Göttingen, Göttingen

In order to further develop treatments and cures for cardiovascular diseases (CVDs), the workings of individual components of the heart must be better understood. Cardiac fibroblasts (CFs), a primary constituent of the heart, contribute to the mechanical properties, normal homeostasis, and cell-cell communication within the heart. However, CFs were widely ignored in the past, thus creating a barrier in the development of future CVD treatments. Here, we focus on the mechanical properties of primary and stem-cell derived CFs, and how they respond to commonly used cardiac drugs. Single CFs are probed via active rheometry in a dual optical trap where a cell in suspension is caught between two beads via focal adhesions. This allows us to determine an effective cell stiffness by approximating the cell as a linear-elastic element. The optical trap is combined with a microfluidic chip permitting for a real-time readout of the response and recovery of individual cells to an applied drug. Integrating optical tweezers and microfluidics allows us to probe, for the first time, the mechanical properties of a cell in a quasi-3D environment in response to drugs in real-time.

BP 10.3 Mon 17:30 P2/3OG

Effect of channel geometry on RBC shape in microfluidic devices — •Mohammed Nouaman[1], Alexander Kihm[1], Steffen Recktenwald[1], Lars Kaestner[1,2], and Christian Wagner[1] — [1]Saarland University, Experimental Physics, Dynamic of Fluids, Campus E2 6, Saarbrücken, Germany. — [2]Saarland University, Theoretical Medicine & Biosciences, Campus University Hospital, Homburg, Germany

Red blood cells (RBCs) exhibit a broad range of different shapes in capillary flows depending on various parameters, such as flow velocity, applied pressure drop, and lateral position. In microfluidic flows in small rectangular channels (e.g. 10x12 microns), two main stable RBC shapes exist. For low-pressure drops, RBCs preferentially show a croissant-like shape, a transition toward slipper-like RBCs can be observed with the increase of pressure drop. However, the effect of the channel dimensions on this transition remains vaguely unknown. Therefore, we perform detailed statistical analysis of the RBC shapes, covering a range of microfluidic channel height and width (e.g. 10-30 microns). In order to enable an unbiased analysis of RBC shape, we further use a convolutional neuronal network CNN, which provides fast data processing and determination of the transition point between the two main stable RBC shapes.

BP 10.4 Mon 17:30 P2/3OG

Spherical harmonics analysis of *in-vivo* force probes for tissue stress quantification — •Alejandro Jurado, Bernhard Wallmeyer, Christoph Engwer, and Timo Betz — Institute of Cell Biology, ZMBE, University of Münster

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

[1] Wieczorek M.A., Meschede M., 2018. SHTools: Tools for working with spherical harmonics, Geochem. Geophys. Geosyst. 19(8), 2574-2592

BP 10.5 Mon 17:30 P2/3OG

Characterization of an ultrasonic transmitter for mechanical manipulation of cancer cells in vitro — •Simon Sommerhage[1], Hsiao-Ching Tsai[1], Monika Illenseer[1], Paul Dunst[2], Tobias Hemsel[2], and Mathias Getzlaff[1] — [1]Institute of Applied Physics, Heinrich Heine University Düsseldorf — [2]Dynamics and Mechatronics, Paderborn University

Ultrasound is a well-established medical application for diagnostic and therapeutic purposes (e.g. HIFU). In this study the effect of unfocused ultrasound with lower intensities compared to HIFU on human oral squamous cancer cells (UD-SSC-1) was investigated. Recent studies have shown that cancer cells exhibit a significantly lower Young's modulus than their healthy counterparts. This should cause a different response to external mechanical stimuli by ultrasound. According to recent study's theoretical analysis the frequency-response of a cell should show a resonance-like characteristic with a peak frequency lying within the range 10^4-10^6 Hz. To be able to test this hypothesis, the electrodynamical properties of an ultrasonic transmitter must be characterized. Therefore, the vibration velocity depending on the adjusted electrical current was measured using a laser Doppler vibrometer (Polytec LSV 60). This was done for different resonance frequencies yielding two suitable resonance modes at about 24 and 67 kHz. The UD-SCC-1 cells were irradiated and observed with an inverted light-microscope in vitro. At constant distance and vibration velocity the qualitative effect was higher for the 67 kHz than for the 24 kHz mode. These results may be a proof of principle for the cell-resonance hypothesis.

BP 10.6 Mon 17:30 P2/3OG

Endothelial cell mechanics in inflammation under shear stress inflicted by flow — •Matthias Brandt[1], Volker Gerke[2], and Timo Betz[1] — [1]Institut für Zellbiologie, ZMBE, Universität Münster — [2]Institut für Medizinische Biochemie, ZMBE, Universität Münster

Localized and tightly controlled leukocyte extravasation is a hallmark of the early inflammatory response. Whereas many cell and protein interactions regulating this process are well described, here we focus on the mechanical role of the endothelium in inflammation prior to leukocyte transmigration. Mimicking inflammation in a human umbilical vein endothelial cell (HUVEC) monolayer via chemical stimulants such as TNF-alpha, traction force and intramonolayer stress microscopy reveal a rapid (30 min) response in traction stress and even more in cell-cell stresses. The majority of cells is found to transfer increasing amounts of internal stress to their neighbors. Intuitively, the quickly altered mechanical state of the endothelium may help in guiding arriving leukocytes. As differences in mechanics for cells under flow as opposed to static conditions have been reported for HUVEC layers in a non-inflammatory state, using a microfluidic setup allowing for the preparation of micropatterned gels inside a flow chamber, we expose the endothelial cells to different levels of shear stress induced by flow. Potential contributions of altered forces among the endothelium to the transmigration process itself will be studied in future experiments via transmigration assays of human neutrophils and a controlled activation of contractility by pharmacologic and optogenetic tools.

BP 10.7 Mon 17:30 P2/3OG

Neutrophil mechanotransduction during durotaxis — •Fatemeh Abbasi, Matthias Brandt, and Timo Betz — Institute of Cell Biology, ZMBE Institute, Münster, Germany

Cell migration based on the environment stiffness gradient towards the stiffer substrate is called durotaxis. Durotaxis might be important for immune cells, since they migrate from bone marrow to the cite of infection. We hypothesized that durotaxis might be a leading factor of immune cells migration from the blood circulation to the infected tissue, since inflammation leads to swelling and stiffness increase. To investigate this hypothesis, we developed a biomimetic system to reconstitute both, the mechanical and the chemical environment of neutrophils. Cells are confined between two elastic polyacrylamide (PAA) hydrogels with controlled elastic moduli and functionalized surface chemistry. By controlling the distance between the PAA hydrogel surfaces, we vary the compression forces exerted by the substrates on the cells. We engineered a sandwich-like configuration of two elastic PAA layer with stiffness between 1 and 10 kPa and confined neutrophils in between these layers, giving them the chance of attaching to both layers simultaneously. Consistent with durotaxis, we find a striking tendency of neutrophils to detach from soft and attach to stiffer layers. We are able to track cell behavior and the cytoskeletal reorganization during the shifting from soft to stiff substrates while measuring the forces.

BP 10.8 Mon 17:30 P2/3OG

Calcium as a key regulator in Physarum polycephalum — •Björn Kscheschinski[1], Mirna Kramar[1], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen — [2]Technical University of Munich

The tubular network-forming slime mold *Physarum polycephalum* is able to maintain long-scale contraction patterns driven by an actomyosin cortex forming the tube walls. The resulting flow transports mass effectively in the organism. Recent models suggest feedback mechanisms for self-oragnized contractions by coupling the actomyosin activity to a regulating chemical, which is in turn advected by the flow. These models predict system sized contraction patterns. However, the exact effect of the regulating chemical is not yet fully understood. Here, we present ratiometric measurements of free intracellular calcium in single *Physarum* tubes suggesting an inhibitory effect of calcium on the acto-myosin activity. The spatio-temporal patterns of the free calcium concentration reveal an anti-correlated relation to the tube diameter, while the main patterns of the contractions are preserved. By controlling the morphology of *Physarum* we can relate our experimental data directly to numerical simulations with simple geometries. Our results suggest that calcium is a key regulator of the acto-myosin activity enabling the organized flow patterns emerging in *Physarum* networks. Thus, our findings might allow further insights into processes in *Physarum* related to the flows.

BP 10.9 Mon 17:30 P2/3OG

Elastic beads as tension sensors to measure the spatial force distribution in reconstructed muscle — •Tamara Limón, Arne Hofemeier, Alejandro Jurado, Bernhard Wallmeyer, and Timo Betz — University of Münster, ZMBE, Institute for Cell Biology

The quantification of forces within the niche of skeletal muscles has gained an increasing importance in the field of regenerative medicine especially in terms of satellite cell (SC) activation. Recent studies have shown that force sensors based on known material properties are a useful tool to analyze cell mechanics. Here, we present a technique using characterized elastic beads as tension sensors to measure forces in reconstructed muscle. The elastic beads are seeded together with the myoblast cell line C2C12 into a fibrin-geltrex scaffold on a silicon substrate to generate a three-dimensional *in vitro* muscle. Due to the deformation of incorporated beads we calculated the tension present in 7-day old muscles by a custom-made bead analysis software. First results indicate differences in force axes and in magnitude of bead deformation giving rise to a spatial force distribution ranging between 1.6 - 4.1 kPa tension in the muscle. A possible explanation might be related to dissimilar stress fiber formation with thicker stress fibers at the lateral sides. Understanding the aspects of a spatial force distribution in muscles could enlighten mechanisms involved in SC activation and improve handling with SC for gene therapy.

BP 10.10 Mon 17:30 P2/3OG

Active and passive microrheology for measurement of intracellular mechanics — •Till Münker, Sebastian Hurst, and Timo Betz — Institute of Cell Biology, University of Muenster, Muenster, Germany

Active mechanics that arises from ATP consuming processes like molecular motors or cytoskeletal polymerization have been shown to play an important role for fundamental cellular processes such as proliferation, migration or morphology. However, studies on understanding the more general principles that dictate force generation in this complex structure are missing. Using an optical tweezers based active-passive microrheology approach we determine the viscoelastic shear modulus and the free fluctuations of phagocytosed particles in different cell types. These measurements give access to an effective energy that is indicative for the cellular activity. By comparing the results from different cell types such as epithelial, carcinoma, muscle and immune cells we observe that all cell types follow a similar energy-frequency dependency. We then compared the outcome of these experiments to a simplified model that describes the cytoskeleton as a viscoelastic cage. In our model, we assumed the cytoskeleton to be a soft glassy material which is displaced by a single random force on a distinct timescale. In this approach the functional dependence of the effective energy is determined by the viscoelastic material properties. First experiments confirm this model where a small set of parameters can describe the overall mechanical activity within the cytosol across various cell types.

BP 10.11 Mon 17:30 P2/3OG

Determining the viscoelastic shear modulus of zebrafish embryos during embryogenesis on the tissue scale — •Julian Vondereck, Sebastian Hurst, Bart Vos, and Timo Betz — University of Münster, ZMBE, Institut of Cell Biology

Understanding the physical principles of collective cell movements is key to acquiring deeper knowledge about fundamental biological processes ranging from wound healing over metastatic cancer invasion to development. A distinguished model to study these processes is collective cell migration in embryogenesis. The first coordinated tissue motion in a zebrafish embryo is called epiboly, where the blastocyte cells spreads over the yolk cell. To understand the mechanical properties during this process, we use in vivo, optical tweezer based microrheology. Epiboly can be described by the behavior of the three embryonic regions: the epithelial monolayer or enveloping layer (EVL), the yolk syncytial layer (YSL) and the deep cells (DEL) of the blastoderm. EVL, YSL and DEL all undergo epiboly. 10 micrometer sized particles are microinjected in these regions as tissue-based probes. Microrheology in vivo allows to determine the viscoelastic shear modulus on the tissue scale, while resolving spatial and temporal changes during development. Illuminating cell and tissue differentiation on the different regions in general and at certain key points is to be expected. This provides new insights into the biomechanical processes controlling collective cell movements, of which a detailed understanding yet remains elusive.

BP 10.12 Mon 17:30 P2/3OG

Microrheology of human umbilical vein endothelial cells using Acoustic Force Spectroscopy — •Alfred Nguyen and Timo Betz — Institute of Cell Biology, University of Münster, Münster, Germany

We present a novel method for microrheology using acoustic forces in the range of pN-nN to oscillate particles inside a microfluidic chip. For this method we used the Acoustic Force Spectroscope (AFS) which was introduced as a single-molecule technique to measure mechanochemical properties of biomolecules in parallel. Our new application for the AFS enables the measurement of the dynamics of the viscoelastic properties of cells exposed to different conditions, such as flow shear stresses or drug injections. To validate our new method for microrheology on living cells in vitro, we cultured a monolayer of human umbilical vein endothelial cells (HUVEC) inside the measurement chip and exerted oscillatory forces on particles attached on top of the cells. By determining the force and measuring the position of the particle, the complex shear modulus $G^*(\omega)$ could be measured. We confirm a decrease in shear modulus after perturbing actin polymerization by cytochalasin B. This effect was reversible after washing the drug out. Although these measurements are possible, we provide a critical discussion of the AFS showing its advantages as well as its drawbacks and how to process the obtained data.

BP 10.13 Mon 17:30 P2/3OG

Elastic beads as cellular tension sensors within muscle tissue — •Arne Hofemeier[1,2], Tamara Limon[1], Till Münker[1], Alejandro Jurado[1], Bernhard Wallmeyer[1], Penney Gilbert[2], and Timo Betz[1] — [1]Institute of Cell Biology, University of Münster, Germany — [2]Donnelly Centre, University of Toronto, Canada

Mechanical tension has recently been recognized as a key element to understand many biological processes such as cell fate determination or collective cell migration. For instance, muscle stem cells are known to strongly react to changes of physical properties of their microenvironment in vitro. However, direct experimental access to determine mechanical tension in cellular niches remains a major challenge. Here, we present a novel experimental approach that allows direct measurement of mechanical stress inside in vitro and in vivo muscle tissue. By injecting fluorescent polyacrylamide (PAA) beads of known size and elasticity into muscle tissues, we are able to measure the deformation of their surface and obtain the resulting force exerted on the bead. With this in hand, we show three applications of this novel technique. Firstly, PAA beads were incorporated into biomimetic muscle tissue in order to trace cellular tension during development and diseased tissues. Secondly, elastic beads were injected into zebrafish embryos to investigate tissue stress on muscle cells during late embryogenesis in vivo. Lastly, we transplanted PAA beads into injured EDL muscles of mice to evaluate local forces after 3 weeks of muscle regeneration for the first time.

BP 10.14 Mon 17:30 P2/3OG

Three-dimensional modeling of a viscous active cell cortex — •Christian Bächer[1], Diana Khoromskaia[2], Guillaume

Salbreux[2], and Stephan Gekle[1] — [1]Biofluid Simulation and Modeling, Theoretische Physik VI, Universität Bayreuth, Germany — [2]The Francis Crick Institute, London, UK

In a biological cell active mechanical stresses in the cortex can lead to flows resulting in strong deformations. We use a thin shell formulation of an active gel in the viscous limit [1] to build a numerical model of a fully three dimensional viscous, active cell cortex. For given active stress distribution, we numerically determine the flow field in the cortex, which directly gives the triggered deformation. Our algorithm consists of two parts: first, a minimization ansatz solves the force balance in presence of viscous and active stresses on the triangulated, three-dimensional cortex. Second, the viscous stresses at a node are expressed in terms of the velocity vectors of the neighboring nodes using an analytically inverted parabolic fitting procedure. Together, this leads to a system of equations which we solve numerically for the flow field on the discretized cortex. Our algorithm provides a versatile and flexible tool, which can easily be extended, e.g., to an active stress coupled to a concentration field, and furthermore allows for a dynamic coupling of the cell cortex to an inner and surrounding fluid.

[1] G. Salbreux, F. Jülicher, Phys. Rev. E 96(3), 2017

BP 10.15 Mon 17:30 P2/3OG

Cryo Scanning Electron Microscopy investigations on penetration of Titanium dioxide particles in human skin — •Hanna-Friederike Poggemann[1], René Gustus[1], and Wolfgang Maus-Friedrichs[1,2] — [1]Clausthal Centre of Material Science, Agricolastraße 2, 38678 Clausthal-Zellerfeld, Germany — [2]Institute of Energy Research and Physical Technology, Leibnizstraße 4, 38678 Clausthal-Zellerfeld, Germany

Titanium dioxide nanoparticles can be found in a lot of cosmetically products as for example sunscreen. Titanium dioxide (TiO2) is not toxic for humans in micrometer size but the Nano sized particles have different material properties. TiO2 nanoparticles are for example photocatalytic active and so able to damage human cells if they get in to the living dermal layers. Previous studies have pointed out that most particles cannot penetrate the topmost dermal layer, the stratum corneum. Accordingly only a small amount of the TiO2 gets into the living cell area. But several studies also underlined the necessity of further research especially in the case of previously damaged skin. (According to actual statistics 14 % of all children und up to 3 % of the adults in Germany suffer from neurodermatitis and particularly for those persons it is inevitable to use sunscreen on their skin) In this regard we analyzed the TiO2 nanoparticles of commercially available sunscreens in our FE-SEM by SEM and EDX. Furthermore we examined samples of human skin with and without sunscreen treatment by Cryo-SEM and Focused Ion Beam to prove that out method is appropriate for continuing research on this subject.

BP 10.16 Mon 17:30 P2/3OG

Measuring intracellular stiffness in epithelial cells — •Bart E. Vos[1], Sebastian Hurst[1], Ying Zhang[2], Paul H.J. Kouwer[2], and Timo Betz[1] — [1]Institute of cell biology, ZMBE, Münster, Germany — [2]Spectroscopy and Catalysis, Radboud University, Nijmegen, the Netherlands

Epithelial cells form the boundary between an organ (or an entire organism) and its environment. Hence, epithelial cells experience a strong asymmetry in their environment: "out" versus "in". It is therefore not surprising that epithelial cells are strongly polarized; for example, the actin meshwork is denser at the apical, or "outward facing"-side of the cell, while the nucleus is always located at the basal, or "inward facing"-side of the cell. However, to date it remains unclear if and how polarity is established and maintained by a gradient in intracellular stiffness and/or motor activity. Furthermore, since the extracellular matrix (ECM) is of crucial importance to cells, we hypothesize that variations in the extracellular matrix also have an influence on intracellular mechanics.

Here I will present a project that focuses on measurement of intracellular stiffness and activity in MDCK-cells. Using both active and passive microrheology, we obtain cellular stiffness and activity as a function of position within the MDCK-cell. Using a synthetic, biomimicking ECM, we systematically vary the mechanical environment of the epithelial cells, where we observe a strong response in the shape and growth rate of the cells.

BP 10.17 Mon 17:30 P2/3OG

Target size dependency of cellular resolution limits during phagocytosis — •Manuel Eisentraut, Adal Sabri, and Holger Kress — Biological Physics Group, Department of Physics, University of Bayreuth, Germany

Antibodies can interact with phagocytic receptors on macrophages and trigger signalling cascades which initiate phagocytosis. A large number of the molecular components of these signalling networks are well known, but it remains unclear how fast and how far the corresponding signals propagate in the cell.

To address this issues, we investigated the spatial spreading of phagocytic signalling by measuring how well cells can resolve whether one or two particles are attached to the cell membrane. In our experiments, we attach pairs of equally-sized polystyrene beads opsonized with antibodies to single macrophages. We were able to precisely control the distance of the beads during the attachment by utilizing holographic optical tweezers. The subsequent uptake into two separate or one joint phagosome was distinguished by analysing the intracellular particle trajectories after the uptake. We found that the probability for separate uptake is very high for large distances and very low for small distances, with a transition between these regimes at surface-to-surface distances of several hundreds of nanometers. A comparison between measurements with different bead sizes suggests that the separate uptake probability not only depends on the bead distance, but also on the total size of the target bead pair. Our results provide quantitative insights into the spatial spreading of signalling during phagocytosis.

BP 10.18 Mon 17:30 P2/3OG

Characterization of cell deformability in patients with major depressive disorder — •Lisa Kwapich[1], Tobias Neckernuss[1,2], Daniel Geiger[1,2], Jonas Pfeil[1,2], Patricia Schwilling[1], Alexander Karabatsiakis[3], Iris-Tatjana Kolassa[3], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Sensific GmbH — [3]Institute of Psychology and Education, Ulm University

Major depressive disorder is a debilitating disease that affects more than 300 million people worldwide. Despite advances in the understanding of the etiology of major depression, no established mechanism can explain all aspects of the disease. A promising approach in this context is the analysis of mechanical cell properties by deformability cytometry. The method probes cell stiffness at high throughput by exposing cells to a shear flow in a microfluidic channel, allowing for mechanical phenotyping based on single-cell deformability. The advantage of this method is that cells are purely deformed by hydrodynamic interactions and without contact with channel walls. The deformability of cells is indicative of underlying membrane, cytoskeletal, or nuclear changes associated with changes in cell state and various disease processes. We investigated differences in deformability of peripheral blood mononuclear cells between patients with major depressive disorder and non-depressed control subjects. A custom-built algorithm (ODIN technology) was used for image analysis, data collection, and postprocessing analysis. The algorithm detects the presence of a cell, determines its contour, and quantifies several parameters.

BP 10.19 Mon 17:30 P2/3OG

What thermal fluctuations of an optically trapped bead can tell us about the properties of an interface — •Tetiana Udod, Felix Jünger, and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, IMTEK, University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

Thermal position fluctuations of optically trapped beads can be measured in 3D with nanometer precision at MHz rates with back focal plane interferometry. The bead fluctuations change in amplitude and time upon interaction with interfaces, which can be characterized by different surface potentials or viscosities. Bead position fluctuations encode the hydrodynamic momentum transfer and repulsion at plane glass coverslips, giant unilamellar vesicles or even living cells, with complex and dynamic surface structures. However, defining and determining the contact between the fluctuating bead and an interface is far from trivial. When studying particle binding and induction of the phagocytic uptake pathway, the following question is of particular interest: When does a cell start to feel an approaching particle? To better understand such processes taking place on very small length and time scales, we first analyze the position fluctuation at simplified interface systems. Therefore, we use combination of experiments with Photonic Force Microscopy, Brownian Dynamic simulation and analytical theory to model and explain the impact of surface potentials and viscosities on the 3D bead position fluctuations. This allows us to identify the contact point and thereby to measure distance -dependent interactions even of living cells.

BP 10.20 Mon 17:30 P2/3OG

Adherent Cell Optical Stretcher: Quantifying Laser Induced Heating — •Alexander Janik[1], Tobias Neckernuss[1], Cornelius Maurer[1], Seiichi Uchiyama[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Graduate School of Pharmaceutical Sciences, The University of Tokyo

Cell stiffness is a valuable indicator for cell functionality, especially in cell types that naturally undergo strong mechanical deformation, such as alveolar epithelial cells. We therefore recently developed a method to stretch adherent cells with a parallel laser beam to determine their viscoelastic properties.

The impact on cells is kept low, for they are stretched uniformly, and the procedure does not require fluorescent labeling. However, heating induced by the 800 nm stretching laser is a side effect. Our contribution focuses on quantification and real-time monitoring of intracellular temperature change during the stretching process. A ratiometric temperature dependent fluorescent dye is used whose two emission bands are detected simultaneously on two cameras. Improvements of the setup for cell height detection, which currently employs beads as markers, are also discussed.

BP 10.21 Mon 17:30 P2/3OG

Why do rigid tumors contain soft cancer cells? — •Thomas Fuhs[1], Franziska Wetzel[1], Anatol W. Fritsch[1], Dapeng Bi[2], Roland Stange[1], Steve Pawlizak[1], Tobias R. Kiesling[1], Erik Morawetz[1], Steffen Grosser[1], Frank Sauer[1], Jürgen Lippoldt[1], Fred Renner[1], Sabrina Friebe[1], Mareike Zink[1], Bahriye Aktas[3], Lars-Christian Horn[3], Klaus Bendrat[4], Axel Niendorf[4], Michael Höckel[3], and Josef A. Käs[1] — [1]Leipzig University, Germany — [2]Northeastern University, Boston, USA — [3]University Hospital Leipzig, Germany — [4]Pathology Hamburg-West, Germany

Palpatation used since acient times, utilizes that solid tumors are stiffer than surrounding tissue. However, cancer cell lines are softer, which facilitates invasion. This paradox raises several questions: Does softness emerge from adaptation to mechanical and chemical cues in the external microenvironment? Or are soft cells already present inside a rigid primary tumor? We investigate primary samples from patients with mammary and cervical carcinomas on multiple length scales from tissue level down to single cells. We show that primary tumors a highly heterogeneous in their mechanical properties on the tissue level as well as cells do exhibit a broad distribution of rigidities, with a higher fraction of softer and more elongated cells compared to normal tissue. Mechanical modelling based on patient data reveals that tumors remain solid containing a significant fraction of very soft cells. Moreover, it predicts that in such tissues, softer cells spontaneously self-organize into multicellular streams, which we observe experimentally.

BP 10.22 Mon 17:30 P2/3OG

Using real-time fluorescence and deformability cytometry and deep learning to transfer molecular specificity to label-free sorting — •Ahmad Ahsan Nawaz[1], Marta Urbanska[1,2], Maik Herbig[1], Martin Kraeter[1], Marketa Kubankova[1], Salvatore Girardo[1], Angela Jacobi[1], and Jochen Guck[1] — [1]Max Planck Institute for the Science of Light, Erlangen — [2]Biotec, Technische Universität Dresden

The identification and separation of specific cells from heterogeneous populations is an essential prerequisite for further analysis or use. Conventional passive and active separation approaches rely on fluorescent or magnetic tags introduced to the cells of interest through molecular markers. Such labeling is time- and cost-intensive, can alter cellular properties, and might be incompatible with subsequent use, for example, in transplantation. Alternative label-free approaches utilizing morphological or mechanical features are attractive, but lack molecular specificity. Here we combine image-based real-time fluorescence and deformability cytometry (RT-FDC) with downstream cell sorting using standing surface acoustic waves (SSAW). We demonstrate basic sorting capabilities of the device by separating cell mimics and blood cell types based on fluorescence as well as deformability and other image parameters. In addition, the classification of blood cells using established fluorescence-based markers provides hundreds of thousands of labeled cell images used to train a deep neural network. The trained algorithm is then used to identify and sort unlabeled blood cells. This approach transfers molecular specificity into label-free sorting.

BP 10.23 Mon 17:30 P2/3OG

A Machine Learning Approach to Computing the Traction Field of Adherent Cells — •Martin Kolaczek, Timo Betz, and Christoph Engwer — Institute for Cell Biology, University of Münster

Adherent cells exert tractions on their surrounding in the course of a variety of cell functions including contraction, spreading, crawling and invasion. Using Traction force microscopy, these forces can be measured by observing the displacements of beads embedded on a flexible hydrogel gel substrate. Computing the traction field algorithmically is computationally intensive, hence making a real time evaluation of traction forces impossible. To overcome this challenge, we pursue a different data-intensive approach to solve this task by harnessing the power of machine learning. Our first and utmost objective is to speed up the computation of the traction field to get a near-instantaneous computation of the traction field during measurement accepting a trade-off for accuracy. Since observing the displacement of beads is time-consuming, an assessment of the measurement right at the beginning is desirable. First attempts with artificially generated data was a success. Using ensembles of white pixels on a black background and generating single pixel and more complex displacements and to a field allowed training a deep neuronal network. This neural network was able to compute displacements with high accuracy with high speed. The next step will be to extend the given model to process real data. Noise and vanishing particles are some of the obstacles to cross.

BP 10.24 Mon 17:30 P2/3OG

Visualisation of cytoplasmic flows in epithelial cells by single particle tracking — •Christoph Engwer, Mariam Ristau, and Timo Betz — Institute of Cell Biology, Center for Molecular Biology of Inflammation, Münster, Germany

Correct polarization of epithelial cells is highly important for tissues to perform their respective function. Failure during polarity formation is connected to different diseases such as polycystic kidney disease and malignant cancers. Whereas biochemical signalling, responsible for establishing cellular polarity is well understood, only little is known about the mechanical processes that play a role during polarity formation. In this project, we investigate how cytoplasmic flows may influence cellular polarity or vice versa. As model system, we use spherical cysts made from kidney epithelial cells from domestic dog (MDCK). These cysts form within three to four days when grown in a pseudo-3D environment of extra cellular matrix components. Prior to cyst formation, far-red labelled nanoparticles that serve as tracers for intracellular flows, are ballistically injected into the cells. For the analysis of intracellular flows, we develop a Python based single particle tracking software based using Trackpy. Cysts are imaged over time and particle tracks are obtained from maximum intensity projections around the equatorial plane. To gain average values, cells are registered using labelled nuclei and F-actin. After rotating and projecting each cell into a unit cell, we obtained activity maps of intracellular particle movement.

BP 10.25 Mon 17:30 P2/3OG

stress stiffening of suspended cells — •elham mirzahossein[1], sebastian muller[2], stephan geckle[2], and ben fabry[1] — [1]University of Erlangen-Nuremberg — [2]Department of Physics, university of Bayreuth

The stiffness of adherent cells has been shown to increase linearly with contractile (pre-) stress of the cytoskeleton and externally applied stress. Previous studies of suspended cells that are forced through small microfluidic constrictions reported the same stress stiffening behavior as in adherent cells, however, the mechanical loading of cells in a microfluidic constriction is complex. to overcome these limitations, here we measure the deformations of adherent suspended cells in response to simple shear stress. nih-3t3 fibroblasts are mixed in shear-thinning 2% alginate solution and are pressed at 1-3 bar through a $200 \times 200\ \mu m$ and 5 cm long microfluidic channel. the shear stress is zero in the channel center and increases linearly towards the walls. as a consequence, cells appear round in the channel center and become elongated towards the walls, with aspect ratios of up to 3. the Taylor strain,ϵ , of the cells versus fluid shear stress, σ, shows a non-linear relationship. This relationship is well described by a differential cell stiffness of the form $E = \frac{\partial \sigma}{\partial \epsilon} = E_0 + \alpha \cdot \sigma$. Cell stiffness is$E_0 = 100Pa$ at low shear stress and linearly increases with shear stress with a factor $\alpha = 8$. at the highest shear stress value of 300 Pa that we apply in our study, differential cells stiffness increases to 1700 pa on average. thus, our measurements of suspended cells show a pronounced stress stiffening that is similar to the behavior found in adherent cells.

BP 10.26 Mon 17:30 P2/3OG

A dynamic model for proteome partitioning — •Anne-Lena Moor, Kalok Kam, and Stefan Klumpp — Institut für Dynamik komplexer Systeme Georg-August-Universität Göttingen

To reproduce as efficiently as possible, bacteria adapt their proteome and metabolism to different environments with different nutrient availability. A key ingredient of this adaptation is the regulation of the fraction of ribosomes in the proteome, which is subject to simple growth laws. In this work, the growth laws are used to analyze the dynamics of cell growth and proteome adaptation, specifically how the ratio of ribosomes to metabolic proteins is modulated to achieve the maximal growth rate. A model is presented that describes the dynamics of this regulation.

BP 10.27 Mon 17:30 P2/3OG

Coupling of growth, replication and division in E. coli — Mareike Berger and •Pieter Rein ten Wolde — AMOLF, Amsterdam, the Netherlands

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

BP 10.28 Mon 17:30 P2/3OG

Robust ligand discrimination by dimeric membrane receptors — •Patrick Binder[1,2,3], Nikolas Schnellbächer[1,2], Nils Becker[2,3], Thomas Höfer[2,3], and Ulrich Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, Heidelberg, Germany — [2]BioQuant, Heidelberg University, Heidelberg, Germany — [3]Division of Theoretical Systems Biology, German Cancer Research Center, Heidelberg, Germany

Many cytokine pathways transduce signals across the cell membrane via ligand-induced receptor dimerization. As differences in cellular response show, the dimeric Interferon-I receptor system can not only sense ligand concentration, but also discriminate between different types of ligand that all bind to the same receptor type. Here we investigate, using information-theoretic methods, which architectural features optimize the ligand discrimination performance of receptor systems. By defining a basic ligand discrimination task and comparing monomeric, homodimeric and heterodimeric receptors, we find that each step in complexity improves the sensory mutual information. We first observe that monomeric receptors are insufficient to sense the ligand presence and type simultaneously. Second, due to the bell-shaped activation curve, the affinity of dimeric receptors is encoded in the maximal activation. Third, asymmetric binding of ligand to heterodimeric receptors broadens the maximum into a plateau, which buffers concentration fluctuations in the physiological range of the type-I interferon system. Fourth, additional turnover of receptors further steepen the response and broaden the plateau.

BP 10.29 Mon 17:30 P2/3OG

Exploring theoretical limits for the lifespan of C. elegans dauer larvae under periodic feeding — xingyu zhang[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

Extending lifespan of organisms has long been an appealing topic of biological sciences. Recent experimental work demonstrated that the lifespan of C. elegans dauer larvae could be extended by providing them with external ethanol solution as a carbon source. A mathematical model for the simplified metabolic network of the dauer allowed us to explain the lifespan prolongation and two possible mechanisms leading to the death of the worm. The model relates the well-being of the worm to its mitochondria, which can be irreversibly damaged either by starvation or toxic compounds accumulated during metabolism. However, by incorporating two omitted but important mechanism into the model, namely degradation of toxic compounds and regeneration of mitochondria, we can extend the survival of dauers even further by choosing an optimal feeding protocol. Thus, modified model reproduces the experimental observation when the feeding ethanol concentration stays constant in time. However, when the feeding ethanol concentration varies as a sinusoidal function, the model gives rise to solutions where the worm lives forever. Detailed analysis of the model suggests that large amplitude and moderate frequency of the periodic feeding give better chances for the worm to have an infinite lifespan, which we now plan to test experimentally.

BP 10.30 Mon 17:30 P2/3OG

Embryonic lateral inhibition as optical modes — •Jose Negrete Jr and Andrew C Oates — École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland

Spatial gene expression patterns define regions where specialised cells emerge within an embryo. Lateral inhibition is a common mechanism that creates fine grained patterns with a characteristic wavelength of the size of 2 cells. Here we developed a generic model for patterning with lateral inhibition, and study its characteristics by making an analogy with crystal phonons from solid state physics. The tissue is redefined in terms of a Bravais lattice where the basis of the crystal contains two to three cells. The steady states are analogous to the optical modes of phonons. The model predicts that there are two different lateral inhibition states that can coexist in a certain parameter regime. Finally, our work suggests that gene expression patterns can be thought as crystal phonons, where long wavelength (Turing like) patterns corresponds to accosting modes and lateral inhibition patterns to optical modes.

Reference: Negrete Jr J and Oates AC, Phys Rev E 99, 042417 (2019)

BP 10.31 Mon 17:30 P2/3OG

Nonlinear response of noisy neurons with spike-triggered adaptation — •Christoph H. Egerland[1] and Benjamin Lindner[1,2] — [1]Humboldt-Universität zu Berlin, Berlin, Germany — [2]Bernstein Center for Computational Neuroscience, Berlin, Germany

A basic question in neuroscience is how a noisy neuron responds to an external stimulus signal. For weak stimuli, typically only the linear response in the firing rate has been considered. More recently, the weakly nonlinear response to periodic stimulu has been in the focus, demonstrating pronounced effects in particular for stimuli consisting of two harmonic signals [1]. Here we extend this analysis to neurons with adaptation currents because it is unclear how these slow currents that are present in many cells will affect the weakly nonlinear response. We show results obtained from simulations and compare them to analytically obtained expressions in the appropriate limits.

[1] Voronenko & Lindner New J. Phys. 19, 033038 (2017)

BP 10.32 Mon 17:30 P2/3OG

Influence of the mechanical environment on neuronal maturation — •Eva M. Kreysing, Hélène O. B. Gautier, Ragnhildur T. Káradóttir, and Kristian Franze — University of Cambridge

During the development of the nervous system, neurons extend long axons as well as shorter and highly branched dendrites to connect to other cells. Once integrated in the neuronal network, neurons mature and the conductivity of their cell membrane changes for certain ion types, resulting in their electrical activity. While mechanical interactions between neurons and their environment are crucial for axon growth and pathfinding, the influence of mechanical signals on neuronal maturation is currently poorly understood. Here, we cultured primary hippocampal neurons on polyacrylamide gels of different stiffness and studied how substrate mechanics impacts the electrical maturation of the cells using Patch-Clamp measurements. Currents through voltage-gated sodium channels, potassium channels, as well as spontaneous activity all started several days earlier in neurons cultured on soft substrates if compared to stiff substrates. These differences in the onset of electrical activity were accompanied by increased synaptic densities on soft substrates as assessed by immunocytochemistry. Our results suggest that mechanical signals play an important role in neuronal maturation, and that local brain tissue stiffness may thus be a key parameter for proper brain development.

BP 11: Data analytics for dynamical systems I (Focus Session joint with DY and BP) (joint session SOE/DY/CPP/BP)

Data analytics is often focussed on (generalized) regression to create models of the structure of complex systems. Here we focus on data-driven approaches of data analytics for complex systems that take into account their intrinsic nonlinear dynamics. Applications to natural and human-made systems, from cardiac dynamics to human mobility, illustrate recent progress and current methodological challenges. (Session organized by Marc Timme)

Time: Tuesday 9:30–13:15 Location: GÖR 226

Topical Talk BP 11.1 Tue 9:30 GÖR 226

One model to rule them all — •Jens Timmer — Institute of Physics, University of Freiburg, Germany

A major goal in systems biology is to reveal potential drug targets for cancer therapy. A common property of cancer cells is the alteration of signaling pathways triggering cell-fate decisions resulting in uncontrolled proliferation and tumor growth. However, addressing cancer-specific alterations experimentally by investigating each node in the signaling network one after the other is difficult or even not possible at all. Here, we use quantitative time-resolved data from different cell lines for non-linear modeling under L1 regularization, which is capable of detecting cell-type specific parameters. To adapt the least-squares numerical optimization routine to L1 regularization, subgradient strategies as well as truncation of proposed optimization steps were implemented. Likelihood-ratio tests were used to determine the optimal penalization strength resulting in a sparse solution in terms of a minimal number of cell-type specific parameters that is in agreement with the data. The uniqueness of the solution is investigated using the profile likelihood. Based on the minimal set of cell-type specific parameters experiments were designed for improving identifiability and to validate the model. The approach constitutes a general method to infer an overarching model with a minimum number of individual parameters for the particular models.

BP 11.2 Tue 10:00 GÖR 226

Volatility and Fractionality in Power-Grid Frequency — •Leonardo Rydin Gorjão[1,2], Anton Yurchenko-Tytarenko[3], and Dirk Witthaut[1,2] — [1]Forschungszentrum Jülich, Institute for Energy and Climate Research - Systems Analysis and Technology Evaluation (IEK-STE), 52428 Jülich, Germany — [2]Institute for Theoretical Physics, University of Cologne, 50937 Köln, Germany — [3]Department of Mathematics, University of Oslo, P.O. Box 1053 Blindern, N-0316 Oslo

Power-grid frequency is a key indicator of stability in power grids. The trajectory of power-grid frequency embodies several processes of different natures: the control systems enforcing stability, the trade markets, production and demand, and the correlations between these. In this article, we study power-grid frequency from Central Europe, the United Kingdom, and Scandinavia under the umbrella of fractional stochastic processes. We introduce an estimator of the Hurst index for fractional Ornstein–Uhlenbeck processes. We show that power-grid frequency exhibits time-dependent volatility, driven by daily human activity and yearly seasonal cycles. Seasonality is consistently observable in smaller power grids, affecting the correlations in the stochastic noise. The United Kingdom displays daily rhythms of varying volatility, where the noise amplitude consistently doubles its intensity, and displays bi- and tri-modal distributions. Both the Scandinavian and United Kingdom power-grids exhibit varying Hurst indices over yearly scales. All the power grids display highly persistent noise, with Hurst indices above $H > 0.5$.

Topical Talk BP 11.3 Tue 10:15 GÖR 226

Gaming the system - Analyzing Uber price data reveals anomalous supply shortages — •Malte Schröder[1], David Storch[1], Philip Marszal[1], and Marc Timme[1,2] — [1]Chair for Network Dynamics, Institute for Theoretical Physics and Center for Advancing Electronics Dresden (cfaed), TU Dresden — [2]Lakeside Labs, Klagenfurt

Dynamic pricing schemes are ubiquitously employed across industries to balance demand and supply. One well-known example is the ride-hailing platform Uber and their *surge pricing* intended to incentivize drivers to offer their service during times of high demand. However, recent reports [WJLA, Uber, Lyft drivers manipulate fares at Reagan National causing artificial price surges (2019)][Möhlmann and Zalmanson, ICIS 2017 Seoul (2017)] indicate that this surge pricing may instead cause demand-supply imbalances by incentivizing drivers to switch off their app to increase their revenue. Analyzing price estimate time series for trips from 137 locations in 59 urban areas across six continents, we identify locations with strong, repeated price surges. Correlations with demand patterns demonstrate that the observed price surges are indeed driven by supply anomalies instead of demand fluctuations. Moreover, we capture the minimal incentives driving the supply dynamics in a simple game-theoretic model, illustrating that such incentives constitute generic consequences of dynamic pricing schemes.

BP 11.4 Tue 10:45 GÖR 226

Estimation of Langevin equations with correlated noise for signals of complex systems — •Clemens Willers and Oliver Kamps — Institut für Theoretische Physik, Westfälische Wilhelms-Universität Münster, Germany

Over the last years, the estimation of stochastic evolution equations of complex systems has been applied in many scientific fields ranging from physics to biology and finance. Especially, Langevin models with delta-correlated noise terms, which realize a Markovian dynamic, have been used successfully in this context [1]. However, many real world data sets exhibit correlated noise and a non-Markovian dynamic, for example data sets from turbulence [2].

To tackle this problem, we use Langevin models containing an added hidden component which realizes a driving correlated noise. We develop two methods for the systematic estimation of the drift- and diffusion functions, parameterized through spline functions. The first method is based on a likelihood function which is constructed by a short-time propagator for the measured values of the visible component. For the second method, we use a comparison of transition probabilities via Jensen-Shannon divergence. Both methods are demonstrated using real world data sets as the turbulent air flow of a free jet [3], stock market prices [4] and wind energy production [5].

[1] Friedrich et al., Phys. Rep. 506, 87 (2011) [2] Friedrich et al., Phys. Rev. Lett. 78, 863 (1997) [3] Renner et al., J. Fluid Mech. 433, 383 (2001) [4] Nawroth et al., Eur. Phys. J. B 50, 147 (2006) [5] Kamps, in Wind Energy-Impact of Turbulence, Springer 2014, p. 67.

BP 11.5 Tue 11:00 GÖR 226

Hyper-Parameter Optimization for Identification of Dynamical Systems — •Tobias Wand[1], Alina Steinberg[1], Tim Kroll[2], and Oliver Kamps[2] — [1]Institut für Theoretische Physik, Universität Münster, Deutschland — [2]Center for Nonlinear Science, Universität Münster, Deutschland

In recent years, methods to identify dynamical systems from experimental or numerical data have been developed [1,2]. In this context, the construction of sparse models of dynamical systems has been in the focus of interest and has been applied to different problems. These data analysis methods work with hyper-parameters that have to be adjusted to improve the results of the identification procedure. If more than one hyper-parameter has to be fine-tuned, simple methods like grid search are computationally expensive and due to this, sometimes not feasible. In this talk, we will introduce different approaches to optimally select the hyper-parameters for the identification of sparse dynamical systems.

[1] Brunton et al. Proceedings of the National Academy of Sciences, 2016, 113, 3932-3937
[2] Mangan et al. Proceedings of the Royal Society A, 2017, 473, 20170009

Topical Talk BP 11.6 Tue 11:15 GÖR 226

Data driven modelling of spatio-temporal chaos in extended dynamical systems — •Ulrich Parlitz[1,2], Sebastian Herzog[1,3], Florentin Wörgötter[3], Roland S. Zimmermann[1,2],

Jonas Isensee[1,2], and George Datseris[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institut für Dynamik komplexer Systeme, Georg-August-Universität Göttingen, Germany — [3]Drittes Physikalische Institut, Georg-August-Universität Göttingen, Germany

Many spatially extended nonlinear systems, an example being excitable media, exhibit complex spatio-temporal dynamics. We shall present machine learning methods to predict the temporal evolution of these systems or estimate their full state from limited observations. The applied techniques include Reservoir Computing [1] and a combination of a Convolutional Autoencoder with a Conditional Random Field [2,3], whose perfomance will be compared to Nearest Neighbours Prediction based on dimension reduced local states [4]. Examples for demonstrating and evaluating the methods employed include the Lorenz-96 model, the Kuramoto-Sivashinsky equation, the Barkley model, and the Bueno-Orovio-Cherry-Fenton model, describing cardiac (arrhythmia) dynamics.

[1] R. S. Zimmermann and U. Parlitz, Chaos 28, 043118 (2018)
[2] S. Herzog et al., Front. Appl. Math. Stat. 4, 60 (2018)
[3] S. Herzog et al., Chaos (to appear) (2019)
[4] J. Isensee, G. Datseris, U. Parlitz, J. of Nonlinear Sci. (2019)

BP 11.7 Tue 11:45 GÖR 226

Predicting Spatio-Temporal Time Series Using Dimension Reduced Local States — •Jonas Isensee[1,2], George Datseris[1,2], and Ulrich Parlitz[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institut für Dynamik komplexer Systeme, Georg-August Universität Göttingen, Germany

Understanding dynamics in spatially extended systems is central to describing many physical and biological systems that exhibit behaviour such as turbulence and wave propagation. Correctly predicting dynamics is advantageous in experimental settings and data-driven approaches are useful, particularly when no adequate mathematical models are available. We present an approach to iterated time series prediction of spatio-temporal dynamics based on local delay coordinate states and local modeling using nearest neighbour methods [1]. A crucial step in this process is to find predictive yet low-dimensional descriptions of the local dynamics . We discuss how imposing symmetries on the dynamics can be used to increase the predictiveness of our approach. The efficacy of this approach is shown for (noisy) data from a cubic Barkley model, the Bueno-Orovio-Cherry-Fenton model.

[1] J. Isensee, G. Datseris, U. Parlitz, J. of Nonlinear Sci. (2019)

Topical Talk BP 11.8 Tue 12:00 GÖR 226

Limits to predictability of complex systems dynamics — Jonathan Brisch and •Holger Kantz — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Motivated by the challenges of weather forecasting and the well known fact that atmospheric dynamics takes place on many temporal and spatial scales, we discuss the possibility of scale dependent error growth and its consequences for predictions. In case that the growth rate of small errors depends on the error magnitude as an inverse power law, we can explain why forecasts of macroscopic observables can be successful on time scales which are orders of magnitude longer than the (estimated) Lyapunov time, and at the same time we find a strictly finite prediction horizon even for arbitrary accuracy of the initial condition. We propose a hierarchical model class, which is able to generate such an error growth behaviour, and finally we re-analyze published data of error-growth in a numerical weather forecast system to present evidence that the error growth rate there is indeed consistent with a power law with diverging growth rate for infinitesimal errors. It is plausible that the same mechanism is active in other complex phenomena which live on a variety of spatial and temporal scales.

BP 11.9 Tue 12:30 GÖR 226

Network inference from event sequences: Disentangling synchrony from serial dependency — •Reik Donner[1,2], Forough Hassanibesheli[2,3], Frederik Wolf[2,3], and Adrian Odenweller[4,5] — [1]Magdeburg-Stendal University of Applied Sciences, Magdeburg — [2]Potsdam Institute for Climate Impact Research — [3]Department of Physics, Humboldt University, Berlin — [4]Center for Earth System Research and Sustainability, University of Hamburg — [5]Max Planck Institute for Meteorology, Hamburg

Inferring coupling among interacting units or quantifying their synchronization based on the timing of discrete events has vast applications in neuroscience, climate, or economics. Here, we focus on two prominent concepts that have been widely used in the past - event synchronization (ES) and event coincidence analysis (ECA). Numerical performance studies for two different types of spreading processes on paradigmatic network architectures reveal that both methods are generally suitable for correctly identifying the unknown links. By further applying both concepts to spatiotemporal climate datasets, we demonstrate that unlike ECA, ES systematically underestimates linkages in the presence of temporal event clustering, which needs to be accounted for in network reconstruction from data. In turn, for spike train data from multi-channel EEG recordings (with relatively narrow inter-event time distributions), the obtained results are practically indistinguishable. Our findings allow deriving practical recommendations for suitable data preprocessing in the context of network inference and synchronization assessment from event data.

BP 11.10 Tue 12:45 GÖR 226

Reconstruction of nonlinear correlations and dynamical laws — Mirko Rossini, Konstantin Schmitz, and •Jürgen Stockburger — ICQ, Ulm University, Germany

Time series taken from a stationary process may feature dependencies far more subtle than linear correlations. We introduce a method based on non-linear feature extraction which can uncover and quantify such dependencies. Its utility is demonstrated using both synthetic and real-world data.

BP 11.11 Tue 13:00 GÖR 226

Collective Response of Reservoir Networks — •Arash Akrami, Fabio Schittler Neves, Xiaozhu Zhang, Malte Schröder, and Marc Timme — Chair for Network Dynamics, Institute for Theoretical Physics and Center for Advancing Electronics Dresden (cfaed), TU Dresden

Reservoir Computing constitutes a paradigm of bio-inspired machine learning relying on dynamical systems theory, that exploits high dimensionality of a large network of processing units (reservoir). However, as the collective dynamics of artificial neural networks is far from understood, their learning outcome is hardly predictable or transparent.

In Reservoir Computing systems, learning occurs exclusively in a read-out layer, with the intrinsic reservoir dynamics freely evolving.

Here we study reservoirs of processing units with linear activation functions, i.e., linear reservoirs and analytically predict the dynamic responses of all network units as a function of general, distributed and time-dependent input signals. These insights may help identifying nodes especially suitable for receiving input signals, and finding minimal reservoirs capable of performing a given task.

BP 12: Active Matter II (joint session BP/DY/CPP)

Time: Tuesday 9:30–13:00 Location: HÜL 386

BP 12.1 Tue 9:30 HÜL 386

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

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

In the state diagram of these parameters, for neutral squirmers we observe sedimentation at strong gravitational forces and inverted sedimentation at finite torques, when activity dominates. In between, we identify plumes of collectively sinking squirmers that feed convective rolls of circling squirmers at the bottom of the simulation cell. At

velocity ratios slightly above one and large torques squirmers form a spawning cluster, which floats above the bottom wall and from which squirmers occasionally escape. For strong pushers and pullers, we find that the dipolar flow fields weaken the formation of plumes and convective rolls.

[1] M. Hennes, *et al.*, PRL **112**, 238104 (2014)
[2] J.-T. Kuhr, *et al.*, Soft Matter **13**, 7548 (2017).
[3] H. Jeckel, *et al.*, PNAS **116**, 1489 (2019).
[4] T.J. Pedley, and J.O. Kessler, Annu. Rev. Fluid Mech. **24**, 313 (1992).

BP 12.2 Tue 9:45 HÜL 386

Sculpting vesicles with active particles — Masoud Hoore[1], Clara Abaurrea-Velasco[1], Hanumantha Rao Vutukuri[2], Thorsten Auth[1], Jan Vermant[2], Gerhard Gompper[1], and •Dmitry Fedosov[1] — [1]Institute of Complex Systems and Institute for Advanced Simulation, Forschungszentrum Jülich, 52425 Jülich, Germany — [2]Department of Materials, ETH Zürich, 8093 Zürich, Switzerland

Biological cells are able to generate intricate structures and respond to external stimuli, sculpting their membrane from inside. Simplified biomimetic systems can aid in understanding the principles which govern these shape changes and elucidate the response of the cell membrane under strong deformations. We employ a combined simulation and experimental approach to investigate different non-equilibrium shapes and active shape fluctuations of vesicles enclosing self-propelled particles. Interestingly, the most pronounced shape changes are observed at relatively low particle loadings, starting with the formation of tether-like protrusions to highly branched, dendritic structures. At high volume fractions, globally deformed vesicle shapes are observed. The obtained state diagram of vesicles sculpted by active particles predicts the conditions under which local internal forces can generate dramatic cell shape changes, such as branched structures in neurons.

BP 12.3 Tue 10:00 HÜL 386

Diffusing Activity: Active Particles in Evolving Environments — •Nima H. Siboni, S. Mohsen J. Khadem, and Sabine H. L. Klapp — Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstrasse 36, 10623 Berlin, Germany

We study the dynamics of a single active Brownian particle (ABP) and the collective behavior of interacting ABPs in a heterogeneous medium. We apply the idea of the diffusing diffusivity model [1] to mimic the environmental heterogeneity in the equation of motion of the ABPs via a time-dependent activity and diffusivities. In our model, the fluctuations of the environment affect simultaneously and similarly the motility and diffusion coefficients. We obtain analytically the probability distribution function of the particle displacement and its moments and support our results via particle-based simulations. We finally investigate the impact of the introduced fluctuations on the collective behavior of ABPs. We obtain the phase diagram of motility-induced phase separation [2,3] for a wide range of noise strength and compare our results with that for the conventional ABPs [4].

[1] M. V. Chubynsky and G. W. Slater, Phys. Rev. Lett. **113**, 098302 (2014).
[2] I. Buttinoni, J. Bialké, F. Kümmel, H. Löwen, C. Bechinger, and T. Speck, Phys. Rev. L. **110**, 238301 (2013).
[3] J. Stenhammar, A. Tiribocchi, R. J. Allen, D. Marenduzzo, and M. E. Cates, Phys. Rev. L. **111**, 145702 (2013).
[4] S. M. J. Khadem, N. H. Siboni, and S. H. L. Klapp, in preparation.

BP 12.4 Tue 10:15 HÜL 386

Phoretic interactions of two chemically-active particles — •Babak Nasouri[1] and Ramin Golestanian[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Goettingen, Germany — [2]Rudolf Peierls Centre for Theoretical Physics, University of Oxford, Oxford OX1 3PU, United Kingdom

Catalytically-coated active particles in a viscous medium interact with one another by altering the chemical and hydrodynamic fields in their surroundings. Such phoretic interactions may drive particles in motion and are strongly dependent on the physico-chemical properties of the system, namely: the response of the particles to the interaction fields, and geometric factors such as inter-particle distances and particle sizes. In this work, we discuss an analytical approach which can accurately capture the dynamical behaviour of two phoretic spherical particles, for any given configuration.

BP 12.5 Tue 10:30 HÜL 386

Axisymmetric spheroidal squirmers and self-diffusiophoretic particles — Ruben Poehnl[1], •Mihail Popescu[2], and William Uspal[1] — [1]Dept. of Mech. Eng., Univ. of Hawai'i at Manoa, 2540 Dole St., Honolulu, HI 96822, USA — [2]Max Planck Institute for Intelligent Systems, Heisenbergstr. 3, 70569 Stuttgart, Germany

By using previously published analytical solutions for Stokes flow around a spheroid, here we investigate the motion of a spheroidal, axisymmetric squirmer in an unbounded fluid and the low Reynolds number hydrodynamic flow induced by the squirmer.

In contrast to the case of a spherical squirmer, for the spheroidal squirmer each slip mode either contributes to the velocity, or contributes to the stresslet. Additionally, and also distinct from the case of a spherical squirmer, each slip mode excites either all of the fore-aft symmetric or fore-aft asymmetric components of the flow field, respectively. Accordingly, with small modifications of the squirming pattern, a microrganism could maintain its velocity unchanged but dramatically alter the topology of the flow around it. This raises the interesting speculative question as whether the spheroidal shape is providing an evolutionary advantage, i.e., a spheroidal squirmer possesses simple means – not available to a spherical one – for acting in hydrodynamic disguise, which can be advantageous as either predator or prey.

The results are straightforwardly extended to the self-phoresis of axisymmetric, spheroidal, chemically active particles with phoretic slip.

BP 12.6 Tue 10:45 HÜL 386

Active particle penetration through a planar elastic membrane — •Abdallah Daddi-Moussa-Ider[1], Benno Liebchen[1,2], Andreas M Menzel[1], and Hartmut Löwen[1] — [1]Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, Germany — [2]Theorie Weicher Materie, Fachbereich Physik, Technische Universität Darmstadt, Germany

Active penetration of nanoparticles through cell membranes is an important phenomenon which has various biomedical and clinical applications. Using particle-based computer simulations and theory, we study the penetration mechanism of an active or externally driven particle through a planar elastic membrane. We model the membrane as a self-assembled sheet of particles embedded in a viscous fluid. We introduce a coarse-grained model to describe the mutual interactions between the membrane particles. We identify three distinct scenarios, including trapping of the active particle, penetration through the membrane with subsequent self-healing, in addition to penetration with permanent disruption of the membrane. The latter scenario may be accompanied by a partial fragmentation of the membrane into bunches of isolated or clustered particles. Our approach might be helpful for the prediction of the transition threshold between the trapping and penetration states in real-space experiments involving motile swimming bacteria or artificial self-propelling active particles. Reference: Daddi-Moussa-Ider *et al.*, Theory of active particle penetration through a planar elastic membrane, *New J. Phys.* **21**, 083014 (2019).

30 min. coffee break

Invited Talk BP 12.7 Tue 11:30 HÜL 386

Physics of Growth: Another Form of Active Matter — •Jens Elgeti — Foschungszentrum Jülich, Germany Theoretical Soft Matter and Biophysics

Active matter is matter, driven out of equilibrium by its microscopic constituents. Growing mater is also active matter, but activity does not enter via the stress, but in material conservation. The material generates itself – think cells dividing or a tumor growing. Growth implies a change in volume. In physical terms, the conjugate force to volume is pressure. Thus, in order to grow, cells must exert mechanical pressure. In turn, pressure influences growth. This yields to interesting novel phenomena like infinite compressibility, self contracting materials and steady tread-milling states.

We use particle based simulations to study mechanical properties and effects in growing matter. These simulations have been helpful in understanding, interpreting and designing experiments. I will present an overview of the simulation technique, and several examples of how this model helped to gain insight in mechanical processes underlying tissue growth, ranging from growth of cancer spheroids under pressure [1], to *in silico* competition experiments [2-5] and tumor evolution [6].

[1] Montel et al., PRL **107**, 188102 (2011)
[2] Podewitz et al., EPL **109**, 58005 (2016)
[3] Basan et al., Phys. Biol. **8**, 026014 (2011)

[4] Podewitz et al., New J. Physics **18**, 083020 (2016)
[5] Ganai et al., New J. Phys. **21** 063017 (2019)
[6] Büscher et al., arxiv:1910.03263 (2019)

BP 12.8 Tue 12:00 HÜL 386

The effect of hydrodynamic interactions on self-propulsion of multiple swimmers — •Sebastian Ziegler[1], Maxime Hubert[1], Thomas Scheel[2], Jens Harting[2], and Ana-Sunčana Smith[1,3] — [1]PULS Group, Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Helmholtz Institute Erlangen-Nürnberg for Renewable Energy, Forschungszentrum Jülich, Germany — [3]Division of Physical Chemistry, Ruder Bošković Institute Zagreb, Croatia

A common theoretical approach to model systems of microswimmers is to prescribe the swimming stroke of each individual. If the system consists of more than one device, such models, however, underestimate the impact of one swimmer's stroke on the stroke of all others, reducing the problem of hydrodynamic interactions to a purely geometric one. Furthermore, a number of experimental systems are associated with imposing the forces driving each of the devices. This situation is, from a theoretical point of view, significantly more demanding and has not been investigated so far for multiple swimmers. This issue is addressed in this presentation where we employ a recently developed perturbative calculation and numerical modeling to study the effects of nearby swimmers on the stroke, swimming speed and direction. Notably, we find that for two swimmers, a significant fraction of the parameter space results in both swimmers experiencing a boost from one another. We identify the key characteristics that yield this effect.

BP 12.9 Tue 12:15 HÜL 386

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

Active propulsion as performed by bacteria and Janus particles, in combination with hydrodynamic interaction at boundaries, can lead to the breaking of time reversibility. One typical example of this is the accumulation of bacteria on a flat wall. However, in microfluidic devices with pillars of sufficiently small radius, self-propelled particles can slide along the surface of a pillar without becoming trapped over long times. Using simulations and theory, we study the impact of different modes of obstacle interaction on the diffusive transport of active particles in a lattice of such obstacles. We find that sliding along obstacles can result in large diffusivities even at high obstacle density, unlike particles that undergo classical specular reflection, as in the Lorentz gas. We introduce a microscopically derived run-and-tumble model, which describes the macroscopic transport for different scattering rules very well, and test it in microfluidic channels for E.coli. Finally, we discuss the role of tumbling in structured and random environments.

BP 12.10 Tue 12:30 HÜL 386

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

Nature provides a plethora of microswimmers, which can be rather elongated, filament- or polymer-like. Examples are bacteria swarmer cells or marine phytoplankton dinoflagellates assembling in a linear fashion. In order to address the relevance of hydrodynamic interactions for the collective behavior of such organisms, we study the swimming properties of linear polymer-like assemblies by mesoscale hydrodynamic simulations, where an active unit (monomer) is described by a spherical squirmer -which can be a pusher, a neutral swimmer, or a puller. We find that the monomer hydrodynamic flow field leads to correlations in the relative orientation of adjacent monomers, and consequently the swimming efficiency differs from that of active Brownian linear assemblies. In particular, puller chains show a pronounced increase in the rotational diffusion coefficient compared to pushers, while for neutral squirmers, the rotational diffusion coefficient is similar to that of active Brownian particles. Hence, the large-scale conformational and dynamical properties depend on the specific propulsion mechanism. Refs.: [1] J. Elgeti, R. G. Winkler, G. Gompper, Rep. Prog. Phys. 78, (2015). [2] R. G. Winkler, J. Elgeti, G. Gompper, J. Phys. Soc. Jpn. 86, (2017). [3] A. Martin-Gomez, T. Eisenstecken, G. Gompper, R. G. Winkler, Soft Matter 15, (2018).

BP 12.11 Tue 12:45 HÜL 386

The step-wise induction of transcription drives morphological changes in aggregates of RNA polymerase II — Agnieszka Pancholi[1], Roshan Prizak[1], Tim Klingberg[2], Weichun Zhang[1], Amra Noa[1], Gerd Ulrich Nienhaus[1,3], Vasily Zaburdaev[2], and •Lennart Hilbert[1] — [1]Karlsruhe Institute of Technology — [2]Friedrich-Alexander University Erlangen-Nuremberg — [3]University of Illinois at Urbana-Champaign

In eukaryotic cells, a main control point of transcription is the transient pausing of engaged RNA polymerase II (Pol II) just before transcript elongation. Paused Pol II forms transient polymeric aggregates that exhibit diverse morphologies. Here, we use super-resolution microscopy in embryonic zebrafish cells to show how entry into and exit from Pol II pausing determines these aggregate morphologies. Instant structured illumination microscopy (iSIM) in live embryos revealed that aggregates initially are morphology complex, round up as they grow, and unfold again when actual transcript elongation begins. Using transcription inhibitors, we confirm that Pol II pausing indeed drives aggregate rounding. Further resolving aggregates by STimulated Emission Double Depletion (STEDD) microscopy, we found a granular fine-structure that suggests clustering aggregation rather than liquid-liquid compartmentalization. We currently develop a theoretical model to explain what underlying macro-molecular interactions could result in the observed morphologies.

BP 13: Cell Mechanics I

Time: Tuesday 9:30–12:45 Location: SCH A251

Invited Talk BP 13.1 Tue 9:30 SCH A251

On another plane: curling and buckling in epithelia — •Guillaume Charras[1], Jonathan Fouchard[1], Tom Wyatt[1], Ana Lisica[1], Nargess Khalilgharibi[1], Pierre Recho[2], Amsha Proag[3], Magali Suzanne[3], Buzz Baum[1], and Alexandre Kabla[4] — [1]University College London, London, UK — [2]Universite Grenoble Alpes, Grenoble, France — [3]Universite Paul Sabatier, Toulouse, France — [4]Cambridge University, Cambridge, UK

During embryonic development and adult life, epithelia are constantly subjected to external forces. The resulting deformations can have a profound impact on tissue development and function. In particular, compressive deformations are central to tissue morphogenesis as they can trigger cell extrusion or differentiation via mechanosensory mechanisms. These processes are all controlled by the relationship between compression and the mechanical state of the tissue, however, this remains poorly understood. Using suspended epithelia, we uncover the response of epithelial tissues to the application of large in-plane compressive strains.

While most epithelia must withstand mechanical stresses without rupture, some developmental epithelia need to rupture allow emergence of mature organs. In Drosophila leg imaginal disks, the peripodial membrane breaks to release the leg. As it breaks, the peripodial membrane curls basally, indicating the presence of spontaneous curvature. Similar curling is observed suspended epithelia. We investigate the biology and physics of monolayer curling to estimate the contribution of active torques to out-of-plane deformation in epithelia.

BP 13.2 Tue 10:00 SCH A251

Bridging microtubules promote centering of kinetochores by length-dependent pulling forces — Agneza Bosilj[1], Iva Tolic[2], and •Nenad Pavin[1] — [1]Department of Physics, Faculty of Science, University of Zagreb — [2]Ruder Bošković Institute, Zagreb

The mitotic spindle, by exerting forces, segregates chromosomes into two daughter cells during cell division. During metaphase, chromosome are positioned in the equatorial plane of the mitotic spindle, which is necessary to prevent lagging chromosomes and abnormal nuclear enve-

lope reformation. It has been proposed that two centering mechanisms play a key role here, microtubule catastrophe promoted by kinesin-8 motors and pushing forces exerted by chromokinesins. Here we show, by combining a theoretical model and quantitative experiments, that kinetochore microtubules cross-linked by bridging microtubules exert length-dependent centering pulling forces. Our model also shows that length-dependent catastrophe and rescue regulated by motor proteins and passive cross-linkers are necessary for well defined length of microtubules and their antiparallel overlap, respectively. We predict that stable antiparallel overlaps exert length-dependent forces on kinetochores to navigate their positioning in the center of the metaphase plate.

BP 13.3 Tue 10:15 SCH A251

Intracellular activity and mechanics in dividing epithelial cells — •Sebastian Hurst, Bart E. Vos, Matthias Brandt, Till Münker, and Timo Betz — Institute of Cell Biology, ZMBE, Münster, Germany

While there is a good understanding of cortical mechanics during cell division, surprisingly little is known about the intracellular mechanics and activity during this fundamental process. Nevertheless, intracellular mechanics have a tremendous impact on both chromosome and organelle distribution. Furthermore, an increase in intracellular activity would help to distribute organelles before cytokinesis. This so-called active diffusion is achieved by random, undirected fluctuations, e.g. generated through motor protein activity.

To quantify the intracellular mechanics, we perform active and passive microrheology measurements using optical tweezers on phagocytosed exogenous particles inside dividing MDCK cells. We obtain the frequency-dependent complex shear modulus and the effective energy, which quantifies the activity in units of thermal energy. We observe global differences between interphase and mitosis. Focusing on mitosis, current results suggest that the cells become more fluid-like in pro- and metaphase, while they become more solid-like towards the end of mitosis. Compared to interphase, the effective energy drops in mitosis, whereas it does not change drastically during cell division. Moreover, experiments with cells in mitotic arrest show that the activity is mostly myosin driven. This data supports a published model connecting mechanics to intracellular activity.

BP 13.4 Tue 10:30 SCH A251

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

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

BP 13.5 Tue 10:45 SCH A251

Rayleigh-Plateau instability of anisotropic biological interfaces — •Katharina Grässel, Christian Bächer, and Stephan Gekle — Biofluid Simulation and Modeling, Theoretische Physik VI, Universität Bayreuth

Tubular vesicles under tension are known to undergo a pearling instability similar to the Rayleigh-Plateau instability of a liquid jet. We extend the classical model for this Rayleigh-Plateau instability to treat complex interfaces with anisotropic surface tension, as found in cells. We do so both in the limit of high and low Reynolds number and accordingly cover both liquid jet and vesicle behaviour. Combining theory and simulations we show that the dominant instability wavelength is determined by the anisotropy of the surface tension. We further show that including bending elasticity of vesicle membranes has negligible influence for isotropic tension, but strongly affects or even completely suppresses the instability if the tension is anisotropic. Our results can be highly relevant for vesicles or tissues with anisotropic interfacial properties.

30 min. coffee break

BP 13.6 Tue 11:30 SCH A251

Measuring Viscoelasticity of Cells by Atomic Force Microscopy — Sandra Perez Dominguez, Shruti Kulkarnie, Carmela Rianna, Prem Kumar Viji Babu, and •Manfred Radmacher — Universität Bremen

Mechanical properties of cells are important for understanding many cellular processes like cell division, cell migration or wound healing. From a mechanical point of view, the most important component of a (mammalian) cell is the actin cytoskeleton, which is an active polymeric network able to generate internal stresses and external forces. If a local deformation is applied to a cell, e.g. by an AFM tip, the response will be viscoelastic, where the elastic forces are mainly generated by the cytoskeleton, and the viscous forces may stem from the interaction of the cytoskeleton with the highly viscous cytoplasm. There are various experimental methods to determine this viscoelastic response by AFM: the simplest are applying a jump in force or a modulating force. The former measures the creep of the sample, the latter is conceptually related to polymer rheology. We will discuss and compare both methods in AFM to determine the viscoelastic response of different cell types.

We have investigated several cell types, including cancer and normal cells, but also various types of fibroblasts, which are related to wound healing or Dupuytren's disease. In all cases we could quantify differences in the mechanical properties: in the elastic and the loss modulus, and in the power law exponents of these quantities as a function of frequency.

BP 13.7 Tue 11:45 SCH A251

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

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

BP 13.8 Tue 12:00 SCH A251

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

To undergo mitosis successfully, animal cells need to acquire a round shape to provide space for the mitotic spindle. This mitotic rounding relies on mechanical deformation of surrounding tissue and is driven by forces emanating from actomyosin contractility. Cancer cells are able to maintain successful mitosis in mechanically challenging environments such as the increasingly crowded environment of a growing

tumor, thus, suggesting an enhanced ability of mitotic rounding in cancer. Here, we show that epithelial mesenchymal transition (EMT), a hallmark of cancer progression and metastasis, gives rise to a cell-cycle dependent cell-mechanical switch and enhanced mitotic rounding strength in breast epithelial cells. Furthermore, we show that this cell-mechanical change correlates with a strong EMT-induced change in the activity of Rho GTPases RhoA and Rac1. Accordingly, we identify Rac1 as a cell-cycle dependent regulator of actin cortex mechanics. Our findings hint at a new role of EMT in successful mitotic rounding and division in mechanically confined environments such as a growing tumor.

BP 13.9 Tue 12:15 SCH A251

Estimating biomechanical properties of Head and Neck Squamous Carcinoma Cells (HNSCC) with single-molecular force microscopy — •Hsiao-Ching Tsai[1], Julia Kristin[2], Jörg Schipper[2], and Mathias Getzlaff[1] — [1]Institue of Applied Physics, Heinrich-Heine-Universität Düsseldorf — [2]Hals-Nasen-Ohren-Klinikum Düsseldorf

AFM is one of the most common approach to access the loading deformation behavior of different soft materials such as tissue or cells. With AFM, a complete data base of biomechanical properties like displacement or deformation could be easily established. The progress of the fundamental biomechanical discovery engages further investigation of living matters. To our knowledge, cancer is one of the most lethal diseases lacking effective treatment. Thus, the development of supplementary or improvement of therapeutic methods lead to an urgent requirement of biomechanics in detail. By means of AFM, cytoskeleton network changing due to the disease progression which is closely associated to the biomechanics is confirmed. In this study, we cultured different head and neck squamous cells from the same area (tongue) at different cancer stages (healthy, benign, cancerous and metastatic) and examined them using a nanoindentation technique. The Hertz model of contact mechanics is adopted to extract the elastic modulus by analyzing the force-indentation curves. Our results present a quantitative model to distinguish the disease conditions of head and neck squamous cells. Three dimensional images of living cells in liquid environment can be visualized simultaneously.

BP 13.10 Tue 12:30 SCH A251

Elucidating cell mechanics regulators from mechano-transcriptomics data using unsupervised machine learning — •Marta Urbanska[1,2], Yan Ge[1], Maria Winzi[1], Konstantinos Anastasiadis[1], Jochen Guck[1,2], and Carlo V. Cannistraci[1] — [1]Biotechnology Center, CMCB, TU Dresden, Dresden, Germany — [2]Max Planck Institute for the Science of Light, Erlangen, Germany

Mechanical properties of cells determine their capability to perform many physiological functions, such as migration, cell-fate specification or circulation through vasculature. Identifying the molecular factors that govern the mechanical phenotype is therefore a subject of great interest. Here we present an approach that enables establishing links between mechanophenotype changes and the genes responsible for driving them. In particular, we employ an unbiased machine learning method termed PC-corr to correlate cell mechanical states, measured by real-time deformability cytometry (RT-DC), with large-scale transcriptome datasets across different biological systems. We validate the obtained functional gene module in silico on four further datasets and show that the five identified genes have the capacity to discriminate between stiffer and softer cell states of 70 to 93%. Finally, we validate experimentally the influence of the top scoring gene on cell mechanics by its down- and up-regulation. The data-driven approach presented here has the power of de novo identification of genes involved in the regulation of cell mechanics and will extend the toolbox for tuning the mechanical properties of cells on demand to enable biological function or prevent pathologies.

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

Stem cells have the remarkable capacity to differentiate into multiple cell types and therefore play pivotal roles in our understanding of tissue maintenance and disease. Theoretical and experimental approaches from physics have advanced our understanding of stem cell dynamics, while at the same time stem cell biology has led to questions at the frontier of non-equilibrium physics. In this session, we will show how mechanical signalling influences cell fate and how concepts from physics can yield understanding of the collective phenomena underlying stem cell behaviour on the molecular and cellular scales.

Time: Tuesday 9:30–12:45 Location: ZEU 250

BP 14.1 Tue 9:30 ZEU 250

Salt-dependent rheology and surface tension of protein condensates using optical traps — Louise Jawerth[1], Mahdiye Ijavi[1], Martine Ruer[1], Shambaditya Saha[1], Marcus Jahnel[1,4], Anthony Hyman[1], Frank Jülicher[2,3], and •Elisabeth Fischer-Friedrich[4,5] — [1]MPI CBG, Pfotenhauerstr. 108, 01307 Dresden, Germany — [2]MPI PKS, Nöthnitzerstr. 38, 01187 Dresden, Germany — [3]Center for Systems Biology Dresden, Pfotenhauerstraße 108, 01307 Dresden, Germany — [4]Biotec, TU Dresden, Tatzberg 47-49, 01307 Dresden, Germany — [5]Excellence Cluster Physics of Life, TU Dresden, Dresden, Germany

An increasing number of proteins with intrinsically disordered domains have been shown to phase separate in buffer to form liquid-like phases. These protein condensates serve as simple models for the investigation of the more complex membrane-less organelles in cells. To understand the function of such proteins in cells, the material properties of the condensates they form are important. However, these material properties are not well understood. Here, we develop a novel method based on optical traps to study the frequency-dependent rheology and the surface tension of PGL-3 condensates as a function of salt concentration. We find that PGL-3 droplets are predominantly viscous but also exhibit elastic properties. As the salt concentration is reduced, their elastic modulus, viscosity and surface tension increase. Our findings show that salt concentration has a strong influence on the rheology and dynamics of protein condensates suggesting an important role of electrostatic interactions for their material properties.

BP 14.2 Tue 9:45 ZEU 250

Protein condenstates as aging Maxwell fluids — •Louise Jawerth[1], Elisabeth Fischer-Friedrich[2], Anthony Hyman[3], and Frank Julicher[1] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Biotec, TU Dresden, Tatzberg 47-49, 01307 Dresden, Germany — [3]Max Planck Institute of Molecular Cell Biology and Genetics

Protein condensates (PC) are intracellular compartments that segregate material without the use of a membrane. The liquid-like behavior of the condensates is a defining characteristic and the material properties of condensates are tuned to their biological function. It has become increasingly clear that some condensates do not have time-independent material properties, but can, instead, transition to more solid, gel-like materials. Here, we present our efforts to quantify these new materials as they age in vitro. We measure the visco-elastic material properties of several proteins by means of a combination of active and passive microrheology. At early times, we find that the droplets behave much like simple liquids but gradually become more elastic. Surprisingly, the changing mechanical properties can all be scaled onto a single master curve using one characteristic time scale which grows as the sample ages. We consider protein condensates as soft glassy materials with age dependent material properties that we call Maxwell glasses. To gain insight into the molecular origins of this behavior, we present electron microscopy images of the condensates at different ages. Furthermore, we demonstrate how salt concentration tunes the characteristics of the aging process.

BP 14.3 Tue 10:00 ZEU 250

Phase separation provides a mechanism to reduce noise in cells — •Florian Oltsch[1,2], Adam Klosin[1], Tyler Harmon[1,3],

Alf Honigmann[1,4], Frank Jülicher[2,3,4], Anthony Hyman[1,2,4], and Christoph Zechner[1,2,4] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany — [2]Center for Systems Biology Dresden, 01307 Dresden, Germany — [3]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [4]Cluster of Excellence Physics of Life, TU Dresden, 01062 Dresden, Germany

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

BP 14.4 Tue 10:15 ZEU 250

Phase Separation of Active Polymers — •Antoine Deblais[1], Daniel Bonn[1], and Sander Woutersen[2] — [1]Van der Waals-Zeeman Institute, Institute of Physics, University of Amsterdam, 1098XH Amsterdam, The Netherlands. — [2]Van 't Hoff Institute for Molecular Sciences, University of Amsterdam, Science Park 904, 1098XH Amsterdam, The Netherlands.

Here, we investigate the aggregation and phase separation of thin, living T.Tubifex worms that behave as active polymers. Randomly dispersed active worms spontaneously aggregate to form compact, highly entangled blobs, a process similar to polymer phase separation, and for which we observe power-law growth kinetics. We find that the phase separation of active polymer-like worms does not occur through Ostwald ripening, but through active motion and coalescence of the phase domains. Interestingly, the growth mechanism differs from conventional growth by droplet coalescence: the diffusion constant characterizing the random motion of a worm blob is independent of its size, a phenomenon that can be explained from the fact that the active random motion arises only from the worms at the surface of the blob. This leads to a fundamentally different phase-separation mechanism, that may be unique to active polymers.

Invited Talk BP 14.5 Tue 10:30 ZEU 250

Could the cytoskeleton influence liquid-liquid phase separation? — •Eric Dufresne — ETH Zürich, Department of Materials

We have recently demonstrated using synthetic polymers that mechanical stresses can have a dramatic impact on the phenomena of liquid-liquid phase separation [1-3]. Shin *et al* [4] recently revealed a coupling of condensation to chromatin density, suggesting that similar effects may play a role in the condensation of liquid droplets in the nucleoplasm.

Here, I will describe our new experiments exploring the interaction of phase-separated domains to elements of the cytoskeleton.

[1] Style, R. W. *et al, Phys. Rev. X*, **8**, 011028 (2018)
[2] Kim, J.-Y. *et al, arXiv:*1811.00841 (2019)
[3] Rosowski, K. A. *et al, arXiv:*1907.08465 (2019)
[4] Shin, Y. *et al, Cell* **175** 1481 (2018)

30 min. coffee break

BP 14.6 Tue 11:30 ZEU 250

Theory of dissolution front dynamics predicts droplet distribution in stiffness gradients — •Estefania Vidal-Henriquez and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Liquid-liquid phase separation is an important mechanism for compartmentalizing the cell's cytoplasm, allowing the dynamic organization of the components necessary for survival. However, it is not clear how phase separation is affected by the complex viscoelastic environment inside the cell. Here we study theoretically how stiffness gradients influence droplet growth and arrangement. Since elastic gradients imply concentration gradients in the dilute phase, droplet material is transported from stiff to soft regions. This process drives a dissolution front invading the stiff region. Using a mean-field theory, we predict how the front emerges and how it propagates. This elastic ripening occurs at a rate much faster than classical Ostwald ripening, thus driving the dynamics. Our work shows how spatial differences in elastic properties could control liquid compartments inside cells.

BP 14.7 Tue 11:45 ZEU 250

Structure and development of patterned silica in the diatom frustule. — •Maria Feofilova and Eric Dufresne — ETH Zurich, Zurich, Switzerland

Diatoms are single-celled organisms, which make an amazing multi-scale silica structure called the frustule as their cell wall. While much is known about the biochemistry involved, currently it is not clear what is the physical mechanism by which the structure is achieved. One of the proposed models is templating by phase separation.

In this work, we observe both the developing structure in living cells and the completely formed structure in extracted frustules of the diatom *Coscinodiscus granii*. By characterizing the development of structural features over time, we hope to gain insight into the mechanism by which ordering of the structure occurs.

BP 14.8 Tue 12:00 ZEU 250

Formation of pilus induced cellular aggregates and their rheological properties — •Hui-Shun Kuan[1,3], Frank Jülicher[2], and Vasily Zaburdaev[1,3] — [1]Department of Biology, Friedrich-Alexander Universität Erlangen-Nürnberg, Erlangen, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

Aggregates of living cells are an example of active materials with unconventional material properties. The rheological properties of cellular aggregates can, therefore, be markedly different from those exhibited by passive soft systems. Motivated by colonies of Neisseria gonorrhoeae bacteria, we develop a continuum theory to study cellular aggregates formed by attractive pili–pili intercellular interactions which introduce active stresses in the system. The formation of cellular aggregates can be explained by an active phase separation process, and the activity-induced viscoelastic properties of such aggregates are coupled with pili–pili interactions. By studying the behaviour of aggregates under oscillatory shear, the loss and storage moduli of the aggregates can be linked to the dynamics of the active intercellular forces. Due to the turnover of pili, the aggregates show a liquid-like behaviour at large times and strong shear-thinning effect under the large amplitude oscillatory shear. Our theory provides an essential insight on how pilus mediated intercellular forces in cellular aggregates govern their material properties which in the future could be tested experimentally.

BP 14.9 Tue 12:15 ZEU 250

Active growth and degradation of coacervate droplets controlled by enzymatic reactions — •Karina Nakashima, Alain André, Merlijn van Haren, and Evan Spruijt — Radboud University, Institute for Molecules and Materials, Heyendaalseweg 135, 6525 AJ Nijmegen, The Netherlands

Liquid-liquid phase separation plays an important role in the organization of biochemical processes in the cell. Control over phase separation by enzymatic reactions and the localization of biomolecules inside different droplet compartments is essential for many cellular functions. To elucidate the physicochemical principles that govern the nucleation, growth and coarsening of droplet organelles, we use coacervate droplets that we control by enzymatic reactions. Here, we present two experimental model systems, in which we achieve dynamic control over condensation and dissolution of coacervate droplets by changing either the charge density or the length of the constituent biomolecules. We track the coacervates by microscopy and follow their active growth and degradation at a single-droplet level. Our results indicate that droplets grow faster with increasing reaction-diffusion rate, while degradation of droplet material leads to a gradual dissolution of all droplets simultaneously. We also find that Ostwald ripening is suppressed in complex coacervates. We quantify the partitioning of all components in our system by HPLC and fluorescence labelling to support our results with a kinetic model. Our findings suggest that controlling phase separation in biological systems through enzymatic reactions may lead to a wide variety of droplet growth and degradation behaviours.

BP 14.10 Tue 12:30 ZEU 250

Protein storage vacuoles and autophagosomes form by similar physical mechanisms — •Roland L. Knorr — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany — The University of Tokyo, Tokyo 113-0033, Japan — Max Planck Institute of Molecular Plant Physiology, Potsdam, Germany

Proteins are components and nutrients essential for the growth and maintenance of the human body. The most important protein source worldwide are plants and the majority of plant protein consumed is packed in protein storage vacuoles (PSVs) of seeds in all major crops including wheat and soy. How highly fragmented PSVs storing protein derive from a single, vegetative vacuole functioning in protein degradation is little understood. Here, we investigate the mechanisms of PSV generation. We find in living embryos that vacuolar phase separation generates storage protein droplets with liquid-like properties. A physical model combined with reconstituted droplet-membrane interactions shows that partial wetting of proteinaceous droplets on membranes determines droplet engulfment by a process we call liquid scaffolding. We thus demonstrate that phase separation and engulfment are the mechanisms underlying the formation of physically separated droplets of storage proteins, which may be important to reprogram degradative vacuoles into storage vacuoles by restricting the access of vacuolar proteases to developing protein reservoirs. Further, we demonstrate that the autophagosomal sequestration of cytosolic droplets underlies similar physical principles.

References: Fujioka, Y; Alam, J.M.D.; Noshiro, D.; Mouri, K.; Ando, T.; Okada, Y.; May, A.I.; Knorr, R. L.; Suzuki, K.; Ohsumi, Y; Noda, N.N.; Nature, accepted. Knorr, R. L.*; Franzmann, T.; Feeney, M.; Kittelmann, M.; Frigerio, L.; Dimova, R.; Hyman, A. A.; Lipowsky, R.; submitted. Agudo-Canalejo, J.; Schultz, S.W.; Chino, H.; Migliano, S.; Saito, C.; Koyama-Honda, I.; Stenmark, H.; Brech, A.; May, A.I.; Mizushima, N.; Knorr, R. L.*; submitted.

BP 15: Active Matter III (joint session DY/BP/CPP)

Time: Tuesday 14:00–16:00 Location: ZEU 160

BP 15.1 Tue 14:00 ZEU 160

Uncovering novel phase transitions in dense dry polar active fluids using a lattice Boltzmann method — David Nesbitt, Gunnar Pruessner, and •Chiu Fan Lee — Imperial College, London, U.K.

The dynamics of dry active matter have implications for a diverse collection of biological phenomena spanning a range of length and time scales, such as animal flocking, cell tissue dynamics, and swarming of inserts and bacteria. Uniting these systems are a common set of symmetries and conservation laws, defining dry active fluids as a class of physical system. Many interesting behaviors have been observed at high densities, which remain difficult to simulate due to the computational demand. Here, we devise a new method to study dry active fluids in a dense regime using a simple modification of the lattice Boltzmann method. We apply our method to an active model with contact inhibition of locomotion, which has relevance to collective cell migration, and uncover multiple novel phase transitions: two first-order and one potentially critical. We further support our simulation results with an analytical treatment of the hydrodynamic equations.

Reference: D Nesbitt, G Pruessner, and CF Lee. Preprint: arXiv:1902.00530.

BP 15.2 Tue 14:15 ZEU 160

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

We consider a Brownian particle, which, in addition to being in contact with a thermal bath, is driven by active fluctuations. These active fluctuations do not fulfill a fluctuation-dissipation relation and therefore play the role of a non-equilibrium environment. Using an Ornstein-Uhlenbeck process as a model for the active fluctuations, we derive the path probability of the Brownian particle subject to both, thermal and active noise. From the case of passive Brownian motion, it is well-known that the log-ratio of path probabilities for observing a certain particle trajectory forward in time versus observing its time-reserved twin trajectory quantifies the entropy production in the thermal environment. We calculate this path probability ratio for active Brownian motion and derive a generalized "entropy production", which fulfills an integral fluctuation theorem. We show that those parts of this "entropy production", which are different from the usual dissipation of heat in the thermal environment, can be associated with the mutual information between the particle trajectory and the history of the non-equilibrium environment.

BP 15.3 Tue 14:30 ZEU 160

Rheotaxis of active drops in confinements — •Ranabir Dey[1], Carola M. Buness[1,2], Chenyu Jin[1], and Corinna C. Maass[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, 37077 Goettingen — [2]Institute for the Dynamics of Complex Systems, Georg August Universitaet Goettingen

Biological microswimmers commonly navigate confinements having liquid flows, e.g. locomotions of spermatozoa through the reproductive tract and bacteria in the gut or in blood vessels. The directed motion of the microorganisms in response to the gradients in external flow velocity is classically called 'rheotaxis'. Recently, rigorous efforts have been made to understand the rheotaxis of microorganims, specifically bacteria. In contrast, there is very little quantitative understanding of rheotaxis of artificial microswimmers. It must be noted that artificial microswimmers, e.g. those designed for drug delivery, are often required to navigate confinements having external flows. Here, we elucidate the swimming dynamics of a common type of artificial microswimmer, i.e. active drops, in micro-confinements having Poiseuille flow. We experimentally quantify the rheotaxis of these droplet microswimmers, intrinsically undergoing Marangoni stress dominated 'self-propulsion', in response to velocity gradients of varying strength. We try to understand the observed rheotaxis of the active drops in confinements in the context of a hydrodynamic model– the active Jeffery-Bretherton model. We strongly feel that detailed understanding of artificial active matter rheotaxis will make significant contributions towards better design optimization for practical applications.

BP 15.4 Tue 14:45 ZEU 160

Multiple Particle Correlation Analysis of Many-Particle Systems: Formalism and Application to Active Matter — •Rüdiger Kürsten[1], Sven Stroteich[1], Martín Zumaya Hérnandez[2], and Thomas Ihle[1] — [1]Universität Greifswald, Institut für Physik, Felix-Hausdorff-Str.6 — [2]Instituto de Ciencias Físicas, Universidad Nacional Autónoma de México, Apartado Postal 48-3, Código Postal 62251, Cuernavaca, Morelos, México

We introduce a fast spatial point pattern analysis technique which is suitable for systems of many identical particles giving rise to multi-particle correlations up to arbitrary order. The obtained correlation parameters allow to quantify the quality of mean field assumptions or theories that incorporate correlations of limited order. We study the Vicsek model [1] of self-propelled particles and create a correlation map marking the required correlation order for each point in phase space incorporating up to ten-particle correlations. We find that multi-particle correlations are important even in a large part of the disordered phase. Furthermore, the two-particle correlation parameter serves as an excellent order parameter to locate both phase transitions of the system, whereas two different order parameters were required before [2].

[1] Phys. Rev. Lett. 75, 1226 (1995). [2] Phys. Rev. Lett. 92, 025702 (2004); Phys. Rev. E 77, 046113 (2008).

BP 15.5 Tue 15:00 ZEU 160

Nonuniversality in scalar active matter with diffusivity edge under periodic confinement — •Benoît Mahault[1] and Ramin Golestanian[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Germany — [2]University of Oxford, United Kingdom

Scalar active matter is often described at the mean field level by nonlinear Fokker-Planck equations with density-dependent diffusion coefficients integrating fast degrees of freedom, as well as various equilibrium and/or nonequilibrium processes. A generic class, characterized by a diffusivity vanishing above some threshold density, was recently introduced [Golestanian, Phys. Rev. E 100, 010601(R)]. In presence of harmonic confinement, such 'diffusivity edge' was shown to lead to condensation in the ground state, with the associated transition exhibiting formal similarities with Bose-Einstein condensation (BEC).

Many active systems, such as self-propelled Janus particles, can however self-assemble into finite-size coexisting clusters. To account for such feature in the diffusivity edge framework, a periodic egg-crate

confinement, that provides multiple sites for condensation, is considered in arbitrary dimensions. While for high barriers separating two minima the system essentially behaves as in the single harmonic trap case, for shallow potentials the transition is qualitatively different as the exponent associated to the scaling of the condensate fraction with an effective temperature is found to be nonuniversal. We nevertheless show from a generalized thermodynamic description that the overall phenomenology of BEC, such as the divergence of the isothermal compressibility at the transition, holds in both cases.

BP 15.6 Tue 15:15 ZEU 160

Anomalous fluctuations accompany dynamical arrest in a cluster of chemically active colloids — •Supriya Saha, Prathyusha K R, and Ramin Golestanian — Max Planck Institute for Dynamics and Self Organisation

Recent years have seen enormous scientific activity exploring the ability of catalytic colloids to collectively form patterns and clusters. However, fluctuations of individual colloids within a cluster remains unstudied, and is the focus of our work. Using the simplest example of active colloids, hard spheres that generate an isotropic chemical field, we find that an interplay of non-local interactions and finite system size results in the formation of a core and a surface layer in the cluster, both of which exhibit dynamics distinct from one another. The simplicity of our model suggests that aspects of the fluctuations revealed here are generic to matter driven phoretically, including enzymes.

BP 15.7 Tue 15:30 ZEU 160

Transport coefficients of active particles: Reverse perturbations and response theory — •Thomas Ihle[1], Arash Nikoubashman[2], Alexander Unruh[1], Sven Stroteich[1], and Rüdiger Kürsten[1] — [1]Institute for Physics, Greifswald University — [2]Institute of Physics, Johannes-Gutenberg-University Mainz

Müller-Plathe's reverse perturbation method [Phys. Rev. E 59, 4894 (1999)] for shearing simple liquids is extended to the Vicsek model (VM) of self-propelled particles. It is shown how the shear viscosity ν and the momentum amplification coefficient λ, can be extracted from simulations by fitting to an analytical solution of the hydrodynamic equations for the VM. The viscosity consists of two parts, a kinetic and a collisional contribution. While analytical predictions already exist for the former [T. Ihle, J. Stat. Mech. 2016, 083205], a novel expression for the collisional part is derived by an Enskog-like kinetic theory [A. Nikoubahsman, T. Ihle, Phys. Rev. E 100, 042603 (2019)]. Using several methods to measure transport coefficients such as reverse perturbations, Green-Kubo relations and transverse current correlations, we find excellent agreement between the different methods and good agreement with theory. We introduce a novel kind of response theory that allows us to not only verify the analytical predictions of kinetic theory but also to efficiently obtain expressions for nonlocal (wavevector dependent) transport coefficients of active systems, avoiding tedious multiple-scale methods like the Chapman-Enskog expansion. The method is applied to the VM with metric and topological interactions as well as to a model with continuous time dynamics.

BP 15.8 Tue 15:45 ZEU 160

Effect of Vicsek-like Activity on the collapse of a Flexible Polymer — •Subhajit Paul[1], Suman Majumder[1], Subir K Das[2], and Wolfhard Janke[1] — [1]Institüt für Theoretische Physik, Universität Leipzig, IPF 231101, 04081 Leipzig, Germany — [2]JNCASR, Jakkur P.O., Bangalore- 560064, India.

Dynamics of various biological filaments can be understood within the framework of active polymer models. In this context, we construct a bead-spring model for a flexible polymer chain in which the activity or self-propulsion of the beads has been defined in the Vicsek-like manner. Following a quench from a high-temperature coil phase to the low-temperature state we have studied the nonequilibrium dynamics of this model by solving the Langevin equation via molecular dynamics (MD) simulations. The low-T equilibrium state for the passive polymer in which the interaction among the beads modeled via standard LJ potential, is a compact globular one. Results from our MD simulations reveal that the globular state is also likely to be the final equilibrium in the active case also, the nonequilibrium dynamics is quite different than the passive case. We observe that the deviation from the intermediate 'pearl-necklace' arrangement and the formation of elongated structures for the polymer increases with activity. Also, it appears that whether smaller values of the activity makes the coarsening faster, activity beyond a certain value makes it slower. On this nonequilibrium front we also compare various results with that of the passive case, viz., scaling laws related to collapse time, cluster coarsening, etc.

BP 16: Poster IV

Active Matter (BP 14.1 – BP 14.19)

Time: Tuesday 14:00–16:00 Location: P2/EG

BP 16.1 Tue 14:00 P2/EG

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

Transport inside living systems or biofluid droplets is governed by diffusion and energy-dependent active transport. Speeding up these processes remains challenging: here we report on an easy way to gently stir biofluid droplets. We produce micrometer long magnetic stir bars (NBs) by aligning Fe_3O_4 nanoparticles and stabilizing them by a biocompatible silica coating. The successful production of these NBs is confirmed by scanning electron microscopy. The rotating magnetic field is achieved by using two pairs of Helmholtz-like coils with a custom build controller, which can tune both the frequency and the strength of the magnetic field. As the rotation frequency is increased, we observed the generation of superdiffusive transport in a NBs suspension of 200 nm fluorescent beads up to an optimum frequency. The range of frequencies we looked at is from 0.01 to 10 Hz and the magnetic field is around 10 mT. The frequency dependence of the transport property can be connected to the dynamics at the single NB level, which is also characterized in parallel experiments. We finally look at their stirring effects on the out of equilibrium self-organization of *Xenopus laevis* egg extract.

BP 16.2 Tue 14:00 P2/EG

Stability and noise of metachronal waves in cilia carpets — •Anton Solovev[1] and Benjamin M. Friedrich[1,2] — [1]Center for Advancing Electronics Dresden (cfaed), Germany — [2]Cluster of Excellence 'Physics of Life' (PoL), Dresden, Germany

Motile cilia on ciliated epithelia in mammalian airways, brain and oviduct display coordinated beating in the form of metachronal waves, presumably due to mutual hydrodynamic coupling. Metachronal coordination is important for efficient fluid transport.

How the shape of the cilia beat determines the direction and wavelength of metachronal waves is not fully understood, nor is robustness with respect to noise.

We developed a multi-scale modelling approach, where a cilia carpet is modeled as an array of noise phase oscillators, similar to a Kuramoto model with local coupling. Importantly, pair-wise hydrodynamic interactions between cilia are accurately computed from hydrodynamic simulations of the Stokes equation, using experimentally measured cilia beat patterns. We numerically determine the set of all possible synchronized states, as well as their linear stability.

Remarkably, while we find multiple metastable metachronal wave states, analysis of global dynamics reveals that only few of them have sizable basins of attraction. In the presence of noise, corresponding to active fluctuations of cilia beating, we observe stochastic transitions between different synchronized states. While strong noise reduces synchronization, weak noise biases the dynamics towards a single synchronized state of metachronal coordination.

BP 16.3 Tue 14:00 P2/EG

Synchronization of flagella at finite Reynolds numbers in viscoelastic fluids — •Chaojie Mo and Dmitry Fedosov — Institute of Complex Systems, Forschungszentrum Jülich, Jülich 52428, Germany

Recent experimental and numerical studies show that viscoelasticity can significantly promote clustering of sperm cells, implying its key

role for the behavior of microswimmers. To better understand the effects of viscoelasticity, we conduct numerical simulations of the synchronization of two parallel 2-D flagella, where inertial effects, flagellum elasticity and fluid viscoelasticity are taken into account. We find that the characteristic time for synchronization due to inertia scales as $\tau^s \propto 1/(f\mathrm{Re})$. In addition, in-phase and anti-phase synchronization can be achieved through the competition between fluid inertial effects and other factors, such as flagellum elasticity, viscoelasticity and compressibility. The fluid viscoelasticity leads to very strong synchronization forces at large beating amplitudes and $\mathrm{De} \gg 1$. Viscoelasticity-induced synchronization generally requires a lower output energy and does not impede the swimming speed. Therefore, a viscoelasticity of suspending medium can promote synchronization by a significant enhancement of the synchronization forces. This can be an advantage for the synchronized sperm cells, as it facilitates their migration.

BP 16.4 Tue 14:00 P2/EG

Dynamic force measurements on actively beating flagella by means of micropipette force sensors — Thomas J. Böddeker, Stefan Karpitschka, Christian T. Kreis, Quentin Magdelaine, and •Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, 37077 Göttingen, Germany

Flagella and cilia are cellular appendages that mediate essential functions such as transport, motility and sensing of the environment. Using a novel experimental technique based on micropipette force sensors, we present the first direct measurement of the oscillatory forcing exerted by the beating flagella of the unicellular model organism *Chlamydomonas*. This method relies on partially aspiring a motile microbe at the tip of a micropipette cantilever. Through Fourier analysis of the deflection spectrum of the cantilever, we isolate the signal originating from the beating flagella from external noise, resulting in a force resolution of a few piconewtons. The method offers full optical access to the microbe at any time and high flexibility regarding varying experimental parameters. We demonstrate the versatility of this novel experimental approach by measuring the oscillatory forcing at varying distance of the beating flagella to a solid surface and identify the length over which hydrodynamic and steric flagella-surface interactions play a role (T.J. Böddeker et al., arXiv:1908.03602).

BP 16.5 Tue 14:00 P2/EG

Magnetic swimmers in confined, porous environments — •Omar Muñoz[1,2,3], Mohammad Charsooghi[4], Agnese Codutti[5,6], Vitali Telezki[1], Damien Faivre[4,7], and Stefan Klumpp[1] — [1]Faculty of Physics, Georg-August Universität Göttingen, Göttingen, Germany — [2]Department of Biology, Friedrich-Alexander Universität Erlangen-Nürnberg, Erlangen, Germany — [3]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [4]Department of Biomaterials, Max Planck Institute of Colloids and Interfaces, Postdam, Germany — [5]Department of Theory and Biosystems, Max Planck Institute of Colloids and Interfaces, Postdam, Germany — [6]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [7]Aix-Marseille University, CNRS, CEA, BIAM, Saint Paul lez Durance, France

Magnetic swimmers are a class of microswimmers, which can be steered and/or propelled by a magnetic field. We proposed a minimal model for independent magnetic swimmers in porous environments, whose orientation aligns passively with an external magnetic field. The porous environment is implemented via coarse-grained interactions with confining walls and circular obstacles. By numerical integration of the respective Langevin equations, we studied the interactions of the swimmers with the environment, as well as their global behavior in a large, confined environment with a magnetic field present. For the specific case of magnetotactic bacteria swimming in sediment-like environments we present a first comparison with experimental data from *Magnetospirillum gryphiswaldense* swimming in a quasi-2D channel.

BP 16.6 Tue 14:00 P2/EG

Absorption Induced Geometry Change in Porous Media — •Carl Becker[1] and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization — [2]Technical University of Munich

Solute transport through natural porous media is often strongly incoherent throughout the medium due to random pore-sizes and connections. This can be improved either by creating artificial porous media layer by layer or by actively changing the network geometry in a random porous medium. One method to change the geometry in a random porous medium with little effort is by flushing a solute through the medium which is absorbed at the pore-walls and thereby changes the pore-size (e.g.˜an acid etching away the pore-walls). It would be highly time- and energy-efficient if this method could be used to optimise the transport properties of porous media. Recently, it has been shown that porous media with low porosity can be approximated by tubular networks with varying radii. Here, we use this approximation to analytically investigate the solute dynamics in single pores with absorbing walls. This is used to predict the impact of small solute concentration peaks travelling through the network which get absorbed at the walls and change the pore-sizes. We show a first numerical example where absorption induced geometry change is used to improve the transport properties of a toy-model of a porous medium.

BP 16.7 Tue 14:00 P2/EG

Gliding motility and self-organization of *Chlamydomonas* populations on surfaces — •Sebastian Till, Alexandros Fragkopoulos, and Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany

Green microalgae are photoactive microorganisms that inhabit porous environments, e.g. wet soils and the interstitial space of rocks, where they constantly interact with surfaces. *Chlamydomonas reinhardtii*, a unicellular biflagellated microbe, can adhere and colonize essentially any surface under exposure to blue light. In this surface-adhered state, the flagella are attached in a widespread configuration and the cooperative effort of molecular motors translocates the cell parallel to them. This type of motion is known as gliding motility. We find that for a sufficiently high density of adhered cells, a motility-induced self-organization effect may be observed leading to areas of locally increased cell densities.

In order to understand this clustering, we quantify the surface-based gliding motility of single cells as well as the spatio-temporal evolution of the surface-associated microbial population. The dynamics of single cells is characterized by rapid movements, followed by states of prolonged inactivity. Due to the predominant directionality induced by the initial flagella configuration, the motility can't be described as a run-and-tumble process, as in their free-swimming state, but rather as a slow rotational diffusion.

BP 16.8 Tue 14:00 P2/EG

Chiral symmetry breaking in viscous environments — •Jonas Neipel[1], Stephan W. Grill[2,3], 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 — [3]Biotechnology Center, Technical University Dresden, Dresden, Germany

The body plan and organs of most animal species show a consistent handedness. During the development of these organisms and structures, chiral flows of molecules and cells in thin fluid films are often observed. These flows suggest the presence of torques. In particular, chiral flows in the acto-myosin cortex of the *Caenorhabditis elegans* embryo have been linked to active torque generation by the acto-myosin system. Due to angular momentum conservation, a torque in such an active surface has to be balanced by an opposing torque somewhere in the surrounding. Hence, the material properties of the environment and its interaction with the active surface are of crucial importance. Here, we study ensembles of torque dipoles in viscous environments. We demonstrate that the resulting flow fields in the active surface show striking differences to torque generation on a rigid substrate. We also study the dynamics of torque dipoles in the presence of active isotropic and nematic stresses. We observe that the presence of even weak torque dipoles can bias chiral symmetry breaking in active nematics. We then ask the question, whether the mutual action of nematic stress and torque dipoles can account for the appearance of chiral flows in avian embryos in the absence of cilia.

BP 16.9 Tue 14:00 P2/EG

Simulations of polymers in crowded environments — •Niklas Butkevich, Ali Malek, and Stefan Klumpp — Georg-August-Universität Göttingen, Institut für Dynamik komplexer Systeme, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Biopolymers, such as DNA, RNA and proteins, are essential components in all living organisms. In cells, these polymers are subject to a crowded environment as well as to active processes. In the present work, molecular dynamics simulations in 3D are performed to study static and dynamical properties of flexible polymer chains in a bath of passive and active crowders. The model is based on the Rouse model with additional repulsive interactions. The active bath has a

pronounced effect on the configurational dynamics of the polymer: by increasing the density of the passive crowders, the squared end-to-end distance decreases, the motion of the center of mass slows down and the chain relaxation is delayed. The model is extended to self-propelled active particles that drive the system out of equilibrium.

BP 16.10 Tue 14:00 P2/EG

Turbulence in a suspension of active rods — •Osamah Sufyan, Josua Grawitter, and Holger Stark — Technische Universität Berlin, Institut für Theoretische Physik, Hardenbergstraße 36, 10623 Berlin, Germany

Self-organizing active systems can exhibit non-equilibrium phase transitions, e.g., from ordered collective motion to spatio-temporal chaos as in motility assays of biofilaments and bacterial suspensions. An interesting phenomenon in such systems is the emergence of active turbulence at small Reynolds numbers [1].

Here, we investigate the collective dynamics of a dilute suspension of active rods in a viscous fluid using the incompressible Navier-Stokes equation coupled to the dynamic equation for the local tensorial order parameter, which quantifies the liquid-crystal nematic order of the active rods [2,3]. We numerically solve the model equations. With increasing activity, we identify a transition from an isotropic to a turbulent phase. We characterize this phase by the scaling law of the local nematic order parameter, the power spectrum of the flow-field fluctuations, as well as the dynamics and statistics of the topological defects in the nematic director field.

[1] L. Giomi, Phys. Rev. X **5**, 03100 (2015).
[2] S. Ramaswamy, Annu. Rev. Condens. Matter Phys. **1**, 323 (2010).
[3] E. L. C. VI M. Plan, S. Musacchio, and D. Vincenzi, Phys. Rev. E **96**, 053108 (2017).

BP 16.11 Tue 14:00 P2/EG

Can the Motility of Magnetotactic Bacteria be Measured by Means of Magnetization Curves? — Sophia Nagelstrasser[1], Frank Mickoleit[2], Dirk Schüler[2], Ingo Rehberg[1], and •Reinhard Richter[1] — [1]Experimentalphysik 5, Universität Bayreuth, 95447 Bayreuth, Germany — [2]Mikrobiologie, Universität Bayreuth, 95447 Bayreuth, Germany

The magnetization of a paramagnetic gas, like oxygen, increases with the applied magnetic field H and saturates if all magnetic moments m are aligned. This curve is described by $M(H) = \Phi L(\xi)$, where Φ denotes the volume fraction of the molecules, $L(\xi)$ the Langevin function, and $\xi = mH/(k_\mathrm{B}T)$ the ratio of magnetic and thermal energy. This function should also apply to a dispersion of magnetotactic bacteria, like the model organism *Magnetospirillum gryphiswaldense*. However, whereas the molecules have identical magnetic moments, those bacteria biomineralize a variing number of magnetite crystals (so called magnetosomes), with 20-60 particles per cell [1]. Moreover, in contrast to the molecules, which are passively kicked by $k_\mathrm{B}T$, the bacteria are *actively* swimming in their environment. In a series of measurements we are elucidating, whether the $M(H)$-curves of this active suspensions can still be described by a superposition of Langevin functions [2], capturing their motility by an enhanced effective temperature.

[1] R. Uebe and D. Schüler, *Nat. Rev. Microbiol.*, 14 (2016) 621.
[2] I. Rehberg, R. Richter, S. Hartung, N. Lucht, B. Hankiewitz, T. Friedrich, *Phys. Rev. B*, 100 (2016) 134425.

BP 16.12 Tue 14:00 P2/EG

Quantifying the flexural rigidity of filamentous cyanobacteria — •Mixon Faluweki and Lucas Goehring — Nottingham Trent University, Nottingham, UK

The structural and mechanical properties of biofilms contribute to their successes in a wide variety of ecological niches; filamentous cyanobacteria show an increase in complexity from single cells towards multicellular structures. We study how the microscopic activity of these organisms gives rise to the macroscopic properties of their colonies, including biofilms and biomats. One of the most important mechanical properties is the flexural rigidity, also known as the bending modulus. Direct measurement of the flexural rigidity of filamentous cyanobacteria is a challenging task due to their small size. Here, we quantify the flexural rigidity of three cyanobacteria species via bending tests in a microfluidic flow device, where single cyanobacteria filaments are introduced into the microfluidic channel and deflected by fluid flow. This measurement is confirmed separately by measuring the Young*s modulus and cell wall thickness using atomic force microscopy and scanning electron microscopy, respectively. These mechanical properties will control how individual filaments of cyanobacteria bend or curve when they interact with each other, or their environment, for example in their alignment into bundles, or with flows or physical boundaries.

BP 16.13 Tue 14:00 P2/EG

Anisotropic exclusion effect between photocatalytic Ag/AgCl Janus particles and passive beads in a dense colloidal matrix — •Tao Huang[1,2], Xu Wang[2], Vyacheslav Misko[3,4], Franco Nori[3], Jürgen Fassbender[2], Denys Makarov[2], Gianaurelio Cuniberti[1], and Larysa Baraban[1,2] — [1]TU Dresden, Dresden, Germany — [2]Helmholtz-Zentrum Dresden-Rossendorf e.V. — [3]RIKEN Cluster for Pioneering Research, Saitama, Japan — [4]Vrije Universiteit Brussel, Brussels, Belgium

Synthetic nano- and micromotors interact with each other and their surroundings in a complex manner. Here, we report on the anisotropy of the active-passive particles interaction in a soft matter system containing an immobile yet photochemical Ag/AgCl-based Janus particle embedded in a dense matrix of passive beads in pure water. The asymmetry in the chemical gradient around the Janus particle, triggered upon visible light illumination, distorts the isotropy of the surrounding electric potential and results in the repulsion of adjacent passive beads to a certain distance away from the Janus particle. This exclusion effect is found to be anisotropic with larger distances to passive beads in front of the Ag/AgCl cap of the Janus particle. We provide an insight into this phenomenon by performing the angular analysis of the radii of exclusion and track their time evolution at the level of a single bead.[1,2] 1. X. Wang. et al., Small,1803613 (2018). 2. X. Wang. et al., Small,1802537 (2018).

BP 16.14 Tue 14:00 P2/EG

Imaging protein-based artificial molecular motors — •Ivan Unksov[1], Pradheebha Surendiran[1], Chapin Korosec[2], Peter Jönsson[3], Roman Lyttleton[1], Damiano Verardo[1], Roberta Davies[4], Till Böcking[5], Nancy Forde[2], Paul Curmi[4], and Heiner Linke[1] — [1]Solid State Physics and NanoLund, Lund University, Lund, Sweden — [2]Department of Physics, Simon Fraser University, Burnaby, British Columbia, Canada — [3]Department of Chemistry, Lund University, Lund, Sweden — [4]School of Physics, University of New South Wales, Sydney, Australia — [5]Single Molecule Science and ARC Centre of Excellence in Advanced Molecular Imaging, University of New South Wales, Sydney, Australia

We are working on two concepts of artificial molecular motors: the Tumbleweed, a protein motor built from DNA-binding protein repressors (Bromley et al. HFSP J 2009), and the Lawnmower, a motor based on a microbead decorated with trypsin protease (Kovacic et al. IEEE Trans Nanobioscience 2015). The Tumbleweed is designed to make steps as small as 10 nm along a DNA upon switching of buffers which enable ligand-specific binding of motor to DNA. We show the binding using silica beads with attached multiple DNA tracks: we add motors with fluorescent labels and track the changes in the intensity and radius of fluorescence patterns; with this approach, we aim at seeing motor motion with sub-diffraction precision. For the Lawnmower, using fluorogenic peptides as the surface-bound substrate, we demonstrate the substrate cleavage by trypsin, which is expected to allow for the motion of motor based on rectified diffusion.

BP 16.15 Tue 14:00 P2/EG

Emergent activity of motile phytoplankton in nutrient landscapes — •Francesco Danza and Anupam Sengupta — Physics of Living Matter Group, University of Luxembourg, Luxembourg

Phytoplankton, microscale photosynthetic organisms that constitute base of most of the aquatic food webs, inhabit dynamic environments where nutrients, alongside light and fluid flow, mediate phytoplankton activity, fitness and succession. Nutrient availability has long been associated with plankton physiology, which due to the shifting environmental trends, is undergoing a major makeover. Currently we lack a biophysical framework that could link nutrient availability to phytoplankton behavior, and crucially, predict if motile species could thrive in shifting nutrient conditions. Using a combination of micro-scale imaging, microbiology and fluid dynamic models, we investigate how nutrient availability regulates single-cell physiology and motility, and scale it up to uncover emergent collective behavior of phytoplankton populations. By quantifying the biophysical traits over ecologically relevant nutrient levels, we extract the time-scales over which phytoplankton actively regulate swimming and morphological characteristics, thus shedding light on the finely tuned biophysical mechanisms that equip them to tackle spatial and temporal heterogeneity of nu-

trient landscapes. Beyond the ecological context, our results propose local nutrient levels as a handle to control the activity of motile phytoplankton species, promising an exciting model of motile active matter where spontaneous changes in motility and morphology trigger a rich phase space over different cell concentrations.

BP 16.16 Tue 14:00 P2/EG

Shape-shifting intelligent active swimmers — •Arkajyoti Ghoshal and Anupam Sengupta — Physics of Living Matter Group, University of Luxembourg, Luxembourg City, Luxembourg

Shape, a key phenotypic trait in living systems, underpins crucial functions across different biological taxonomies. The ability of microbes (e.g., bacteria or algae) to dynamically shape-shift enables them to respond to external cues, optimize resources, and ultimately enhance fitness. Recent studies on microplankton have revealed exquisite mechanisms that allow cells to rapidly tune their shape and modulate motility under environmental perturbations [1]. Such adaptive traits play out over seconds to minutes timescales, offering biophysical insights that could be harnessed to engineer intelligent active swimmers. Combining single and population scale imaging, automation and tracking techniques, we catalogue active behavioral response of microbial species exposed to hydrodynamic cues over respective life cycles. Our results indicate that, for individual level, shape is a fundamental determinant of motility over cell lifecycle. At a population scale, variabilities in shape lead to intrinsic heterogeneity in motility traits, leading to an activity landscape that elicit a rich collective behavior over different flow regimes. These results provide quantitative insights which can be harnessed, on the one hand to elucidate niche composition in aquatic ecosystems, and on the other hand, tailor intelligent active matter based on adaptive biomechanics across scales. [1] A. Sengupta et al., Nature 543, 555, 2017. [2] Dynamic shape-motility coupling in active biological swimmers: A. Ghoshal & A. Sengupta (in prep).

BP 16.17 Tue 14:00 P2/EG

Reinforcement Learning with Artificial Microswimmers — Frank Cichos[1], Viktor Holubec[2], and •Ravi Pradip[1] — [1]Molecular Nanophotonics, Peter Debye Institute for Soft Matter Physics, Leipzig, Germany — [2]Charles University in Prague, Faculty of Mathematics and Physics

Artifical microswimmers are designed to mimic the motion of living microorganisms. The adaptive behavior of the latter is based on the experience they gain through the interactions with the environment. They are also subjected to Brownian motion at these length scales which randomizes their position and propulsion direction making it a key feature in the adaptation process. However, artificial systems are limited on their ability to adapt to such noise and environmental stimuli. A novel solution to this problem has already been demonstrated by incorporating machine learning algorithms: self thermophoretic artificial microswimmers are employed in a real-world environment controlled by a real-time microscopy system to introduce reinforcement learning. It has also been shown that the learning process in these noisy environments contributes to a decline in learning rate and varied optimal behavior. In addition, as a consequence of non zero delay between sensing and responding to external stimuli in such an environment an optimal velocity emerges for these microparticles which ensure the expected behavior. Therefore an effort to lower the current delay is made which will enable the particles to exploit the learned knowledge for a wider range of velocities.

BP 16.18 Tue 14:00 P2/EG

Environmental applications of high-motility visible light-driven Ag/AgCl Janus microswimmers — •xu wang[1], tao huang[2], larysa baraban[2], vyacheslav r misko[3,4], franco nori[3], gianaurelio cuniberti[2], jurgen fassbender[1], and denys makarov[1] — [1]Helmholtz-Zentrum Dresden-Rossendorf — [2]Technische Universität Dresden — [3]RIKEN Cluster for Pioneering Research — [4]Vrije Universiteit Brussel

Active photochemically-driven microswimmers show a great potential for the applications of environment remediations, such as the dye-solution degradation.[1] Previous reports focus on the favourable stimuli of visible light for driving microswimmers only show limited propulsion ability.[1] Here, we demonstrate Ag/AgCl-based spherical Janus microswimmers that reveal an efficient propulsion under visible light illumination.[2,3] They can boost the MSD to a remarkable value of 800 um2 (over 8 s) in pure H2O when activated by blue light (λ = 450-490 nm). We also demonstrates the potential of using visible light-driven plasmonic Ag/AgCl-based Janus micromotors in human saliva, phosphate-buffered saline solution, the most common isotonic buffer that mimics the environment of human body fluids, and Rhodamine B solution.

1. Simmchen, J., et al., ChemNanoMat 2017, 3, 65. 2. Wang, X., et al., Small 2018, 14, 1803613. 3. Wang, X., et al., Small 2018, 14, 1802537.

BP 16.19 Tue 14:00 P2/EG

Self-assembly of magnetic cubic nanomotors — •Martin Kaiser[1], Sofia Kantorovich[1,3], Yeimy Martinez[2], and Annette Schmidt[2] — [1]Faculty of Physics, University of Vienna, Boltzmanngasse 5, 1090 Vienna, Austria — [2]Chemistry Department, University of Cologne, D-50939 Cologne, Germany — [3]Ural Federal University, Lenin Av. 51, Ekaterinburg 620000, Russian Federation

Microscopic active particles, including self-propelled cells, microorganisms and artificial swimming colloids, have gained a lot of attention due to their relevance in such important fields as biology, biomedicine, nanoscience and nanotechnology. The term "active" is usually used in order to underline the ability of particles or units to gain the kinetic energy and move by converting the energy from their environment.

In this study, we use active matter to create a new type of nanomotor, based on active particle propulsion, that can be oriented by an applied magnetic field. Such a nanomotor consists of two units: one is a magnetic cube that can be directed due to its interaction with a magnetic field, whereas a second non-magnetic active particle with a propulsion force directed into the cubes centre of mass.

In the present contribution, we discuss the self-assembly of the aforementioned magnetic nanomotors, employing the combination of Molecular Dynamics Simulations and experiments. Due to competing propulsion and magnetic forces we observe striking differences in cluster size distribution and topology if compared to the self-assembly of non-active magnetic cubes.

BP 17: Poster V

Biomaterials and Biopolymers (BP 15.1 – BP 15.10); Focus: Biological Cells in Microfluidics (BP 15.11 – BP 15.31)

Time: Tuesday 14:00–16:00 Location: P2/1OG

BP 17.1 Tue 14:00 P2/1OG

Surface Analysis of (Bioactive) Glasses and pH-dependent Protein Adsorption observed by X-ray Reflectometry — •Annemarie Prihoda, Michail Goldes, and Tobias Unruh — Institute of Crystallography and Structural Physics (ICSP), Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Staudtstr. 3, 91058 Erlangen, Germany

Since 1977 bioactive glass has been used in medicine and dentistry as a bone implant or toothpaste ingredient. In contact with liquids a hydroxyapatite layer forms on the glass surface by releasing alkali metal ions from the glass surface. Osteoblasts adhere to this layer and thus form new bone structure (1). A basic understanding of the medical compatibility on a molecular level has, however, not been achieved yet.

We have tried to simulate the first steps of glass interaction after implantation by studying protein adsorption on glasses. We present X-Ray Reflectivity (XRR) data showing the adsorption of BSA on glasses (soda lime and borosilicate glass). We were able to identify protein layers whose thickness and roughness we determined on angstrom scale. Furthermore, we show the dependence of the degree of coverage on the pH-value of the protein solution. In addition, we are sensitive to aging effects of the glass surface, e.g. glass corrosion, which occurs when the glasses are immersed in liquids. For the first time we were able to

characterize the surface of Bioglass 45S5 with XRR and compared the results to non-bioactive glasses.

(1) Baino F. et al. Journal of functional biomaterials 2018, 9 (1)

BP 17.2 Tue 14:00 P2/1OG

Tailoring Network Structure of Collagen Type 1 by High-Energy Electron Irradiation — •Catharina Krömmelbein[1], Stefanie Riedel[1], Tom Kunschmann[2], and Stefan Mayr[1,2] — [1]Leibniz-Institut für Oberflächenmodifizierung e. V., Leipzig, Germany — [2]Fakultät für Physik und Geowissenschaften, Universität Leipzig, Leipzig, Germany

Imitating mammalian's extracellular matrix is essential to investigate cell behavior like adhesion and migration *in vitro* and is of great importance for biomedical applications as well. Collagen as main component of the mammalian's extracellular matrix is well suited as biomimetic material due to its excellent biocompatibility and biodegradability. Mostly, the fabrication of collagen type 1 matrices with defined network pore size involves the usage of cytotoxic chemicals. Herein, we adjust the pore size by covalent crosslinking, using high-energy electron irradiation of 0 kGy, 50 kGy and 100 kGy. Thereby, electron beam treatment is an effective and noninvasive method to ensure biocompatibility without the need for further chemicals. In addition, the pore size dependence of collagen type 1 networks on protein concentration is examined, using 1 mg/ml, 2 mg/ml and 3 mg/ml. In this contribution, we present a method to tailor the hydrogel's pore size by adjusting the gel concentration and the irradiation dose.

BP 17.3 Tue 14:00 P2/1OG

Observing polymer conformations at the 2D theta point — •Julian M. Philipp[1], Joachim O. Rädler[1], and Eugene P. Petrov[2] — [1]LMU, Munich, Germany — [2]PTB, Berlin, Germany

Important biological processes at cellular membranes involve interaction of biopolymers with the elastic deformable lipid bilayer. It has been found previously that conformations of DNA macromolecules adsorbed to freestanding cationic lipid membranes are controlled by the DNA-membrane attraction: whereas at low membrane charge densities membrane-bound DNA molecules behave as 2D swollen chains, an increase in the DNA-membrane attraction leads to membrane-driven coil-globule transition [1, 2]. These two regimes should be separated by the theta point, at which electrostatic and steric repulsion and membrane-mediated attraction of polymer segments compensate each other. Although theoretical predictions for the scaling of the macromolecule dimensions at the 2D theta-point are known [3]: $R_g \sim L^{4/7}$, the 2D theta-point behavior has never been observed directly in experiments. Using fluorescence microscopy we study conformations of single DNA molecules on freestanding cationic lipid bilayers at the membrane compositions close to those inducing the coil-globule transition and find that the dependence of R_g on L follows the scaling predicted for polymers at the theta-point in 2D. This represents the first direct experimental observation of polymer conformations at the 2D theta point. [1] C. Herold, P. Schwille, E.P. Petrov, Phys.Rev.Lett. 104(2010)148102; [2] A.G. Cherstvy, E.P. Petrov, Phys.Chem.Chem.Phys. 16(2014)2020; [3] B. Duplantier, H. Saleur, Phys.Rev.Lett. 59(1987)539.

BP 17.4 Tue 14:00 P2/1OG

Interaction of Neuronal Cells with Electrode Materials — •Alice Abend, Chelsie Steele, and Mareike Zink — Universität Leipzig, Peter Debye Institut für Physik der weichen Materie, Leipzig, Deutschland

Deep brain stimulation of neuronal cells with neuroelectrodes is already employed for medical treatment of different diseases such as epilepsy and Parkinson's. Additionally, coupling of neuronal cells to multielectrode and lab-on-a-chip materials offers new perspectives in in-vitro assessments ranging from neuronal network formation to drug testing. However, many biomaterials lack the ability to promote adhesion of neurons important for biomaterial performance. Employing the human glioblastoma cell line U87-MG as well as the human neuroblastoma cell line SH-SY5Y, we investigate the neuronal cells' adhesion dynamics, bioactivity as well as network formation on custom-made electrode materials composed of gold, indium tin oxide, titanium nitride with and without nanocolumnar surface patterning.

BP 17.5 Tue 14:00 P2/1OG

The Inhomogeneous Chain Ensemble Model for Semiflexible Polymer Networks — •Constantin Huster and Klaus Kroy — Universität Leipzig, Institut für theoretische Physik

When considering the theoretical descriptions of the mechanical properties of semiflexible polymer networks one might conclude that they suffer from a severe case of multi personality disorder: They can appear viscoelastic, plastic or inelastic, have been called time-fractals, can be self-heal and may soften or harden. Here we introduce a new perspective on semiflexible polymer networks called the inhomogeneous chain ensemble model which combines the bottom-up approach for biomechanics with ideas from super-statistics and core principles underlying the theory of soft glassy materials as well as the theory of floppy modes and non-affine deformation to show that the multi personality disorder of semiflexible polymer networks might not be as severe as it seams.

BP 17.6 Tue 14:00 P2/1OG

Analysis of protein secondary structure in silkworm and spider silk fibroins using Raman spectroscopy — •Emilia Pozarowska[1], Tomasz Runka[2], and Jan Ingo Flege[1] — [1]BTU Cottbus - Senftenberg, Germany — [2]Poznan University of Technology, Poland

Spider silks carry outstanding mechanical properties, such as the combination of high strength and large extensibility. The aim of this work is to investigate the protein secondary structure, in particular β - sheets, occurring in silkworm and spider silk fibers from different species, by Raman spectroscopy. The analysis of the Raman spectra provides information about characteristic conformations, such as amide I, III and protein secondary structure. A Steatoda grossa spider silk was compared with a silk of the Bombyx mori silkworm. The former shows smaller amount of β - sheets and more random coil and/or α - helix, suggesting better elastic properties. Furthermore, the analysis of dragline silks of 16 different spider species was performed resulting in specific Raman fingerprints corresponding to the silk structure and the sequence of amino acids within. Dragline silks of P. alticeps and S. grossa exhibit a larger contribution of proline and carbonyl (C=O) groups compared to other species. Data of polarized Raman spectroscopy confirmed the parallel alignment of the molecular chains to the fiber axis for all spider silks. Stress-strain curve measurements of one selected spider silk, tubiliform silk of S. grossa, revealed very good mechanical properties, i.e. a maximal strain of approximately 12.2% and final tensile stress at break of 1575 MPa.

BP 17.7 Tue 14:00 P2/1OG

Mechanoradicals in tensed tendon collagen as a new source of oxidative stress — •Christopher Zapp[1,2], Agnieszka Obarska-Kosinska[1,3], Reinhard Kappl[4], and Frauke Gräter[1,5] — [1]Heidelberg Institute for Theoretical Studies, Heidelberg — [2]Institute for Theoretical Physics, Heidelberg University — [3]Unit c/o DESY, European Molecular Biology Laboratory, Hamburg — [4]Institute for Biophysics, Saarland University Medical Center, Homburg — [5]Interdisciplinary Center for Scientific Computing, Heidelberg University

Mechanoradicals originate from homolytic bond scission in polymers. The existence, nature and biological relevance of mechanoradicals in proteins, instead, are unknown. We show that mechanical stress on collagen, a biopolymer, produces radicals and subsequently reactive oxygen species, essential biological signaling molecules. Electron-paramagnetic resonance (EPR) spectroscopy of stretched rat tail tendon, atomistic Molecular Dynamics simulations and quantum calculations show that radicals form by covalent bond scission in collagen due to mechanical stress. Radicals migrate to adjacent clusters of oxidized aromatic residues radicals, giving rise to a distinct and stable EPR spectrum consistent with a stable dihydroxyphenylalanine (DOPA) radical. The protein mechanoradicals, as a yet undiscovered source of oxidative stress, finally convert into hydrogen peroxide. Our study suggests collagen I to have evolved as a radical sponge against mechano-oxidative damage and proposes a new mechanism for exercise-induced oxidative stress and redox-mediated pathophysiological processes.

BP 17.8 Tue 14:00 P2/1OG

High Coverage Inductive Interface for Implants in Small Animals — •Ana Domingues[1], Christian Bentler[2], and Thomas Stieglitz[3] — [1]anadomingues53@gmail.com — [2]christian.bentler@imtek.de — [3]thomas.stieglitz@imtek.uni-freiburg.de

In Biomedical Engineering inductive wireless power transfer (IWPT) has been investigated by many researchers to charge active implantable medical devices (AIMDs) since IWPT is safe and avoids the implementation of cables, preventing infections through the skin and movement limitations.

This research develops a high coverage inductive interface to build a cage that works as a tool to acquire and study the neuronal activity in small animals. The coverage is constituted by big transmitter coils in order to charge homogeneously implants in free-moving small animals, where the receiver coil is fully implanted. Different approaches as the implementation of bigger coils, segmentation technique, multicoil array were combined to maximize the covered area and optimize the power distribution homogeneity as well as the power transfer efficiency.

It was found that segmentation technique significantly mitigated the power losses. Another important finding was that larger distances between transmitter and receiver coils decreased the misalignment sensitivity. Finally, after testing three different arrangements of multicoil arrays, it was concluded that overlapped coils provided the most homogeneous magnetic flux over the inductive surface compared with separated and adjacent coils.

BP 17.9 Tue 14:00 P2/1OG

Structural Dynamics Correlation of Peptides derived from Nucleoporins: Time-resolved X-ray Scattering and Computational Modelling — •Naireeta Biswas[1] and Simone Techert[1,2] — [1]FS-SCS, Deutsches Elektronen-Synchrotron (DESY), Notkestraße 85, 22607 Hamburg, Germany — [2]University of Göttingen, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Nuclear pore complexes (NPCs) form aqueous conduits along the nuclear membrane, controlling exchange of macromolecules between the cytoplasm and the cell nucleus is built up of ~ 30 different types of proteins called as nucleoporins(Nups) which contain phenylalanine-glycine (FG) repeating motifs know as FG repeat domains. FG repeat domains are intrinsically disordered. The FG domains facilitate a highly selective, bidirectional passage of macromolecules through the NPCs thus forming the permeability barrier. Several models for the highly selective nature of the permeability barrier of the NPCs have been proposed. According to the selective phase model, the NPC permeability barrier is constructed through cohesive meshwork of the FG domains by weak hydrophobic interactions between the phenylalanine residues forming a sieve like 3D hydrogel within the central channel of the NPCs.

To get an insight in the structural dynamics of these FG Nups, we are investigating the molecular dynamics of the FG repeat domains and their interactions during the gelation process using time-resolved small/wide-angel X-ray scattering (TR-SAXS/WAXS) techniques and molecular dynamics simulation.

BP 17.10 Tue 14:00 P2/1OG

First passage method to thermal fragmentation of amyloid fibrils — •Mohammadhosein Razbin[1], Panayotis Benetatos[2], and Ali Akbar Moosavi-Movahedi[3] — [1]Department of Energy Engineering and Physics, Amirkabir University of Technology, 14588 Tehran, Iran — [2]Department of Physics, Kyungpook National University, 80 Daehakro, Bukgu, Daegu 41566, Republic of Korea — [3]Institute of Biochemistry and Biophysics, University of Tehran, Tehran, Iran

Using the mean first passage method, we calculated the fragmentation rate in a given position along an amyloid fibril. We consider the fibril as one dimensional Rouse chain. The thermal fluctuations define the first passage time (FPT) associated to the fragmentation of the chain. The fragmentation rate is the inverse of the average of the FPT. Our expression for the rate is a function of the number of monomers, the position of the fragmentation along the filament, the ratio of the bond energy to the thermal energy, and the Rouse relaxation time. Our model predicts the fragmentation rate of insulin fibrils under optimal growth conditions which is consistent with the experimental data.

BP 17.11 Tue 14:00 P2/1OG

X-ray measurements of bovine red blood cells in continuous flow — •Jan-Philipp Burchert[1], Gerrit Brehm[1], Rita Graceffa[1], Manfred Burghammer[2], and Sarah Köster[1] — [1]Institut für Röntgenphysik, Georg-August-Universität Göttingen, Germany — [2]European Synchrotron Radiation Facility, Grenoble, France

Due to their high penetration depth and resolution, X-rays are ideally suited to study structures and structural changes within biological samples. For this reason, X-ray-based techniques have been used by various authors to investigate adhesive cells on solid supports. However, these techniques cannot conveniently study suspended cells in flow. We developed an X-ray compatible microfluidic device that serves as a sample delivery system and measurement environment. In our experiments, this device is applied to measure fixed bovine red blood cells by small-angle X-ray scattering (SAXS). We find a good agreement between in-flow and static SAXS data. Thus, we demonstrate that suspended cells can be measured with SAXS in continuous flow.

BP 17.12 Tue 14:00 P2/1OG

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

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

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

BP 17.13 Tue 14:00 P2/1OG

DNA origami encoded shaping of synthetic cells — •Julius Fichtler[1,2], Kevin Jahnke[1,2], Dimitris Missirlis[3], and Kerstin Göpfrich[1,2] — [1]Biophysical Engineering Group, Max Planck Institute for Medical Research, Jahnstraße 29, 69120 Heidelberg, Germany — [2]Department of Physics and Astronomy, Heidelberg University, 69120 Heidelberg, Germany. — [3]Department of Cellular Biophysics, Max Planck Institute for Medical Research, Jahnstraße 29, 69120 Heidelberg, Germany

Over the past decades, DNA nanotechnology, especially DNA origami, has developed a ever-increasing opportunities to create arbitrary two- or three-dimensional nanoscale objects out of DNA. Here, we report a strategy in bottom-up synthetic biology to qualitatively as well as quantitatively establish a link between information and compartment shape of synthetic cells. This is achieved via the deformation of giant unilamellar vesicles (GUVs) with information-encoding DNA origami. Variants of a squared-shaped two-layer DNA origami plate, displaying different degrees of polymerisation, were attached onto the surface of GUVs resulting in quantitatively clearly distinguishable membrane deformations that were evaluated by statistical analysis of the GUV's circularity. The strength of deformation correlates with the respective degree of polymerisation of DNA origami, induced by blunt end stacking, ranging from 100% nonspherical GUVs for the highest to 45% nonspherical GUVs for the lowest degree of polymerisation.

BP 17.14 Tue 14:00 P2/1OG

Flow-accelerated platelet biogenesis is due to an elasto-hydrodynamic instability — •Christian Bächer[1], Markus Bender[2], and Stephan Gekle[1] — [1]Biofluid Simulation and Modeling, Theoretische Physik VI, Universität Bayreuth, Germany — [2]Institute of Experimental Biomedicine I, University Hospital and Rudolf Virchow Center, Würzburg, Germany

Blood platelets form out of long protrusions, which are extended by stem cells into blood vessels of the bone marrow. After extension, these protrusions form swellings which eventually mature into blood platelets. Interestingly, experiments show a strong acceleration of platelet genesis in presence of blood flow. We use a newly developed 3D Lattice-Boltzmann/Immersed-Boundary method for active elastic cell membranes in presence of fluid flow [1] to provide a biophysical understanding of the swelling formation and its connection to blood flow. Our simulations show that actomyosin contractility triggers a pearling instability, which is similar to the Rayleigh-Plateau instability of a liquid jet and leads to the platelet-like swellings along the protrusion. Instability dynamics strongly accelerate as function of the blood flow velocity. Rather than to a biochemical regulation of platelet size, this points to a pure physical regulation, namely by the dominant wavelength of the instability.

[1] C. Bächer, S.Gekle, Phys. Rev. E 99, 062418, 2019

BP 17.15 Tue 14:00 P2/1OG

Dynamics of light-sensing microbial populations in microfluidic model habitats — •Sebastian Raum, Alexandros Fragkopoulos, and Oliver Bäumchen — Max Planck Institute for

Dynamics and Self-Organization (MPI-DS), D-37077 Göttingen, Germany

The natural habitats of many microorganisms are complex porous environments, where surface interactions of the cells play an important role, e.g., for navigation and survival of cell populations. By performing phototaxis, photosynthetic microbes are able to migrate towards optimal light conditions, where they can eventually adhere to surfaces. The goal of our work is to study the competition between surface interactions, light-regulated motility and surface adhesion. We designed an experimental setup that mimics the natural environment of the microorganisms and simultaneously allows for precisely tailoring the light conditions. A suspension of the light sensing *Chlamydomonas reinhardtii* cells is confined in a quasi-two-dimensional microfluidic compartment consisting of randomly distributed circular pillars. We account for natural light gradients by using an optical density filter for the illumination of the model habitat. Measurements of the spatial cell distributions are conducted in blue and red light, in order to switch the cellular light responses on and off. We test the hypothesis that the interplay of phototaxis and light-regulated adhesiveness represents an evolutionary adaptation to optimize the cell's photosynthetic efficiency in their natural habitat.

BP 17.16 Tue 14:00 P2/1OG

Label-free, High Throughput, Optical Characterization and Sorting of Particles and Cells in Microfluidic Channels — •Daniel Geiger, Tobias Neckernuss, Jonas Pfeil, Lisa Kwapich, Patricia Schwilling, and Othmar Marti — Ulm University, Institute of Experimental Physics

We present ODIN, a high performance, label-free optical sensing system for real-time detection, analysis and sorting of biological and synthetic particles and complex structures in a continuous flow. It combines a fast and sensitive CMOS camera sensor and a field programmable gate array, a high-performance data processing unit, with smart evaluation algorithms in a single device. Our algorithms reduce the dimensionality of the data from the camera, which condenses the amount of data tremendously but maintains all important information and in addition decreases noise. This enables ODIN to perform advanced image analysis in real-time at very high frame rates without buffering so that it can run continuously. Hence, we can analyze a large number of objects at very high throughput rates of several thousand objects per second. ODIN analyzes properties like size, shape and morphology of different kinds of particles like microplastic, cells, droplets, algae or complex structures like encapsulated objects. Since our modular analysis toolkit runs in real-time, we can control a microfluidic sorting device to sort objects and cells based on predefined conditions. We show the base technology as well as selected applications from the fields of Lab-on-a-Chip testing, drug delivery and cell mechanics.

BP 17.17 Tue 14:00 P2/1OG

Mechanical phenotyping beyond geometrical constraints using virtual channels — •Muzaffar H. Panhwar, Venkata A.S. Dabbirru, Yesaswini Komaragiri, Ricardo H. Pires, and Oliver Otto — ZIK HIKE, University of Greifswald, Greifswald, Germany

Microfluidic techniques have proven to be of key importance for achieving high-throughput cell mechanical measurements. However, their design modifications require sophisticated cleanroom equipment. Here, we introduce virtual fluidic channels as a flexible and robust alternative to Poly-dimethylsiloxane chips. Virtual channels are liquid-bound fluidic systems that can be created in almost arbitrary fluidic systems, e.g. standard flow cytometer cuvettes, and tailored in three dimensions within seconds for rheological studies on a wide size range of biological samples. We show that cell deformation in narrow virtual channels inside micrometer-sized systems is mainly driven by shear stress. By contrast, cells inside virtual channels of a large cuvette or capillary are deformed by an interfacial normal stress originating from the liquid-liquid interface. We demonstrate that this liquid-liquid interface acts as a high-frequency liquid cantilever for probing cell rheology on a millisecond timescale. As a proof-of-principle, cells are treated with the actin depolymerizing drug cytochalasin D. A significant reduction in elastic modulus is found compared to untreated cells. In summary, we show that virtual channels might offer the ability for high-throughput mechanical cell characterization in almost arbitrary geometries.

BP 17.18 Tue 14:00 P2/1OG

The effect of oxygen deprivation on mechanical properties of HEK293 cells — •Giulio Bianchi[1,2], Doreen Biedenweg[3], Ricardo H. Pires[2], and Oliver Otto[2] — [1]Physiolab, University of Florence, Florence, Italy — [2]ZIK HIKE, University of Greifswald, Greifswald, Germany — [3]University of medicine of Greifswald, Greifswald, Germany

Hypoxia plays an important role in triggering a variety of diseases and is also an important stimulus during embryogenesis. Despite our detailed understanding of the molecular events associated with oxygen starvation, its consequences to the mechanical stability of the cell remain to be fully scrutinized. Using recombinant expression of fluorescently labeled Hypoxia Inducible Factor-1 (HIF-1) in HEK293 cells, we have monitored inducement of cellular response to a 1% oxygen atmosphere by epifluorescence microscopy to study modifications in the cytoskeleton. We link this molecular state of the cells to changes in the mechanical phenotype as a label-free functional parameter. Performing real-time deformability cytometry on HEK293 cells at different times after inducing hypoxia, our results demonstrate a significant increase in the elastic modulus after 12h, an effect that becomes reversed after 48h. Using fluorescence-based methods we have correlated our findings to an increased number of apoptotic cells 24h after induction of hypoxia.

BP 17.19 Tue 14:00 P2/1OG

The role of substrate contacts in 2D and 3D microenvironments for cell mechanical properties — •Venkata Dabbiru[1], Emmanual Manu[1], Huy Tung Dau[1], Nora Bödecker[1], Doreen Biedenweg[2], Ricardo Pires[1], and Oliver Otto[1] — [1]University of Greifswald, Germany — [2]University Medicine Greifswald, Germany

Cells form with their microenvironment a network of biological and physicochemical signals that stem from cell-cell and cell-matrix contacts. Several pathologies including oncological disorders are associated with changes in such contacts but a comparative investigation by different approaches substantiating their relevance towards cell mechanics has, to our knowledge, never been conducted.

Here, we examine the role played by the substrate for the mechanical properties of HEK293T cells grown in 2D monolayers and spheroids as a 3D cell culture model. Experiments are performed using atomic force microscopy (AFM) and real-time deformability cytometry (RT-DC) in comparative assays. Our AFM results show that cells cultured in 2D have a Young's modulus that is significantly higher than that of spheroids. Interestingly, when cells are detached from the 2D substrate or the 3D matrix and captured in suspension, they become considerably stiffer. Comparing our AFM data to RT-DC results, which probes cells in suspension, we observe the same increase in elastic modulus independent of cell culture geometry. Our findings suggest, that the mechanical phenotype of adherent cells is to a large extent dominated by the presence of a substrate and less by the dimensionality of the cell environment.

BP 17.20 Tue 14:00 P2/1OG

Physical properties of cells required for efficient microcirculation — •Martin Krater[1,2], Stefanie Tietze[2], Angela Jacobi[1,2,3], Anna Taubenberger[2], Martin Bornhauser[3], and Jochen Guck[1,2] — [1]MPI for the Science of Light Erlangen — [2]Biotechnology Center TU Dresden — [3]Medical Clinic I, University Hospital TU Dresden

Biological cells in blood encounter successive constrictions smaller than their own diameter when circulating through microcapillaries such as the pulmonary networks. This is relevant for blood cells, circulating tumor cells or cells transplanted for therapeutic purposes such as mesenchymal stromal cells (MSC). While the cell size has been shown to be a relevant parameter to overcome capillary entrapment, the cells mechanical properties have so far not been considered. Here we investigated the microcirculation of MSCs as a function of their physical phenotype quantified using real-time deformability cytometry and atomic force microscopy. When MSCs were expanded in organ-like 3D mesenspheres, as opposed to MSCs classically cultured on 2D surfaces, we found them to be smaller and more compliant. Resulting in a more effective circulation in vitro, using a microfluidic microcirculation mimetic and improved in vivo circulation after intravenous transplantation to NOD/SCID mice. The initially large and stiff MSCs cultured in 2D could be reprogrammed into a physical phenotype suitable for circulation by subsequent culture in 3D systems. Thus, the physical properties of cells are essential to overcome capillary entrapment and are a promising therapeutic target to improve effective circulation.

BP 17.21 Tue 14:00 P2/1OG

High-throughput characterization of the time-dependent

mechanical properties of hydrogel beads, liquid droplets and biological cells — •Felix Reichel[1,2], Lucas Wittwer[1,3], Marta Urbanska[1,2], Shada Abuhattum[1], Sebastian Aland[3], and Jochen Guck[1] — [1]Max Planck Institute for the Science of Light and Max-Planck-Zentrum für Physik und Medizin, Erlangen — [2]Biotechnology Center, Center for Molecular and Cellular Bioengineering, Technische Universität Dresden, Dresden — [3]Hochschule für Technik und Wirtschaft Dresden, Dresden

In recent years, microfluidic tools have emerged that are capable of characterizing the mechanical properties of hundreds of thousands of cells individually within minutes. These tools, termed deformability cytometry, often focus on the deformation of the cell at a single time point once it has reached steady-state. Because of this, the strain information can only be linked to the elastic response of the deformed object. Here, we extend this approach and analyze the time-dependent deformation of spherical objects over a stress profile to determine their viscoelastic response when flowing through a microfluidic channel. Experiments on standardized hydrogel beads, phase-separated liquid droplets, and biological cells are compared to FEM-simulation data to derive both Young's Modulus and bulk viscosity. The simulations are also used to identify suitable mechanical models to describe the stress-strain relation of these different objects. With our approach we are broadening the mechanical information gained from deformation studies of spherical objects in high-throughput microfluidic assays.

BP 17.22 Tue 14:00 P2/1OG

Mechanical dissociation of tissue for real-time deformability cytometry — •Markéta Kubánková[1], •Despina Soteriou[1], Oana-Maria Thoma[2], Andrea-Hermina Györfi[3], Alexandru-Emil Matei[3], Stefan Scheuermann[4], Felix Dirla[5], Maximilian Waldner[2], Jörg Distler[3], Jens Langejürgen[4], and Jochen Guck[1] — [1]Max Planck Institute for the Science of Light, Erlangen, DE — [2]Dept. of Medicine 1, FAU Erlangen-Nürnberg, DE — [3]Dept. of Medicine 3, FAU Erlangen-Nürnberg, DE — [4]Fraunhofer IPA, Mannheim, DE — [5]BioITix, Frankfurt/Main, DE

Real-time deformability cytometry (RT-DC) is a high-throughput method used for characterizing single cells in suspension. Here we apply RT-DC for analyzing cells obtained from solid tissues. We used an enzyme-free approach based on mechanical dissociation of tissue, TissueGrinder (TG), to obtain heterogeneous single cell suspensions from various mouse tissues. The dissociation procedure resulted in high cell yield and viability and was significantly faster (~ 20 min) compared to conventional enzymatic methods (hours). RT-DC analysis allowed us to distinguish subpopulations of cells in label-free manner and to extract further information from single cell images, such as deformability. A key advantage of this method is that it is non-destructive and cells may be further reused. Moreover, a cell population of interest can be sorted according to image-based parameters. The combination of TG with RT-DC has potential as a fast and high-throughput diagnostic pipeline to detect pathological changes in tissue biopsies and to reveal cell populations invisible to marker-based approaches.

BP 17.23 Tue 14:00 P2/1OG

Droplet-Based Multiplexed Screening of Single NK Cells' Interferon-γ Release and Cytotoxicity — •Tobias Abele[1,2], Silvia Antona[1,2], Kevin Jahnke[1,2], Yannik Dreher[1,2], Ilia Platzman[1,2], and Joachim P. Spatz[1,2] — [1]Max Planck Institute for Medical Research, Heidelberg, Germany — [2]Department of Biophysical Chemistry, University of Heidelberg, Germany

Interferon-gamma (IFN-γ) is a fundamental cytokine secreted by natural killer (NK) cells and activated T cells. The amount of IFN-γ released by cytotoxic cells strongly immunomodulates several antitumor mechanisms. Therefore, single-cell analysis of IFN-γ release can help disentangle the heterogeneity of immune cells, leading to breakthrough findings. Towards this end, we exploited droplet-based microfluidics to investigate IFN-γ secretion from single NK cells in correlation with their cytolytic activity. Our method relies on co-encapsulation of activated NK-92 cells, polystyrene beads conjugated with specific IFN–γ capture antibodies and fluorescently labeled detection antibodies within surfactant stabilized water-in-oil compartments. The secreted cytokines are captured and detected via localized fluorescence at the periphery of the beads. Using this method, we thoroughly correlated the IFN-γ released from activated NK-92 cells with their ability to kill a specific target. We believe that the developed method represents a straight-forward approach to unravel the complex heterogeneity of NK cells. Furthermore, we envision our droplet-based assay to deepen the understanding of further immunological challenges such as aberrant IFN-γ expression related to autoimmune diseases.

BP 17.24 Tue 14:00 P2/1OG

MPI-based multi-GPU extension of the Lattice Boltzmann Method — •Fabian Häusl, Moritz Lehmann, and Stephan Gekle — Biofluid Simulation and Modeling, University of Bayreuth, Germany

The lattice Boltzmann method (LBM) is a highly versatile flow solver which benefits greatly from graphics processing unit (GPU) computing. However, the LBM is very memory-intensive while at the same time the on-board memory of GPUs is quite limited, which directly restricts simulation domain size. This poster presents a muli-GPU implementation based on the framework OpenCL and the Message Passing Interface (MPI) which is able to widen this limitation as well as to gain additional speedup. By using spezialized buffer types and memory layouts as well as applying the concept of templates to OpenCL-kernels in order to reduce memory access, it is precisely tailored to the requirements of GPUs and MPI. It differs from comparable implementations especially in that the domain can be subdivided along all three spatial directions. The communication scheme remains independent of the velocity set selected, can easily be adapted to the various extensions of the LBM and guarantees optimal buffer bandwidth. Communication time consumption can be hidden for the most part by overlapping it with computation, so the algorithm can reach 95% of its theoretical optimum in the weak-scaling and 13000 MLUPs using 4 Radeon VII GPUs for a cubic benchmark setup can be observed.

BP 17.25 Tue 14:00 P2/1OG

Analysis of red blood cells behaviour in a microfluidic device — •Amirreza Gholivand[1,2], Knut Dahlhoff[3], Timo Dickscheid[4], and Minne Paul Lettinga[1,2] — [1]Laboratory of Soft Matter and Biophysics, KU Leuven, Leuven, Belgium — [2]ICS-3 Soft Condensed Matter, Forschungszentrum Jülich, Jülich, Germany — [3]ZEA-1 Engineering, Electronics and Analytics, Forschungszentrum Jülich, Jülich, Germany — [4]INM-1 Neuroscience and Medicine, Forschungszentrum Jülich, Jülich, Germany

The blood flow dynamics through the micro-vascular system, which is the end of our vascular system, depend on many factors, such as the exact shape of the vessels, the aggregation and disaggregation and deformation of the red blood cells (RBCs). The effects of these parameters have been systematically studied in microfluidics, mainly using 2D channels with rectangular cross section, which are very different from the physiological vessels.

Here we present first data the flow of concentrated dispersions of (attractive) red blood cells in model 3-D microfluidic channels as well as physiologically relevant shaped channels. We used a novel technique, Selective Laser-induced Etching (SLE), to produce 3D structures in glass that allows the design of bifurcations into different planes with any desirable shape. To study the shape memory of the vessels the second generation of the bifurcation has been implemented with a parallel and perpendicular orientation relative to the first bifurcation,

BP 17.26 Tue 14:00 P2/1OG

Rectification of Bacterial Diffusion in Microfluidic Labyrinths — •Ariane Weber[1,2], Marco Bahrs[3], Zahra Alirezaeizanjani[3], Xingyu Zhang[1,4], Carsten Beta[3], and Vasily Zaburdaev[1,4] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg, Deutschland — [2]Max-Planck-Institut für Menschheitsgeschichte, Jena, Deutschland — [3]Universität Potsdam, Deutschland — [4]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Deutschland

Bacteria are able to explore large areas and move through complex environments. Both are of importance in various fields ranging from medicine over ecological sciences to industrial processes. In complex environments, bacteria interact with their surroundings and are strongly guided by confinement. To investigate how the dispersal of bacteria can be augmented by confinement, we study the long-term dispersal of bacteria which exhibit the run-and-tumble motility pattern in microfluidic labyrinths. Here we focus on two labyrinths made of obstacles regularly arranged in a square and a hexagonal lattice. We present an analytical description of the bacterial dispersal and numerical simulations of the underlying random walk for both geometries. To validate our theoretical predictions, we compare our results to experimental data of *E. coli* bacteria swimming through microfluidic labyrinths. Both in theory and experiments we observe enhanced dispersal of bacteria in labyrinths as compared to freely swimming cells for realistic motility and labyrinth parameters. For an extended initial period, the dispersal exhibits non-Gaussian diffusion, where the

geometry of the labyrinth is imprinted in the bacterial density profiles.

BP 17.27 Tue 14:00 P2/1OG

Better, faster, stronger: a new era of measuring cell mechanics and why we should care about strain rates — •Marta Urbanska[1,2], Hector E. Muñoz[3], Josephine Shaw Bagnall[4], Oliver Otto[1,5], Scott R. Manalis[4], Dino Di Carlo[3], and Jochen Guck[1,2] — [1]TU Dresden, Dresden, Germany — [2]MPL, Erlangen, Germany — [3]UCLA, Los Angeles, CA, USA — [4]MIT, Cambridge, MA, USA — [5]University of Greifswald, Greifswald, Germany

The mechanical phenotype of a cell is an inherent biophysical marker of its state and function, with potential value in clinical diagnostics. Several microfluidic-based methods developed in recent years have enabled single-cell mechanophenotyping at throughputs comparable to flow cytometery, thereby opening a new era of cell mechanical characterization. Here we present a highly standardized cross-laboratory study comparing three leading microfluidic-based approaches to measure cell mechanical phenotype: constriction-based deformability cytometry (cDC), shear flow deformability cytometry (sDC), and extensional flow deformability cytometry (xDC). We show that all three methods detect cell deformability changes induced by exposure to altered osmolarity. However, a dose-dependent deformability increase upon latrunculin B-induced actin disassembly was detected only with cDC and sDC, which suggests that when exposing cells to the high strain rates imposed by xDC, other cell components dominate the response. The direct comparison presented here serves to unify deformability cytometry methods and provides context for the interpretation of deformability measurements performed using different platforms.

BP 17.28 Tue 14:00 P2/1OG

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

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

We introduce an extension of RT-DC towards dynamic single cell measurements with the possibility to capture full viscoelastic properties at up to 100 cells/s. Cellular shape-changes along the entire length of the microfluidic channel are tracked in real-time and are subsequently analyzed by a Fourier decomposition discriminating cell responses to interfering stress distributions. We demonstrate that dRT-DC allows for cell mechanical assays at the millisecond time scale independent of cell shape. We use this approach for a comparison of peripheral blood cells based on their Young's modulus and viscosity.

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

BP 17.29 Tue 14:00 P2/1OG

Stimulation Dynamics of Circular Dorsal Ruffles in Fibroblast Cells — •Malte Ohmstede and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen, Bremen

Circular Dorsal Ruffles (CDRs) are ring shaped, propagating protrusions on the dorsal cell surface in - among others - fibroblast cells. These dense actin structures play a major role in macropincytosis and are orchestrated using a complex molecular pathway. The upstream stimulation of CDRs is done by activation of Receptor Tyrosine Kinases using various types of growth factors. In this work, Platelet Derived Growth Factor (PDGF) in conjunction with a microfluidic perfusion chamber is used to perform precise stimulation and re-stimulation of adherent fibroblast cells. Combined with fibronectin micro-contact printing, this method reproducibly yields large amounts of data from equally shaped cells. Through usage of circular kymographs and further image processing, the dynamics of cellular responses to PDGF stimuli are measured. For different PDGF concentrations, various characteristics of CDRs are evaluated. CDRs only form on the lamellipodium of adherent cells and are reflected by the nucleus and the cell edge. Incorporating deep learning based image segmentation, the influence of lammelipodial shape as boundary condition on CDR dynamics is evaluated.

BP 17.30 Tue 14:00 P2/1OG

Impact of cell culture age and structural modifications on the mechanical properties of hiPSCs derived cardiomyocytes. — •Emmanuel Manu[1], Nithya Shree[1], Ricardo Pires[1], Stefan Gross[2], and Oliver Otto[1] — [1]Biomechanics, ZIK HIKE, University of Greifswald, Germany — [2]DZHK, University of Greifswald, Greifswald, Germany

Cardiomyocytes derived from human induced pluripotent stem cell-derived cardiomyocytes (hiPSC-CM) are important biological models in drug screening and in understanding the pathophysiology of many cardiac diseases. Here, using atomic force microscopy, we focus on understanding the mechanical properties of cardiomyocytes as a function of culture age, using Cytochalasin D (CytoD) to promote actin-network depolymerisation. We observed that between the second to the fifteenth day of culture, the Young*s modulus (mean * SEM) of hiPSC-CM increased from 657 * 93 Pa to 1967 * 159 Pa. Exposing hiPSC-CMs to CytoD of varying concentrations, we determined an EC50 of 3.892 *M. Interestingly, the effect of actin depolymerization on the mechanical properties of cells decreases with cell culture age. This indicates that maturation of hiPSC-CMs involves remodelling of the actin network towards increased stability, possibly through the predominant incorporation of actin filaments into sarcomeres. Finally, we compared the elastic modulus of hiPSC-CMs when the cells are characterized in suspension as well as in adherent state. Interestingly, both methods yield elastic modulus values in good agreement.

BP 17.31 Tue 14:00 P2/1OG

Impact of cell culture age and structural modifications on the mechanical properties of hiPSCs derived cardiomyocytes — •Emmanuel Manu[1], Nithya Shree[1], Ricardo Pires[1], Stefan Gross[2], and Oliver Otto[1] — [1]ZIK HIKE, University of Greifswald, Greifswald, Germany — [2]DZHK, University Medicine Greifswald, Greifswald, Germany

Cardiomyocytes derived from human induced pluripotent stem cell-derived cardiomyocytes (hiPSC-CM) are important biological models in drug screening and in understanding the pathophysiology of many cardiac diseases.

Here, using atomic force microscopy, we focus on analysing the mechanical properties of cardiomyocytes as a function of culture age and cytoskeletal modifications, using Cytochalasin D (CytoD) to promote actin-network depolymerisation. We observed that between the second to the fifteenth day of culture, the Young's modulus (mean +/- SEM) of hiPSC-CM increased from 657 +/- 93 Pa to 1967 +/- 159 Pa. Exposing hiPSC-CMs to CytoD of varying concentrations, we determined an EC50 of 3.892 uM. Interestingly, the effect of actin depolymerization on the mechanical properties of cells decreases with cell culture age. This indicates that maturation of hiPSC-CMs involves remodelling of the actin network towards increased stability, possibly through the predominant incorporation of actin filaments into sarcomeres. Finally, we compared the elastic modulus of hiPSC-CMs when the cells are characterized in suspension as well as in adherent state. Interestingly, both methods yield elastic modulus values in good agreement.

BP 18: Poster VI

Cell Adhesion and Migration & Multicellular Systems (BP 16.1 – BP 16.27)

Time: Tuesday 14:00–16:00 Location: P2/2OG

BP 18.1 Tue 14:00 P2/2OG

Altering the early development of Caenorhabditis Elegans via laser ablation — •Vincent Borne, Philipp Strunz, and Matthias Weiss — Experimental Physics I, University of Bayreuth, Germany

While the role of biochemical signaling during embryonic development has been extensively studied, the role of mechanical cues in this process are still only partially understood. For the early development of the model organism Caenorhabditis elegans, mechanical forces have been shown to be key for a proper cell arrangement in the embryo until gastrulation: Based on mutual pushing forces of cells within the confining egg shell, a simple relaxation model was shown to be capable of predicting cell trajectories and final positions. Here we have probed the validity of this model when perturbing the nematode's embryogenesis at very early stages via laser microsurgery. Experimental results observed after ablating early precursor cells suggest that an extension of the model, e.g. updating the cortical stiffness of cells for reproducing correct wetting angles between neighboring cells, is required. Preliminary results on developing such an extended model, based on dissipative particle dynamics simulations, are discussed.

BP 18.2 Tue 14:00 P2/2OG

Morphodynamics in the Foraging of *Physarum polycephalum* — •Lisa Schick, Mirna Kramar, and Karen Alim — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

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

BP 18.3 Tue 14:00 P2/2OG

Network adaptation to transient stroke — •Leonie Bastin[1], Komal Bhattacharyya[1], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Technical University of Munich, Germany

Damage is a risk that all kinds of networks are exposed to. This includes overload in power grids as well as the formation of blood clots in brain microvasculature. The occlusion of a single blood vessel in the brain can cause severe tissue damage and cognitive dysfunction. Experiments and simulations have been done in the past to understand the effect of vessel occlusions on brain blood flow and network architecture. Here, we are interested in the morphological adaptation of a network to occlusion induced flow changes. Is it possible that networks reorganise to minimise the damage caused by lack of flow? For this aim, we use the model organism *Physarum polycephalum*. In the plasmodial stage, the slime mould forms a network of interconnected tubes through which its cytoplasm streams back and fro, driven by peristaltic tube contractions. Previously, morphological changes due to changes in the contraction pattern have been observed. Here, we locally induce stalling of the flow in a tube of the network and analyse the effect of flow changes on network morphology.

BP 18.4 Tue 14:00 P2/2OG

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

Motion and force generation of cell collectives are crucial in many biological processes, including wound healing and cancer metastasis. The first case can be quantitatively investigated in the so-called wound healing assay, when 2D cell monolayers start to move into empty space after removal of a barrier, often by forming protrusions led by so-called leader cells. During recent years it has become clear that these cell monolayers are both dynamic and elastic at the same time, a combination which is hard to model with conventional approaches. Here we introduce a new model that uses phase fields for the dynamical aspects and the theory of thin elastic sheets for the mechanical aspects. Our continuum equations can be solved numerically by a combination of spectral and matrix methods, and they can be compared to analytical solutions. We demonstrate how our approach works for several paradigmatic situations, namely contraction of a 1D bar and a 2D disc, and formation of elastic protrusions for a 2D wound healing situation due to localized forces at the interface.

BP 18.5 Tue 14:00 P2/2OG

Stochastic Cell-Cell Interactions in Confined Systems — •Nicolas Arlt[1], David Brückner[1], Alexandra Fink[2], Joachim Rädler[2], and Chase Broedersz[1] — [1]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, LMU Munich — [2]Faculty of Physics and Center for NanoScience, LMU Munich

Assemblies of motile cells can exhibit distinct behaviors, such as clustering to heal a wound or dispersal in cancer cell invasion. Such collective behaviors have been shown to be intimately related to the local contact interactions between individual cells. Here, we investigate how cell-cell interactions affect the dynamics of confined migrating cells. To this end, we place pairs of highly invasive MDA-MB-231 cancer cells on adhesive micropatterns, consisting of two square patches connected by a thin constriction. In this setup, we observe that the cells repeatedly transition across the constriction, leading to repeated 'cellular collisions' in a standardized microenvironment. By obtaining a large dataset of such collision trajectories, we infer an equation of motion for these interacting cell pairs. This model reproduces the key statistics of the interaction dynamics, such as position- and velocity correlations. Our approach allows us to characterize the cell-cell interactions, which we compare for different celltypes and different types of confinement.

BP 18.6 Tue 14:00 P2/2OG

Collective cell migration in 3D micro-tumours — •Tom Brandstätter[1], David Brückner[1], Yu Long Han[2], Ming Guo[2], and Chase Broedersz[1] — [1]Arnold-Sommerfeld-Center For Theoretical Physics and Center of NanoScience, LMU Munich, Germany — [2]Department of Mechanical Engineering, Massachusetts Institute of Technology, Cambridge, MA, USA

The coordinated migration of cell collectives is key to many biological processes, including cancer progression. Here, we study the dynamical behaviour of in vitro micro-tumours. Initially, these micro-tumours are in a benign phase, exhibiting strongly correlated and highly persistent collective rotation of nearly all cells inside the spheroid. We investigate local interactions that can induce this collective mode of cell migration, using a physical minimal model for cell migration.

To constrain our models of interacting active particles, we analyse experimental data obtained from in vitro micro-tumours of various sizes. These experimental observations, including correlation functions and spatio-temporally resolved measures of the local persistence, place strong constraints on possible candidate models.

Furthermore, we find that these benign tumours eventually transition to a malignant state, which is characterized by an unconfined, non-definite shape with branches invading the surrounding tissue. Collective rotation is completely lost and the cancer cells show correlated but disordered motion. We aim to understand this drastic change in the collective behaviour in terms of the changes in single-cell behaviour and in cell-cell interactions.

BP 18.7 Tue 14:00 P2/2OG

Unravelling the biomolecular mechanism of light-switchable adhesion of *Chlamydomonas* to surfaces — •Antoine Girot, Rodrigo Catalán, Alexandros Fragkopoulos, Anaëlle Chrétien, Line Holtzer, and Oliver Bäumchen — Max Planck Institute

for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, 37077 Göttingen, Germany

Bioadhesion is a ubiquitous phenomenon for many living systems such as mussels, bacteria or microalgae. In this work, we focus on the adhesion of the flagellated microalga *Chlamydomonas reinhardtii*. We discovered that *Chlamydomonas* exhibits light-switchable adhesion, in which the flagella of the cells stick to surfaces under blue but not under red light. Our goal is to unravel the biomolecular mechanism of this specific light-regulated behaviour. In order to characterise the adhesiveness of *Chlamydomonas* to surfaces, two different experimental approaches are carried out. First, the kinetics of the adsorption and desorption of a cell suspension to a surface in response to a light switch is recorded. Second, *in vivo* micropipette force spectroscopy experiments are performed to precisely measure the adhesion force of single cells. By applying these methods for different wild-type as well as genetically modified strains, we aim at identifying characteristic gene sequences associated to the cells adhesiveness. To unravel the blue-light photoreceptor that triggers the light-switchable adhesion, experiments with specific photoreceptor-deleted mutants are performed. Finally, we also investigate how the glycosylation of the flagella membrane proteins affects the adhesiveness of *Chlamydomonas*.

BP 18.8 Tue 14:00 P2/2OG

Mechanisms behind growth and locomotion of *Physarum polycephalum* — •Nico Schramma[1] and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization — [2]Technical University of Munich

The unicellular slime mould *Physarum polycephalum* is able to find and efficiently connect multiple food sources by reorganising its network-like morphology. Acto-myosin driven peristaltic contractions of the networks' tubes enable this efficient mass transport. Moreover, this organism is known to respond to a huge variety of stimuli by altering its body plan and the contraction patterns.
However, it is not understood how this slime mould moves and which mechano-chemical parameters are varied in order to modulate the contractions driving the migration. Here, we present a multi-timescale approach including brightfield-, birefringence- and fluorescence microscopy, particle image velocimetry, and a non-invasive air-jet indentation method to observe the contraction patterns, acto-myosin organisation, local flow-profile and spatial variations in cortex elasticity in small *Physarum* during migration.

BP 18.9 Tue 14:00 P2/2OG

Energetic cost of morphological states of Physarum polycephalum — •Leonie Kemeter[1], Mirna Kramar[1], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization — [2]Technical University of Munich

An interconnected network of tubes forms the flow-driven plasmodial networks of the unicellular slime mould Physarum polycephalum and provides an astonishing example of self-organization in biological systems: the tubes' oscillatory activity is responsible for driving the flow of endoplasm through the network, thus forming the morphology via the contractions. Changes in oscillations and the resulting morphological changes help Physarum react to its environment. For example, it increases effective Taylor dispersion by pruning of small tubes during foraging. Recent experiments show two distinct morphological states - one fan-like slower state and one lightning-like faster state. Interestingly, the slime mould seems to switch randomly between the two states. Knowing the energetic cost of those morphological states would allow for possible explanations for this behaviour, e.g. a high energetic cost of the lightning strike suggests that it is used only when advantages of this state such as the higher speed are necessary. We model the elastic and dispersive energy of a network showing both morphological states. The model uses the tried and tested approach that the tube's contractions result in a peristaltic wave across the network and needs only the time-averaged radii of the tubes as input from the experiments. The modelled contractions can later be compared to the measured contractions to check the validity of the model.

BP 18.10 Tue 14:00 P2/2OG

The effect of blue light on *Physarum polycephalum* cytoplasm flow for different topologies — •Siyu Chen[1], Felix Bäuerle[1], Jean-Daniel Julien[1], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Technische Universität München, München, Germany

The network-forming unicellular slime mould *Physarum polycephalum* adapts to external stimuli in a coordinated manner over an extended body plan in space and time. This is achieved by sharing information and resources across the body plane in a peristaltic wave that adapts to body size.
Among the common external stimuli, one of the most studied stimuli is blue light, which triggers a retreat response in *P. polycephalum*. This change of the slime mould's environment are met with an adaptation of its tubes' oscillatory activity.
In this project we focus on the relationship between the topology of the network and their responses towards the external stimuli. We suspect that, when *P. polycephalum* was exposed to the blue light, it regulates the fluid properties of the endoplasm, and this process diversifies with different topology. Here we experimentally observe how *P. polycephalum* in different topologies responses to blue light stimuli. We quantify its contraction pattern and flow information such as velocity and viscosity to compare with our theoretical expectations.

BP 18.11 Tue 14:00 P2/2OG

Flow reorganisation in the brain microvasculature during a stroke — •Agnese Codutti[1] and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]Physik-Department, Technische Universität München, Garching, Germany

Ischemic brain strokes are a major concern for public health. Major strokes obstructing main arteries cause reorganisation of flows throughout the microvasculature, likely with a long lasting influence on brain microvasculature behaviour and topology. Strikingly flow reorganisation is different in different parts of the brain vasculature. While the loopy surface arteriole network undergoes stops and reversals during a stroke, the penetrating arterioles exhibit steady flow direction. One hypothesis is that the flow reorganisation at the surface prevents changes in the penetrating arterioles. Here, we investigate if network topology and hierarchy of the system drives penetrating arterioles to be robust asking: Is the network designed to be resilient to such changes? To test this hypothesis, we analytically solved the flows in a toy model of an H- shaped network module showing that flow reversal in the penetrating arterioles can happen in principle for great pressure instabilities, due to the hierarchy and topology of the network. In two dimensional irreg- ular networks optimised for transport, the pressure difference needed for the reversal yet is even higher, supporting the hypothesis of the in-built resilience of the network. Currently, we are testing the dependence on different network properties to identify the main factor inducing the resilient behaviour.

BP 18.12 Tue 14:00 P2/2OG

Parameter Optimization of a Cellular Potts Model using Multiple Micro-Pattern Cell Migration Experiments — •Sophia Anna Schaffer[1], Andriy Goychuk[2], Christoph Schreiber[1], Erwin Frey[2], and Joachim Rädler[1] — [1]Fakultät für Physik, Ludwig-Maximilians-Universität, Geschwister-Scholl-Platz 1, 80539 München — [2]Arnold Sommerfeld Center, Ludwig-Maximilians-Universität, Theresienstraße 37, 80333 München

Modelling cell migration is important to simplify and understand the highly complex machinery of cells. Cellular Potts Models (CPMs) have been successfully used to reproduce cell migration patterns in two dimensions. They are capable to reproduce cell behavior with increasing levels of complexity and biological accuracy from single cells to collective migration. A particular challenge for computational simulations is to optimize model assumptions and parameters so that many experimental data sets are fitted simultaneously. Cells in confining geometries show restricted motion and various properties of cell behavior such as deformation, persistence, adhesion and polarization can be separately probed. Here, we still present a rational approach to use a set of geometries with complementary properties to determine parameter values successively in a systematic manner using one specific cell line. The general concept is to determine model parameters successively by using the emergent properties of the different geometry designs.

BP 18.13 Tue 14:00 P2/2OG

Evaluation of cancer spheroid growth in synthetic hydrogels with light sheet microscopy — •Viktoria Zieger, Timo Betz, and Bart E. Vos — Institute of Cell Biology, ZMBE, Münster, Germany

Tumours of cancer cells are in constant interaction with their surroundings, where physical forces are applied to the extracellular matrix (ECM) to eventually allow the cancer cell to migrate and to form

metastasis. We evaluate cancer spheroid growth and cell invasion over time as a function of the rigidity of a non-linear ECM. To achieve this, the extracellular matrix is mimicked by a synthetic hydrogel, which is biocompatible, strain-stiffening and can be finely mechanically tuned without affecting the structural properties. This allows control of the physical properties and the mechanoenvironment.

To gain 3D timeseries of spheroid evolution as well as hydrogel deformation, an in-house scanning light-sheet microscope is built, which allows rapid imaging while reducing photo-bleaching for long-time measurements. To avoid sample motion, the set-up combines axial light-sheet movement via a scanning galvanometer mirror system and simultaneous focus adjustment via an electrically tunable lens. This prevents the necessity to move the sample and enables precise time-resolved 3D images of spheroid growth and cell invasion.

BP 18.14 Tue 14:00 P2/2OG

The effect of lidocaine and calcium signaling on the adhesion of *Chlamydomonas* to surfaces — •Marzieh Karimi, Henning Lührs, Antoine Girot, and Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany

Photosynthetic microorganisms are ubiquitous in nature and applied in photobioreactor technologies for molecular farming and as a sustainable source of biofuels. However, the formation of microbial biofilms in such photobioreactors appears as a major technological issue, which could be solved by tuning the adhesion of the cells. In this context, we discovered that the adhesion of the microalga *Chlamydomonas reinhardtii* to surfaces is switchable by light (Kreis et al., Nature Physics, 2018). Under blue light, the cells stick to surfaces, while under red light they do not show any adhesion. Previous experiments suggest that this change in adhesion is based on the translocation of the adhesion-mediating protein FMG-1B within the flagella membrane. In this work, we study the influence of lidocaine as a signal inhibitor on the light-switchable adhesion of *Chlamydomonas*. Using in vivo micropipette force spectroscopy experiments, we find that the light-switchable adhesion of the flagella is completely inhibited in the presence of lidocaine in any light condition. Since lidocaine is known to inhibit calcium ion channels, we hypothesize that such a photocurrent is involved in the signal transduction from the blue-light photoreceptor to the flagella membrane.

BP 18.15 Tue 14:00 P2/2OG

Fluid flow controls morphological changes — •Noah Ziethen[1] and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Technical University of Munich, Garching, Germany

The morphology of biological transport networks is often regarded as a result of optimization under a given demand. As demands may change rapidly in life, biological flow networks continuously adapt. The shear rate inside the flow network is largely assumed to be the control mechanism of this adaptation. However, direct experimental evidence for this hypothesis is still missing, and the theoretical implication of such local adaptation on the network dynamics is not fully understood.

Here, the model organism *Physarum polycephalum* allows to directly test causality between flow shear rate change and vessel pruning. *P. polycephalum* forms a network of connected tubes exhibiting a complex oscillatory shuttle streaming inside them. We image and quantify the time evolution of single vessels in *Physarum* by extracting the vessel diameter evolution and the corresponding flow field using particle image velocimetry. These measurements reveal a time-delayed response in the tube diameter trend on the average flow magnitude, which results in some data sets in a pruning behavior and for others in an oscillatory interplay between the two quantities. Motivated by the experimental result, we build a feedback model taking into account the local minimization of energy dissipation and the coupling to the network, which is able to reproduce the bistability found in the data.

BP 18.16 Tue 14:00 P2/2OG

Quantification of the collective dynamics of endothelial cells in a two-dimensional confluent layer — •Anselm Hohlstamm, Mats Leif Moskopp, Andreas Deussen, and Peter Dieterich — Institut für Physiologie, Medizinische Fakultät, TU Dresden

Collective dynamics of confluent cells results from a complex interplay of single cell dynamics and cell-to-cell interactions. In order to better understand these processes, a quantitative analysis of cell movements is essential. Hence, we aim to quantify the migration activity of single cells influencing the whole cell collective. Human umbilical vein endothelial cells (HUVECs) were seeded and stained with low concentrations of a fluorescent dye. The cells were observed for up to 48 hours via time-lapse microscopy (dt = 10 min) and trajectories were obtained with an in-house developed image processing software. Typically, several 10.000 cell trajectories per experiment were detected within an area of 6 x 7 mm. HUVECs showed lively proliferation generating a confluent two-dimensional monolayer in a non-equilibrium situation. This process can be characterized by an exponential velocity distribution of the cells where the mean squared velocity showed a slow decrease. The mean squared displacement indicated a sub-diffusive behaviour. This is consistent with an increasing cell density forcing cells to localize their positions. Besides, the spatial velocity correlation function showed an exponential-like decrease with correlation lengths of around 60 μm ($\sim$3 cell diameters). In conclusion, we quantified the dynamics of confluent cells allowing us to evaluate the effects of humoral or pharmaceutical stimulations in future.

BP 18.17 Tue 14:00 P2/2OG

The Physics of Carcinomas: A multi-scale analysis on primary tumor tissues — •Frank Sauer[1], Steffen Grosser[1], Erik W. Morawetz[1], Thomas Fuhs[1], Frederic Renner[1], Benjamin Wolf[3], Sonja Kallendrusch[4], Hannah-Marie Scholz Margraf[1], Jürgen Lippoldt[1], Heiko Tzschätzsch[6], Jürgen Braun[7], Ingolf Sack[6], Claudia T. Mierke[2], Ingo Bechmann[4], Susanne Briest[3], Lars-Christian Horn[5], Michael Höckel[3], Bahriye Aktas[3], and Josef A. Käs[1] — [1]Soft Matter Physics Division, Peter-Debye-Institute for Soft Matter Physics, Leipzig, Germany — [2]Biological Physics Division, Peter Debye Institute for Soft Matter Physics, Leipzig, Germany — [3]Department of Gynaecology and Obstetrics, Universitätsklinikum Leipzig, Germany — [4]Institute of Anatomy, Universitätsklinikum Leipzig, Germany — [5]Institute of Pathology Ad Interim, Universitätsklinikum Leipzig, Germany — [6]Department of Radiology, Charité-Universitätsmedizin, Berlin, Germany — [7]Institute of Medical Informatics, Charité-Universitätsmedizin, Berlin, Germany

Cancer is a heterogeneous disease and most fatalities from solid tumors arise from their ability to systematically metastasize. This metastatic cascade is a multi-scale process. In cooperation with the University Hospital Leipzig, we are realizing a full-scale biophysical analysis on selected primary tumor tissue samples. Covering a range from macroscopic bulk properties down to single cell features, we are aiming at an interdisciplinary tumor characterization to contribute to a better understanding of the systemic nature of the disease cancer.

BP 18.18 Tue 14:00 P2/2OG

Stick-slip motion for a cellular glider with translational and rotational friction — •Pintu Patra[1,2], Anna Battista[1,2], and Ulrich S. Schwarz[1,2] — [1]BioQuant, Heidelberg University & University Medical School, Heidelberg, Germany — [2]Institute for Theoretical Physics, Heidelberg University, Heidelberg, Germany

Cellular movement over planar surfaces is often limited by sliding friction at the cell-substrate interface. A typical feature of sliding friction is stick-slip motion which consists of periods of slow (stick phase) and fast movement (slip phase). Stochastic multi-contact models explain the observed stick-slip motion at intermediate speeds of the translational motion. These models consider an ensemble of molecular bonds that form and rupture at the interface between two surfaces moving relative to each other. Here we extend this theoretical framework to include also the effect of rotational motion, a situation which arises e.g. for malaria parasites gliding on flat substrates. First, we derive analytical force-velocity and torque-angular velocity relations for pure translation and pure rotational driving, respectively. Then we show that a critical region of large bond fluctuations observed for the combined driving smoothly connects the corresponding regimes that exist for the purely translational and purely rotational cases. We also find an additional regime at small translational but high rotational velocities in which large deviations occur in the circularity of the cellular glider.

BP 18.19 Tue 14:00 P2/2OG

One-dimensional active gel models for optogenetic control of cell locomotion — •Oliver Max Drozdowski[1,2], Falko Ziebert[1,2], and Ulrich Sebastian 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

Cell motility is essential in all domains of life, including development,

wound healing and cancer. In order for a cell to start moving, a transition from a symmetric non-motile state to a polarized moving state has to occur. One-dimensional models of active gels based upon continuum mechanics have resulted in a quantitative understanding of how the interplay between contraction and flow in the actin cytoskeleton can lead to this transition. Recently, optogenetics has emerged as a promising experimental tool to control these processes. In this work we theoretically investigate if and how optogenetics could be used to control cell locomotion. We find that effects from external optogenetic signals can be incorporated in existing models as perturbations of solutions to the governing equations. We investigate an active Maxwell model with elastic boundary conditions, which cannot sustain the broken symmetry on its own, and show that asymmetric signals can lead to motility that then stops when the optogenetic activation ends. Additionally, we discuss models that also couple to a dynamic concentration field of motor proteins. Here optogenetic perturbations can both initiate and arrest steady states of motility. Together these results suggest that optogenetics could indeed be used to control cell movement.

BP 18.20 Tue 14:00 P2/2OG

Spatio-temporal characteristics of eukaryotic single-cell motility on fibronectin coated micro-lanes — •Johannes Heyn, Christoph Schreiber, and Joachim Rädler — Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, D-80539 Munich, Germany

Studying cell migration in naturally occurring environments, such as metastasising cancer in cell tissue or stem cells during embryonic development, proves immensely complex from an experimental point of view. Additionally, the external cues of the complex environment makes it difficult to develop a consistent mathematical description of the cell trajectories. To simplify the system, we constrain single cells to a quasi-one-dimensional migration by using micropatterned substrates that only allow cell movement along a fibronectin coated lane. The defined geometry facilitates quantitative read-out of locomotion, allows for large number statistics and simplifies theoretical models. In order to capture all relevant timescales of cell migration we observe cells for several days with a time-resolution in the order of seconds. From this we extract the memory kernel for a generalised Langevin equation approach. By comparing memory kernels, we are able to discriminate between different cell lines. In the next step we are interested in how external cues influence the characteristic memory kernels of cells. In particular, chemical gradients can be studied to get a better understanding of the cell migration process and its dependence on the microenvironment.

BP 18.21 Tue 14:00 P2/2OG

Quantitative Phase Imaging for Studying Cell Migration and Bone Resorption in Periodontitis — •Felix Peter Sanchez Klose, Agnes Dahlstrand Rudin, Karin Christenson, Maria Ransjö, and Johan Bylund — Göteborgs Universitet, Göteborg, Sweden

Periodontitis is a chronic inflammation of the tooth supporting structures caused by a prolonged immune reaction to bacteria resulting in tooth loss if left untreated. As an inflammatory disease, the migration of neutrophils to the site of infections is of interest to study periodontitis. Besides the inflammatory lesions, periodontitis is characterized by loss of the bone structures surrounding the teeth. Imaging of the cell cultures was performed with a quantitative phase imaging (QPI) microscope. We demonstrate that a QPI microscope can be used to measure neutrophil chemotaxis and to perform cell tracking on a cellular level. The system allows for statistical analysis of various chemotactic parameters. In an osteoclast model system, the live imaging allowed for identification of early osteoclast-like cell formation and helped us to pinpoint the ideal culture length for cell quantification. QPI offers a valuable tool to observe neutrophil migration in a label-free system directly in cell cultures. In contrast to conventional methods, QPI can give insights in the neutrophil migration on a single-cell level and it enables analysis of cell movement parameters, e.g., motility. In addition, this method can aid in investigating the processes of cell differentiation, e.g., formation of osteoclasts.

BP 18.22 Tue 14:00 P2/2OG

Engineering motile amoeboid cells toward precise and targeted microtransport — •Setareh Sharifi Panah[1], Oliver Nagel[1], Valentino Lepro[1,2], Robert Grossmann[1], and Carsten Beta[1] — [1]Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]Max Planck Institute of Colloids and Interfaces, 14476 Potsdam, Germany

Over the past decades, growing efforts have been invested on biohybrid microsystems. However, applications such as targeted drug delivery through complex environments remain challenging. Inspired by leukocytes, we propose to exploit the potential of eukaryotic cells for microtransport, using the Dictyostelium discoideum cells as model. Our experiments highlight the ability of amoeboid cells to displace cargo particles with faster spreading cargo-loaded cells, suggesting cell-particle interactions as a stimulus promoting cell motility. Further, we developed a physical model which captures the main motility aspects of our system. Chemotaxis experiments reveal a guided transport driven by both single and collective cells. Remarkably, active microtransport across 3D collagen matrices suggest reliability of our system also in complex environments. To get an insight into the cell-particle dynamis, the approximate pulling force exerted on a cargo by the cell, is being estimated using microfluidics. Interestingly, under constant drag force of up to a few nano Newton, agent cells maintain their adhesion site to the cargo while being pulled downstream, suggesting limited yet considerable applied force to the cargo. These findings serve as a basis for undestanding underlying mechanics of such microtransport.

BP 18.23 Tue 14:00 P2/2OG

Physical interaction of tumor spheroids with the ECM — •Eliane Blauth, Steffen Grosser, Frank Sauer, and Josef A. Käs — Soft Matter Physics Divison, Peter Debye Institute for Soft Matter Physics, University of Leipzig, Germany

The interaction between tumors and the extracellular matrix is an important factor during cancer progression. Most experimental assays that are used to study this interaction are rather designed with single cells or have a complex three-dimensional structure.

Here, we present a simple, but efficient setup to characterize how model tumors interact with their surroundings. To mimic the physiological conditions in a more realistic manner we use three-dimensional tumor spheroids and put them on collagen matrices to model the extracellular matrix. With this approach our ECM-model gains a third dimension and complex interactions such as three-dimensional cell migration or the nonlinear viscoelastic behavior of the ECM are observed. By using multicellular spheroids as model tumors we detect not only the interaction of cell clusters with the ECM but also the different migration modes of cells that left the original spheroid. Still we can use basic brightfield microscopy to measure all of these properties sufficiently.

Our data demonstrate the invasiveness of different cell lines, including healthy epithelial ones, which is characterized by the traction forces and the collective migration behavior of the spheroids on different collagen matrices.

BP 18.24 Tue 14:00 P2/2OG

Bacterial adhesion and biofilm inhibition on nanopatterned surfaces — •Claudia Arbeitman[1,2], Magalí Lingenfelder[3], Karla Banjac[3], Pablo Rojas[2], Virginia Albarracín[1], and Martín García[2] — [1]CONICET, Argentina — [2]Theoretical Physics, University of Kassel, Germany — [3]Max Planck - EPFL, Switzerland

The ability of the bacteria to associate into communities in biofilms -as it happen in medical devices- is central to their pathogenicity as they confer protection from antimicrobial agents and bactericidal molecules present on host tissues. Here, we developed a hierarchical antibacterial nanopatterning, that is able to control bacterial biofilm formation. We successfully tested this nanopatterned surface against multi resistant bacteria, proving a long standing protection with improved biocompatibility. In order to unveil the underlying mechanisms, we applied a set of advanced microscopy tools and mathematical models. Our results indicate further details in the realm of bacteria-surface interactions.

BP 18.25 Tue 14:00 P2/2OG

Active gel model of onset of the movement in one-dimensional cell motility — •Yuan-Heng Tseng[1] and Hsuan-Yi Chen[1,2] — [1]Department of Physics, National Central University, Zhongli, Taiwan — [2]Institute of Physics, Academia Sinica, Nankang, Taiwan

To understand how the intracellular mechanical mechanism affects the motion of a cell, we develop a one-dimensional model for cell migration on a solid substrate. This model includes contractile force from actomyosin network, viscous stress in the cytoskeleton, actin polymerization at the ends of the cell, drag force due to substrate and drag force due to cell-substrate bonds. Our numerical solutions show that in addition to the contractility, polymerization-cell-movement feedback, and

spontaneous symmetry breaking in the distribution of cell-substrate bonds helps to initiate cell crawling. This is illustrated by phase diagrams for static and motile states.

BP 18.26 Tue 14:00 P2/2OG

Motility of aggregated *Neisseria gonorrhoeae* cells influences cell death and response to antibiotic treatment — •Marc Hennes, Tom Cronenberg, and Berenike Maier — Institute for Biological Physics, AG Maier, University of Cologne, Germany

Like most procaryotic unicellular organisms, members of the genus Neisseriaceae polymerize hair-like appendages that protrude from the cell body. In the case of *N. gonorrhoeae*, the pathogen responsible for the sexually transmitted disease gonorrhoea, the so-called type IV pili (T4P) allow the cell to bind to surfaces and move on them through retraction, but also enable the uptake of extracellular DNA. Cooperatively, intercellular network binding by dynamic T4P-T4P interactions leads to the formation of spherically shaped cell aggregates which may fuse and deform like water drops and play a crucial role in the infection of host tissues. Here, we investigate the temporal dynamics of these aggregates at the single-cell level by tracking the positions and velocities of each bacteria. We find that bacterial motility inside the colonies is highly heterogeneous and sensitive to translation inhibitors, which hyper-motilize bacteria and homogenize their dynamics. Strikingly, we find that cell motility correlates negatively with the fraction of dead cells in the absence of bactericidal antibiotics, and positively in their presence.

BP 18.27 Tue 14:00 P2/2OG

A large scan are AFM with convolutional neural network image segmentation for live cell measurements — •Todor Krastev and Tilman E. Schäffer — Universität Tübingen, Institut für Angewandte Physik, Auf der Morgenstelle 10, 72076 Tübingen

The atomic force microscope (AFM) has become a robust and versatile tool for the investigation of mechanical properties of single cells. We have developed an AFM with a large scan range of 25 mm in xy-direction. This enables us to access high numbers of cells for mechanical measurements. In order to harness the full potential of our setup we employ state of the art convolutional neural networks for single cell detection, thereby facilitating high throughput measurements on single cells. To demonstrate the setup's potential we investigate the influence of common live fluorescent dyes on single cell mechanics. Our investigation is focused on SiR-actin and SiR-tubulin as these dyes target principal components of the cytoskeleton.

BP 19: Poster VII

Computational Biophysics (BP 17.1 – BP 17.11); Protein Structure & Dynamics (BP 17.12 – BP 17.17); Single Molecule Biophysics (BP 17.18 – BP 17 .25); Statistical Physics of Biological Systems (BP 17.26 – BP 17.32)

Time: Tuesday 14:00–16:00 Location: P2/3OG

BP 19.1 Tue 14:00 P2/3OG

How to Pare a Pair: Topology Control and Pruning in Intertwined Complex Networks. — •Felix Kramer[1,2] and Carl Modes[1,2] — [1]Center for Systems Biology Dresden (CSBD), Dresden, Germany — [2]Max Planck Institut for Molecular Cell Biology and Genetics (MPI-CBG), Dresden, Germany

Recent work on self-organized remodelling of vasculature in slimemold, leaf venation systems or vessel systems in vertebrates has provided a plethora of potential adaptation mechanisms. All these have in common the underlying hypothesis of a flow driven machinery, meant to prune primary plexi in order to optimize the system's dissipation, flow uniformity or more, with different versions of constraints. Nevertheless, the long-term dynamics of adapting networks whose architecture and function is particularly dependent of their respective environment have not been properly understood. Therefore, interwoven capillary systems such as found in the liver, kidney and pancreas, present a novel challenge regarding the field of coupled distribution networks. We here present an advanced version of the discrete Hu-Cai model, coupling two spatial networks in 3D. We show that spatial coupling of two flow adapting networks can control the onset of topological complexity given the system is exposed to short-term flow fluctuations. Further, our approach results in an alternative form of Murray's law, which incorporates the local vessel interactions and flow fluctuations.

BP 19.2 Tue 14:00 P2/3OG

Foamlike network of bundled semiflexible polymers — •Tobias A. Kampmann and Jan Kierfeld — TU Dortmund University, Germany

We applied the EC algorithm to a system of many (semiflexible) harmonic chains, where the simulation efficiency is comparable to optimized molecular dynamics simulations, while still incorporating the essential features of the actual dynamics. This algorithm allows the simulation of polymer melts, where reptation can be clearly observed. When the polymers interact via a short range, attractive square well potential bundled structures are assembled. We analyse time series of quasi-two-dimensional systems, where foam-like structures arise. This can be linked to the attractive interaction which leads to a minimization of the overall bundle length similar to surface tension in the case of foams. The low mobility and the bending stiffness of polymers lead to structural differences in comparison to soap foams.

BP 19.3 Tue 14:00 P2/3OG

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

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

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

BP 19.4 Tue 14:00 P2/3OG

Personalized numerical modeling for stent implantation in the aorta — •Dandan Ma[1,3], Yong Wang[2,3], Michael Steinmetz[1], and Martin Uecker[1,3] — [1]University Medical Center Göttingen, 37075 Göttingen, Germany — [2]MPI for Dynamics and Self-Organization, 37077 Göttingen, Germany — [3]German Center for Cardiovascular Research (DZHK), Partner Site Göttingen, Germany

The coarctation of the aorta (CoA) accounts for 7% of all congenital heart defects. Stent implanted is a recommended therapy to reduce the pressure gradient and restore blood flow. Computational fluid dynamic (CFD) can provide valuable insight for flows in a patient-specific model, and thereby predict therapy outcome. In this study, the flow within an aorta, reconstructed from magnitude resonance imaging (MRI) data, was numerically modeled firstly, using lattice Boltzmann method. Both large eddy simulation (LES) and direct numerical simulation (DNS) were adopted to resolve the turbulent blood flow, with boundary condition extracted from phase-contrast MRI (PC-MRI) measurement. Numerical results such as flow velocity,

pressure drop and wall shear stress (WSS) were obtained. By comparing the results from LES, DNS and PC-MRI, we conclude that the LES is capable of obtaining accurate aortic flow within acceptable simulation time. In silico stent implantation for a child with CoA was then performed, by predicting the deformed geometry after implantation and modeling the flow therein with LES. It is shown from the numerical results that both pressure drop and maximum WSS are reduced. Such methodology will be used to optimize patient-specific therapy.

BP 19.5 Tue 14:00 P2/3OG

AI Developer: a general tool for deep-learning image classification in life science and beyond — Martin Kräter[1,2], Shada Abuhattum[1,2], Despina Soteriou[1], Jochen Guck[1,2], and •Maik Herbig[1,2] — [1]Max Planck Institute for the Science of Light, Erlangen — [2]Biotechnology Center of the TU Dresden, Dresden

The publication record on artificial intelligence (AI) -based image analysis has increased drastically over the last years. However, all application cases consist of individual solutions with high specificity for a particular use. Here, we present an easy-to-use, adaptable, open source software, called AIDeveloper (AID) to train neural nets (NN) for image classification without the need for programming. The software provides a variety of NN-architectures that can be simply selected for training. AID allows the user to apply trained models on new data, obtain metrics for classification performance, and export final models to different formats. The working principles of AID are first illustrated by training a convolutional neural net (CNN) on a large standard dataset consisting of images of different objects (CIFAR-10). We further demonstrate the range of possible applications on selected biophysical and biomedical problems, such as distinguishing differentiated and non-differentiated stem cells, performing a whole blood cell count, and classifying B- and T-cells, all based on cell images alone. Thus, AID can empower anyone to develop, train, and apply NNs for image classification. Moreover, models can be generated by non-programmers, exported, and used on different devices, which allows for an interdisciplinary use.

BP 19.6 Tue 14:00 P2/3OG

Parallel Network-Based Biocomputation using molecular motors- Solving Exact cover — •Pradheebha Surendiran[1], Aseem Salhotra[2], Till Korten[3], Alf Månsson[2], and Heiner Linke[1] — [1]Nanolund and Solid state physics, Lund university, Lund, Sweden — [2]Department of chemistry and biomedical sciences, Linnaeus university, Kalmar, Sweden — [3]B-cube, Centre for molecular bioengineering, Technische universität Dresden, Dresden, Germany

Computational problems of a combinatorial nature requires exponential time to explore the solution, making traditional serial computation intractable, and parallel computation a necessity. The subset sum problem was recently solved [1] encoding them into a graphical network of channels ingrained onto a nanofabricated device which was then explored by molecular motors to find all possible solutions to the problem. This approach of network based parallel-computation (NBC) could be potentially used to solve other problems by scaling in an energy efficient manner compared to that of the conventional computer. In this work, we focus on solving Exact Cover(ExCov) which is a decision problem applying the same strategy. We fabricate the problem encoded nanodevice with upscaled network of channels and observe the motility of molecular motors using fluorescence microscopy. Thus scaling of these devices has led to the interest of developing different architectural elements and also employ methods such as deep learning for the automatic evaluation of the huge amount of data obtained. [1] Nicolau et al, PNAS 113 (10), 2591-2596 (2016) Funding: EC-H2020 Bio4Comp Grant-No. 732482

BP 19.7 Tue 14:00 P2/3OG

Morphogenesis in Viscoelastic Tissues via Planar Deformations — •Abhijeet Krishna[1,2], Jana Fuhrmann[1], Joris Paijmans[1,2,3], Suzanne Eaton[1,2,3], Frank Jülicher[1,2], Natalie Dye[1], and Carl Modes[1,2] — [1]Max Planck Institute of Cell Biology and Genetics, Dresden, Germany — [2]Center for Systems Biology Dresden, Dresden, Germany — [3]Max Planck Institute of Physics of Complex Systems, Dresden, Germany

The mechanisms by which tissue surfaces develop to form complex 3D morphologies is an interesting question from the perspective of developmental biology. A model system for answering this question is the Drosophila wing imaginal disc which is a flat epithelial tissue that everts out of the plane to form a surface with non-zero Gaussian curvature. We are interested in understanding the mechanics of this eversion. It has been shown that before eversion, the cells in the wing disc elongate anisotropically and orient themselves in concentric circles around the central region of the tissue. Our hypothesis is that during eversion, cells lose their anisotropic characters which would lead to inhomogeneous and patterned planar deformations. Such inhomogeneous planar deformations can lead to change in the Gaussian curvature of the tissue. We build a spring-dashpot lattice model to simulate a viscoelastic and thick epithelial tissue. Using our model, we try to explain the robustness of the event of eversion. We also propose a mechanism by which eversion could be temporally controlled by the tissue.

BP 19.8 Tue 14:00 P2/3OG

mRNA secondary structure on cationic lipid membrane surfaces — •Mohd Ibrahim and Nadine Schwierz — Department of Theoritical Biophysics, Max Planck Insitute of Biophysics,Max-von-Laue-Str. 3, 60438 Frankfurt, Germany

RNA based therapeutics have emerged as promising candidates for treating currently untreatable diseases like cancer or diabetes. Since RNA is highly charged and degradable it needs a carrier to be transported into the cells. Lipid nanoparticles (LNPs) hold great promise and have been extensively studied for such purposes. However, the delivery efficiency of existing LNPs is very low and the structure of RNA-LNP systems remains poorly understood. A powerful technique to elucidate the structure of nanoparticles are scattering experiments (SAXS and SANS). However, interpreting scattering intensities for a complex systems like LNP is non-trivial. Molecular dynamic simulations in conjunction with scattering experiments can serve as a powerful method to overcome this hurdle. In this work, we use coarse-grained MD simulations to elucidate the conformations of mRNA on the cationic lipid membrane surface. Using existing secondary prediction tools to model mRNA structures, we show that SAXS intensities can be used to differentiate between different RNA conformations on cationic lipid membrane surfaces. By comparing our scattering intensities with experiments we will be able to identify the most probable RNA conformation on the lipid membrane surface or inside lipid nanoparticle thus aiding our understanding of RNA loaded LNP structures.

BP 19.9 Tue 14:00 P2/3OG

Uncertainty quantification for electromagnetic models of biological cells based on dielectric spectroscopy data — •Julius Zimmermann[1], Fukun Shi[2,3], Jürgen Kolb[2,3], and Ursula van Rienen[1,4] — [1]Institut für allgemeine Elektrotechnik, Universität Rostock, 18051 Rostock — [2]Institut für Physik, Universität Rostock, 18059 Rostock — [3]Leibniz-Institut für Plasmaforschung und Technologie (INP), 17489 Greifswald — [4]Department Life, Light & Matter, Universität Rostock, 18051 Rostock

Developing reliable models to understand the interaction between electromagnetic fields and biological cells is a challenging task due to a lack of precise data. We present an approach to estimate the induced transmembrane potential. The approach is based on the electroquasistatic formulation of Maxwell's equations and requires knowledge of the conductivity and relative permittivity of the different constituents of the system under investigation (that is cell membrane, cytoplasm and extracellular medium). We estimate the required parameters from dielectric spectroscopy data. Based on the estimate's uncertainty, the uncertainty of the model output is estimated in a mathematically rigorous fashion.

Acknowledgement: This research was supported by the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG) within the Collaborative Research Centre 1270 ELAINE.

BP 19.10 Tue 14:00 P2/3OG

Physical Analysis of One-Component Signalling in Bacteria — •Linda Martini and Ulrich Gerland — Physics of Complex Biosystems, Technical University of Munich, Garching, Germany

Adaptation to changing environments is of vital importance to bacterial cells and is enabled by sophisticated signal transduction systems. While classical two-component signalling is well studied, the mechanisms of one-component systems, where a single protein implements both sensing and response regulation, are mostly uncharacterized. One such one-component system is the membrane-integrated protein CadC, which is part of the pH-stress response system in E. Coli. As it directly binds to the genomic DNA to regulate transcription, it faces a target search problem the dynamics of which are still to be understood. Using kinetic Monte Carlo simulations of a lattice model, we focus on a char-

acterization of the coupled stochastic dynamics of the DNA and the proteins, and its dependence on the system parameters. Understanding the kinetics of membrane-localized proteins specifically binding to a dynamic DNA will be important to interpret corresponding in vitro experiments and more generally to understand the biophysics of one-component signal transduction.

BP 19.11 Tue 14:00 P2/3OG

Metaheuristic Optimization of Biomolecular Simulation Parameters — •Marie Weiel[1], Markus Götz[1], and Alexander Schug[2] — [1]Karlsruhe Institute of Technology, Karlsruhe, Germany — [2]Jülich Supercomputing Centre, Jülich, Germany

Owing to the structure-function paradigm, a wealth of structural information on proteins has been accumulated. Experimental data might be ambiguous and have to be interpreted to access their actual content. A common way is to integrate them into molecular simulations via an energetic bias favoring conformations concordant with the data. Data-assisted simulations often rely on parameters, the choice of which is far from trivial but crucial for performance. A central question is how to weight experimental information with respect to prior knowledge in the underlying physical model. We propose a metaheuristic particle-swarm based optimization method. In our setup, a particle corresponds to a simulation using a particular combination of parameters to be optimized. To assess simulation outcome, the ensemble's physicality and its agreement with the data are considered. We use Rosetta and bias energy, respectively, out of which the objective function is constructed. To assign equal importance, each contribution has to be rescaled to the same order of magnitude. As the related objective function hyperparameters are a priori unknown but have a critical impact on the search-space topology, they are refined on the fly while the algorithm proceeds. The better different contribution ranges are known from complete simulations, the more accurate values can be chosen, improving optimization efficiency and thus simulation quality.

BP 19.12 Tue 14:00 P2/3OG

Markov Modeling of an Allosteric Transition — •Georg Diez, Daniel Nagel, Benjamin Lickert, and Gerhard Stock — Albert-Ludwigs-Universität Freiburg, 79104 Freiburg, Germany

Allostery plays a fundamental role in regulatory biological processes, in which a functional change of a protein is triggered at one site by the binding of a ligand to another, distant site. It yet remains unclear what forces drive the underlying mechanisms, especially if they are of structural or dynamical nature. In order to investigate allostery, here we study molecular dynamics data of a PDZ domain, in which the binding of a ligand causing an allosteric transition is mimicked by an azobenzene photoswitch.

Markov State Models are a powerful tool for accessing the full dynamics of a system since they only require locally converged trajectories instead of one single long trajectory. This allows us to analyze an ensemble of equilibrium and non-equilibrium trajectories which in total cover more than 400 μs [1].

The chances to make predictions about the dynamical and conformational change of the system will be illustrated. At the same time, the virtues and shortcomings of constructing a Markov State Model will be addressed.

[1] S. Buchenberg, F. Sittel, and G. Stock, "Time-resolved observation of protein allosteric communication," Proc. Natl. Acad. Sci. U.S.A. 114,E6804 (2017)

BP 19.13 Tue 14:00 P2/3OG

Finding Pathways of Markov State Models — Daniel Nagel and •Gerhard Stock — Albert-Ludwigs-Universität Freiburg, 79104 Freiburg, Germany

In numerous fields of research, the population dynamics of states is described in terms of a master equation or a Markov state model (MSM). Given Markovian dynamics, we can define a transition matrix T_{ij} for a certain lagtime τ_{lag} which determines completely the time evolution of the system. Often we are interested in the pathways of the MSM, that lead from an initial to a final state. E.g., the in protein folding these paths account for the mechanism the molecular reaction evolves. These paths naturally arise in a Markov chain Monte Carlo simulation, where we draw random numbers which determine the next step depending on the transition matrix T_{ij}. The catch is the slow convergence. As a remedy, Vanden Eijnden and co-workers have proposed transition path theory. However, this method is designed to only give the most important pathways correctly. In systems of biological interest, e.g. protein folding, allostery etc., many pathways may arise and may also be important to understand the mechanism. To cope with these problems, we suggest a new method which directly considers the path probabilities. In contrast to Markov chain Monte Carlo, it samples the path space more efficiently and gives a well-defined error. We demonstrate the performance and discuss the insights revealed by adopting the folding of villin headpiece.

BP 19.14 Tue 14:00 P2/3OG

Quantitative analysis of protein binding curves — •Lukas Refisch and Clemens Kreutz — Institute of Medical Biometry and Statistics, Faculty of Medicine and Medical Center - University of Freiburg, Germany

New measurement techniques for the quantification of reaction rate constants are continuously emerging. Usually, densely sampled time courses of labeled or unlabeled protein intensities are measured to observe a change from one equilibrium state which relaxes to another one. Traditional analysis approaches commonly assume simplifications of the underlying effects and select subsets of measured data to perform the analysis on. Instead, we propose using comprehensive ordinary differential equation (ODE) models that describe the entire protein binding process and can therefore be fitted to the full time series of obtained data.

We present advances for the analyses of two different experimental settings (i) microscale thermophoresis and (ii) reflectometric interferometry utilizing ODE models. They explicitly incorporate assumptions about the underlying processes and are fitted directly to the experimental data. These models contain several parameters that are estimated from data, some of them specifying time points at which experimental conditions change. The parameter estimates also contain information about spatial effects, like e.g. the flow of a solution across a microarray which is estimated from time course data. Our approach finds reliable characterization of binding curves and automates the data analysis, thus increasing the rate of data analysis considerably.

BP 19.15 Tue 14:00 P2/3OG

Targeted Molecular Dynamics Calculations of Free Energy Profiles of Gramicidin A Using a Nonequilibrium Friction Correction — •Miriam Jäger, Gerhard Stock, and Steffen Wolf — Albert-Ludwigs- Universität Freiburg

Standard unbiased molecular dynamics (MD) simulations are impractical to sample rare events due to their high computational costs. An economic approach to simulate such processes are biased MD simulations. We here use targeted MD simulations, which apply a moving distance constraint along some prechosen reaction coordinate to enforce rare transitions. Free energy profiles can be calculated on the fly from such simulations by dissipation-corrected targeted MD, which combines a second-order cumulant expansion of Jarzynski's equality with an interpretation within the framework of Langevin equations of motion [1]. We here applied dissipation-corrected targeted MD to potassium diffusion through ion channels, using the Gramicidin A channel as a test system. Performing a non-equilibrium principal component analysis on backbone dihedral angles to separate different protein conformations appearing during the transfer, we find that the dissipation-corrected free energy profiles correspond well to barriers predicted by other methods. Further, the friction profiles give insight into ion-protein and ion-water molecule interactions.

[1] S. Wolf and G. Stock, Targeted molecular dynamics calculations of free energy profiles using a nonequilibrium friction correction, J. Chem. Theory Comput. 14, 6175 (2018).

BP 19.16 Tue 14:00 P2/3OG

Optimizing aerodynamic-lens-stack geometries for nanoparticle injection — Lena Worbs[1,3], •Jannik Lübke[1,2,3], Armando Estillore[1], Amit Kumar Samanta[1], and Jochen Küpper[1,2,3] — [1]Center for Free-Electron Laser Science, Deutsches Elektronen-Synchrotron (DESY), Hamburg, Germany — [2]Center for Ultrafast Imaging, Universität Hamburg, Germany — [3]Department of Physics, Universität Hamburg, Germany

Single-particle imaging (SPI) experiments at x-ray free-electron lasers (XFELs) promise high-resolution-imaging of the structure and dynamics of nanoparticles. By guiding isolated sample molecules to the focus of an XFEL, diffraction patterns of individual particles can be collected. Sufficient amounts of patterns of identical nanoparticles are needed to overcome the inherently small signal-to-noise ratio and reconstruct the underlying 3D structure [1]. To achieve atomic resolution, a beam of identical particles needs to be delivered into the XFEL focus, which necessitates sample-control methods. We develop various

control techniques, such as particle beam focusing using fluid dynamics [2], temperature control [3], charge state selectivity using electric fields, and further methods. Here, we present theoretical and experimental studies for improving of aerodynamic-lens geometries [3] to create high-density particle beams for SPI experiments.

[1] M. M. Seibert et al., *Nature* **470**, 78 (2011)
[2] N. Roth et al., *J. Aerosol Sci.* **124**, 17 (2018)
[3] A. K. Samanta et al., *arXiv*:1910.12606 (2019)

BP 19.17 Tue 14:00 P2/3OG

Domain Swapping in Crystallin Proteins Can Drive Early Stages of Cataract Formation — •Govardhan Reddy Patluri and Balaka Mondal — Indian Institute of Science, Bangalore, India

Crystallins (Crys) are densely packed, long-lived eye lens proteins responsible for the ocular functions of the lens. Physicochemical perturbations in the cellular environment disrupt the native state stability of Cry proteins and populate aggregation prone misfolded states. These misfolded states gradually accumulate to produce high molecular weight amorphous aggregates, which scatter visible light resulting in lens opacity or cataract. The molecular mechanism of cataract formation or structure of these aggregation prone precursors remain elusive to date. Using molecular dynamics simulations and coarse-grained protein model of human γC and γD Crys, we identified the aggregation prone misfolded states present in the unfolding pathways of these proteins. We further show that these partially misfolded conformations readily undergo dimerization by domain swapping revealing the early stages of aggregation leading to cataract formation.

BP 19.18 Tue 14:00 P2/3OG

High-yield fabrication of DNA and RNA constructs for single molecule force and torque spectroscopy experiments. — •Flavia Stal Papini, Mona Seifert, and David Dulin — Junior Research Group 2, Interdisciplinary Center for Clinical Research, Friedrich-Alexander-University Erlangen-Nürnberg (FAU), Cauerstraße 4, 91058 Erlangen, Germany

Single molecule biophysics experiments have enabled the observation of biomolecules with a great deal of precision in space and time, e.g. nucleic acids mechanical properties and protein*nucleic acid interactions using force and torque spectroscopy techniques. The success of these experiments strongly depends on the efficient design and fabrication of complex nucleic acid structures, as the outcome of the experiment strongly depends on the high quality of the final construct. Though the molecular biology techniques involved are well known, the fabrication of nucleic acid constructs for single molecule experiments still remains a difficult task. We developed new protocols to generate high-yield and high-quality coilable double-stranded DNA and RNA constructs, as well as DNA and RNA hairpins with *500*1000 bp long stems (Papini et al., NAR 2019). A new approach based on single-stranded DNA annealing is presented and its efficiency in the fabrication of complex DNA constructs is shown in magnetic tweezers assays. Our protocols enable the design of a large range of nucleic acid constructs for single molecule biophysics experiments.

BP 19.19 Tue 14:00 P2/3OG

Temperature controlled high-throughput magnetic tweezers assay for viral RNA-dependent RNA polymerase study — •Mona Seifert[1], Pauline van Nies[1], Flávia Stal Papini[1], Jamie Arnold[2], Minna Poranen[3], Craig Cameron[2], Martin Depken[4], and David Dulin[1] — [1]IZKF, FAU Erlangen-Nürnberg — [2]The University of North Carolina Chapel Hill — [3]University of Helsinki — [4]TU Delft

The viral RNA-dependent RNA polymerase (RdRp) is an essential factor for the virus to establish a successful infection as it generates all viral RNA. As enzymatic kinetic processes follow the Arrhenius law, polymerase nucleotide addition rate is expected to be temperature sensitive. We previously introduced high-throughput magnetic tweezers to study RdRp kinetics using kilobases long templates, i.e. a length similar to the viral genome, with near single base resolution. To perform experiments at in vivo temperature, we developed a temperature controlling system for our magnetic tweezers assay and performed in situ temperature calibration by leveraging the temperature dependence of DNA twist. We applied the temperature controlled setup to study the elongation kinetics of different RdRps at several temperatures and we observed that the increase in temperature correlates with a higher nucleotide addition rate and short pause exit rate, confirming the catalytic nature of these pauses. Non-catalytic backtrack pauses however are temperature insensitive. The assay we present here simultaneously provides high throughput and temperature control, which will be essential for future studies of complex viral replicases.

BP 19.20 Tue 14:00 P2/3OG

Probing Nucleosome Dynamics in Magnetic Tweezers — •Yi-Yun Lin[1], Willem Vanderlinden[1], Lori Van de Cauter[1], Tine Brouns[1,2], and Jan Lipfert[1] — [1]Department of Physics, Nanosystems Initiative Munich, Center for NanoScience, LMU Munich, Amalienstrasse 54, 80799, Munich, Germany — [2]KU Leuven, Division of Molecular Imaging and Photonics, Celestijnenlaan 200F, 3001, Leuven, Belgium

Nucleosomes are the fundamental unit of chromatin. They control eukaryotic genome accessibility and can regulate expression, replication and repair of the genome by organizing chromatin. Multiple factors affect chromatin dynamics and control the unwrapping and assembly of nucleosomes. Lens epithelium-derived growth factor (LEDGF) p75 is a co-activator of general transcription. In vivo LEDGF/p75 can recognize transcriptionally active genomic regions by specific binding of its PWWP domain to tri-methylated histone H3 lysine 36 (H3K36me3). To investigate how LEDGF/p75 affects chromatin structure, we applied single molecule magnetic tweezers. Our results suggest that LEDGF/p75 alters nucleosome unwrapping and inter-nucleosome interactions, and help us understand the cellular mechanisms of LEDGF/p75 as a transcriptional co-activator.

BP 19.21 Tue 14:00 P2/3OG

Deep Learning for DNA Reads through 2D Solid-state Nanopores — •Angel Diaz Carral[1], Chandra Shekar Sarap[1], Ke Liu[2], Aleksandra Radenovic[2], Maria Fyta[1], and Elka Radoslavova[3] — [1]Institute for Computational Physics, Universität Stuttgart, Germany — [2]Laboratory of Nanoscale Biology, Institute of Bioengineering, School of Engineering, EPFL, Switzerland — [3]Fundamental Physics Department, Faculty of Science UNED, Spain

DNA molecules can electrophoretically be driven through nanopores giving rise to measurable electronic current blockades important for DNA sensing. In this work, experimental ionic traces from 2D molybdenum disulfide nanopores DNA translocations are used to train a Deep Learning model for interpreting the DNA events and improving the identification of different nucleotides threading the nanopore. We propose a methodological approach to train a Clustering model for identifying molecular events related to different conformations of DNA nucleotides threading the nanopore. This approach has revealed the efficiency of using the height of the ionic blockade as the training feature. This can lead to a clear clustering of the nanopore events over the use of the traditionally used dwell time. In order to eventually predict the type of molecule threading the pore, the features selected in the clustering analysis are used to train a Convolutional Neural Network capable of optimizing and accelerating the nanopore read-out. Our approach allows for a deep insight into characteristic molecular features in 2D nanopores and provides a feedback mechanism to tune these materials and interpret the experimentally measured signals.

BP 19.22 Tue 14:00 P2/3OG

Avidity of multivalent DNA binding to DNA origami — •Maximilian Voggenthaler[1], Ricarda Berger[1], Joachim Rädler[1], Ralf Jungmann[2], Florian Schüder[2], Alexander Auer[2], Eugene Petrov[1], and Tim Liedl[1] — [1]Department of Physics and Center for Nanoscience, Ludwig Maximillian University, Munich, Germany — [2]Max Planck Institute of Biochemistry, Martinsried, Germany

Multivalent binding is a frequently occurring theme in biological recognition that enables both tight binding and high specificity. DNA nanotechnology employs this concept when higher order assemblies are designed by multivalent hybridization sites. However, the effective binding affinity of multiple linkages with both steric as well as electrostatic constraints has not been studied in a quantitative manner. Here, we study the binding affinity of a double stranded DNA helix with two single stranded overhangs to a DNA origami block equipped with two complementary strands as multivalent receptor. We use fluorescence correlation spectroscopy, thermophoresis, total internal reflection fluorescence microscopy and gel electrophoresis to study avidity as a function of spacing and salt concentration. Our findings are important for better engineering of super selective linkages in origami self-assembly and medical nanoagents.

BP 19.23 Tue 14:00 P2/3OG

In situ magnetic tweezers force calibration for all tether

length — •Eugeniu Ostrofet, Flavia Stal-Papini, and David Dulin — FAU, Erlangen, Germany

Magnetic tweezers are a powerful technique to perform high-throughput and high-resolution force spectroscopy measurements at single-molecule level. The camera-based detection of magnetic tweezers enables the observation of hundreds of magnetic beads in parallel, and therefore the characterization of the mechanochemical behavior of hundreds of nucleic acids and enzymes. The accuracy of force spectroscopy measurements relies on a precise force calibration. In magnetic tweezers, the forces are quantified from the lateral fluctuations of the tethered magnetic bead. Such measurements are difficult to perform on short tethers, i.e. less than 4 kbp DNA, and therefore often rely on calibration tables, i.e. magnetic force versus magnets distance, performed using long DNA molecules, i.e. ~8 kbp and longer. However, the bead-to-bead variation in magnetic content leads to force dispersion, which biases the force spectroscopy measurement. To solve this issue, we present a new and simple strategy to perform in situ force calibration for hundreds of tethered magnetic beads simultaneously, for any tether length, and for the whole accessible force range for a given magnets-magnetic bead configuration. We illustrate the usefulness of our approach by characterizing the force dependence of protein-DNA interactions using a DNA hairpin-based force jump assay.

BP 19.24 Tue 14:00 P2/3OG

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

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

BP 19.25 Tue 14:00 P2/3OG

A proof-of-principle set-up linking ion channel conformation and function by combining single-molecule FRET and single-channel recording — •Steven Vanuytsel, Christopher Parperis, and Mark Wallace — Department of Chemistry, King's College London, London, UK

Building a bridge between static high-resolution membrane protein structures and the kinetic information obtained via patch-clamping remains challenging due to significant incompatibilities in the experimental conditions required to measure these two signals. Nevertheless, when successful, such a method would provide a plethora of information by allowing the construction of a molecular movie that links function to conformation.

Optical single-channel recording (oSCR) shifts the measurement of ionic current from an electrical to an optical readout, allowing parallel interrogation of multiple channels simultaneously. Furthermore, shifting from an electrical to an optical set-up allows a straightforward route to measure function and conformation in parallel by interrogating the latter using single-molecule Förster Resonance Energy Transfer (smFRET).

Here, we report on our recent work to establish parallelized smFRET and oSCR recordings in a proof-of-principle set-up that allows control over single-molecule *gating* kinetics of a protein nanopore that stochastically senses fluorescently labelled DNA, thereby allowing us to record well-controlled simultaneous events.

BP 19.26 Tue 14:00 P2/3OG

Modeling meiotic chromosomes - random walk bridges in a confinement — •Tim Klingberg[1,2], Meng Wang[1,2], Xingyu Zhang[1,2], Hui-Shun Kuan[1,2], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Max-Planck-Zentrum für Physik und Medizin

The alignment and correct pairing of homologous chromosomes is a crucial step during meiosis. In its early stages, the chromosomes are tethered with their telomeres to the nuclear envelope. Telomers may interact with the cytoskeleton while the fluctuations of chromosomes in the nucleus are affected by the physical properties of the chromatin and the state of the nucleoplasm. Overall, it is largely not understood how the homologous chromosomes manage to align and pair with the exquisite precision and in a short period of time. Our goal is to understand physical limitations of the pairing and homologous search process. To this end, we focus on quantifying possible configurations of tethered chromosomes in the confinement of the nucleus. We use the bead-rod polymer model for numerical simulations and the theory of random walk bridges for analytical calculations. We show that a smaller persistence length leads to smaller polymer fluctuations but also to a higher entropic force acting on tethered ends. We argue that such an optimization problem may determine physical properties of chromosomes in meiosis.

BP 19.27 Tue 14:00 P2/3OG

Bayesian gradient-sensing in the presence of noise — •Maja Novak and Benjamin M. Friedrich — TU Dresden (CFAED, PoL), Dresden, Germany

Chemotaxis, the navigation of biological cells in external concentration fields, guides foraging bacteria to food patches, immune cells to inflammation sites, or sperm cells to the egg. Chemotaxis strategies must be adapted to sensing and motility noise, inevitable at the microscopic scales of cells, by optimal filtering of chemosensorial input and choice of chemotaxis strategy. A key question is: how to combine most recent and previous sensory input?

We present an information-theoretic framework of optimal gradient-sensing and chemotactic navigation, based on Bayesian sequential estimation. Remarkably, the Bayesian strategy optimally combines "temporal comparison" and "spatial comparison", two distinct gradient sensing strategies employed by biological cells. The width of likelihood estimates of individual agents provides a reliable proxy for the dispersion of direction angles of an ensemble, reflecting the consistency of our approach.

We investigate a search strategy that maximizes the expected information gain in each time step, generalizing the previously proposed "infotaxis" strategy [1] to the case of multiple sensors. We find that agents move slower at locations with low local signal-to-noise ratio to increase the fidelity of gradient measurements.

[1] Vergassola et al. 2007

BP 19.28 Tue 14:00 P2/3OG

Pitfalls in statistical data analysis — •Thomas John and Christian Wagner — Experimentalphysik, Universität Saarland

During your studies, you learned various ways of evaluating and displaying data. We would like to introduce some further statistical evaluation methods. After the presentation, you may no longer generate histograms with bars and you will never again try to fit a Gaussian curve to an empirical probability distribution. Even if both methods are intuitively clear, it delivers less precise results as more indirect methods. As keywords, we would mention: kernel density estimators and fitting to empirical cumulative distribution functions.

[1] D. W. Scott, Multivariate Density Estimation: Theory, Practice and Visualization, Wiley Series in Probability and Statistics 2015.

BP 19.29 Tue 14:00 P2/3OG

Tracing non-equilibrium signatures in time series obtained from biological systems — •Samuel Salinas-Almaguer, Florian Rehfeldt, and Matthias Weiss — Experimentalphysik I, Universität Bayreuth

Revealing whether a stationary time series originated from an out-of-equilibrium system is, in general, a non-trivial task. While living biological systems surely are far away from thermal equilibrium, this might not be directly visible in a given experimentally acquired time series of some accessible observables. Therefore, probing whether time reversibility and detailed balance are broken in such time series, and quantifying a putative net entropy production is mandatory in the analysis. Using analytical and numerical toy systems as well as experimental data acquired in living cells, we compare different methods to uncover and quantify the non-equilibrium nature of time series.

BP 19.30 Tue 14:00 P2/3OG

Theory of Active Transport by DNA-relaying — •Christian Hanauer[1,2], Silke Bergeler[1], Erwin Frey[1], and Chase

Broedersz[1] — [1]Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität, 80333 Munich, Germany — [2]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany

Robust and faithful segregation of chromosomes is essential for the replication of bacterial cells. In recent years, experiments have identified the biochemical and mechanical properties of the chromosome as key ingredients for active transport in bacterial cells. Intracellular cargos, such as chromosomal ori, are thought to use chromosome fluctuations to transport themselves along a guiding concentration gradient of DNA-binding ATPases. However, a theory for this DNA-relaying is still lacking. Here, we present a theoretical framework that allows us to calculate the relaying force on the cargo. We test our predictions by Brownian Dynamics simulations. Our analytical model provides insight into how the system parameters determine this active transport mechanism.

BP 19.31 Tue 14:00 P2/3OG

Maximum entropy model for the spatial organization of the E. coli chromosome — •Lucas Tröger, Joris Messelink, and Chase Broedersz — LMU, Munich, Germany

Bacterial chromosomes lack many proteins that are central for the spatial structuring of eukaryotic DNA. Despite this, bacterial chromosomes are not just randomly folded within the cells; recent Hi-C experiments that quantify spatial interactions between pairs of regions of the chromosome reveal a high degree of organization. However, extracting a 3D model from such data remains a major challenge. To address this problem, we use a statistical mechanics approach. Specifically, we infer a least-biased 3D representation of the chromosome of Escherichia coli by developing a maximum entropy model based on Hi-C data. This allows us to derive the full joint probability distribution of spatial chromosome configurations in E. coli. From this, novel organizational features can be extracted.

BP 19.32 Tue 14:00 P2/3OG

Reconciliation of controversial death pattern of starved cells — •Hamid Seyed-Allaei, Elena Biselli, Zara Gough, Felix Fleschhut, and Ulrich Gerland — Department of Physics, Technical University, Munich, Germany

During carbon starvation of isothermal batch culture of E. Coli, viability of the cells as a function of time decreases exponentially for approximately 10 days. This behavior is the result of a collective behavior where living starved cells use the leaked nutrients from dead cells and can be explained by the balance of the nutrient flux of the leaking dead cells and the maintenance of the living starved cells. The single cell level study of isolated starved cells, however, indicates that the death rate of the cells follow the Gompertz law of mortality which relates the death rate to the age. The greater the time since a cell has received nutrients, the higher its death rate. The observation of Gompertz law of mortality in isolated starved cells with increasing death rate over time seems controversial with the observation of exponential decay with a constant death rate in isothermal batch culture. In this study we reconcile these two seemingly controversial results by the help of theoretical modeling.

BP 20: Poster VIII

Bioimaging and Biospectroscopy (BP 18.1 – BP 18.26)

Time: Tuesday 14:00–16:00 Location: P2/4OG

BP 20.1 Tue 14:00 P2/4OG

High-throughput scanning SAXS of desmin-expressing cells — •Chiara Cassini[1], Manfred Burghammer[2], Harald Herrmann[3], and Sarah Köster[1] — [1]IRP, Georg-August-Universität Göttingen, Germany — [2]ESRF, Grenoble, France — [3]DKFZ, Heidelberg, Germany

Desmin is the main intermediate filament (IF) protein in muscle cells. Recently, a large number of mutations in the desmin gene have been discovered to be pathogenic. In order to assess the structures formed in cells by normal and mutant desmin, a high resolution method, capable of retrieving structural information at sub-cellular length scales, without the need for slicing the cells, is preferable. Thus, we used scanning small angle X-ray scattering (SAXS) on three different cell lines generated from IF-free mouse fibroblasts: one expressing wild type desmin, one expressing R406W-desmin, and the IF-free mother cell clone itself. The cells were grown on silicon nitride windows and measured in freeze-dried state. Each window contained tens to hundreds of cells. Each cell scan used to take minutes to hours; recently, we were able to employ a special fast scanning mode that allowed us to image an entire window in about 8 hours only. This approach ensured the collection of a statistically significant pool of data in a reasonable time span. The large quantity of data thus collected was treated with a combination of semi-automated segmentation of the dark field images and parallel computations. In the end, we were able to carry out a statistically relevant comparison of local structure-related parameters of the three cell lines, such as anisotropy and orientation.

BP 20.2 Tue 14:00 P2/4OG

Studying molecular interactions with a combination of microfluidics and FFS — •Eleonora Perego and Sarah Köster — IRP, Georg-August-Universität Göttingen, Germany

Assembly and aggregation of biomolecules into larger complexes are fundamental processes in living organisms. Ordered protein assembly is vital for the organism, as for example the assembly of the cytoskeletal filaments, however sometimes disordered aggregates, which can be toxic as fro example alpha-synuclein fibrils, are also produced. It is fundamental to study both the ordered assembly and the disordered aggregation with high spatial resolution (on a single molecule level) and good temporal precision (in the order of ms) to gain a complete knowledge of these reactions. Here, we combine fluorescence fluctuation spectroscopy (FFS), employed to measure the interactions, with microfluidics to access the temporal information. We focus on studying the ordered assembly of vimentin, an intermediate filament (IF) protein which is part of the cytoskeleton, using a multi-layer microfluidic device that prevents the protein from coming in contact with the channel walls. This type of device also provides a controlled diffusive mixing of assembly buffer and protein solution. Employing FFS in these devices enables us to precisely measure the labelling stoichiometry of the assembling protein, which allow us to follow the very first time steps of vimentin assembly. Our results show that the combination of microfluidics and FFS provides a suitable approach for studying the aggregation of biomolecules in real time, which is important for understanding cellular behavior.

BP 20.3 Tue 14:00 P2/4OG

Imaging single glycans — •Xu Wu[1], Martina Delbianco[2], Kelvin Anggara[1], Stephan Rauschenbach[1,3], Sabine Abb[1], Peter Seeberger[2], and Klaus Kern[1] — [1]Max-Planck-Institut für Festkörperforschung, Stuttgart — [2]Max-Planck-Institut für Kolloid und Grenzflächenforschung, Potsdam — [3]Chemistry Research Laboratory, Department of Chemistry, University of Oxford

Imaging biomolecules guides the understanding of their diverse structures and functions [1]. Real space imaging at sub-nanometer resolution by cryo-electron microscopy has provided key insights into proteins and their assemblies. Direct molecular imaging of glycans, the predominant biopolymers on earth with a plethora of structural and biological functions, is currently not possible. Inherent glycan complexity and backbone flexibility requires single molecule approaches for real space imaging. Glycan characterization using mass spectrometry and nuclear magnetic resonance provides insights into size, sequence, branching, and connectivity but rely on structure reconstruction from indirect information. Here, we show direct low temperature scanning tunneling microscopy (STM) imaging of single glycan molecules that are isolated by mass-selective, soft-landing electrospray ion-beam deposition [2]. Sub-nanometer resolution allows for the visualization of glycan connectivity and discrimination between regio-isomers. Direct glycan imaging is an important step towards a better understanding of the structure of carbohydrates.

[1] Unwin, P. N. T, et. al. J. Mol. Biol. 94, 425-440 (1975). [2] Rauschenbach, S., et. al. Annu. Rev. Anal. Chem. 9, 473-498 (2016).

BP 20.4 Tue 14:00 P2/4OG

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

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

BP 20.5 Tue 14:00 P2/4OG

The relative densities of cell cytoplasm, nucleoplasm, and nucleoli are robustly conserved during cell cycle and drug perturbations — •Kyoohyun Kim and Jochen Guck — Max Planck Institute for the Science of Light, 91058 Erlangen, Germany

The cell nucleus is an essential cellular compartment as the location of gene expression and DNA replication. While the large amount of its chromatin confined in the finite nuclear space could install the picture of a particularly dense organelle surrounded by less dense cytoplasm, recent studies have begun to report the opposite. However, the generality of this observation has so far not been tested. Here, we used combined optical diffraction tomography (ODT) and epi-fluorescence microscopy to systematically quantify the mass densities of cytoplasm, nucleoplasm, and nucleoli of HeLa-FUCCI and RPE-FUCCI cells being challenged by various perturbations. We found that the nucleoplasm maintains a lower mass density than cytoplasm, but lower than nucleoli, during cell cycle progression by scaling its volume to match the increase of dry mass during cell growth. Moreover, actin and microtubule depolymerization and changing chromatin condensation altered volume, shape and dry mass of the various cellular compartments, while the relative distribution of mass densities was still robustly conserved. Our findings suggest that cells regulate relative mass densities across membrane-bound and membrane-less compartments, likely by different as of yet unknown mechanisms. This surprising robustness of mass densities contributes to the increasing importance of physical properties of biological cells in current biological research.

BP 20.6 Tue 14:00 P2/4OG

Biocompatible fluorescence modulating nanocoatings for sharper and faster screening applications — •Deyan Nestorov[1], Julia Fender[2], Kristina Lorenz[2], and Katrin G. Heinze[1] — [1]Rudolf Virchow Center, University of Würzburg, 97080 Würzburg, Germany — [2]Institute of Pharmacology and Toxicology, University of Würzburg, 97078 Würzburg, Germany

Biocompatible metal-dielectric nanocoatings have been shown to act as versatile fluorescence modulators. They can be customized to different spectral ranges and biological architectures of interest. Here, we explore such coatings for dual-color high-throughput screening (HTS) applications highlighting ligand-receptor interactions. Culturing adherent cells directly on nanocoated substrates allows to enhance both the signal-to-noise ratio of the detected fluorescence from the fluorescenctly tagged membrane proteins as well as the Förster resonance energy transfer (FRET) efficiency as a measure of the protein conformational changes upon ligand binding. Our simulations show that the signal contrast could be enhanced by a factor of 2.7, and thus the screening rate accelerated by a factor of 1.6. We plan to experimentally establish such an approach for high-throughput ligand screening of G-Protein coupled receptors which comprise over 30% of all drug targets. A major advantage of this approach is that it could be directly integrated into common setups with ease and thus offers new perspectives for pharmacological research.

BP 20.7 Tue 14:00 P2/4OG

Metal Induced Energy Transfer for Structural Analysis of Focal Adhesions via Actin Stress Fiber Angles — •Lydia Rebehn, Fabian Port, and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Ulm, Germany

Focal adhesion (FA) structures physically anchor cells to the extracellular matrix and facilitate cell interactions with their environment. They are composed of different protein components assembled in a highly regulated conformation. Intracellularly, FAs couple with actin to transfer external forces into internal mechanical and biochemical signals. Their structure is difficult to resolve since the components interact in the nanometer range [1],requiring localization of molecular components with nanometer-range resolution in x-, y-, and z- axes. Analyzing the actin stress fibers of cells in 2D culture can give information on the FA attachment to the surface based on angle analysis. The technique we use is Metal Induced Energy Transfer (MIET) [2]. We have provided an initial analysis of the angles between actin stress fibers and a 2D substrate, demonstrating the worth of MIET for cellular structure analyses near the basal membrane with nanometer accuracy.

References:

[1] Kanchanawong, P., Shtengel, G., Pasapera, A. M., Ramko, E. B., Davidson, M. W., Hess, H. F., & Waterman, C. M.,Nature, 468(7323), 580-584 (2010)

[2] Chizhik, A. I., Rother, J., Gregor, I., Janshoff, A., Enderlein, J., Nature Photonics, advance on(January), 1-8 (2014)

BP 20.8 Tue 14:00 P2/4OG

Investigating nanoplasmonic membranes as cellular strain sensors — •Peter Kolb and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Ulm, Germany

Metallic nanoparticles (NPs) display specific electromagnetic resonances, known as localized surface plasmon resonances (LSPR). These LSPRs strongly depend on the size and geometry of the NPs [1], as well as the local environment of the particles. Coupling between closely spaced NPs creates resonance dependence on their inter-particle distances. Since a change in this distance leads to a shift of the LSPR, nanoplasmonic membranes can be used as strain sensors [2]. The combination of gold NPs and polydimethylsiloxane (PDMS) substrate offers a biocompatible membrane that can be used for in vitro studies. Combining electron beam lithography, electron beam evaporation, dry lift-off, and reactive ion etching, we produce gold NP arrays on PDMS membranes. These nanoplasmonic membranes are analysed via scanning electron microscopy, atomic force microscopy, and spectroscopy. Supported by electromagnetic simulations, we investigate their properties and suitability as cellular strain sensors.

References:

[1] Chen, Yiqin, et al., Reliable fabrication of nanostructures without an adhesion layer using dry lift-off. Nanotechnology 26.40 (2015): 405301.

[2] Maurer, Thomas et al., The beginnings of plasmomechanics: towards plasmonic strain sensors. Frontiers of Materials Science 9.2 (2015): 170-177.

BP 20.9 Tue 14:00 P2/4OG

Investigation of Actin near the Basal Membrane of Living Cells using Metal Induced Energy Transfer — •Fabian Port, Ulla Nolte, Peter Kolb, Carolin Grandy, and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Germany

Focal adhesions function as anchoring points to the extracellular matrix, and also enable cells to sense and exert forces on their environment [1]. Focal adhesions are complex structures consisting of a multitude of different proteins. Despite the important role of the focal adhesion complex in cellular adhesion, its structure and dynamics remain difficult to resolve [2]. Knowing the exact position of the proteins in the focal adhesion complex in live cells is necessary to understand their working principles. For a detailed analysis of the focal adhesions dynamic architecture, we require a method to measure small distances that may be applied over a variable time scale. To meet this challenge, we use Metal Induced Energy Transfer (MIET) [3] to resolve protein positions at the nanoscale level in live cells. Using MIET, we analyse the dynamics of focal adhesion associated actin with ultra high resolution.

[1] Geiger, B. et al., Nature Reviews. Molecular Cell Biology, 10(1), 21-33 (2009)

[2] Kanchanawong, P. et al., Nature, 468(7323), 580-584 (2010)

[3] Chizhik, A. I. et al., & Enderlein, J., Nature photonics, advance on(January), 1-8 (2014)

BP 20.10 Tue 14:00 P2/4OG

Micropatterning on Gold Surfaces for Biophysical Applications — •Carolin Grandy, Peter Kolb, Fabian Port, and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Ulm, Germany

Cells change their shape based on their environment and are highly sensitive to mechanical and geometric factors. Micropatterning is a simple method to manipulate and control cell shape [1]. Our primary goal was to develop a reproducible method to manipulate and normalize cell shape on gold with micropatterning for quantitative super-resolution imaging. We use methoxy polyethylene glycol (PEG) thiol to create a self-assembled monolayer on gold, due to the strong bonds formed between thiol groups and gold [2], and the protein repellent nature of PEG. This monolayer can be oxidised through a photomask with deep UV-light [1]. The oxidised PEG pattern is no longer protein repellent, and can be coated with extracellular matrix proteins and seeded with cells. The surfaces we developed and analyzed can be used in a wide range of biophysical applications, including metal induced energy transfer and surface enhanced raman scattering.

References:

[1] M Thery, Micropatterning as a tool to decipher cell morphogenesis and functions, Journal of Cell Science 2010 123 (24), 4201-4213.

[2] R.G. Nuzzo et al, Fundamental studies of the chemisorption of organosulfur compounds on gold(111). Implications for Molecular self-assembly on gold surfaces, Journal of the American Chemical Society 1987 109 (3), 733-740.

BP 20.11 Tue 14:00 P2/4OG

Surface functionalization of Nanodiamonds — •Svenja Maurer, Frederike Erb, Karolina Zeh, and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Germany

Fluorescent Nanodiamonds (FNDs), due to their properties, find application in various areas and can be used for fluorescence bioimaging. FNDs contain photostable nitrogen vacancy centers. Their fluorescence shows neither blinking nor photobleaching. The NV-center absorbs green light and emits photons in the near-infrared range. FNDs can be used in vitro as well as in vivo due to their biocompatibility. The fluorescence characteristics can be influenced by the environment such as an external magnetic field and thus FNDs can be used in versatile nanosensors [1]. Various surface modifications of FNDs are possible and necessary for different experiments. We present techniques to functionalize the FND's surface [2].

[1] Hsiao, Wesley Wei-Wen, et al. "Fluorescent nanodiamond: a versatile tool for long-term cell tracking, super-resolution imaging, and nanoscale temperature sensing." Accounts of chemical research 49.3 (2016): 400-407.

[2] Krüger, Anke, et al. "Surface functionalisation of detonation diamond suitable for biological applications." Journal of Materials Chemistry 16.24 (2006): 2322-2328

BP 20.12 Tue 14:00 P2/4OG

Fluorescent nanodiamond as a detector for magnetic field fluctuations — •Frederike Erb and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Germany

Fluorescent nanodiamonds (FNDs) offer various new imaging and metrology approaches, especially in the life sciences. Nanodiamonds containing nitrogen-vacancy centers (NV-centers) as fluorophores emit light in the near-infrared window of bioimaging. Their luminescence properties depend on the environment and thus FNDs cannot only be used for bioimaging but also find an application as part of various nanosensors. A nanodiamond sensor can be smaller than 50 nm in diameter and read-out optically without contact. As they are biocompatible and non cytotoxic, they can be used for many experiments in biological samples.

We present experiments using the NV-center in nanodiamond as a magnetic field detector. Gd^{3+} ions in the surrounding of the nanodiamond introduce magnetic field fluctuations, which affect the NV's spin relaxation time T_1 [1]. Reading-out this T_1-Time with a commercial confocal microscope gives a measure of the Gd^{3+} concentration in the sample.

References:

[1] Kaufmann, S. et al. (2013): Detection of atomic spin labels in a lipid bilayer using a single-spin nanodiamond probe. In: Proceedings of the National Academy of Sciences 110 (27), S. 10894-10898.

BP 20.13 Tue 14:00 P2/4OG

Nanomechanics of collagen fibrils in native tendon — •Martin Dehnert[1], Anke Bernstein[2], and Robert Magerle[1] — [1]Fakultät für Naturwissenschaften, Technische Universität Chemnitz, Germany — [2]G.E.R.N. Tissue Replacement, Regeneration & Neogenesis, Department of Orthopedics and Trauma Surgery, Medical Center and Faculty of Medicine, Albert-Ludwigs-University of Freiburg, Germany

We use atomic force microscopy to determine the three-dimensional depth profiles of the local nanomechanical properties of collagen fibrils and their embedding interfibrillar matrix in native (unfixed), hydrated tendon. AFM imaging in air with controlled humidity preserves the tissue's native water content and allows for high-resolution imaging the assembly of collagen fibrils beneath an approximately 5 to 10-nm-thick layer of the fluid components of the interfibrillar matrix. We collect pointwise force–distance (FD) data from which we construct 3D depth profiles of the local tip–sample interaction forces. We observe diversity in the nanomechanical properties of individual collagen fibrils in their adhesive as well as their repulsive, viscoelastic mechanical response. The contact points between adjacent collagen fibrils are discovered to be twice as stiff as the fibrils. Furthermore, the 3D depth profiles of the tip–sample interaction allow for accurate measurements of the fibrils' shape within the interfibrillar matrix. With a newly developed force–distance measuring scheme, we separate the viscoelastic deformation from the elastic response of the hydrated collagen. This sheds new light on the role of interfibrillar bonds, the mechanical properties of the interfibrillar matrix, and the biomechanics of native tendon.

BP 20.14 Tue 14:00 P2/4OG

Femtosecond laser cell surgery and wound healing on Drosophila embryos — •Elena Ramela Ciobotea, Ruby van Dijk, Bastian Zielinski, Mostafa Aakhte, Cristian Sarpe, Arne Senftleben, H.Arno J. Müller, and Thomas Baumert — Heinrich-Plett-Straße 40, 34132 Kassel, Germany

In this work we combine fluorescence microscopy and fs laser tissue ablation on a living Drosophila melanogaster embryo to investigate the wound closure in different stages of development. In contrast to typical larger scale UV laser damage, single cells or membranes can be targeted. Pulses from an 800nm Ti:Sapphire high energy oscillator were selected by the Pockels cell and coupled into a Leica confocal fluorescent microscope with a 63x oil immersion objective (NA: 1.32). 3h old embryos were dechorionated, washed, mounted in halocarbon oil between a microscope slide and a cover slip and imaged with a 488 nm Ar laser for up to 30 minutes after fs treatment. Images were assembled and analyzed using ImageJ software and a preliminary LabVIEW program. Firsts experiments were performed on embryos with cell nucleus marker and plasma membrane. Enhancement of the setup lead to well defined control of the energy deposition on the target tissue by varying exposure time and burst sequence with the Pockels cell, as well as optimizing temporal pulse length of the ultrashort laser pulses. Recent experiments on Myosin-GFP-labeled embryo with ablation in different stages show a larger migration of the myosin towards the damage over time for early stages in comparison with late stages of development.

BP 20.15 Tue 14:00 P2/4OG

Development of a fast real time sub-pixel accurate multi particle tracking system — •Jonas Pfeil, Daniel Geiger, Tobias Neckernuss, and Othmar Marti — Institute of Experimental Physics, Ulm University, Ulm, Germany

A multitude of functions in the human body depend on the rheological behaviour of the tissue and hence of the single cells involved. To determine the microscopical cell properties there is a need for microrheological measurement devices. An established technique is the passive and active microrheology. Small beads with known properties embedded in the probed material are tracked by an imaging system. By comparison with theoretical models, mechanical properties of the cells can be computed.

We present a new implementation of a system for particle tracking which can track up to 8 particles with sub pixel precision at high speeds of up to 10,000 frames per second. We will discuss the setup, the implemented method for subpixel tracking and the hardware consisting of an FPGA and a CMOS sensor.

In addition we will show a fast and fixed latency algorithms for the approximative multi-parameter fitting of 2D surfaces.

BP 20.16 Tue 14:00 P2/4OG

Local membrane height dynamics of live cells — •Max Ulbrich[1], Christian Völkner[1], Regina Lange[1], Heiko Lemcke[2], Robert David[2], Martina Grüning[3], Barbara Nebe[3], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, Physics of Surfaces & Interfaces, University of Rostock, 18059 Rostock —

[2]University Medical Center, Cardial Regeneration, University of Rostock, 18057 Rostock — [3]University Medical Center, Dept. of Cell Biology, University of Rostock, 18057 Rostock

Cellular membrane fluctuations are considered for monitoring physiologic and pharmacologic effects [1]. Scanning Ion Conductance Microscopy (SICM) is a nanoprobing method to acquire morphologies on live cells. We operate the nanopipette-probe on fixed lateral locations and record SICM time traces in order to assess membrane fluctuations and cell activities with regard to processes [2]. Height variations of live osteoblasts and cardiomyocytes are analyzed in time and frequency domain. Cardiomyocytes show a pronounced frequency response behavior due to the electromechanical action, which can get modulated upon change of location or environment. Osteoblasts show rather strict 1/f behavior, with varying amplitude among different cells or cell surface regions. Close inspection points towards low frequency modulations in the course of migration. We discuss possible correlations with cell activity obtained by supporting optical microscopy.

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

BP 20.17 Tue 14:00 P2/4OG

High throughput sorting in droplet-based microfluidics — •Patricia Schwilling[1], Tobias Neckernuss[1,2], Daniel Geiger[1,2], Jonas Pfeil[1,2], Ralf Schuster[1], Lisa Kwapich[1], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Sensific GmbH

Droplet-based microfluidics offer a method to meet the ever-increasing demand for cost-efficient high-throughput analysis and experiments by fabricating up to thousands of nanoliter-sized water-in-oil droplets per second. Each droplet serves as a tiny reaction chamber in which for example specific biochemical reactions may take place. One field, among others, that utilizes this technique is single-cell RNA sequencing by encapsulating functionalized beads with cells to capture the cells' RNA for subsequent sequence analysis. It is therefore inevitable to encapsulate single cells with single beads to ensure the highest resolution. Here, we present a setup to eliminate droplets containing more than one cell together with more than one bead using dielectrophoretic force and ODIN - a high-performance optical sensing system for real-time counting, analysis, and sorting. The setup is further capable to sort biological and synthetic particles and complex structures in a continuous flow based on their respective mechanical or phenotypical properties.

BP 20.18 Tue 14:00 P2/4OG

Wavelength and pressure dependent measurement of the retinal radiation exposure during diaphanoscopic illumination — •Nicole Sieber[1], Philipp Kölbl[1], Christian Lingenfelder[2], Kathrin Stucke-Straub[3], Sebastian Kupferschmid[4], and Martin Hessling[1] — [1]Institute of Medical Engineering and Mechatronics, Ulm University of Applied Sciences, 89081 Ulm, Germany — [2]Pharmpur GmbH, 86343 Koenigsbrunn, Germany — [3]Department of Mathematics, Natural and Economic Sciences, Ulm University of Applied Sciences, 89081 Ulm, Germany — [4]Clinic of Ophthalmology, Bundeswehrkrankenhaus Ulm, 89081 Ulm, Germany

In vitreoretinal surgery the imaging of the ocular fundus is of great interest. Therefore, sufficient bright illumination of the intraocular space is necessary. However, excessive irradiance can cause irreversible photochemical and thermal damage to the retina. In the international standard DIN EN ISO 15007-2: 2014 limit values for the irradiance of the retina are given. These values must not be exceeded during surgery. In fact, the actual intraocular irradiance caused by ophthalmological illumination systems has never been determined. In this study the retinal irradiances during diaphanoscopic illumination through the porcine eye wall is investigated. The irradiance is wavelength and pressure dependent if the illuminator is pressed against the eyeball. The irradiance is measured spectrally resolved for different pressures inside eyes to assess the photochemical and thermal retinal hazard. These data also permit calculating the appropriate application time of the illumination system during eye surgery.

BP 20.19 Tue 14:00 P2/4OG

First steps toward reversible protein immobilization on conductive carbon nanomaterials — •Lara Jorde[1], Zehao Li[2,3], Jacob Piehler[2], Changjiang You[2], and Carola Meyer[1] — [1]Department of Physics, University of Osnabrück, Germany — [2]Department of Biology, University of Osnabrück, Germany — [3]College of Life Science, Beijing University of Chemical Technology, China

The surface immobilization of biomolecules is indispensable for most characterization techniques and therefore a goal in structure analysis. Fundamental understanding of the effects of immobilization on proteins functionalized to these conductive carbon nanomaterials thus enables the development of new types of electronic biosensors. Graphene is used as a calibration material for the CNT functionalization. Here, we achieved the Graphene-functionalization by a pyrene-linker compound binding to Green Fluorescent Protein (GFP) exemplary for a wide range of proteins. Reflectance interference- and total internal reflectance fluorescence spectroscopy reveals a specific and reversible protein binding on graphene with well-defined binding kinetics. Fluorescence quenching caused by graphene is determined by fluorescence lifetime imaging microscopy, confirming a tight yet reversible immobilization of the GFP-fluorophore on graphene. Challenges with regard to the application of this functionalization route and characterization techniques on CNTs are discussed, which have great transport properties for a later analysis of different protein configurations that allow for one-dimensional alignment and high sensitivity of sensing.

BP 20.20 Tue 14:00 P2/4OG

Single molecule localization microscopy in front of a tuned mirror — •Hannah S. Heil[1], Marie-Christine Dabauvalle[2], Sven Höfling[3], Martin Kamp[3], Markus Sauer[2], and Katrin G. Heinze[1] — [1]Rudolf Virchow Center, University of Würzburg — [2]Biocenter, University of Würzburg — [3]Technische Physik, University of Würzburg, Würzburg, Germany

Single-molecule localization microscopy (SMLM) methods have evolved as powerful tools to image cellular structures with virtually molecular resolution. We have demonstrated that higher photon yield at lower background on biocompatible metal-dielectric coatings substantially improves the SMLM performance, and significantly increases the localization precision and, thus, the image resolution (Heil HS et al., Light Sci Appl 7 (99), 2018).

The strength of the approach is that - except for the coated cover glass - no special microscope setup is required. We show that biocompatible metal-dielectric nanostructures fabricated on microscopy coverslips improve the resolution of direct stochastic optical reconstruction microscopy (dSTORM). The enhanced signal-to-noise ratio induced by the metal-dielectric coating sharpens the localization precision, and exceeds Widefield and Total Internal Reflection Fluorescence (TIRF) dSTORM performance without the need for a special TIRF objective lens in a much simpler setup. The resolution improvement is spectrally and spatially tunable as experimentally demonstrated for dual-color SMLM in cells and allows to access additional spatial information in the axial dimension.

BP 20.21 Tue 14:00 P2/4OG

The Structure of Red Blood Cells' Aggregates — •Mehrnaz M. Babaki[1,2] and Minne Paul Lettinga[1,2] — [1]ICS-3 Soft Condensed Matter, Forschungszentrum Jülich GmbH, Jülich, Germany — [2]Laboratory for Soft Matter and Biophysics, KU Leuven, Leuven, Belgium

Red Blood Cells (RBCs) aggregate in blood plasma due to presence of proteins like fibrinogen, immunoglobulin M and C-reactive protein. The characteristic face-to-face morphology of RBC's aggregates is similar to stacks of coins, which is referred to as rouleaux. The first step in understating rouleaux formation is the aggregation of two RBCs, which is called doublet. The formation and shape of a doublet is governed by bending and shear elasticity and adhesion energy of RBCs.

We induce aggregation of RBCs by adding different type of particles to RBCs dispersed in a density matched buffer. The ideal long rage attraction is induced by rod-like fd-viruses. Rode-like fd-viruses with a high length to diameter ratio are used as a depletant agent. The interaction is tuned by varying the concentration of the fd-virus. We employ ultra-fast confocal microscope to image the aggregates of RBCs to investigate the 3D shape of doublets.

By increasing the concentration of fd-virus, we observe a transition between line contacted doublets, where RBCs do not deform but touch along a circle, to doublets, where individual RBCs deform and are in full contact. The full surface contacted doublets can have different shapes which we developed a fingerprint to distinguish between these shapes.

BP 20.22 Tue 14:00 P2/4OG

Divergence-free smoothing for 3D direct traction force microscopy — •Johannes Blumberg[1,2] and Ulrich Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University —

[2]BioQuant, Heidelberg University

In traction force microscopy (TFM), the mechanical forces of cells adhering to an elastic substrate are estimated from the substrate displacements as measured by the movement of fiducial markers. Usually this estimate is obtained by minimizing the mean squared distance between experimentally observed and predicted displacements (inverse TFM). In direct TFM, in contrast, the stress tensor and the surface tractions are calculated directly and locally from the deformation field using the underlying material law. This procedure makes it easier to estimate not only tangential, but also normal forces, and to deal with non-planar substrates. However, it is not clear how accurate direct TFM performs compared with inverse TFM. We develop a new method to estimating the local inaccuracy, based on the divergence-freeness of the stress tensor in an equilibrium setup. This improves the usability of this method and possibly allows traction force microscopy to be used in a wider range of settings.

BP 20.23 Tue 14:00 P2/4OG

XPS evaluation of enzymatically oxidized nanocellulose from tunicate biomass — •Philipp Moritz[1,2], Oliver Höfft[1], Anthi Karnaouri[3], Paul Christakopoulos[3], Ulrika Rova[3], Georgia Sourkouni[2], and Wolfgang Maus-Friedrichs[1,2] — [1]Institute of Energy Research and Physical Technologies, Clausthal University of Technology, 38678 Clausthal-Zellerfeld — [2]Clausthal Centre of Material Technology, Clausthal University of Technology, 38678 Clausthal-Zellerfeld — [3]Department of Civil, Environmental and Natural Resources Engineering, Luleå University of Technology, 97187 Luleå

The use of highly crystalline oxidized nanocellulose has recently increased considerably, particularly in biomedicine. The exact physicochemical and mechanical properties of cellulose nanocrystals depend primarily on their origin and the manufacturing process.

The aim of our experiments is to obtain highly crystalline and oxidized nanocellulose from the invertebrate tunicate species Ciona intestinalis. A novel process consisting of an organosolv pre-treatment and a subsequent enzyme treatment was developed for this purpose. The biocatalyst lytic polysaccharide monooxygenase (LPMO) is known to oxidatively cleave the glycosidic bond of cellulose without reducing its crystallinity. To evaluate the oxidizing effect of the novel pretreatments, X-ray photoelectron spectroscopy (XPS) was used.

Compared to the untreated raw nanocellulose, XPS indicates a significant increase of the oxidized "C=O/O-C-O" and "O-C=O" species achieved by the novel physicochemical pre-treatment. An additional in-situ enzyme treatment leads to further oxidation of the material.

BP 20.24 Tue 14:00 P2/4OG

Point Spread Function engineering in real time for iSCAT — •Vivien WALTER and Mark WALLACE — Department of Chemistry, King's College London, London, United Kingdom

Interferometric scattering (iSCAT) microscopy extends the limits of traditional optical microscopy by imaging the interference pattern between light scattered by an object and a reference beam reflected from a surface. Efficient subtraction of the large reference signal and its magnitude relative to the scattering of the object is key to high-speed high-sensitivity imaging. However, subtraction of the reference signal in complex biological samples requires more sophisticated processing to detect single biomolecules.

Optical processing of images is commonly used in microscopy to optimise the collected signals by increasing contrast or decreasing noise. Fourier plane processing is a common method to select specific image properties and while powerful the application of optical processing to iSCAT has typically been limited to static apodising filters. Adaptive Fourier filtering can be performed using Spatial Light Modulators (SLM), computer controlled high resolution devices capable of applying any type of filter in real-time.

We demonstrate here the application of real time SLM processing applied in iSCAT microscopy to obtain a 6-fold increase of the signal-to-noise ratio. We investigate a range of optical processing methods, and demonstrate that this optical pre-processing reduces the molecular weight threshold of detectable label-free proteins and polymers.

BP 20.25 Tue 14:00 P2/4OG

Development of a flat-top laser excitation for TIRF microscopy-based single molecule FRET experiments — •Wubulikasimu Yibulayin and David Dulin — Junior Research Group 2, Interdisciplinary Center for Clinical Research, Friedrich-Alexander-University Erlangen-Nürnberg (FAU), Erlangen, Germany.

Total internal reflection fluorescence microscopy (TIRFM) is a widely used technique for single molecule fluorescence spectroscopy studies, in particular in combination with single molecule fluorescence resonance energy transfer (smFRET). The advent of large detector scientific CMOS camera has enabled high throughput observation of single molecule using TIRFM. However, the Gaussian distribution of intensity in the excitation laser renders the illumination inherently inhomogeneous, whereas a flat-top intensity distribution would be ideal. Several approaches have been developed to convert the Gaussian laser excitation beam into a flat-top beam, such as injecting the excitation laser(s) into a mechanically vibrated multimode fiber (MMF). Here, we have assembled a custom two-colors TIRF microscope with the excitation lasers (532 nm and 640 nm) are injected into a MMF. To remove the speckle added by the MMF to the laser intensity profile, we couple to the MMF a piezo element that vibrates at high frequency, enabling a uniform flat-top illumination, while maintaining the TIR conditions. This all-custom microscope will provide a platform for hybrid force-fluorescence spectroscopy measurements, e.g. TIRFM-magnetic tweezers.

BP 20.26 Tue 14:00 P2/4OG

Low-budget High-resolution Fluorescence Microscope — •Leon Claassen[1], Lukas Lechler[1], Florian Schwarz[1], and Jens Pflaum[1,2] — [1]Experimental Physics VI, Julius Maximilian University of Würzburg, 97074 Würzburg — [2]ZAE Bayern, Würzburg

Non-destructive optical methods are vital for the determination of material properties in various fields of application. In particular, fluorescence microscopy has become an established technique which can be used for analyzing solid state properties such as the optical band-gap of semiconductors or in biology to identify and spatially resolve labeled constituents in cells or cellular processes. However, fluorescent microscope setups are usually very expensive and thus, financially hardly viable for schools or technical classes. Here, we present a low-cost laser-scanning version of such a setup based on two DVD-scanners driven by an Arduino controller and slightly modified optics, which offers a resolution up to 15 μm within a scanning range of 5 x 5 cm^2. We demonstrate the characteristics of the relevant electronic and optical components and show first results obtained by operating the microscope in a neat reflection mode. Thereafter, the necessary conversions to run the setup in fluorescent mode are presented together with preliminary studies on fluorescent organic single crystals as well as labeled biological structures. Based on these achievements we will discuss future optimizations to improve the performance and, in particular, the lateral resolution of the setup down to the micrometer length scale. The University of Würzburg is acknowledged for financial support within the Fund for Innovative Projects in Teaching.

BP 21: Cell Adhesion and Migration, Multicellular Systems I

Time: Wednesday 9:30–13:00 Location: HÜL 386

Invited Talk BP 21.1 Wed 9:30 HÜL 386

Cellular mechanosensing within synthetic 3D extracellular matrices — •Britta Trappmann — Max Planck Institute for Molecular Biomedicine, Münster, Germany

Cell fate decisions are influenced by many cues, which together constitute the cell microenvironment. One critical regulator is the extracellular matrix (ECM), which varies not only in composition, but also in physical properties such as stiffness. The impact of matrix stiffness on cell spreading and differentiation has been studied intensively on 2D surfaces using synthetic hydrogels, but very little is known about stiffness sensing within more complex 3D matrices.

Here, a major hurdle is to isolate the role of ECM stiffness from other matrix properties, in particular degradability. If cells are fully encapsulated, changes in bulk stiffness also influence the amount of matrix crosslinks that a cell has to cleave in order to spread and interact with its surroundings, impacting cell shape and function. Here, we

have developed a sugar-based hydrogel system that offers independent control over mechanical properties, adhesive ligand density and matrix degradation rates. Using this system, we study the impact of matrix stiffness and degradability on cell spreading, mesenchymal stem cell differentiation and angiogenic sprouting. In particular, we demonstrate that matrix degradability, mechanics and adhesivity jointly control the multicellularity of 3D endothelial cell invasion.

BP 21.2 Wed 10:00 HÜL 386

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

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

BP 21.3 Wed 10:15 HÜL 386

Relation between tissue homeostasis and mechnosensitivity in model epithelium — •Maxime Hubert[1], Sara Kaliman[1], Carina Wollnik[2], Simone Gehrer[1], Damir Vurnek[1], Diana Dudziak[3], Florian Rehfeldt[2], and Ana-Suncana Smith[1,4] — [1]PULS Group, Friedrich Alexander University Erlangen-Nurnberg, Erlangen, Germany — [2]Cell & Matrix Mechanics Group, Georg-August-University Gottingen, Gottingen, Germany — [3]Group for the Biology of Dendritic Cells, University Clinic Erlangen-Nurnberg, Erlangen, Germany — [4]Group for Computational Life Sciences, Ruder Boskovic Institute, Zagreb, Croatia

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

BP 21.4 Wed 10:30 HÜL 386

Stress Fiber vs. Cortical Contractility and its Relevance for Tissue and Cancer Development — •Enrico Warmt, Steffen Grosser, Eliane Blauth, and Josef Käs — Uni Leipzig, Soft Matter Physics, Leipzig

It is the current perception that cell contractility is solely based on a force dipole like interaction requiring stress fibers that pull between cellular adhesion sites for migratory and invading purposes. However, our observations suggest a clear differentiation between stress fiber and cortical contractility. We investigate on one hand suspended cells, lacking stress fibers and adhesion points, regarding active cortical contractility and on the other hand adhered cells, in an ECM environment displacing biomechanical properties based on oriented actin stress fiber contractility. Epithelial cells assemble a strong actomyosin cortex providing cortical tension exhibiting mechanosensitive contractile behavior. In contrast mesenchymal cell cortices behave less contractile, while they express more prominent stress fibers generating stronger contractile forces in 3D collagen gels. We propose an actomyosin rearrangement from cortical to stress fiber structures during epithelial*mesenchymal transition. We investigate the formation of cell-cell contacts up to the formation of cell spheroids, which is accompanied, for epithelial cells, with rearrangement of their contractile actomyosin cortices building up a collective actomyosin cortex surrounding the aggregates. In contrast, mesenchymal cells, do not form stable cell-cell contacts neither collective actomyosin rims, due to lacking cortical contractile potential, suggesting low surface tension like behavior.

BP 21.5 Wed 10:45 HÜL 386

On moving nuclei and membranes - interkinetic nuclear migration on the cell level — •Anne Herrmann and Raymond E. Goldstein — Department of Applied Mathematics and Theoretical Physics, University of Cambridge, Cambridge, United Kingdom

In developing pseudostratified epithelia, nuclei move repeatedly between the apical and basal surfaces of cells. This process is termed interkinetic nuclear migration (IKNM) and has been studied extensively in the brain, retina and spinal cord of multiple organisms. But despite these efforts many questions about the precise mechanism of IKNM remain. Based on *in vivo* light sheet microscopy we previously developed a quantitative model for the phenomenological properties of IKNM on the tissue level [1]. In this talk, we now examine the properties of IKNM on the level of individual cells. First, we investigate the random walk behaviour of individual nuclei within the tightly packed tissue environment to make estimates of the forces involved in this process. Secondly, we aim to understand the role of the interaction between nucleus and cell membrane. This not only appears to influence IKNM but possibly even has implications for the overall cell architecture.

[1] Afnan Azizi, Anne Herrmann, Yinan Wan, Salvador J. R. P. Buse, Philipp J. Keller, Raymond E. Goldstein, William A. Harris. *sub judice* (2019), arXiv: 1903.05414

30 min. coffee break

BP 21.6 Wed 11:30 HÜL 386

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

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

BP 21.7 Wed 11:45 HÜL 386

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

Remembering sources of food and threat is essential for survival. While higher animals rely on their nervous system, even very simple organisms are able to encode sensory information that aids them in tackling complex environments. The true slime mould *Physarum polycephalum* is a giant unicellular eukaryote whose body consists of a protoplasm-filled network of tubes which undergoes constant reorganization.The mechanism behind the reorganization of *P. polycephalum* body upon food encounter has not been explained previously. Here, we identify the imprint the food stimulus leaves on network morphology as memory and show that the network relies on tube growth and flows to encode stimulus information. We hypothesise an encoding mechanism introducing a local release of a chemical agent that affects the mechanical properties of the tubes and spreading through the network by protoplasmic flows. Using a theoretical model, we test our hypothesis

and find the model yields a correct prediction of flow-dependent stimulus response. Finally, we investigate the role of network hierarchy in memory encoding and show that both hierarchy and the orientation of tubes are relevant in stimulus encoding. Our findings demonstrate *P. polycephalum*'s ability to encode memory and likely open doors to the use of the organism in bioinspired design.

BP 21.8 Wed 12:00 HÜL 386

Relation between long- and short-time wave dynamics in Physarum polycephalum — •Adrian Fessel and Hans-Günther Döbereiner — Universität Bremen, Bremen, Germany

In the recent past, the slime mold Physarum polycephalum has attracted considerable attention due to its behavioral complexity, which is unparalleled in unicellular systems. However, the interplay of mechanisms giving rise to the non-neural information processing observed in the slime mold still lacks detailed understanding. The physical processes believed to be at the basis include mechanochemical oscillations. These organize as peristaltic wave patterns propagating on, and simultaneously modifying, a time-variant network topology. Comparable stable patterns are observed in micrometer-sized fragments and on extended networks, and share some visual similarity with spatiotemporal modulation of neuron activity in the brain. Here, we present a quantitative computational approach for the analysis of travelling waves on centimeter-sized network topologies. Employing a clustering method, we characterize recurring patterns. This leads to the identification of a functional link between wave dynamics at very different time-scales, extending to the migratory behavior of the slime mold.

BP 21.9 Wed 12:15 HÜL 386

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

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

BP 21.10 Wed 12:30 HÜL 386

Identifying the blue-light photoreceptor underlying light-switchable adhesion of *Chlamydomonas* to surfaces. — •Rodrigo Catalán[1], Antoine Girot[1], Theresa Büttner[1], Alexandros Fragkopoulos[1], Simon Kelterborn[2], Peter Hegemann[2], and Oliver Bäumchen[1] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, 37077 Göttingen, Germany. — [2]Humboldt University of Berlin, Institute of Biology, Invalidenstrasse 42, 10115 Berlin, Germany.

Photosynthetic microorganisms have developed several photoactive responses to spatial and temporal light variations. Interestingly, the unicellular, eukaryotic microalga *Chlamydomonas reinhardtii* swims freely in red light but exhibits flagella-mediated adhesion to surfaces when exposed to blue light (Kreis *et al.*, Nature Physics, 2018). We performed adsorption experiments to establish the spectral sensitivity of the adhesiveness of wild-type *Chlamydomonas* and found a maximum of the cell adsorption rate at 470 nm. These results provide evidence that a blue-light photoreceptor triggers light-switchable adhesiveness. There are 18 known photoreceptors in *Chlamydomonas*, most of which are blue-light sensitive. We use targeted gene editing tools to establish photoreceptor-deletion mutants and perform adsorption experiments and complementary micropipette force spectroscopy experiments on these strains. We find that channelrhodopsin 1 and 2 as well as phototropin are not the functional photoreceptors mediating light-switchable adhesion, which is interesting since they account for other important responses, namely phototaxis and the cell's life cycle.

BP 21.11 Wed 12:45 HÜL 386

Characterization of Spider Silk for Elucidating the Reasons Behind its Medical Success in Nerve Regeneration Applications — •Aida Naghilou[1], Lena Pöttschacher[2], Flavia Millesi[1], Anda Mann[1], Paul Supper[1], Ellen Backus2[2], and Christine Radtke[1] — [1]Research Laboratories of the Division of Plastic and Reconstructive Surgery, Medical University of Vienna, Vienna, Austria — [2]Department of Physical Chemistry, University of Vienna, Vienna, Austria

Spider silk has been established as a fascinating materials due to its unique strength, toughness, and elasticity [1]. One of the more remarkable applications of the spider silk is its use for nerve growth and nerve regeneration [2]. The Schwann cells, which are a crucial part of the nerve regeneration process, adhere well to spider silk and migrate along it [3]. However, the reasons behind the medical success of the silk is unclear.

In this work, we performed systematic studies for the material characterization and medical performance of various spider silks. The characterization experiments focus on the Raman spectroscopy, morphology, and wettability of the silk. The medical assessment of the silk in evaluated by in vitro experiments with Schwann cells, where the adhesion, motility, and the proliferation of the cells on the spider silk in monitored. [1] L. Römer, T. Scheibel, Prion, 2 (2008) 154. [2] C. Radtke, Int J Mol Sci, 17 (2016) 1754. [3] T. Kornfeld, P.M. Vogt, V. Bucan, C.-T. Peck, K. Reimers, C. Radtke, J Funct Biomater, 7 (2016) 30.

BP 22: Single Molecule Biophysics (joint session BP/CPP)

Time: Wednesday 9:30–13:00 Location: SCH A251

BP 22.1 Wed 9:30 SCH A251

Magnetic tweezers reveal the mechanism of directional transcription termination in human mitochondria — Eugen Ostrofet[1], Flavia Stal Papini[1], Britney Johnson[2], Jamie Arnold[2], Craig Cameron[2], and •David Dulin[1] — [1]Junior Research Group 2, IZKF, FAU Erlangen-Nürnberg, Germany — [2]Department of Microbiology and Immunology, The University of North Carolina Chapel Hill, USA

Transcription termination is essential to synthesize functional RNA and to prevent transcription interference with downstream promoters. Therefor, it must be performed efficiently despite the stability of the elongating RNA polymerase (RNAP) on DNA. One approach adopted by eukaryotic cells is directional transcription termination upon collision of RNAP with a termination factor bound to DNA, as for human mitochondria RNAP (mtRNAP) and Pol I. How the termination factor senses the direction of transcribing RNAP remains to be found. We propose that the termination factor senses DNA unwinding, and consequently terminates transcription directionally. To interrogate this hypothesis, we employed a high throughput magnetic tweezers instrument and a hairpin-based force jump assay to mimic DNA unwinding and look into the human mitochondria transcription termination factor 1 (MTERF1). We found that MTERF1 blocks directionally hairpin opening, explaining directional transcription termination. Performing in situ force calibration, we determined accurately the energy landscape of MTERF1 bound to its termination site.

BP 22.2 Wed 9:45 SCH A251

Magnetic Tweezers Protein Force Spectroscopy — •Jan Lipfert[1], Achim Löf[1], Philipp Walker[1], Steffen Sedlak[1], Sophia Gruber[1], Tobias Obser[2], Maria Brehm[2], and Martin Benoit[1] — [1]Department of Physics, LMU Munich — [2]Department of Pediatric Hematology and Oncology, University Medical Center Hamburg Eppendorf

The physiological function of proteins is often critically regulated by mechanical forces acting on them. Single-molecule manipulation techniques such as atomic force microscopy or optical tweezers have enabled unprecedented insights into the molecular mechanisms underlying such force regulation. However, these techniques have limited throughput and lack resolution at low forces. We have developed a versatile and modular approach for force measurements on proteins in magnetic tweezers [Löf et al. PNAS 2019] that enables ultra-stable (> days) and parallel measurements (> 50) of single molecules in a wide force range including very low forces (<1 pN). Leveraging our new assay, we directly probe regulatory low-force transitions within von Willebrand factor, a vascular protein that is activated for its critical role in hemostasis by hydrodynamic forces in the bloodstream. Or results reveal fast (˜250 ms) opening and closing transitions in the dimeric VWF stem at a critical force of 1 pN, which like constitute the first steps in VWF mechano-activation.

BP 22.3 Wed 10:00 SCH A251

Real-time imaging of DNA loop extrusion by condensin and their mutual interactions — •Eugene Kim[1], Jacob Kerssemakers[1], Indra Shaltiel[2], Christian Haering[2], and Cees Dekker[1] — [1]Department of Bionanoscience, Kavli Institute of Nanoscience Delft, Delft University of Technology, Delft, Netherlands. — [2]Cell Biology and Biophysics Unit, Structural and Computational Biology Unit, European Molecular Biology Laboratory (EMBL), Heidelberg, Germany.

How is DNA spatially organized in our cells? By what mechanisms do chromosomes fold over long distances? In this talk, I will discuss our work on understanding the looping structures of DNA using fluorescence imaging assay at the single-molecule level. The major focus is on condensin, that is one of the SMC (Structural Maintenance of Chromosomes) complexes. This ring-shaped protein is the molecular motor that can extrude large loops of DNA, a mechanism thought to be the basis of the chromosome structures at various stages of the cell cycle. I will firstly show how a single condensin can extrude loops at a force-dependent speed of up to 2 kbp/s and it does so in a strictly asymmetric manner. I will then show how these individual condensins can form a dimeric structure by traversing one over the other, in turn forming a novel type of loop structure that we name as Z loop. This condensin dimer can extrude DNA in a symmetric fashion, thus may be able to contribute to chromosomal compaction in a more efficient way. We believe that our work will allow to disentangle the fundamental looping architecture of chromosomes, that is essential to all life.

BP 22.4 Wed 10:15 SCH A251

Magnetic tweezers reveal two coexisting and interconverting bacterial RNA polymerase conformations with different open complex stability — •Subhas Chandra Bera[1], Mona Seifert[1], Santeri Maatsola[2], Eugen Ostrofet[1], Monika Spermann[1], Flavia Stal-Papini[1], Anssi M. Malinen[2], and David Dulin[1] — [1]Junior Research Group 2, Interdisciplinary Center for Clinical Research, Friedrich Alexander University Erlangen-Nürnberg (FAU), Cauerstr. 3, 91058 Erlangen, Germany — [2]Department of Biochemistry, University of Turku, Tykistökatu 6A, 6th floor, 20520 Turku, Finland

To start transcription, the RNA polymerase (RNAP) recognises the promoter, to form the closed complex (CC), and eventually unwinds the DNA to form the open complex (OC), and is then ready for RNA synthesis. OC stability decides the yield of expression in many genes, and is therefore of great importance to regulate expression of a given gene. Using high throughput magnetic tweezers, we investigated OC dynamics. Surprisingly, we observed two OC populations with nearly 10-fold difference in lifetime, where the stability of the OC varies as a function of the nature and the concentration of the anions, as well as the temperature. We further noticed that the RNAP completely dissociates upon return to CC and therefore the two OC populations do not originate from a single interconverting RNAP, but rather from two conformations of RNAP. Our study shows the power of single molecule techniques to resolve two interconverting populations of RNAP that have remained elusive to bulk assays so far.

BP 22.5 Wed 10:30 SCH A251

Towards the Label-free Plasmonic Detection of Single Untethered Proteins — •Martin D. Baaske, Peter S. Neu, Nasrin Asgari, and Michel Orrit — Huygens-Kamerlingh Onnes Laboratory, Leiden University, Postbus 9504, 2300 RA Leiden, The Netherlands

Label-free optical detection schemes so far rely on specific chemical interactions between receptor and target molecules in order to facilitate analyte recognition. Here we present our first step towards the label-free recognition of untethered nanoscale analytes. We show that via a polarization selective technique and careful optimization of a confocal microscope, single gold nanorods, which are commonly used as labels, can be transformed into high-speed nanoscale sensors. We demonstrate the performance of our system by detecting microemulsion nanodroplets which mimic 250 kDA proteins as they diffuse through the near field of a single gold nanorod on nanosecond timescales.

BP 22.6 Wed 10:45 SCH A251

How to gain reliable information from short trajectories — •Marie Schwebs[1], Torsten Paul[2], Marius Glogger[1], Philip Kollmannsberger[2], Markus Engstler[1], and Susanne Fenz[1] — [1]Department for Cell and Developmental Biology, Biocenter, University of Würzburg, Germany — [2]Center for Computational and Theoretical Biology, University of Würzburg, Germany

Trypanosoma brucei expresses a dense coat of GPI-anchored variant surface glycoproteins (VSGs). The fluidity of this coat is fundamental for the evasion of the host‘s immune system and thus for the survival of the parasite. So far, the VSG dynamics on living trypanosomes has been studied at the micron and second scale for the whole ensemble. In this project, we want to elucidate the dynamics of individual VSGs in relation to the flagellar pocket, the sole site for endo- and exocytosis, with single-molecule fluorescence microscopy. For this purpose, we have recently introduced super-resolution imaging of intrinsically fast-moving flagellates based on cyto-compatible hydrogel embedding. Building on this work, we are now able to track VSG dynamics on living trypanosomes at high spatial (localization precision ˜30 nm) and temporal resolution (f = 100 Hz). The length of gained trajectories is mainly limited by the shape and size of trypanosomes (approx. 18 μm in length and 3 μm in width). Therefore, we use a self-written program based on an approach from Hoze and Holcman [Biophys. J., 2014] to make reliable statements about local forces and the diffusion tensor. The information is gained from a large number of short trajectories and will be presented in directed motion and diffusion maps.

30 min. coffee break

Invited Talk BP 22.7 Wed 11:30 SCH A251

The mechanical stability of proteins regulates their translocation rate into the cell nucleus — •Sergi Garcia-Manyes — Department of Physics, Randall Centre for Cell and Molecular Biophysics King's College London

The translocation of mechanosensitive transcription factors (TFs) across the nuclear envelope is a crucial step in cellular mechanotransduction. Yet the molecular mechanisms by which mechanical cues control the nuclear shuttling dynamics of TFs through the nuclear pore complex (NPC) to activate gene expression are poorly understood. Here, we show that the nuclear import rate of myocardin-related transcription factor A (MRTFA) * a protein that regulates cytoskeletal dynamics via the activation of the TF serum response factor (SRF) * inversely correlates with the protein*s nanomechanical stability and does not relate to its thermodynamic stability. Tagging MRTFA with mechanically-stable proteins results in the downregulation of SRF-mediated gene expression and subsequent slowing down of cell migration. We conclude that the mechanical unfolding of proteins regulates their nuclear translocation rate through the NPC and highlight the role of the NPC as a selective mechanosensor able to discriminate forces as low as *10 pN. The modulation of the mechanical stability of TFs may represent a new, general strategy for the control of gene expression.

BP 22.8 Wed 12:00 SCH A251

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

Chlorophyll a (Chl a) is one of the most abundant pigments on earth, responsible for the green color of plants. Despite extensive research, the composition of its visible Q absorption band is yet not well understood. Here, we apply polarization resolved femtosecond Vis pump - IR probe spectroscopy, providing a detailed insight into Q band mixing

of Chl a. Vis excitation was tuned to various wavelengths scanning the Q band absorption. We show that the dichroic ratio of the keto-C=O stretching vibration at 1698 cm-1 strongly depends on the excitation wavelength. Hence, the angle between the excited electronic transition dipole moment (tdm) and the vibrational keto-C=O tdm changes significantly across the Q band. Tracing the relative angle Θ for different excitation wavelengths allows to determine the Qx contribution along the Q band region. In this way, Qx is found to contribute 40-60% to absorption of the lower energetic peak at 618 nm and to 75-100% to the absorption of the high energy flank at around 580 nm. Complementary measurements on the C=C stretching vibration at 1608 cm-1 provide corroborating evidence for our findings. Further, we show that from our recent results the three-dimensional orientation of the Qx and Qy tdms can be resolved under guidance of quantum chemical calculations.

BP 22.9 Wed 12:15 SCH A251

Power law decays of ligand concentrations in single-molecule kinetic experiments. — •Aykut Erbas[1], Monica Olvera de la Cruz[2], and John F. Marko[2] — [1]Bilkent University- UNAM, Ankara 06800, Turkey — [2]Northwestern University, Evanston 06202, USA

SPR (Surface Plasmon Resonance) or single-molecule kinetic methods rely on the relaxation of initially surface-bound ligands into a confined reservoir to measure the dissociation rates of the corresponding ligands. Similarly, biological processes such as exocytosis (emission of small molecules into the intracellular void for cellular communication) can be considered as a similar relaxation problem. Using molecular dynamics simulations and scaling arguments, we studied a model system closely related to the above cases. In our model, Brownian particles are released from their binding sites into a confined volume. Then, within this volume, we tracked how the concentration of particles throughout the volume changes as a function of time. Our results show that the dissociation process (more specifically rebinding rates of released particles) exhibits various power laws at times longer than the initial exponential decay. Interestingly, the cumulative rebinding number, which is robust against the concentration fluctuations, exhibits a distinct plateau regime as a result of the three-dimensional escape process of the particles from their initial binding sites. Overall our results can be used for new sensor applications to probe molecular kinetics at long tines.

BP 22.10 Wed 12:30 SCH A251

Narrow escape: How long does it take for a camel to go through the eye of a needle? — •Elisabeth Meiser[1], Reza Mohammadi[2], Nicolas Vogel[2], and Susanne Fenz[1] — [1]University of Würzburg, Biocenter: Cell- and Developmental Biology, Würzburg, Germany — [2]Friedrich-Alexander University Erlangen-Nürnberg, Institute of Particle Technology, Erlangen, Germany

The narrow escape problem is a common problem in biology and biophysics. It deals with Brownian particles confined to a given domain with reflecting borders and only a small escape window where particles are absorbed. The mean first passage time (MFPT), the time it takes a set of particles to escape, can be analytically calculated in 2D and 3D for several geometries. It depends on the area of the domain, the size of the escape window and on the diffusion coefficient of the particle. We aim to systematically test the analytical solution of the NEP in 2D by variation of the relevant parameters. Experiments are being complemented by matching random walk simulations. For the experimental test, we prepared micro-patterned phospholipid bilayers from a combination of colloid lithography and vesicle fusion. We imaged fluorescently labeled lipids diffusing in circular membrane patches with diameters of 1-5 um using single-molecule microscopy at 100 Hz and a localization precision of 14 nm. While the area of the membrane was tuned during colloid lithography, the size of the escape window was adjusted in the course of the analysis. We will present our first results on membrane patterning as well as a comparison of our experimental and simulation results with the theoretical prediction for the MFPT.

BP 22.11 Wed 12:45 SCH A251

Probing single molecular surface interactions on electroactive surfaces — •Julia Appenroth, Laura Mears, Pierluigi Bilotto, Alexander Imre, and Markus Valtiner — TU Wien, Applied Physics, Vienna, AT

Adhesive interactions between hydrophobic, charged and electroactive moieties steer ubiquitous processes in aqueous media, including the self-organization of biologic matter and adhesive interfaces in general. Recent decades have seen tremendous progress in understanding these interactions for macroscopic adhesive interfaces. Yet, it is still a challenge to experimentally measure interactions at the single-molecule scale and thus to compare with theory, especially on electroactive surfaces. Here, we directly measure and quantify the sequence dependence and additivity of charge-mediated and electroactive interactions at the single-molecule scale. We combined dynamic single-molecule force spectroscopy with MD simulations and show how electroactive surfaces can be probed with single molecules using force probe techniques.

BP 23: Focus: Physics of Stem Cells

Time: Wednesday 9:30–12:45 Location: ZEU 250

BP 23.1 Wed 9:30 ZEU 250

Multi-scale imaging and analysis identify pan-embryo cell dynamics of germlayer formation in zebrafish — Gopi Shah[1], Konstantin Thierbach[2], Benjamin Schmid[1], Johannes Waschke[3], Anna Reade[4], Mario Hlawitschka[3], Ingo Roeder[2], •Nico Scherf[1,2], and Jan Huisken[1] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany. — [2]Institute for Medical Informatics and Biometry, TU Dresden, Germany — [3]Faculty of Computer Science and Media, Leipzig University of Applied Sciences, Germany — [4]Department of Biochemistry and Biophysics, University of California San Francisco, USA

The coordination of cell movements across spatio-temporal scales ensures precise posi- tioning of organs during vertebrate gastrulation. Mechanisms governing such morphogenetic movements have been studied only within a local region, a single germlayer or in whole embryos without cell identity. Scale-bridging imaging and automated analysis of cell dynamics are needed for a deeper understanding of tissue formation during gastrulation. Here, we report pan-embryo analyses of formation and dynamics of all three germlayers simultaneously within a developing zebrafish embryo. We show that a distinct distribution of cells in each germlayer is established during early gastrulation via cell movement char- acteristics predominantly determined by position within the embryo. The differences in initial germlayer distributions are amplified by a global movement, organizing the organ precursors along the embryonic body axis and giving rise to the blueprint of organ formation.

BP 23.2 Wed 9:45 ZEU 250

How Tissue Microenvironment Impacts Pluripotent Cell Differentiation — •Allyson Quinn Ryan — MPI-CBG, Dresden, Germany

The importance of stem cell population maintenance throughout both development and adulthood has been evident for several decades. Classically, how these populations are regulated is investigated through genetic and cell biological studies. However, work in the past 20 years has shown forces exerted by tissue microenvironments to be of equal importance as molecular and transcriptional profiles to cell potency and identity.1-3 In the context of the mammalian blastocyst, a multicellular system eventually comprised of three epithelial cell lineages, it has recently been shown that emergence of its asymmetrically localized fluid lumen influences the specification and positioning of the two multipotent interior cell lineages.4 The positioning and size of the blastocyst lumen are controlled through mechanisms favoring physical stability of the embryo in its entirety.5,6 Combined, these results point towards a framework of noncellular tissue entities influencing the specification and maturation of developmental tissues originating from progenitor populations of varying potency.

1. A. J. Engler et al., Cell 126, 677-689 (2005).
2. M. Théry et al. Nat., Cell Biol. 7, 947-953 (2005).
3. A.R. Cameron et al., Biomaterials 32, 5979-5993 (2011).
4. A.Q. Ryan et al. Dev., Cell 51, 1-14 (2019).
5. J.C. Chan et al., Nature 571, 112-116 (2019).
6. J.G. Dumortier et al. Science 365, 465-468 (2019).

BP 23.3 Wed 10:00 ZEU 250

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

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

Invited Talk BP 23.4 Wed 10:30 ZEU 250

Mechanical signalling in cell fate choice — •Kevin Chalut — Wellcome-MRC Stem Cell Institute, University of Cambridge, Cambridge, UK

Abstract. Mechanical signaling in cell fate choice plays a significant role in tuning stem cell function. Specifically, my lab has shown that mechanics tunes the response of stem cells to biochemical signaling to steer fate choice. The feedback loop between mechanics and biochemical signaling has significant impact on cellular plasticity both in development and stem cells. I will show that, by tuning the mechanical microenvironment, we can reverse the loss of plasticity associated with ageing of stem cells in the brain. I will also show that, in vivo, we can *fool* the stem cells in an aged brain into functioning as if they are in a soft, neonatal-like environment, thereby leading them to function like young stem cells. This result could have significant impact on treatments of disease like multiple sclerosis. I will then explore how cell surface mechanics in general contextualizes signalling to drive cell fate choice, both in embryonic stem cells and in vivo.

30 min. coffee break

BP 23.5 Wed 11:30 ZEU 250

Robustness and timing of cellular differentiation through population based symmetry-breaking — Angel Stanoev, Dhruv Raina, Christian Schröter, and •Aneta Koseska — Department of Systemic Cell Biology, Max Planck Institute of Molecular Physiology, Dortmund

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

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

BP 23.6 Wed 11:45 ZEU 250

Embryo segmentation by stem cells with genetic clocks and timers. — •Jose Negrete Jr[1,2], Laurel A Rohde[1], Arianne Bercowsky-Rama[1], Alfonso Martinez-Arias[3], Frank Jülicher[2], and Andrew C Oates[1] — [1]École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]University of Cambridge, Cambridge, United Kingdom

Spatial gene expression patterns define regions where specialized cells emerge within an embryo. Patterning may arise from cell signaling, as in lateral induction/inhibition, or from single cells containing genetic timers, as observed in the daughters of neuroblasts. Here, we study the dynamics of the segmentation clock in zebrafish embryos. We show that isolated stem cells extracted from embryos are able to recapitulate the same behavior as in vivo. Their behavior is consistent with a theoretical model of a noisy genetic timer driving a downstream noisy genetic oscillator. Finally, we show that a spatiotemporal model of sequentially activated genetic timers and oscillators is able to reproduce the dynamics of embryo segmentation under different perturbations. This shows that patterning by the segmentation clock proceeds from a mixture of cell signaling and genetic timers.

BP 23.7 Wed 12:00 ZEU 250

Setting up the epigenome: a collective phenomenon — Fabrizio Olmeda[1], Stephen Clark[2], Tim Lohoff[2], Heather Lee[3], Wolf Reik[2,4], and •Steffen Rulands[1,5] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]The Babraham Institute, Babraham, UK — [3]The University of Newcastle, Callaghan NSW, Australia — [4]University of Cambridge, Cambridge, UK — [5]Center for Systems Biology Dresden, Dresden, Germany

During early development, when cells for the first time differentiate into somatic cell types, the genome undergoes large-scale changes in epigenetic DNA modifications (DNA methylation) and chromatin structure. As a result of these processes cells carry distinct epigenetic marks that assign their fate during later stages of development and adulthood. Aberrations in these marks can lead to the death of the embryo and, in adulthood, are one of the hallmarks of cancer. But how are these epigenetic marks so robustly established? Combining novel methods from single-cell multi-genomics with non-equilibrium physics we find universal scaling behaviour in the processes leading to the establishment of epigenetic marks. We show that these phenomena result from long-range interactions mediated by the interplay between chemical and topological modifications of the DNA. Our work sheds new light on epigenetic mechanisms involved in cellular decision making. It also highlights how mechanistic insights into the molecular processes governing cell-fate decisions can be gained by the combination of methods from genomics and non-equilibrium physics.

BP 23.8 Wed 12:30 ZEU 250

Reversibility and heterogeneity as building principles of hematopoietic stem cell organization — •Ingmar Glauche[1] and Ingo Roeder[1,2] — [1]Institute for Medical Informatics and Biometry, Carl Gustav Carus Faculty of Medicine, Technische Universität Dresden, Germany — [2]National Center for Tumor Diseases (NCT), Partner Site Dresden, Germany

Hematopoietic stem cells (HSCs) retain the ability to maintain their own population while at the same time generate all types of the peripheral blood. In contrast to other somatic stem cells, HSCs undergo periods of extended quiescence, in which they do not proliferate but retain their stemness.

We have been developing conceptual and mathematical models of HSC organization for almost two decades. Central to all these models is the conceptual idea that stem cells can reversibly change between different states of activity, thereby introducing an intrinsic level of heterogeneity. Even the simplest assumption, that HSCs can either be in a proliferative state or a state of extended quiescence, proved sufficient to explain the wide range of phenomena observed in hematopoietic stem cell biology. We successfully apply to this concept to competitive transplantation assays in mouse, to the analysis of label dilution data and to stem cell aging. Most importantly, this concept was also instrumental to describe and predict pathogenesis and treatment in acute and chronic leukemias. We conclude that stemness is not a static feature, but should be understood as an emergent and reversible property resulting from the interaction of cells with their current environment.

BP 24: Active Matter IV (joint session DY/CPP/BP)

Time: Wednesday 10:00–12:30 Location: ZEU 160

BP 24.1 Wed 10:00 ZEU 160

Quantitative Assessment of the Toner and Tu Theory of Polar Flocks — •Benoît Mahault[1,2], Francesco Ginelli[3,4], and Hugues Chaté[1,5,6] — [1]Service de Physique de l'Etat Condensé, CEA, CNRS, Université Paris-Saclay, CEA-Saclay, France — [2]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Germany — [3]University of Aberdeen, United Kingdom — [4]Università degli Studi dell'Insubria, Italy — [5]Beijing Computational Science Research Center, China — [6]LPTMC, CNRS UMR 7600, Université Pierre et Marie Curie, France

We present a quantitative assessment of the Toner and Tu theory describing the universal scaling of space-time correlations functions in polar phases of dry active matter. Using large-scale simulations of the Vicsek model in two and three dimensions, we find the overall phenomenology and generic algebraic scaling predicted by Toner and Tu, but our data on density correlations reveal some qualitative discrepancies. The values of the associated scaling exponents we estimate differ significantly from those conjectured in 1995. In particular, we identify a large crossover scale beyond which flocks are only weakly anisotropic. We discuss the meaning and consequences of these results.

BP 24.2 Wed 10:15 ZEU 160

Swirl formation of active colloids near criticality — •Robert C. Löffler, Tobias Bäuerle, and Clemens Bechinger — Fachbereich Physik, Universität Konstanz, Konstanz D-78464, Germany

Animal groups like flocks of birds or schools of fish normally show a high degree of order. Yet they are also responsive to external factors in order to optimize nutrition and avoid predation. Various observations of such responsiveness have let to the assumption that those systems represent a state of order close to a critical point. In our experiments, we use light-responsive active Brownian particles (ABPs) to which we can apply individual torques in a feedback controlled system to study such behavioral rules. The propulsion applied to each ABP is thereby calculated based on information about its local neighbors. Through the variation of a single parameter in our interaction model, which is related to zonal models used in theoretical biology, we observe a continuous phase transition in the collective motion of the group: The ABPs transition from a disordered swarm to a stable swirl (i.e. milling, vortex-like state). Being able to continuously change our control parameter we can also measure the susceptibility of the collective motion, peaking at a critical point within the transition. Observation of such critical behavior in simple models not only allows for more insight in complex animal behavior but also helps with designing future rules for collective tasks in robotic or other autonomous systems.

T. Bäuerle *et al., Nat. Comm.* **9**, 3232 (2018); F. A. Lavergne *et al., Science* **364**, 70-74 (2019).

BP 24.3 Wed 10:30 ZEU 160

Probing mechanical properties of rod-shaped colloidal suspensions with active particles — •N Narinder and Clemens Bechinger — Fachbereich Physik, Universität Konstanz, Konstanz, Germany

Recently self-propelled colloidal particles have been shown to provide a novel tool to probe the mechanical properties of colloidal glassy states of spherical particles [1]. Unlike conventional micro-rheology, where one studies the coupling between the translational motion of a driven probe particle to a background, here the coupling of the host medium to the rotational dynamics of the self-propelled particle contains information about the mechanical properties of the host medium. Here, we apply this method to study the mechanical properties of assemblies of rod-shaped particles with a mean aspect ratio of 15. Such anisotropic colloidal suspensions exhibit a rather rich phase behavior including a two-step glass transition at the aspect ratio considered here [2]. Our first results demonstrate a strong variation of the rotational dynamics of the active particle with increasing area fraction of the rods.

[1] C. Lozano, J.R. Gomez-Solano, & C. Bechinger Nature Materials 18, 1118-1123 (2019).

[2] Z. Zheng, F. Wang, & Y. Han PRL 107, 065702 (2011).

BP 24.4 Wed 10:45 ZEU 160

Statistical mechanical sum rules for active colloids at surfaces - a touch of equilibrium — •René Wittmann[1,2], Frank Smallenburg[3], and Joseph Brader[2] — [1]Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, Germany — [2]Soft Matter Theory, Université de Fribourg, Switzerland — [3]Laboratoire de Physique des Solides, Université Paris Sud, France

We study the mechanical properties of active particles in the presence of curved walls by computer simulation of Active Brownian Particles (ABPs), Active Ornstein-Uhlenbeck Particles (AOUPs) and a passive system with effective interactions [R. Wittmann, F. Smallenburg and J. M. Brader, J. Chem. Phys. 150, 174908 (2019)]. The effective theory admits analytic results for pressure, surface tension and adsorption of an active ideal gas at a two-dimensional circular wall. It further predicts that an equilibrium sum rule also holds for active fluids, which we confirm numerically for both ABPs and AOUPs in the limit of small curvature.

More precisely, we find within each model that the slope of the pressure as a function of the curvature equals the surface tension and adsorption (up to an effective temperature scale) on a planar wall. Intriguingly, the explicit value of these coefficients is model-dependent, which can be explained by the different velocity distributions. We also discuss the influence of interactions and find that the effect of curvature on the wall pressure is reduced when increasing the density. Within numerical accuracy, the equality of the slope of the pressure and the planar surface tension appears to hold at finite density.

BP 24.5 Wed 11:00 ZEU 160

Lorentz forces induce inhomogeneity and flux in active systems — •Hidde Vuijk[1], Jens-Uwe Sommer[1,2], Holger Merlitz[1], Joseph Brader[3], and Abhinav Sharma[1,2] — [1]Leibniz Institute of Polymer Research, Dresden, Germany — [2]Technische Universität Dresden, Dresden, Germany — [3]Universite de Fribourg, Fribourg, Switserland

We consider the dynamics of a charged active Brownian particle in three dimensions subjected to the Lorentz force due to an external magnetic field. We show that in the presence of a field gradient, a macroscopic flux emerges from a flux-free system and the density distribution becomes inhomogeneous. The flux is induced by the gradient of the magnetic field only and does not require additional symmetry breaking such as density or potential gradients, which stands in marked contrast to similar phenomena in condensed matter such as the classical Hall effect. We further demonstrate that passive tracer particles can be used to measure the essential effects caused by the Lorentz force on the active particle bath, and we discuss under which conditions this diffusive Hall-like effect might be observed experimentally. Lastly, we show that similar effects arise in case of inhomogeneous activity in combination with a constant magnetic field.

15 min. break.

BP 24.6 Wed 11:30 ZEU 160

Interaction of Active Crystallites within the Active Phase-Field-Crystal Model — •Lukas Ophaus[1], Johannes Kirchner[2], and Uwe Thiele[1,2] — [1]Center for Nonlinear Science, Münster, Germany — [2]Institut für Theoretische Physik, Münster, Germany

We use the active phase-field-crystal (PFC) model, developed by Menzel and Löwen as a model for crystallizing self-propelled particles [1], to study the interaction of traveling crystalline patches. Within the active PFC model, these localized states exist besides periodic states, i.e., spatially extended crystals [2]. Due to the activity, crystalline states undergo a drift instability and start to travel while keeping their spatial structure. Using results for the parameter ranges where the individual states exist, we explore how two and more traveling localized states interact by performing numerical collision experiments. We show that a critical minimal free path is necessary to preserve the number of colliding localized states and that the active PFC model fails to exhibit dynamical clustering and motility induced phase separation.

[1] A.M. Menzel and H. Löwen, Phys. Rev. Lett. 110, 055702 (2013)

[2] L. Ophaus, S.V. Gurevich and U. Thiele, Phys. Rev. E 98, 022608 (2018)

BP 24.7 Wed 11:45 ZEU 160

Continuum model for bacterial suspensions with density variations — •Vasco Marius Worlitzer[1], Avraham Be'er[2],

Gil Ariel[3], Markus Bär[1], Holger Stark[4], and Sebastian Heidenreich[1] — [1]Physikalisch-Technische Bundesanstalt — [2]Ben-Gurion University — [3]Bar-Ilan University — [4]Technical University of Berlin

The various dynamical states found in bacterial suspensions are a fascinating illustration of the rich dynamics exhibited by active polar fluids. A recent study explored the phase space experimentally, identifying three major states: single-cell motion, collective swarming, biofilm formation and mixtures between them [1]. While a continuum model presented in [2] has been proven to describe the statistical features of the swarming phase quite successfully, it is not applicable outside this regime as a constant density is assumed. We show that new dynamical states are accessible by relaxing this assumption. In particular a regime similar to the mixed state of swarming and biofilm formation is covered, showing the same anomalous statistics as found experimentally. The new model is inspired by work on scalar active matter [3] and consist of a generic continuity equation for the density. The density is coupled to a local polar order parameter through a density dependent self-propulsion speed and an active pressure.

[1] H Jeckel et al., PNAS 116 (5) (2019) [2] J Dunkel et al., Phys. Rev. Lett. 110 (2013) 228102. [3] J Bialké et al., EPL 103 (2013) 30008.

BP 24.8 Wed 12:00 ZEU 160

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

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

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

BP 24.9 Wed 12:15 ZEU 160

Self-propelled thermophoretic colloidal swimmers — •Sergi Roca-Bonet and Marisol Ripoll — Theoretical Soft Matter and Biophysics, Institute of Complex Physics, Forschungszentrum Jülich, Germany

Self-propelled phoretic colloids have recently emerged as a promising avenue for the design of artificial microswimmers. We employ a hydrodynamic fluctuating mesoscale simulation approach to study both single and collective swimming. We investigate self-propelled colloidal multimers in which one monomer can eventually get higher temperature, and it is linked with one or more other monomers which induce the multimer motion. Single colloid swimming properties are varied by changing the number of the constituting monomers (here two or three), their spatial arrangement (rod-like or v-like) and the relative sizes of such monomers. We have investigated the effect of slid confinement in comparison to the 3d-bulk motion of these dimeric and trimeric colloids. The collective system properties are determined by the competition between hydrodynamic and phoretic interactions which vary as a function of the density, the colloid geometry, and the monomers phoretic affinity (philic or phobic). Examples of the resulting behaviour are clustering, swarming, or rotational motions.

BP 25: Cell Mechanics II

Time: Wednesday 15:00–17:15 Location: HÜL 386

BP 25.1 Wed 15:00 HÜL 386

Chemotherapy interferes with leukocyte deformability in a cancer patient study — Martin Kräter[1,2], Maik Herbig[1,2], Martin Bornhäuser[3], Jochen Guck[1,2], and •Angela Jacobi[1,2,3] — [1]MPL, Erlangen, Germany — [2]BIOTEC, TU Dresden, Dresden, Germany — [3]University Hospital Carl Gustav Carus, TU Dresden, Dresden, Germany

Blood cell mechanics, dictated by the cytoskeleton, is essential for circulation in microcapillary networks, where cells need to deform and squeeze through vascular constrictions. If this deformability is attenuated, blood flow can be impeded, leading to thromboembolic complications. Using real-time deformability cytometry (RT-DC), a high-throughput method that determines cell mechanics, we performed a pilot study on blood samples from a cancer patient undergoing chemotherapy with epirubicin/cyclophosphamide (EC) and paclitaxel (P). Over the course of the treatment, we monitored leukocyte count, size and deformability. During the therapy, granulo-/monocytes exhibited a dramatic decrease in deformability. However, 45 weeks post treatment, leukocyte deformability was restored to normal levels, indicating that blood cell mechanics is tightly regulated in homeostatic conditions. Intriguingly, the treatment did not alter cell size, which emphasises the advantage of measuring blood cell deformability when monitoring poor circulation in chemotherapy patients. Finally, our study suggests that reduced blood cell deformation could favour vascular complications encountered during chemotherapy.

BP 25.2 Wed 15:15 HÜL 386

Investigating the red blood cells (dis)aggregation mechanism using optical tweezers — •Francois Yaya[1,2], Olivera Korculanin[3], Mehrnaz Babaki[3], Kisung Lee[4], Pavlik Lettinga[3,5], and Christian Wagner[1] — [1]1Experimentalphysik, Saarbrücken, Germany — [2]Interdisciplinaire de Physique, Grenoble, France — [3]ICS-3 Forschungszentrum, Jülich, Germany — [4]Korean Institute for Basic Science, Ulsan, South Korea — [5]Laboratory for Soft Matter and Biophysics, KU Leuven, Belgium

Red blood cells (RBC) in our body circulate, while continuously aggregating and disaggregating under low shear rates. RBC aggregation is a reversible process that can only be observed in the presence of macromolecules (i.e. large plasma proteins like fibrinogen or non-ionic polymers). The potential description of the RBC interaction was studied, mainly from the scope of polymer induced aggregation and predominantly with dextran. Despite the favored model based on the depletion forces, one can find that, conclusive experimental affirmations of the model are still lacking. Hence, we aimed to investigate the RBC interaction mechanism utilizing holographic optical tweezers (HOT). We assessed RBC interaction forces in two model solutions, namely dextran and a pure depletant (Fd virus). Aggregation and disaggregation of multiple pairs of RBC, in dextran, revealed that forces differ by more than 3 fold. For Fd virus, interaction forces are in the same order of magnitude. Combining HOT with a microfluidic platform, we finally show that adsorption of macromolecules takes place onto a single RBC membrane.

BP 25.3 Wed 15:30 HÜL 386

Dynamics of Circular Dorsal Ruffles as a Function of Cellular State — •Merthe Schwachenwald, Julia Lange, Malte Ohmstede, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

Circular Dorsal Ruffles (CDRs) are dense moving actin structures that play an important role in cell propagation and the uptake of growth factors. The occurrence and propagation of CDRs are controlled by a multitude of different proteins and interconnected signaling pathways, the most prominent and well-understood being Arp2/3-mediated actin branching. Thus the dynamics of CDRs can be manipulated by interfering with actin regulators or actin itself. Further, the kinetics of CDRs are influenced by membrane tension. To quantify the impact of the different players, we investigate the dynamics of CDRs under narrowly-controlled conditions. Experimentally, we ensure even boundary conditions by using microcontact printed substrates to enforce an even cell shape. The influences of different proteins and growth-factor stimulation on CDR dynamics are controlled employing a microfluidic set-up, and examined using light microscopy. The dynamics of the occurring CDRs are analyzed via kymographs or the use of machine-learning alghorithms.

BP 25.4 Wed 15:45 HÜL 386

Stochastic bond dynamics induce optimal alignment of

malaria parasite — •Anil Kumar Dasanna, Sebastian Hillringhaus, Gerhard Gompper, and Dmitry Fedosov — Institute of Complex Systems and Institute for Advanced Simulation, Forschungszentrum Jülich, Germany

Malaria parasites invade healthy red blood cells (RBCs) to escape from the immune response and multiply inside the host by utilizing its machinery. The invasion only occurs when the parasite apex is aligned with RBC membrane, which makes the alignment a crucial step. Recent experiments also demonstrated that there is a considerable membrane deformation during the alignment process which are thought to speed up the alignment process. In this work, using mesoscopic simulations we try to assess the exact roles of RBC deformations and parasite adhesion during the alignment. Using deformable RBC and a rigid parasite, we show that both RBC deformation and parasite's adhesion work together to induce an optimal alignment. By calibrating our parasite's movement with experiments, we show that our alignment times match quantitatively with the experimental alignment times. Here we stress that the stochastic nature of our adhesion bond kinetics is the key for inducing optimal alignment times rather than too fast times such as in case of smooth potentials or too slow such as in case of purely rotational diffusion. We also show that alignment times increase drastically for rigid RBC which signifies that parasite invasion is less probable with already infected RBC and signifying the role of membrane deformations during the parasite alignment.

BP 25.5 Wed 16:00 HÜL 386

Unbiased recovery of frequency-dependent mechanical properties from noisy time-dependent data — •Shada Abuhattum[1], Paul Müller[1], Vasily Zaburdaev[2], Jochen Guck[1], and Hui-Shun Kuan[2] — [1]Max Planck Institute for the Science of Light — [2]Department of Biology, FAU-Universität Erlangen-Nürnberg

The mechanical response of materials to dynamic loading has great significance in various applications, ranging from performance and failure of engineered setups to exploring the structure of biological matter. This mechanical response is quantified using the frequency-dependent complex modulus. Probing materials directly in the frequency domain faces technical challenges such as a limited range of frequencies or lengthy measuring times. Therefore, it is common practice to extract frequency-dependent properties by fitting predefined mechanical models to measurements done in time-domain. Fitting these models circumvents problems with noise handling and signal shape imperfections. However, it precludes the probing of unique and unexplored material properties. Here, we demonstrate that the frequency-dependent complex modulus can be properly derived from stress-strain time-domain measurements even in the presence of random noise and systematic offset. We apply signal blurring methods to eliminate the systematic offset and to clean the complex modulus at lower frequencies. We then extend the range of reliable frequencies by employing a local averaging method to the complex modulus data. Finally, we propose an alternative probing procedure to increase the signal-to-noise ratio and further extend the frequency range for a reliable mechanical characterization.

15 min. coffee break

BP 25.6 Wed 16:30 HÜL 386

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

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

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

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

BP 25.7 Wed 16:45 HÜL 386

Quantification of size-dependent organelle transport in cells — •Simon Wieland[1], David Gitschier[1], Marius M Kaiser[1], Solange Hoffbauer[1], Magdalena Haaf[1], Adam G Hendricks[2], and Holger Kress[1] — [1]Universität Bayreuth, Arbeitsgruppe Biologische Physik, Bayreuth — [2]McGill University, Department of Bioengineering, Montreal

Intracellular organelle transport is a vital process for a large variety of cellular functions, like exocytosis and endocytosis, including phagocytosis. Recently, it was found that organelle transport during phagocytosis is not only regulated biochemically, but also by the size of the organelle [1]: In macrophages, larger phagosomes are transported very persistently towards the nucleus, whereas smaller phagosomes exhibit highly irregular motion. To unravel the molecular causes of this behavior, we systematically quantified the size-dependence of the intracellular transport of phagosomes. Using magnetic tweezers, we found that intracellular transport forces of organelles strongly depend on the cargo size. Immunofluorescence experiments performed on isolated phagosomes allowed us to identify and partially quantify dynein, kinesin-1, and kinesin-2 on the organelles. The scaling behavior of the numbers of dyneins on the organelles together with the scaling behavior of measured stall forces implies cooperation between the molecular motors. These findings can lead to a more fundamental understanding of intracellular transport and the dynamics of molecular motors.

[1]: Keller, S., Berghoff, K., & Kress, H. (2017). Scientific reports, 7(1), 17068.

BP 25.8 Wed 17:00 HÜL 386

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

Cytotoxic T lymphocytes (T) and natural killer cells are the main cytotoxic killer cells of the human body to eliminate pathogen-infected or tumorigenic cells (target cells). Once T-cell has identified a target cell, they form a tight contact zone, the immunological synapse (IS). One then observes a re-polarization of the cell involving the rotation of the microtubule (MT) half-spindle and a movement of the microtubule organizing center (MTOC) to the IS. Concomitantly a massive relocation of organelles attached to MTs is observed. Since the mechanism of this relocation remains elusive we devise a theoretical model for the molecular motor driven motion of the MT half-spindle confined between membrane and nucleus. We analyze different currently discussed scenarios, the cortical sliding and the capture-shrinkage mechanisms, and compare quantitative predictions about the spatio-temporal evolution of MTOC position and spindle morphology with experiments. Model predicts the experimentally observed biphasic nature of the repositioning and confirms the dominance of the capture-shrinkage over the cortical sliding mechanism when MTOC and IS are initially diametrically opposed. We find that the two mechanisms act synergetically reducing the resources necessary for repositioning. Localization of dyneins in the pSMAC facilitates their interaction with MTs. Model opens a way to infer details of the dynein distribution from the experimentally observed features of the MT half-spindle dynamics.

BP 26: Focus: Biological Cells in Microfluidics I

Microfluidic devices have a great potential to enable precise label-free analysis and manipulation of heterogeneous cell suspensions based on the intrinsic properties of the cell. This focus session will discuss recent advances in the behavior of biological cells and cell-mimicking systems in microfluidic flow, and represent a forum of theoretical and experimental contributions.

Time: Wednesday 15:00–17:30 Location: SCH A251

BP 26.1 Wed 15:00 SCH A251

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

In 3D bioprinting, cells suspended in hydrogel are deposited through a fine nozzle, creating three dimensional biological tissues. Due to the high viscosity of the hydrogel, the cells experience hydrodynamic stresses that deform or damage the cells and can ultimately affect the viability and functionality of the cells in the printed construct.
Using numerical methods, we quantify these deformations in dependency of the flow parameters and cell elasticity. We consider shear thinning fluid rheology and validate our Lattice Boltzmann flow calculations with microfluidic flow experiments of typical hydrogel materials. Our hyperelastic cell, modeled as purely elastic continuum with neo-Hookean force calculations, is validated with experimental data for cells obtained via AFM indentation measurements.
By coupling our cell model with the fluid simulations, we investigate the cell deformation in typical flow scenarios, like capillary and shear flow. As essential part of the printing process, we further simulate the cell flowing through the transition from the printer nozzle into the free hydrogel strand, where additional radial flow components stretch the cell at short time scale.

BP 26.2 Wed 15:15 SCH A251

Geometry-induced focusing of red blood cells in a contraction-expansion microfluidic device — •Steffen Michael Recktenwald[1], Asena Abay[1,2], Thomas John[1], Lars Kaestner[1,3], and Christian Wagner[1] — [1]Saarland University, Saarbruecken, Germany — [2]Landsteiner Laboratory, Amsterdam, Netherlands — [3]Saarland University Medical Center, Homburg, Germany

Constrictions in blood vessels of the cardiovascular system can dramatically change the spatial distribution of passing cells or particles. To study the flow of red blood cell (RBC) suspensions in obstructed vessels, constricted microfluidic devices are commonly used. However, the three-dimensional nature of cell focusing in the channel cross-section remains poorly investigated. Here, we explore the cross-sectional distribution of living and rigid RBCs passing a constricted microfluidic channel. Therefore, individual cells are tracked in multiple layers across the channel depth and across the channel width. While cells are homogeneously distributed in the channel cross-section pre-contraction, we observe a strong geometry-induced focusing post-contraction. The magnitude of this cross-sectional focusing effect increases with increasing Reynolds number for both living and rigid RBCs. We discuss how this non-uniform cell distribution results in an apparent double-peaked velocity profile in particle image velocimetry analysis and show that trapping of RBCs in the recirculation zones of the abrupt constriction depends on cell deformability, highly relevant for biomedical cell-sorting applications.

BP 26.3 Wed 15:30 SCH A251

Optical Detection, Characterization and Sorting of Cells and Vesicles in Microfluidics — •Tobias Neckernuss[1,2], Daniel Geiger[1,2], Jonas Pfeil[1,2], Lisa Kwapich[1], Patricia Schwilling[1], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Sensific GmbH

High-speed video microscopy is used for many particle or cell detection applications. In order to measure the mechanical properties of cells or to identify their type. With standard equipment none of these tasks can be accomplished in a real-time and in a label-free environment, let alone if a subsequent sorting step is required.
With our new ODIN technology, we are able to assess important parameters like size, shape, velocity, and morphology of different kinds of particles in microfluidic channels and in Lab-on-a-Chip environments. The optical and label-free measurement delivers relevant parameters immediately after the particle passes the sensor. Due to the fixed latency times we are able to set a trigger signal as soon as the particle or cell matches freely configurable, predefined parameters. ODIN enables new measurement applications for particles and cells, leading to potentially groundbreaking changes in Lab-on-a-Chip designs and their throughputs. We present different experiments and sorting tasks regarding cell stiffness, droplet size, particle encapsulation, bacterial analysis, and antibiotic screening performed with ODIN. Simultaneous real-time detection, categorization and sorting enables novel multifunctional Lab-on-a-Chip designs leading to a multifunctional microfluidic factory.

BP 26.4 Wed 15:45 SCH A251

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

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

BP 26.5 Wed 16:00 SCH A251

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

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

15 min. coffee break

Invited Talk BP 26.6 Wed 16:30 SCH A251

3 D Classification of Red Blood Cells in microchannels — •Christian Wagner — Universität des Saarlandes

Red blood cells (RBCs) are very soft objects that can pass capillaries smaller than the cells diameter. Due to their high deformability, they couple strongly with the flow and can adopt many different shapes. For their quantitative characterization we developed a new confocal 3D imaging technique for fluorescent stained RBCs. We found two equilibrium cell shapes under certain flow condition: the so called 'slipper' and the 'croissant' shape. Numerical simulations are in good agreement with experimental observations. In addition, high throughput data of classical 2-D microscopy combined with an adaptive neural network allow us to obtain the full phase diagram of red blood cell shapes as a function of the flow rate. In larger channels, we use the confocal technique to characterize the margination of single rigidified RBCs in a suspension of healthy RBCs. Margination of e.g. white blood cells or platelets at the vessel walls is a haemodynamic key mechanism of our immune system. Our confocal observation technique allows us to characterize the distribution of hard vs. soft cells in full time and space resolution for the first time. Again numerical simulations are in good agreement although some quantitative differences remain that need further investigations.

BP 26.7 Wed 17:00 SCH A251

Simulation of cell deformation inside a microfluidic channel under the influence of a non-Newtonian fluid. — •Ralf Schuster[1], Bob Fregin[2], Oliver Otto[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University, D-89081 Ulm — [2]Humorale Immunreaktionen bei kardiovaskulären Erkrankungen, Universität Greifswald, D-17489

The mechanical characterization of certain cell types is important to obtain physiological insights. For instance, tumor and normal cells can be distinguished by elasticity, indicated by the amount of deformation under given stress. Simulations help to understand, verify and improve the analysis of deformation-based cell characterization such as flow-based cytometry. We achieve efficient computations using a 2D-rotational symmetric model, based on Fluid-Structure-Interaction with a hyper-elastic material. The deformation of a cell along an entire microfluidic channel can be tracked for a variety of elasticities, viscosities, cell sizes, channel geometries and flow rates. The aim is to model typical experimental conditions [1] and compare simulated and measured results. In the study HL60 cells undergo a shear stress in a fluid with shear dependent viscosity, which can be described by a power law. Simulations are carried out for three different flow rates and additionally for Newtonian fluids with constant viscosity. The results help to find appropriate parameters and models to describe and interpret the behavior of certain cell types.

[1]Fregin et al, High-throughput single-cell rheology in complex samples by dynamic real-time deformability cytometry. Nat Com(2019)

BP 26.8 Wed 17:15 SCH A251

ROS induces intracellular acidosis associated with increased cell stiffening — •Yesaswini Komaragiri[1], Huy Tung Dau[1], Doreen Biedenweg[2], Ricardo H Pires[1], and Oliver Otto[1] — [1]Biomechanics, ZIK-HIKE, University of Greifswald, Greifswald, Germany — [2]University medicine Greifswald, Greifswald, Germany

Reactive oxygen species (ROS) are a primary source of superoxides associated with important alterations in cell physiology. Here, it is accepted that ROS affect the cytoskeleton, however, the interplay with cell mechanics has not been thoroughly investigated. This study focuses on understanding the impact of oxidative stress on the mechanical properties of the human myeloid precursor cell line (HL-60). Generation of ROS was induced by exposing cells to varying concentrations of hydrogen peroxide (H2O2). Using real-time fluorescence deformability cytometry we coupled the mechanical characterization of cells with simultaneous fluorometric assessment of intracellular ROS levels. Our work reveals a direct correlation between the elastic modulus of cells and increased levels of superoxides. Interestingly, the changes in the mechanical phenotype cannot be explained by altered structured of F-actin and microtubule. We demonstrate that cell stiffening at elevated levels of ROS is driven by intracellular acidosis and a corresponding decrease in the cytoplasmic pH of our model system.

BP 27: Fluid Physics of Life (joint session DY/BP)

Time: Wednesday 15:00–17:45 Location: ZEU 160

Invited Talk BP 27.1 Wed 15:00 ZEU 160

Light-regulated microbial dynamics and self-organization in complex geometries — •Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, D-37077 Göttingen, Germany

Life on Earth has evolved under the periodic exposure to sunlight and many microorganisms are equipped with a photosynthesis machinery enabling them to convert light into chemical energy. Their habitats include liquid-infused soil, porous rocks and microdroplets, featuring complex geometric architectures that induce strong spatial and temporal light fluctuations. Thus, biological functionalities to sense and rapidly respond to light fluctuations are pivotal for microbial life.

In this presentation I will discuss how concepts from non-equilibrium statistical physics, in conjunction with novel experimental approaches from soft matter and biophysics [1], enable us to decipher fundamental physical principles of microbial responses to light cues. We discovered that light regulates the transition of motile microbes from the free-swimming to the surface-adhered state [2]. I will further elaborate on how interfacial interactions govern the motility and navigation of individual cells in complex geometries [3] and demonstrate that the light-regulated motility controls the emergence of self-organization and phase separation of microbial populations in confinement.

[1] M. Backholm & O. Bäumchen, Nature Protocols 14, 594 (2019).
[2] C. Kreis et al., Nature Physics 14, 45 (2018).
[3] T. Ostapenko et al., Phys. Rev. Lett. 120, 068002 (2018).

BP 27.2 Wed 15:30 ZEU 160

Wet-tip versus dry-tip regimes of osmotically driven bile flow in the liver — Oleksandr Ostrenko, Michael Kücken, and •Lutz Brusch — Center for Information Services and High Performance Computing (ZIH), Technische Universität Dresden, Germany

The secretion of osmolites into a lumen and thereby caused osmotic water inflow drive fluid flows like saliva, sweat and bile in organs without a mechanical pump, as opposed to the heart in blood circulation. The effects of elevated fluid pressure and the associated mechanical limitations of organ function remain largely unknown. We consider the pressure profile of the coupled osmolite-flow problem with combined velocity and pressure boundary conditions. Notably, the entire lateral boundary acts as a fluid source, the strength of which is determined by feedback from the emergent pressure solution itself. Hence, the pressure difference between the boundaries is not imposed but self-organises. Our theoretical results reveal fundamental parameter dependencies and a phase boundary separating the commonly considered "wet-tip" regime with steady flow out of the very tip of a channel from a "dry-tip" regime suffering stalled flow and a self-organised block of osmotic water inflow [1]. We validate model predictions against intra-vital video microscopy data from mouse liver [2] and propose a relation between the predicted phase boundary and the onset of zonated cholestasis, a pathological liver condition [3].

[1] Ostrenko et al. (2019) Scientific Reports 9, 4528. [2] Meyer et al. (2017) Cell Systems 4, 277. [3] Segovia-Miranda et al. (2019) Nature Medicine and bioRxiv 572073.

BP 27.3 Wed 15:45 ZEU 160

Memory capacity of a flow network — •Komal Bhattacharyya[1], David Zwicker[1], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]Physik-Department, Technische Universität München, Garching, Germany

The slime mould *Physarum polycephalum* is a very simple unicellular but seemingly intelligent organism with a network-like body. Its complex behaviour requires the ability to propagate, store and process information. Recently, it has been shown that *Physarum* propagates information about stimuli with the fluid flows throughout its network. Most inspiringly, *Physarum* was observed to adapt its networks tube radii globally in response to stimuli, reaching a steady-state as a long term response that keeps a memory of the stimuli in its network morphology. Inspired by this observation we here investigate the capacity to store information about previous stimuli in the morphology of an

adaptive flow network. We model the organism as a flow network whose radii can change when optimising the network to have the least energy dissipation. We observe how the system reacts to localised changes and the timescale of its responses to applied stimuli by numerical simulation. Through theoretical understanding, we aim to pinpoint the information storing and processing capabilities of adaptive flow networks in general and *Physarum* networks specifically.

BP 27.4 Wed 16:00 ZEU 160

Fluid transport by metachronal waves in cilia chains — •Albert von Kenne, Thomas Niedermayer, and Markus Bär — Physikalisch-Technische Budesanstallt (PTB), Berlin 10587

Motile cilia are hair-like cell extensions that undergo a cyclic motion with the purpose to transport the extracellular fluid at a low Reynolds number, providing crucial functionality of living matter such as cell locomotion or molecular transport in tissue. A striking feature of populations of cilia is a state of collective motion known as metachronal wave. In proximity to a cell surface a symmetry breaking of the flow field is due that affects the properties of metachronal waves and facilitates transport generation. We generalize a simple phase oscillator model for the elastohydrodynamic coupling in ciliated systems [1] to include this asymmetry. We obtain analytical results for the linear stability of metachronal waves in presence of long-range hydrodynamic interactions, illustrate their properties by numerical simulations and relate the change in transport ability to the specific properties of metachronal waves.

[1] Niedermayer et. al., Chaos: 18(3) 2008.

BP 27.5 Wed 16:15 ZEU 160

Boundary conditions for polar active fluids exhibiting mesoscale turbulence — •Sebastian Heidenreich[1], Henning Reinken[2], Daiki Nishiguchi[3], Andrey Sokolov[4], Igor S. Aranson[5], Sabine H. L. Klapp[2], and Markus Bär[1] — [1]Physikalisch Technische Bundesanstalt Braunschweig und Berlin — [2]Technische Universität Berlin — [3]University of Tokyo, Japan — [4]Argonne National Laboratory, USA — [5]Pennsylvania State University, USA

Bacterial suspensions are intriguing examples for active polar fluids which exhibit large-scale collective behaviour from mesoscale turbulence to vortex lattices. The bulk collective motion is well described by a continuum equation with derivatives up to the fourth order [1]. That simple model reproduces experimental findings of mesoscale turbulence and was recently derived from a minimal micro-swimmer model. However, the treatment of boundaries to describe the collective motion in a confinement or near walls remains so far unknown. In the talk, we propose boundary conditions for active polar fluids suitable to describe recent experiments of Bacillus subtilis bacteria moving in an array of lithographic designed pillars [2]. Furthermore, we describe the collective motion of bacteria around single pillars of different sizes in experiments and show that the model with the mentioned boundary conditions reproduces this behavior faithfully.

[1] J. Dunkel, S. Heidenreich, M. Bär and R. E. Goldstein, New. J. Phys. 15, 040516 (2013). [2] D. Nishiguchi, I. S. Aranson, A. Snezhko and A. Sokolov Nat. Comm. 9, 4486 (2018).

15 min. break.

BP 27.6 Wed 16:45 ZEU 160

Artificial topological defects organize bacterial motion — •Henning Reinken[1], Sebastian Heidenreich[2], Daiki Nishiguchi[3], Andrey Sokolov[4], Igor Aranson[5], Markus Bär[2], and Sabine Klapp[1] — [1]Technische Universität Berlin — [2]Physikalisch-Technische Bundesanstalt Berlin — [3]University of Tokyo, Japan — [4]Argonne National Laboratory, USA — [5]Pennsylvania State University, USA

Active systems spontaneously self-organize into complex spatio-temporal structures such as flocks, bands, vortices, and turbulence. These collective states are susceptible to weak geometrical confinement, as has been demonstrated in experiments on suspensions of *Bacillus subtilis*, where turbulent motion is organized into a highly ordered bacterial vortex lattice by arrays of tiny obstacles [1].
Using a continuum-theoretical approach [2], we show how self-induced topological defects imposed by artificial obstacles guide the flow profile of the active fluid and enable the stabilization of vortex patterns with tunable properties. Beyond the stabilization of square and hexagonal lattices, we also provide a striking example of a chiral, antiferromagnetic lattice induced by arranging the obstacles in a Kagome-like array. In this setup, the interplay of lattice topology, activity and length-scale selection generates a net rotational flow. Further, we investigate how the properties of the stabilized patterns impact the transport of tracer particles in the active fluid.

[1] D. Nishiguchi et al., Nat. Commun. **9**, 4486 (2018).
[2] H. Reinken et al., Phys. Rev. E **97**, 022613 (2018).

BP 27.7 Wed 17:00 ZEU 160

Topological defects in growing bacterial colonies — Anh LP Thai, Arkajyoti Ghoshal, and •Anupam Sengupta — Physics of Living Matter Group, University of Luxembourg, Luxembourg

Bacterial populations are known to mediate vital processes in ecology, medicine and industry. Morphology, a key biophysical trait, has been long studied for its biological relevance in uptake, motility and selection. Yet, only recently we have started to uncover the role of morphology in biophysical interactions between cells or with their micro-environment [1]. Here, I will present recent results that elucidate how non-motile bacteria harness morphology to regulate transport processes over colony scales. We examine the geometric and mechanical properties of growing colonies, with a particular focus on the emergence of topological defects. Our results indicate that the number of topological defects depends on the cell physiology and colony dimensions, which in turn regulate the active dynamics of the colony. We compare our experimental results with MD simulations and continuous modelling [2, 3], and demonstrate that an expanding colony of non-motile cells self-organizes into domains of aligned cells. Topological defects mediate the interactions between domains, ultimately yielding an active nematodynamic system. Topology mediated mechanics can potentially lead to physiological functions due to the active hydrodynamics at scales that are orders of magnitude larger than single cells. [1] A. Sengupta, Microbial Active Matter: A Topological Perspective (under rev.); [2] You, Pearce, Sengupta, Giomi, Phys. Rev. X. 8 (2018); [3] You, Pearce, Sengupta, Giomi, Phys. Rev. Lett. 123 (2019).

BP 27.8 Wed 17:15 ZEU 160

Dynamics of Lithium Chloride Solutions in Nanopores of Various Diameters - a NMR Study — •Christoph Säckel, Sarah Schneider, and Michael Vogel — Institut für Physik kondensierter Materie, TU Darmstadt

We analyse ion transport in aqueous salt solutions confined to nanopores as part of a project that aims to develop a new generation of nanosensors by combining the effectiveness of biological ion channels with the robustness of synthetic silica nanopores. To this end it is necessary to understand the influence of the confinement on the temperature-dependent ion transport. We systematically vary the pore parameters and study effects on the dynamics of aqueous LiCl solutions using ^{2}H and ^{7}Li nuclear magnetic resonance (NMR). We combine homogeneous and gradient field NMR to selectively investigate water and ion dynamics on broad time and length scales from room temperature to the supercooled regime. Both the local and long-range dynamics of ions and water show a slowdown in silica confinement. In addition, our data indicates more heterogeneous dynamics for the liquid in confinement than in bulk. Moreover, NMR studies of solutions in functionalized silica pores reveal a significant influence of the chemical nature of the inner pore surfaces. The observed effects can be explained by a slower layer of solution at the pore walls and bulk-like dynamics in the pore centre. Self-diffusion shows an Arrhenius-like behaviour of the solution in confinements, while bulk samples are best described by a VFT fit.

BP 27.9 Wed 17:30 ZEU 160

Self-organization of active microtubule networks — Smrithika Subramani, •Viswa Maitreyi, and Isabella Guido — Max Planck Institute for Dynamics and Self-Organization, Goettigen, Germany

Transport in nature is a crucial task and simple diffusion is insufficient, especially in the intracellular confinement. Relying on cytoskeletal components and their motor proteins is a strategy that have been evolved to tackle this limitation. It was observed that inside large eukaryotic cells microtubule-motor protein networks display an activity that generates a flow, called cytoplasmic streaming, that contributes to transport and distribution of components. Many efforts have been made to understand the features and function of this intracellular streaming. However, the exact mechanism behind its establishment is still unknown. Here we present a study on a synthetic system made of active microtubule networks. When confined, they self-organize and show an interesting emergent behaviour that presents transitions

through different regimes. Such transitions have similarities with the process examined in the intracellular space of Drosophila oocytes during their development. Our results show that the self-assembling of the active network as well as the generated synthetic streaming is dependent on the confinement geometry. This simplified approach allows the characterization of such dependence and can provide a deeper understanding of the natural process.

BP 28: Statistical Physics of Biological Systems II (joint session BP/DY)

Time: Wednesday 15:00–17:30 Location: ZEU 250

Invited Talk BP 28.1 Wed 15:00 ZEU 250

Eavesdropping on fluctuation-driven transport in living matter — •Matthias Weiss — Experimental Physics I, University of Bayreuth, Gemany

The interior of eukaryotic cells is crowded on several length scales by a plethora of macromolecules and membrane-enveloped subcompartments. Self-organization of this complex environment eventually involves fluctuation-driven transport on many scales. Due to a vast number of active processes, living cells are in a genuine non-equilibrium state, endowing fluctuation-driven transport also with a non-thermal noise character.

Using different model systems, from culture cells to developing embryos, we have analyzed fluctuation-driven transport of cell constituents to eavesdrop on the ambient non-equilibrium noise of living matter. In particular, we have used single-particle tracking to quantify the heterogeneous and driven, yet often anomalous diffusion of cellular constituents under varying physiological conditions. Based on a thorough analysis of the experimental data, e.g. in terms of correlation functions and power spectra, and comparison to model simulations, our data provide deep insights into the physics of fundamental steps in cellular self-organization.

BP 28.2 Wed 15:30 ZEU 250

Control of droplet kinetics in active emulsions — •Jacqueline Janssen[1], Marta Tena-Solsona[2,3], Caren Wanzke[2], Fabian Schnitter[2], Hansol Park[4], Benedikt Riess[2], Julianne M. Gibbs[4], Job Boekhoven[2,3], and Christoph A. Weber[1] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Department of Chemistry, Technical University of Munich — [3]Institute for Advanced Study, Technical University of Munich — [4]Department of Chemistry, University of Alberta

Living cells host many membrane-less organelles which originate via liquid-liquid phase separation in both the cytoplasm and the nucleoplasm. Liquid phase separated droplets are crucial in living cells to spatially control chemical reactions. Recent experimental work revealed a new class of active emulsions where the lifetime and the rate of droplet growth can be controlled. This class of active emulsions involves fuel-driven chemical reactions from thermodynamically stable precursor molecules to metastable building blocks. At large enough concentration of building block material, the liquid droplets can form and undergo an anomalously fast ripening towards fewer droplets of larger size. Up to date, there is no theoretical model which would describe such anomalous ripening kinetics of active emulsions. We have derived a theoretical model which quantitively coincides with the experimental measurements conducted in the Boekhoven Laboratory. Our theory allows to understand how the metastable building blocks determine the lifetime and accelerate the droplet kinetics in this new class of phase separated, active systems.

BP 28.3 Wed 15:45 ZEU 250

Plasticity in vertex model of epithelial tissues — •Marko Popović, Valentin Druelle, and Matthieu Wyart — Institue of Physics, École Polytechnique Fédérale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland

In order to properly develop and function living organisms are required to change and maintain shape. This can be achieved by reshaping a liquid-like tissue and then changing its material properties to stabilize the final shape. Alternatively, if the tissue is plastic it will respond elastically to stresses below some critical value but higher values of stress will produce a plastic flow leading to a permanent plastic shape change, allowing it to retain the memory of stresses that have acted on it. Plasticity is exhibited by a wide class of amorphous solids such as: colloidal gels, emulsions and foams where it corresponds to a yielding transition. Are there features of yielding transition, such as strong dependence on system preparation and collective particle rearrangements leading to non-linear rheology, that are relevant during biological morphogenesis? Motivated by similarities of disordered tissues and amorphous solids we study plastic properties of vertex model of epithelial tissues, where mechanical properties of individual cells are prescribed and emerging tissue mechanics is obtained from their collective behaviour. We study mechanical properties of elementary plastic event in epithelial tissues, a so called T1 transition, in which two pairs of cells exchange neighborship. We demonstrate that interactions between T1 transitions are analogous to those of particle rearrangements in amorphous solids and that vertex model belongs to the same class of universality.

BP 28.4 Wed 16:00 ZEU 250

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

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

15 min. coffee break

BP 28.5 Wed 16:30 ZEU 250

Sperm chemotaxis in external flows — •Steffen Lange[1,2] and Benjamin Friedrich[1,2,3] — [1]Center for Advancing Electronics Dresden (cfaed) — [2]Cluster of Excellence Physics of Life (PoL) — [3]Institut Theoretische Physik (ITP), TU Dresden, 01062 Dresden, Germany

Chemotaxis - the navigation of biological cells guided by chemical gradients - is crucial for bacterial foraging, immune responses, and guidance of sperm cells to the egg before fertilization.

Previous work on chemotaxis focused predominantly on idealized conditions of perfect chemical gradients. However, natural gradients are subject to distortions, e.g. by turbulent flows in the ocean.

Recent experiments with bacteria [1] and sperm cells from marine invertebrates [2] have surprisingly revealed the existence of an optimal turbulence strength at which the chemotaxis is more effective than for still water conditions with perfect gradients.

Using sperm chemotaxis in shear flow as a prototypical example, we reproduce an optimal turbulence strength in numerical simulations. We can understand the origin of this optimum and quantify it:

For this we apply a theory of sperm chemotaxis to the concentration filaments, which are typical for scalar turbulence. We explain how external flows distort sperm swimming paths and concentration gradients, but at the same time extend the spatial range of these gradients. Together, these two competing effects set the optimal turbulence strength. We compare our theoretical results to previous experiments and find good agreement.

[1] Taylor, Stocker; Science 2012 [2] Zimmer, Riffell; PNAS 2011

BP 28.6 Wed 16:45 ZEU 250

Extracting the degree of order in the bacterial chromosome using statistical physics — •Joris Messelink[1], Jacqueline Janssen[2], Muriel van Teeseling[3], Martin Thanbichler[3], and Chase Broedersz[1] — [1]Arnold Sommerfeld Center for Theoretical Physics, LMU München — [2]Max Planck Institute for the Physics of Complex Systems, Dresden — [3]Faculty of Biology, Philipps University Marburg

Elucidating the three-dimensional spatial organization of the bacterial chromosome is essential to understand how genomic processes are spatially regulated inside the cell. Recent Hi-C chromosome conformation capture experiments provide contact frequency maps of the chromosome. These experiments reveal structural organization beyond that of an amorphous polymer. However, despite such experimental advances, the degree of spatial organization of the bacterial chromosome remains unclear. To investigate this, we develop a maximum entropy approach to extract the three-dimensional structure of the bacterial chromosome from such data. Using this approach, we obtain a coarse-grained model for the full distribution of chromosome configurations for the bacterium C. crescentus. We validate the predictive power of our model by experiments on the localization of chromosomal loci in the cell. Our model reveals novel features of spatial chromosome organization on various length scales. Our approach is not organism-specific, and opens up a new way of analyzing spatial chromosome organization.

BP 28.7 Wed 17:00 ZEU 250

Rewarding cargo-carrier interactions: cell-mediated particle transport — •Valentino Lepro[1,2], Robert Grossmann[1], Oliver Nagel[1], and Carsten Beta[1] — [1]Institute of Physics and Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]Max Planck Institute of Colloids and Interfaces, 14476 Potsdam, Germany

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

BP 28.8 Wed 17:15 ZEU 250

Effective spin glass theories for gene regulatory networks — •Fabrizio Olmeda[1] and Steffen Rulands[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Center for Systems Biology Dresden, Dresden, Germany

The development and maintenance of complex organs relies on precisely regulated cell fate decisions. Understanding the molecular mechanisms underlying these decisions is one of the central questions in stem cell biology.

The primary layer of regulation is the expression of genes and their interaction in gene regulatory networks. Here, by rigorously mapping the stochastic dynamics of gene regulatory networks to bipartite spin glasses, we develop an effective theory for describing fluctuations in gene regulatory networks during cellular decision making.

Performing a replica calculation, we describe the phase diagram that emerges in terms of the parameters of the gene network and demonstrate the existence of a spin glass phase.

In addition to the highly efficient simulation of gene networks our work, for the first time, allows using single-cell sequencing experiments to link fluctuations in gene expression to mechanisms of cellular decision making.

BP 29: Annual General Assembly

Time: Wednesday 18:00–19:00 Location: HÜL 386

Discussion of division members

BP 30: Cell Adhesion and Migration, Multicellular Systemadhesion and Migration, Multicellular Systems II

Time: Thursday 9:30–13:00 Location: HÜL 386

Invited Talk BP 30.1 Thu 9:30 HÜL 386

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

The actomyosin machinery endows cells with contractility at a single cell level. Within a tissue, cells can show either contractile or extensile stresses based on the direction of pushing or pulling forces exerted by their neighbours or on the substrate. In the first part, I will show how these active behaviours and stresses govern fundamental biological processes such as cell extrusion. By modelling the epithelium as an active nematic liquid crystal and measuring mechanical parameters such as strain rates and stresses measurements within cellular monolayers, we show that apoptotic cell extrusion is provoked by singularities in cell alignments in the form of comet-shaped topological defects. The results highlight the importance of active nematic nature of epithelia. However, cellular monolayers display various active behaviors as exemplified by the contractile nature of fibroblasts and the extensile nature of epithelial cells or neural crest cells. In a second part, I will discuss how these two contradictory modes of force generation can coexist. Through a combination of experiments and in silico modeling, we uncover the mechanism behind this switch in behaviour of cell monolayers from extensile to contractile as the weakening of intercellular contacts. We find that this switch in active behaviour also promotes the buildup of tension at the cell-substrate interface through an increase in actin stress fibers and higher traction forces. Such differences in extensility and contractility act to sort cells, thus determining a general mechanism for mechanobiological pattern formation.

BP 30.2 Thu 10:00 HÜL 386

Embryonic Inversion in *Volvox carteri*: The Flipping and Peeling of Elastic Lips — •Pierre A. Haas and Raymond E. Goldstein — Department of Applied Mathematics and Theoretical Physics, University of Cambridge, United Kingdom

The embryos of the green alga *Volvox carteri* are spherical sheets of cells that turn themselves inside out at the close of their development through a program of cell shape changes. This process of inversion is a simple model for the cell sheet deformations in the development of higher organisms. Inversion starts with four lips opening up at the anterior pole of the cell sheet; these lips then flip over, and peel back to invert the embryo. Experimental studies have revealed that inversion is arrested in mutants or if some of these cell shape changes are inhibited chemically, but the mechanical basis for these observations has remained unclear. We analyze the mechanics of this inversion by deriving an averaged elastic theory for the cell sheet and the lips in particular and we interpret the experimental observations in terms of the mechanics and evolution of inversion [1].

[1] P. A. Haas and R. E. Goldstein, Phys. Rev. E **98**, 052415 (2018)

BP 30.3 Thu 10:15 HÜL 386

Tissue-wide integration of mechanical cues promotes efficient auxin patterning — •João R. D. Ramos[1], Alexis Maizel[2], and Karen Alim[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]Center for Organismal Studies, University of Heidelberg, Heidelberg, Germany — [3]Physik-Department, Technische Universität München, Garching, Germany

New plants organs form by local accumulation of auxin, which is transported by PIN proteins that localize following mechanical stresses. As

auxin itself modifies tissue mechanics, a feedback loop between tissue mechanics and auxin patterning unfolds, yet the impact of tissue-wide mechanical coupling on auxin pattern emergence remains unclear. Here, we use a hybrid model composed of a vertex model for plant tissue mechanics, and a compartment model for auxin transport to explore the collective mechanical response of the tissue to auxin patterns and how it feeds back onto auxin transport. We compare a model accounting for a tissue-wide mechanical integration to a model where mechanical stresses are averaged out across the tissue. We show that only tissue-wide mechanical coupling leads to focused auxin spots, which we show to result from the formation of a circumferential stress field around these spots, self-reinforcing PIN polarity and auxin accumulation.

BP 30.4 Thu 10:30 HÜL 386

(In-)stability of growing tissue interfaces — •Tobias Büscher, Gerhard Gompper, and Jens Elgeti — Theoretical Soft Matter and Biophysics, Institute of Complex Systems and Institute for Advanced Simulations, Forschungszentrum Jülich, 52425 Jülich, Germany

Interfaces of tissues are ubiquitous, between tissue and environment as well as between populations of different cell types. The propagation of an interface can be driven mechanically, e.g. by a difference in the respective homeostatic stress of the different cell types [1,2]. Computer simulations of growing tissues are employed to study the competition of two tissues on a substrate. In particular, we focus on the stability of the interface between them [3]. Two identical tissues of course mix with time. Even a small difference in tissue properties results in competition and demixing. A stable interface emerges for competition driven by a difference in homeostatic stress. However, it becomes unstable above a critical difference for reduced apoptosis rates of the weaker tissue. A finger-like protrusion remains in the stronger, invading, tissue.

A difference in directed bulk motility also suffices to result in competition and a stable interface between them, even for otherwise identical tissues. Larger differences in motility force however result in a clear finite-wavelength instability of the interface. Interestingly, this instability seems to be bound by higher order terms, such that the amplitude of the undulation only grows to a finite value.

[1] Podewitz *et al.*, 2016, *New J. Physics* **18**, 083020
[2] Ranft *et al.*, 2014, *New J. Phys.* **16**, 035002
[3] Williamson *et al.*, 2018, *Phys. Rev. Lett.* **121**, 238102

BP 30.5 Thu 10:45 HÜL 386

Complex fluid flow, cell polarity and cilia beating patterns in the brain ventricles — •Christian Westendorf[1], Shoba Kapoor[2], Yong Wang[1], Gregor Eichele[2], and Eberhard Bodenschatz[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Am Fassberg 17, 37077, Goettingen. — [2]Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, 37077, Goettingen.

The brain ventricles are filled with cerebrospinal fluid (CSF) and are lined with a specialized cilia bundle carrying epithelium. The spatially organized beating of the cilia creates CSF flows along the epithelial surface. Particle tracking shows that these flows are very complex, forming a network of flows that varies little between individual mice (Faubel et al., Science, 2016). Using immunohistochemistry with suitable antibodies, we now show that the flow pattern is grounded on the translational and rotational polarity of the epithelial cells. For example whirl like flows are created above cells, whose cilia bundles are oriented accordingly. Additionally, these investigations revealed highly regular patterns in cell shape and cell size, and eccentricity and orientation of the cilia bundles. We further imaged the beating cilia with DIC microscopy with high spatial and temporal resolution over the expanse of the entire ventricular wall. This allowed us to determine the beating properties of cilia and the coordination of beating between the cilia bundles. Alltogether these data suggest that genetic factors make a major contribution to the organization of the flow patterns along the ventricular wall.

30 min. coffee break

BP 30.6 Thu 11:30 HÜL 386

Migration of immune cells in an obstacle park — •Doriane Vesperini[1], Zeinab Sadjadi[3], Heiko Rieger[3], and Franziska Lautenschläger[1,2] — [1]INM-Leibniz Institute for New Materials, 66123 Saarbrücken, Germany — [2]Experimental Physics, Saarland University, 66123 Saarbrücken, Germany — [3]Theoretical Physics, Saarland University, 66123 Saarbrücken, Germany

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

We investigate how search efficiency is influenced by spatial arrangement of obstacles. A microfluidic device is designed to track HL-60 cells differentiated into neutrophils in confined 2D environments. Our device consists of pillar forests of different diameters distributed in triangular or square arrangements. We calculate the mean first passage time and diffusion properties of the searcher in different densities and geometries of pillars and investigate which key parameters influence the search efficiency.

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

BP 30.7 Thu 11:45 HÜL 386

Cell-cell adhesion and 3D matrix confinement explain plasticity of breast cancer invasion — •Simon Syga[1], Peter Friedl[2], and Andreas Deutsch[1] — [1]Center for Information Services and High Performance Computing, Technische Universität Dresden, Dresden, Germany — [2]Department of Cell Biology, Radboud Institute for Molecular Life Sciences, Radboud University Medical Center, Nijmegen, The Netherlands

Plasticity of cancer invasion and metastasis depends on the ability of cancer cells to switch between collective invasion modes and single cell dissemination, under the control of cadherin-mediated cell-cell junctions. E-cadherin is considered a tumor suppressor, the downregulation of which causes single-cell scattering in 2D environments. In clinical samples, however, E-cadherin expressing and deficient tumors both invade collectively and metastasize equally, implicating additional mechanisms controlling cell-cell cooperation and dissemination.

Using a cellular automaton model we identify physical confinement by the extracellular matrix (ECM) as the dominant physical mechanism that supports collective invasion irrespective of the composition and stability of cell-cell junctions. In particular, we predict that downregulation of E-cadherin results in a transition from coordinated to uncoordinated collective movement along extracellular boundaries, whereas single-cell escape depends on locally free tissue space.

BP 30.8 Thu 12:00 HÜL 386

Confined cell migration: learning a dynamical systems theory from data — •David Brückner[1], Alexandra Fink[2], Matthew Schmitt[1], Nicolas Arlt[1], Joachim Rädler[2], and Chase Broedersz[1] — [1]Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität, München — [2]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-Universität, München

In many biological phenomena, cells migrate through confining environments. However, a quantitative conceptual framework for confined migration has remained elusive. To provide such a framework, we employ a data-driven approach to infer the dynamics of cell movement, morphology and interactions of cells confined in two-state micropatterns. In this confinement, cells stochastically migrate back and forth between two square adhesion sites connected by a thin bridge. By inferring a stochastic equation of motion directly from the experimentally determined short time-scale dynamics, we show that cells exhibit intricate non-linear deterministic dynamics that adapt to the geometry of confinement. This approach reveals that different cell lines exhibit distinct classes of dynamical systems, ranging from bistable to limit cycle behavior. To connect these findings to underlying migratory mechanisms, we track the evolution of cell shape and develop a framework for the dynamics of cell morphology in confinement. Our approach yields a conceptual framework for the motility and morphology of confined cells which we also generalize to more complex environments including multiple interacting confined cells.

BP 30.9 Thu 12:15 HÜL 386

Cell Motility Using Race Tracks on Elastic Substrates — Daniel Meyer[1], Christoph Schreiber[2], Joachim Rädler[2], Matthias Weiss[3], and •Florian Rehfeldt[1,3] — [1]3rd Institute of Physics - Biophysics, Georg-August University, Göttingen, Ger-

many — [2]Faculty of Physics, Soft Condensed Matter Group, Ludwig-Maximilians-University, Munich, Germany — [3]Experimental Physics 1, University of Bayreuth, Bayreuth, Germany

Cell motility and migration processes are vital during biological development and homeostasis. They are essential in tissue regeneration, morphogenesis, but also in pathological mechanisms like tumor metastasis. While migration due to biochemical gradients (e.g. chemotaxis) is very well studied, the influence of other parameters of the microenvironment such as topography and stiffness are less understood.

Here, we use polyacrylamide (PA) hydrogels in combination with a novel microcontact printing (μCP) protocol to generate patterned substrates with well-controlled Young's modulus E . These collagen-coated tracks are used to analyze the migration behavior of human mesenchymal stem cells (hMSC) and NIH3T3 fibroblasts by parallelized life cell microscopy under physiological conditions.

We demonstrate that both, elasticity as well as the geometry of the tracks affect the migration velocity and that the two cell types show distinct motile behavior.

BP 30.10 Thu 12:30 HÜL 386

Morphological and Mechanical Dynamics of Migrating Platelets Investigated with Scanning Ion Conductance Microscopy — •Johannes Rheinlaender, Jan Seifert, and Tilman E. Schäffer — Institute of Applied Physics, Eberhard Karls University Tübingen, Germany

Platelets or thrombocytes are the central element of the hemostatic system as being the first cells adhering to the site of a vessel injury, orchestrating the blood clot formation, and thereby establishing the initial steps of sealing the wound. In addition, platelets have been quite recently identified to be very motile cells, which can actively migrate towards sites of inflammation or bacterial pathogens. However, many aspects of the underlying cellular machinery are still unknown. We therefore studied migrating platelets using scanning ion conductance microscopy (SICM), an imaging technique providing topography images together with quantitative mechanical sample properties at nanoscale resolution. Thereby, we found that migrating platelets exhibit a three-dimensional shape anisotropy, which is directionally correlated with the direction of migration. Furthermore, we used SICM to record time-lapsed maps of the elastic modulus of migrating platelets, which revealed a characteristic subcellular distribution. We show that this distribution is caused by a dynamics reorganization of the platelet's actin cytoskeleton and thereby give direct mechanical evidence that platelet migration is driven by active cytoskeletal reorganization.

BP 30.11 Thu 12:45 HÜL 386

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

Chemical and physical surface gradients to control local cell adhesion and migration may allow to find routes to improve osseointegration of implants. Therefore, the local as well as the mesoscopic responses of living osteoblast-like cells (MG-63) were studied by means of Scanning Ion Conductance Microscopy (SICM) [1] and Fluorescence Microscopy, respectively. To achieve molecular landscapes with a small topographic corrugation height, amine-terminated PAMAM dendrimers and albumin were deposited in a stripe pattern on glass cover slips by direct micro-contact printing [2]. A distinct spindle shape oriented parallel to the surface pattern as well as a preferential adhesion of the cells on the glass site is observed when the width of the stripes is in the regime of 20 microns. We discuss in how far the pre-treatment of the glass and small protruding heights of a few nm are involved in the preference of the cells.

[1] Korchev et al., Biophys. J. 73, 653 (1997)
[2] Whitesides et al., Chem. Rev. 105, 1171 (2005)

BP 31: Computational Biophysics (joint session BP/CPP)

Time: Thursday 9:30–13:00 Location: SCH A251

BP 31.1 Thu 9:30 SCH A251

Effectiveness of Ca^{2+} clearance by PMCA pumps — •Barbara Schmidt[1], Cristina Constantin[2], Bernd Fakler[2], and Heiko Rieger[1] — [1]Center for Biophysics and Department of Theoretical Physics, Saarland University, 66123 Saarbrücken, Germany — [2]Institute of Physiology, University of Freiburg, 79104 Freiburg, Germany

Ca^{2+} influx through voltage-gated (Cav) channels leads to an increase in the intracellular Ca^{2+}-concentration ($[Ca^{2+}]_i$) that can be monitored by BK-type Ca^{2+}-activated K^+ channels. Due to their gating kinetics they may be used as sensors for $[Ca^{2+}]_i$ underneath the plasma membrane. Here, K^+ currents through BK channels were used to determine the Ca^{2+} transport activity of Ca^{2+}-ATPases of the plasma membrane (PMCA), the classical Ca^{2+} pumps. Experimentally we monitored PMCA-mediated Ca^{2+} clearance by the decay of BK-currents following their activation by a short (0.8 ms) period of Ca^{2+}-influx through Cav2.2 channels. Our theoretical model describes the Ca^{2+} diffusion within a spherical cell. Time- and Ca^{2+} concentration-dependent boundary conditions model the initial Ca^{2+} influx and the following outflow via the PMCA pumps. The time scale of this diffusion process is used to predict the strength of the PMCA pumps. Based on the experimentally determined density of Cav channels and PMCA pumps within the membrane we predict a PMCA pump strength that is at least 1.5 orders of magnitude larger than what has been assumed so far.

BP 31.2 Thu 9:45 SCH A251

Talin impacts force-induced vinculin activation by 'loosening' the vinculin inactive state — Florian Franz[1,2] and •Frauke Gräter[1,2] — [1]HITS gGmbH, Schloß-Wolfsbrunnenweg 35, 69118 Heidelberg, Germany — [2]IWR - Interdisciplinary Center for Scientific Computing, Im Neuenheimer Feld 368, 69120, Heidelberg, Germany

Focal Adhesions (FA) are large, multi-protein complexes connecting the cytoskeleton to the extracellular matrix. Their adhesive functionality is tightly regulated by mechanical stress. A key component of FA-associated mechanosensing is vinculin, which can assume either a closed ("inactive") or open ("active") conformation. The underlying activation mechanism, however, remains yet to be fully understood.

Here, we employ molecular dynamics (MD) simulation to demonstrate that vinculin activation is greatly facilitated by the binding of vinculin on talin's vinculin binding site. Steered MD simulations reveal that the force required for activation is drastically reduced upon formation of the vinculin-talin complex. Using correlated motions and force distribution analysis, we illuminate how the force propagation through vinculin changes upon complex formation. Interestingly, after talin dissociation, vinculin returns to its native conformation on a submicrosecond time scale, with 60% of its native contacts restored.

Our results suggest a rapid dynamic equilibrium between 'tight' and 'loosened' inactive vinculin, which depends on talin and determines the level of mechanical stress required for activation. Our study has important implications for our understanding of mechano-sensing mechanisms at FAs.

BP 31.3 Thu 10:00 SCH A251

Protein-ligand dynamics on multisecond timescales from submicrosecond atomistic simulations — •Steffen Wolf, Benjamin Lickert, Simon Bray, and Gerhard Stock — Biomolecular Dynamics, Institute of Physics, Albert Ludwigs University, 79104 Freiburg, Germany

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

timescales and beyond. Adopting the dissociation of solvated sodium chloride and several protein-ligand complexes as test problems, we are able to reproduce rates from atomistic MD simulation and experiments within a factor of 1.5-4 for rates up to the range of milliseconds and 2-10 in the range of seconds.

BP 31.4 Thu 10:15 SCH A251

Active processes in cellular networks and comparison with viscoelastic models — •Joris Paijmans[1], Mandar Inamdar[2], and Frank Jülicher[1,3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Department of Civil Engineering, Indian Institute of Technology Bombay, Mumbai, India — [3]Center for Systems Biology Dresden, Dresden, Germany

During morphogenesis, the collective behavior of many cells determines the emergence of tissue shape. How the mechanical properties and behavior of individual cells lead to a desired morphology is not well understood. Here we use a vertex model, modeling the cellular network, and a hydrodynamic theory, describing the tissue as a continuous viscoelastic material, to study this problem in epithelial tissues.

First, we consider different scenarios for how cells drive local stresses in cellular networks such as orientation dependent edge tensions and oriented cell divisions. Coarse-graining over the cellular dynamics, we find the large scale deformation of the tissue and how cells contributed to this deformation such as cell shape changes and rearrangements in the cell network. This allows us to compare the dynamics of the cellular network to a hydrodynamic model of a viscoelastic material with active and passive contributions to the stress and cell rearrangements in the tissue. We find that the large scale viscoelastic properties of the cellular network depend strongly on the details of how cells locally generate stress. We compare results with the developing wing blade in Drosophila, where phases of active and passive cell rearrangements are observed.

BP 31.5 Thu 10:30 SCH A251

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

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

BP 31.6 Thu 10:45 SCH A251

The role of thickness inhomogeneities in brain folding — •Lucas da Costa Campos[1,2], Svenja Caspers[2,3,4], Gerhard Gompper[1], and Jens Elgeti[1] — [1]Theoretical Soft Matter and Biophysics (ICS-2 / IAS-2), Research Centre Jülich, Jülich, Germany — [2]Institute of Neuroscience and Medicine (INM-1), Research Centre Jülich, Germany — [3]JARA-Brain, Jülich-Aachen Research Alliance, Jülich, Germany — [4]Institute for Anatomy I, Medical Faculty, Heinrich-Heine University, Düsseldorf, Germany

The morphology of the mammalian brain cortex is highly folded. Misfolds of the brain correlate with a long list of cognitive disabilities, such as schizophrenia and epilepsy. Having realistic models of gyrogenesis is the first step in the understanding of these issues. It has been hypothesized that mechanical instabilities play an essential role in gyrogenesis. However, the emergence of higher order folding, one of the main characteristics of the human brain, has not been fully tackled. We perform finite element simulations of rectangular slabs divided into two distinct regions. Differential growth is introduced by growing the top layer (gray matter) tangentially, while keeping the underlying layer (white matter) unchanged. The material is modelled as a Neohookean hyperelastic. Simulations are performed with system with either homogeneous or inhomogeneous cortical thickness. In early stages of development, we obtain structures reminiscent of the deep sulci in the brain, which can be mapped into the primary sulci. As the cortex continues to develop, we obtain secondary undulations whose characteristics are consistent with those of higher order folding.

30 min. coffee break

Invited Talk BP 31.7 Thu 11:30 SCH A251

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

On the molecular level, life is orchestrated through an interplay of many biomolecules. To gain any detailed understanding of biomolecular function, one needs to know their structure. Yet the structural characterization of many important biomolecules and their complexes - typically preceding any detailed mechanistic exploration of their function- remains experimentally challenging. Tools rooted in statistical physics such as Direct Coupling Analysis (DCA) but also increasingly Machine Learning driven approaches take advantage of the explosive growth of sequence databases and infer residue co-evolution to guide structure prediction methods via spatial constraints. Going beyond anecdotal cases of a few protein families, systematic large-scale studies of >1000 protein families are now possible and other information, such as low-resolution experimental information (e.g. SAXS or FRET) can be used as further constraints in simulations.

BP 31.8 Thu 12:00 SCH A251

A machine learning assessment of the two states model for lipid bilayer phase transitions — •Vivien Walter[1], Céline Ruscher[2], Olivier Benzerara[2], Carlos Marques[2], and Fabrice Thalmann[2] — [1]Department of Chemistry King's College London, London, UK — [2]Institut Charles Sadron, Strasbourg, France

We have adapted a set of classification algorithms, also known as Machine Learning, to the identification of fluid and gel domains close to the main transition of dipalmitoyl-phosphatidylcholine (DPPC) bilayers. Using atomistic molecular dynamics conformations in the low and high temperature phases as learning sets, the algorithm was trained to categorize individual lipid configurations as fluid or gel, in relation with the usual two-states phenomenological description of the lipid melting transition. We demonstrate that our machine can learn and sort lipids according to their most likely state without prior assumption regarding the nature of the order parameter of the transition. Results from our machine learning approach provides strong support in favor of a two-states model approach of membrane fluidity.

BP 31.9 Thu 12:15 SCH A251

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

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

BP 31.10 Thu 12:30 SCH A251

Quantifying membrane curvature sensing — •Kai Steffen Stroh[1] and Herre Jelger Risselada[1,2] — [1]Institute for Theoretical Physics, Göttingen, Germany — [2]Leiden Institute of Chemistry, Leiden, The Netherlands

When considering the interplay of lipid membranes and proteins, membrane curvature is an important factor, as it can act as a control mech-

anism for protein function. Several proteins feature subunits that serve as membrane curvature sensors. This sensing ability together with the spatial information provided by membrane curvature allows for site specific binding, and thus regulation of, e.g., transport processes.

Naturally, the curvature-dependent binding free energy provides valuable quantitative information about a protein's curvature sensing abilities. Therefore, we present a novel molecular dynamics simulations protocol to obtain such free energy profiles.

BP 31.11 Thu 12:45 SCH A251

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

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

For predicting the load distribution of spinal structures, we combined experimental and simulation methods. In experiments, we determined the overall stiffness for forward-flexing rotations between the lumbar vertebrae L5 and L4 of subjects lying in sideways position and being bent by a machine, without active muscle resistance. Forward dynamics simulations of this experiment using our detailed musculoskeletal multibody model of the human allowed for a structural resolution of the loads in the L4|5 region. The results indicated that stiffness values of particularly ligaments and passive muscle tissue put in from literature resources were too high. With now corrected values, our model has gained validity for future investigations on human movement dynamics and modelling applications like e.g. exoskeletons.

BP 32: Focus Session: Nonlinear Dynamics of the Heart I (joint session DY/BP)

Time: Thursday 9:30–12:45 Location: ZEU 118

Invited Talk BP 32.1 Thu 9:30 ZEU 118

Nonlinear dynamics of cardiac arrhythmias in the long QT syndrome — •Alain Karma — Northeastern University, Boston, USA

Long QT syndrome is associated with fatal ventricular arrhythmias promoted by triggered activity in the form of early afterdepolarizations (EADs). This talk will review recent progress to understand the genesis of EADs and associated life-threatening arrhythmias at cellular and tissue scales using a combination of computational and experimental studies. Computational studies make use of a physiologically detailed computational model of calcium (Ca2+) cycling and membrane voltage dynamics that bridges the submicron scale of individual couplons of plasmalemmal L-type Ca2+ channels clusters and sarcoplasmic reticulum (SR) Ca2+ release units (CRUs) and the whole cell. Experimental studies make use of large animal transgenic rabbit models that mimic human mutations associated with most common forms of the long QT syndrome types 1 and 2. The results, obtained by iterations between modeling and experiments spanning ion channels, cellular, and organ scales, highlight the important roles of the coupling between intracellular Ca2+ cycling and voltage dynamics in the genesis of cellular EADs and tissue-scale spatial heterogeneities in the initiation of arrhythmogenic premature ventricular contractions.

BP 32.2 Thu 10:00 ZEU 118

Understanding the origin of line defects in heart tissue. — •Marcel Hörning[1], Alessio Gizzi[2], and Alessandro Loppini[2] — [1]University of Stuttgart, Stuttgat, Germany — [2]University Campus Bio-Medico of Rome, Rome, Italy

Spatiotemporal patterns are observed in a wide range of excitable systems. They have important and diverse regulatory functions, such as regulation of cell migration of Dictyostelium cells, synchronization of electrophysiological dynamics in the cerebral neocortex, and maintenance of the contractility and cardiovascular blood circulation in mammalian hearts. In the heart, excitable waves can form complex oscillatory and chaotic patterns even at an abnormally higher frequency than normal heart beats, which increase the risk of fatal heart conditions by inhibiting normal blood circulation. Previous studies suggested that the occurrence of line defects in alternans play a critical role in the stabilizion of those undesirable patterns. However, this nonlinear phenomenon is still poorly understood. It remains to be elucidated, how nodal lines form, what their origin is, and how they stabilises. Here we show new insights in the stability of those by observing and analysing nodal line dynamics in spiral waves that exhibit stable alternans, and giving first clues on the origin of those.

BP 32.3 Thu 10:15 ZEU 118

Optogenetic Control Spiral Wave Dynamics in Cardiac Tissue — •Sayedeh Hussaini[1,2,4], Rupamanjari Majumder[1,4], Valentin Krinski[1,4], Ulrich Parlitz[1,4], Stefan Luther[1,2,3,4], and Claudia Richter[1,4] — [1]Max Planck Institute for Dynamics and Self-Organization, Goettingen, Germany — [2]Institute for the Dynamics of Complex Systems, Goettingen, Germany — [3]Institute of Pharmacology and Toxicology, Goettingen, Germany — [4]German Center for Cardiovascular Research, Goettingen, Germany

Cardiac optogenetics may be used as a tool to elucidate the mechanisms underlying the dynamics and control of the spiral waves in the heart. Here we present a simulation study based on the ionically realistic Bondarenko model of mouse ventricular cardiomyocytes, coupled to a model for the light-activated protein Channelrhodopsin-2. We show that constant global sub-threshold illumination increases the resting membrane voltage, decreases the amplitude and the conduction velocity of the excitation wave. Periodic global illumination of the two-dimensional domain results in the transition of the spiral wave core of the trajectory from circular to epicycloidal and hypocycloidal. Using structured sub-threshold illumination, we induced spiral drift towards the boundary and subsequent termination. In the presence of an intensity gradient, the spiral wave drifts towards higher intensities.

BP 32.4 Thu 10:30 ZEU 118

Dynamics of scroll waves in a cylinder jacket geometry — Christian Bruns[1] and •Marcus Hauser[2] — [1]Institut für Biometrie und Medizinische Bioinformatik, Universität Magdeburg, Magdeburg, Germany — [2]Insitut für Biologie, Universität Magdeburg, Magdeburg, Germany

The dynamics of scroll waves in a narrow cylinder jacket-shaped reactor is investigated experimentally by optical tomography using a chemical model system. The fate of the scroll waves of excitation in the Belousov-Zhabotinsky reaction depend on the thickness of the cylinder jacket. While at sufficiently wide cylinder jackets vertically oriented scroll waves remain stable, the probability that the filaments of the scrolls hit a lateral wall increase with the shrinking width of the cylinder jacket. This may lead to the rupture of the initial filament and pinning of the filament ends at the lateral walls. Filaments that pin to opposite lateral walls shrink and reorient to a horizontal orientation; such a reorientation corresponds to a transition from an intramural to a transmural scroll wave. The kinetics of the reorientation and shrinkage of the scrolls were studied. Furthermore, we find that no new filaments were generated upon collision of excitation waves at the side of the cylinder jacket opposite to the scroll wave. Thus, under the studied conditions, we do not observe any new generation of filaments due to a phenomenon like reentry.

BP 32.5 Thu 10:45 ZEU 118

Synchronization of viscoelastically coupled cardiomyocytes — •Florian Spreckelsen[1,2,3], Stefan Luther[1,2,3], and Ulrich Parlitz[1,2,3,4] — [1]Max Planck Institute for Dynamics and Self-organization, Göttingen, Germany — [2]University of Göttingen, Institute for the Dynamics of Complex Systems, Göttingen, Germany — [3]DZHK (German Center for Cardiovascular Research), Partner Site Göttingen, Germany — [4]University Medical Center Göttingen (UMG), Institute of Pharmacology and Toxicology, Göttingen, Germany

Periodically beating cardiomyocytes coupled mechanically by a viscoelastic extracellular matrix are modelled as viscoelastically coupled

excitable oscillators. Their synchronization dynamics depends on the stiffness of the coupling matrix [1].

Systems of two coupled cells and linear chains are investigated numerically. At high stiffness of the viscoelastic coupling, full in-phase synchronization is found. Partial n:n synchronization is observed in case of intermediate stiffness. In the special case of purely elastic coupling, two cells show antiphase synchronization while antiphase chimera states are found in linear chains.

The conditions necessary for the synchronization of viscoelastically coupled cardiomyocytes may give a mechanistic explanation for the importance of fibroblasts to the engineering of cardiac tissue [2,3].

[1] Spreckelsen, Luther, Parlitz, Phys. Rev. E 100, 2019
[2] Tiburcy et al., Circulation 135, 2017
[3] Schlick et al., Prog Bio Mol Bio 144, 2019

15 min. break.

Invited Talk BP 32.6 Thu 11:15 ZEU 118

Wave-particle duality of dissipative vortices and implications for cardiology — •Irina V. Biktasheva — University of Liverpool, Liverpool, UK

Recent theoretical and experimental advancements in study of dynamics of dissipative vortices (aka spiral waves) brought these studies closer to practical impact and applications than ever before.

A dissipative vortex divides homogeneous system into the core, defined by it's rotation centre, or organising filament, and the periphery synchronised by signals from the core. Perturbed vortex slowly changes frequency and location of the core. Regime synchronises all available space, though it behaves as localised object sensitive only to perturbations affecting the core. The wave-particle duality is due to localisation of vortex's Response Functions (RFs) in immediate vicinity of the core. RFs allow quantitative prediction of drift caused by small perturbations of any nature, which makes RFs as fundamental characteristics for spiral waves as mass is for the matter.

We use cardiac re-entry's RFs to predict iscaemic border zone dynamics, and define basal tissue conditions for re-entry's escape into recovered tissue to either collapse or develop fibrillation. In human atrium, we demonstrate functional effects of anatomical structures on re-entry's spontaneous drift along pectinate muscles (PM) and crista terminalis, anchor to PM-atrial wall junctions or to some locations with no obvious anatomical features. The insights might improve patient specific ablation and low-voltage defibrillation protocols.

BP 32.7 Thu 11:45 ZEU 118

Control and self-termination of spiral wave chaos — •Thomas Lilienkamp[1,2] and Ulrich Parlitz[1,2,3] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]German Center for Cardiovascular Research (DZHK), Göttingen, Germany — [3]Institut für Dynamik Komplexer Systeme, Georg-August Universität, Göttingen, Germany

During life threatening cardiac arrhythmias like ventricular fibrillation the electrical excitation dynamics inside the heart is governed by chaotic spiral/scroll wave propagation. In experiments, it is frequently observed that the chaotic dynamics can also terminate by itself. This phenomenon can also be reproduced in numerical simulations. We demonstrate in simulations, how a system of chaotic spiral wave dynamics can be controlled using small but finite perturbations which are locallized in space and time, by exploiting the state space structure. With this, we show that a control of such systems can be achieved in principle by a minimal interaction with the system.

BP 32.8 Thu 12:00 ZEU 118

Constitutive modeling for failing heart regeneration — Moritz Kalhöfer-Köchling[1,3], Wolfram Zimmermann[2,3], Eberhard Bodenschatz[1,3], and •Yong Wang[1,3] — [1]MPI for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]University Medical Center Göttingen, 37075 Göttingen, Germany — [3]German Center for Cardiovascular Research (DZHK), Partner Site Göttingen, Göttingen, Germany

Heart failure is a common, costly, and potentially fatal condition in which the heart cannot pump enough blood to meet the body's needs. It is mainly caused by myocardial infarction, and associated with changes both in structure and function of the heart. Employing nonlinear solid mechanics, constitutive modeling is adopted to study cardiac mechanics and guide new therapy such as tissue engineered heart repair. To simulate the infarcted tissue as well as implanted engineered heart muscle, a novel class of constitutive models is proposed by considering fiber dispersion. Compared with their predecessors, those models improve the numerical stability, compute faster and are easier to implement. We also investigate the mechanical properties of heart muscle experimentally. This work was supported by the Max Planck Society and the German Center for Cardiovascular Research.

BP 32.9 Thu 12:15 ZEU 118

Synchronization-based reconstruction of the electrical dynamics of the heart — •Baltasar Rüchardt[1,3], Jochen Bröcker[4], Stefan Luther[1,2,3], and Ulrich Parlitz[1,2,3] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Georg-August-Universität Göttingen, Institute for Nonlinear Dynamics, Göttingen, Germany — [3]German Center for Cardiovascular Research (partnersite Göttingen), Göttingen, Germany — [4]University of Reading, Reading, UK

For more than a century, the electrocardiogram (ECG) is the standard diagnostic tool to assess cardiac electrophysiological function. The relation between the electrical excitation of the heart and the electrical potential on the surface of the body is well understood. The reconstruction of the source distribution on the heart from given ECG measurements is challenging, because information is lost when the electrical signal travels through the body in a diffusion-like process. This problem is called inverse problem of electrocardiography.

The standard methods to handle this loss are regularization methods which impose pre-defined assumptions on the problem until a solution can be found. This can exclude the true solution and, in general, does not rely on information of the underlying dynamical processes. In contrast, we show the reconstruction of the electrical state of the heart from sensor signals with reduced spatial information by means of synchronization, based on a model of the spatial-temporal electrical dynamics. We show this for a 2D excitable media heart tissue model and discuss the application to three dimensions.

BP 32.10 Thu 12:30 ZEU 118

Real-time Processing of Optical Fluorescence Videos showing Contracting Hearts using Neural Networks — •Jan Lebert[1,2,3] and Jan Christoph[1,2,3] — [1]University Medical Center Göttingen, Germany — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [3]German Center for Cardiovascular Research, Partnersite Göttingen, Germany

Optical mapping is an established fluorescence imaging technique for studying electrophysiological wave phenomena in isolated, intact hearts and cardiac cell cultures. Mechanical contraction of the cardiac tissue, however, can lead to severe motion artifacts in the recorded optical signals. Pharmacological electromechanical uncoupling agents have been used to compensate for these artifacts. However, recently numerical motion tracking and post-processing algorithms were developed to suppress motion artifacts and separate the recorded electrical waves from mechanical contraction.

Here, we present a deep convolutional neural network (CNN) approach for the real-time tracking of contracting and fluorescing hearts in optical mapping videos. Our approach provides a dramatic speed-up in the processing of optical mapping data and superior performance over conventional optical flow estimation algorithms, which are sensitive to noise and can be irritated by fluorescence-encoded wave patterns, as they assume brightness consistency. After training the network on various experimental and synthetically generated optical mapping data, we evaluated the network's performance and found it to perform robustly under various conditions.

BP 33: Protein Structure and Dynamics

Time: Thursday 9:30–13:00 Location: ZEU 250

BP 33.1 Thu 9:30 ZEU 250

Protein Short-Time Diffusion in a Naturally Crowded Environment — Marco Grimaldo[1], Hender Lopez[1,2,3], •Christian Beck[1,2], Olga Matsarskaia[1], Felix Roosen-Runge[5], Martine Moulin[1], Juliette Devos[1], Valerie Laux[1], Michael Hartlein[1], Stefano Da Vela[2], Ralf Schweins[1], Alessandro Mariani[4], Fajun Zhang[2], Jean-Louis Barrat[3], Martin Oettel[2], V. Trevor Forsyth[1,6], Tilo Seydel[1], and Frank Schreiber[2] — [1]Institut Laue-Langevin, Grenoble, France — [2]University of Tübingen, Germany — [3]LiPhy, Saint Martin d'Hères, France — [4]European Synchrotron Radiation Facility, Grenoble, France — [5]Malmö University, Malmö, Sweden — [6]Keele University, Staffordshire, UK

We employ neutron backscattering spectroscopy to measure the short-time self-diffusion of tracer proteins in a deuterated cell-like environment (cell lysate) with explicit control over crowding conditions. We successfully link coarse-grained Stokesian dynamics simulations with experimental results on these complex, flexible molecules providing a consistent understanding by colloid theories. In the case of immunoglobulin, both experiments and simulations show that tracers in polydisperse solutions close to the effective particle radius $R_{eff} = \langle R_i^3 \rangle^{1/3}$ diffuse approximately as if the suspension was monodisperse [1]. The simulations predict size-dependent deviations from this scaling which was tested by measuring different proteins in lysate with an increased energy transfer range, also allowing to investigate the influence of the lysate on the internal dynamics in more detail. [1] M. Grimaldo *et al.*; J. Phys. Chem. Lett. 10 (2019) 1709

BP 33.2 Thu 9:45 ZEU 250

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

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

BP 33.3 Thu 10:00 ZEU 250

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

Quantum mechanics was initially developed in the field of atomic physics and rapidly extended to quantum chemistry in the early 20th century. The extension of seeking quantum effects in biological systems is of one of the important areas of research, termed as quantum biology. Recent experimental studies reported long-lived quantum coherence in the primary step of energy transfer in photosynthetic protein complexes. However, the origin of the coherence is still under debate. To capture the solid evidence of electronic quantum coherence, we studied the quantum dynamics in Fenna-Matthews-Olson (FMO) complex by two-dimensional (2D) electronic spectroscopy at different temperatures. We clearly observed the electronic coherence with time scale of 500 fs at low temperature (20 K). However, the lifetime of electronic coherence is dramatically reduced with increasing of temperature. We observed, at room temperature, the electronic coherence is too short (~60 fs) to play any functional role in the process of energy transfer in FMO complex. Moreover, we identified that the long-lived oscillations in 2D spectra are mainly contributed by Raman modes on the electronic ground states.

BP 33.4 Thu 10:15 ZEU 250

Following the formation of PYP's photocycle intermediates on a femtosecond to millisecond timescale with a site-specific IR label — •Larissa Blankenburg, Luuk J.G.W. van Wilderen, and Jens Bredenbeck — Goethe-Universität, Institut für Biophysik, Max-von-Laue-Str. 1, 60438 Frankfurt am Main, Germany

The photocycle dynamics of Photoactive Yellow Protein (PYP) that are induced by excitation with blue light occur on a timescale ranging from femtoseconds to seconds. Local dynamic information about the protein can be obtained by the use of the vibrational label thiocyanate (SCN) that can be inserted site-specifically at any desired position by cysteine mutation and cyanylation. The CN stretch vibration is highly sensitive to polarity and hydrogen-bonding interactions and thus allows to probe local structural changes during PYP's photocycle.

With transient fs-ms infrared spectroscopy on SCN-labeled PYP mutants we followed most part of the photocycle from chromophore isomerization (ps) and protonation (μs) to partial unfolding of the protein (ms). The data revealed spectral changes corresponding to alterations in the local environment of the non-perturbing label, providing dynamic site-specific structural information for multiple observed photocycle intermediates. While the site resolution in infrared spectroscopy of unlabeled proteins is generally limited to a few marker bands (e.g. of the chromophore or specific side chains), vibrational labels can be inserted at almost every location improving the structural resolution and investigation of proteins and may resolve new intermediates.

Invited Talk BP 33.5 Thu 10:30 ZEU 250

Atomistic ensembles of proteins and soft matter complexes from MD simulations and solution scattering data — Milos T Ivanovic[1], Markus R Hermann[2], and •Jochen S Hub[1] — [1]Unvierstität des Saarlandes, Saarbrücken, Germany — [2]Georg-August-Universität Göttingen, Germany

Understanding the function of disordered peptides or soft-matter complexes requires understanding of their conformational ensembles. However, experimental data alone is often insufficient for defining all degrees of freedom of such systems, whereas simulations may be biased by poor sampling or force field limitations. We developed a method for coupling atomistic simulations to small- and wide-angle X-ray scattering (SAXS/WAXS) data, based on Jaynes' principle of maximum entropy, with the aim to obtain accurate atomistic ensembles biomolecular and soft-matter systems. As examples, we show that the method is capable of overcoming force field inaccuracies in simulations of an intrinsically disordered protein and of a detergent micelle. In addition, we critically review capabilities and limitations of widely used continuum models in deriving micellar structures.

[1] Hub, Curr Opin Struct Biol, 49, 18-26 (2018)
[2] Hermann and Hub, J Chem Theory Comput, 15, 95103-5115 (2019)
[3] Ivanović, Bruetzel, Lipfert, Hub, Angew Chem Int Ed, 57, 5635-5639 (2018)
[4] Ivanović, Hermann, Wójcik, Pérez, Hub, BioRxiv doi:10.1101/815266

30 min. coffee break

BP 33.6 Thu 11:30 ZEU 250

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

A decisive characteristic of the biomolecular machinery is the access to a rich set of coordinated processes within a small energy window. Most of these processes involve collective conformational changes and occur in an aqueous environment. Conformational changes of (bio)molecules

as well as their interaction with water are thereby largely governed by non-covalent van der Waals (vdW) dispersion interactions. By virtue of their intrinsically collective nature, vdW forces also represent a key influence on collective nuclear behavior. Our understanding of vdW interactions in large-scale (bio)molecular systems, however, is still rather limited [Chem. Soc. Rev. 2019, 48, 4118]. Here, we employ the Many-Body Dispersion framework to investigate the vdW interaction in biomolecular systems and its spatial and spectral aspects. In particular, we show the role of beyond-pairwise vdW forces for protein stability and highlight the delocalized character of the protein-water vdW interaction. We further examine intermolecular electronic behaviors and reveal a coexistence of strong delocalization with spatially-separated, yet correlated, local domains. This, ultimately, forms the basis for a potential, efficient long-range interaction mechanism for coordinated processes in biomolecular systems.

BP 33.7 Thu 11:45 ZEU 250

Investigating the conformational ensembles of intrinsically-disordered proteins with a simple physics-based model — •Yani Zhao, Robinson Cortes-Huerto, Kurt Kremer, and Joseph F. Rudzinski — Max Planck Institute for Polymer Research, Mainz, Germany

The coupled interactions of intrinsically disordered proteins (IDPs) with its partners play an important role in biological processes but present a number of fundamental challenges for computational modeling. This challenge is magnified for proteins due to the variety of competing interactions and large deviations in side-chain properties. In this work, we apply a simple physics-based coarse-grained model for describing largely disordered conformational ensembles of peptides, based on the premise that sampling sterically-forbidden conformations can compromise the faithful description of both static and dynamical properties. The Hamiltonian of the employed model can be easily adjusted to investigate the impact of distinct interactions and sequence specificity on the randomness of the resulting conformational ensemble. Starting with a bead-spring-like model and then adding more detailed interactions one by one, we construct a hierarchical set of models and perform a detailed comparison of their properties. Our analysis clarifies the role of generic attractions, electrostatics and side-chain sterics, while providing a foundation for developing efficient models for IDPs that retain an accurate description of the hierarchy of conformational dynamics, which is nontrivially influenced by interactions with surrounding proteins and solvents.

BP 33.8 Thu 12:00 ZEU 250

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

Motions of biomolecular systems, recorded by molecular dynamics simulations, are often modeled as Markov processes. A very popular approach is given by Markov state models where the conformational space is divided into different states [1]. To be Markovian, the intrastate dynamics need to be significantly faster than the interstate dynamics. On the other hand, the observed dynamics can be modeled as a continuous diffusive process, called Langevin dynamics, on some low-dimensional free energy landscapes $F(\vec{x})$. In this case, Markovianity is given if the system, i.e., $\vec{x}(t)$, evolves substantially slower than the neglected degrees of freedom, i.e., the bath surrounding the system. Recently, a data-driven approach was formulated to estimate such a Langevin model from a given trajectory $\vec{x}(t)$ [2]. Here, we compare the features of both modeling frameworks. While Markov state models are very appealing due to their clearly structured generation and interpretation, Langevin dynamics have the advantage that they allow for the estimation of continuously defined observables, like free energy and autocorrelations. Using molecular dynamics simulations of systems with varying complexity we have a look at these points in practice.

[1]: J.H.Prinz et al., J.Chem.Phys. 134, 174105 (2011)
[2]: N.Schaudinnus et al., J.Chem.Phys. 145, 184114 (2016)

BP 33.9 Thu 12:15 ZEU 250

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

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

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

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

BP 33.10 Thu 12:30 ZEU 250

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

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

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

BP 33.11 Thu 12:45 ZEU 250

Control of (bio)nanoparticles with external fields — •Jannik Lübke[1,2,3], Lena Worbs[1,3], Armando Estillore[1], Amit Kumar Samanta[1], and Jochen Küpper[1,2,3,4] — [1]Center for Free-Electron Laser Science, Deutsches Elektronen-Synchrotron DESY, Hamburg, Germany — [2]Center for Ultrafast Imaging, Universität Hamburg, Germany — [3]Department of Physics, Universität Hamburg, Germany — [4]Department of Chemistry, Universität Hamburg, Germany

Single-particle imaging (SPI) experiments rely on dense streams of isolated nanoparticles that are guided into the focus of free-electron lasers (FELs). Then typically diffraction data from arbitrary spatial orientations of the particles are collected, classified, combined into a three-dimensional (3D) diffraction volume and inverted to the underlying 3D structure of the sample [1].

To achieve atomic resolution, beams of many, ideally identical, particles need to be delivered into the FEL focus, which necessitates sample control methods to select nanoparticles. We develop and characterize various control techniques, such as particle beam focusing using fluid dynamics [2], temperature control [3], charge state state selectivity using electric fields [4], and further techniques. Here, we present novel approaches for the production of pure and high-density beams of a broad variety of biological nanoparticles, using external fields.

[1] M. M. Seibert et al., *Nature* **470**, 78 (2011)
[2] N. Roth et al., *J. Aerosol Sci.* **124**, 17 (2018)
[3] A. K. Samanta et al. *arXiv*:1910.12606 (2019)
[4] Y. P. Chang et al., *Int. Rev. Phys. Chem.* **34**, 557 (2015)

BP 34: Nonlinear Dynamics of the Heart II (joint session DY/BP)

Time: Thursday 14:00–15:45 Location: ZEU 118

Invited Talk BP 34.1 Thu 14:00 ZEU 118

Dyadic structure-function relationships in ventricular cardiac myocytes: from sparks to action potentials — •Martin Falcke[1,2], Filippo G. Cosi[3], Wolfgang Giese[1], Wilhelm Neubert[1], Stefan Luther[3], and Ulrich Parlitz[3] — [1]Max Delbrück Center, Berlin — [2]Dept. of Physics, Humboldt University Berlin — [3]MPI for Dynamics and Self-Organization, Göttingen

Cardiovascular disease is often related to defects in molecular and subcellular components in cardiac myocytes, specifically in the dyadic cleft, which include changes in cleft geometry and channel placement. Modelling of these pathological changes requires both spatially resolved cleft as well as the whole cell level descriptions. We use a multiscale model to create dyadic structure-function relationships in order to explore the impact of molecular changes on whole cell electrophysiology and calcium cycling. This multiscale model incorporates stochastic simulation of individual L-type calcium channels (LCC) and ryanodine receptor channels (RyRs), spatially detailed concentration dynamics in dyadic clefts, rabbit membrane potential dynamics, and a system of partial differential equations for myoplasmic and lumenal free Ca^{2+} and Ca^{2+}-binding molecules in the bulk of the cell.

We create models with varying dyadic cleft properties including RyR and LCC clustering, stochastic opening and closing rates as well as changes in LCC and RyR calcium currents. We investigate biomarkers describing action potential, Ca^{2+} transient and Ca^{2+} spark dynamics. We quantify sensitivity and parameter uncertainty and derive cellular functional implications from molecular level properties.

BP 34.2 Thu 14:30 ZEU 118

Multiscale modeling of dyadic structure-function relation in ventricular cardiac myocytes — •Filippo Cosi[1,4,5], Wolfgang Giese[2], Wilhelm Neubert[2], Stefan Luther[1,4,5], Nagaiah Chamakuri[3], Ulrich Parlitz[1,4,5], and Martin Falcke[2,5] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Max Delbrück Center for Molecular Medicine in the Helmholtz association, Berlin, Germany — [3]Institute of Applied Mathematics, University of Hohenheim, Stuttgart, Germany — [4]Georg-August-Universität Göttingen, Institute for the Dynamics of Complex Systems, Göttingen, Germany — [5]DZHK (German Center for Cardiovascular Research), Partnersites Göttingen and Berlin, Germany

Understanding how defects in the subcellular components of single cardiomyocytes affect the calcium cycling in single cells can help to pin down the origin of cardiovascular disease. A multiscale model is used, which combines the stochastic nature of subcellular components (as Ryanodine Receptors, RyR or L-type Calcium Channels, LCC), their spatial arrangement as well as spatio-temporal calcium and buffer gradients at the whole-cell level. Recent findings regarding the geometrical clustering of RyRs and LCCs inspired us to include the physiological description of it into our mathematical model. The included structure modifications showed a dramatic effect on the model's outputs; in detail the arrangement of RyRs has a strong impact on cell functions. Our study aims to lay a quantitative fundament for the analysis of defect cardiomyocytes under physiologically conditions to deepen the understanding of how diseased heart tissue might be treated.

BP 34.3 Thu 14:45 ZEU 118

Simple mechanism for low-energy antifibrillation pacing — Pavel Buran, Thomas Niedermayer und •Markus Bär — Physikalisch-Technische Bundesanstalt (PTB), Berlin

Rotating excitation waves and electrical turbulence in cardiac tissue are associated with arrhythmias such as life-threatening ventricular fibrillation. Experimental studies have shown that a sequence of low-energy electrical far-field pulses is able to terminate fibrillation with less energy than a single large energy shock [1]. Previous theoretical approaches to understand this low-energy antifibrillation pacing (LEAP) have often focused on unpinning and removal of a small number of rotating spirals in quasi-two-dimensional situations. These theories, however, cannot explain the defibrillation of spatiotemporal chaos. Based on a systematic simulation study, we present an alternative mechanism for the success of LEAP in two dimensions, which explains both, the termination of stable spirals as well as spatiotemporal chaos. It turns out that actually each pulse during LEAP annihilates all excitation fronts, however, that new fronts could arise at the borders between refractory and excitable parts of the tissue. The success probability of each individual pulse can thus be simply interpreted as the probability that no new front arises. Furthermore, we will show that the success probability depends exponentially on the total length of these refractory boundaries and that successful LEAP is characterized by pulses causing a gradual decrease of this length simultaneously increasing the success probability of subsequent pulses until complete defibrillation.
[1] Luther et al., Nature **475**, 235-239 (2011)

BP 34.4 Thu 15:00 ZEU 118

Feedback-based protocol for low-energy defibrillation — •Pavel Buran, Thomas Niedermayer und Markus Bär — Physikalisch-Technische Bundesanstalt (PTB), Berlin

Low-energy antifibrillation pacing (LEAP) is a method where electrical turbulence characteristic for atrial or ventricular fibrillation is suppressed by a series of low energy pulses [1]. Systematic simulation studies show that the choice of the right pacing period is crucial for successful LEAP [2]. However, the range of those successful pacing periods is a priori not known for a given tissue. Methods that efficiently determine the range of successful pacing periods are therefore of high interest. We have found, that termination probability of each individual pulse during LEAP depends exponentially on the total length of the interfaces between refractory and excitable parts of the tissue. Based on this finding, we present a feedback controlled protocol that ensures that pulses are applied in such a way to minimize the mentioned interface length in line with our earlier findings about the mechanism of LEAP. This protocol does not need any a priori information about the system and can thus also be used as an efficient method to determine the optimal pacing period.
[1] Luther et al., Nature **475**, 235-239 (2011)
[2] Buran et al., Chaos **27**, 113110 (2017)

BP 34.5 Thu 15:15 ZEU 118

General equilibrium approach to resolve ventricular calcium homeostais — •Enrique Alvarez-Lacalle[1], Blas Echebarria[1], Angelina Peñaranda[1], Inmaculada R. Cantalapiedra[1], Yohannes Shiferaw[2], and David Conesa[1] — [1]Departament de Física. Universitat Politècnica de Catalunya (UPC-BarcelonaTech), Barcelona, Spain. — [2]Department of Physics. California State University Nortridge, Los Angeles, USA.

The ventricular contraction in the heart is roughly proportional to the amount of calcium released from the Sarcoplasmic Reticulum during systole. The change in the membrane potential triggers the opening of thousands of Ryanodine Receptor clusters in the SR membrane, being the release larger when pre-systolic calcium levels are larger. While it is rather straightforward to measure calcium levels and contractibility under different physiological conditions, the complexity of calcium handling during systole and diastole has made the prediction of its release at steady-state from measurements away from steady-state impossible. In this contribution, we present a general equilibrium framework to understand how homeostasis can be understood and analyzed to make predictions about its level when key properties of ionic channels or buffers (due to phosphorylation, genetic mutation,etc..) involved in calcium handling are changed. This framework should be useful to describe why different animals have such different homeostatic behavior upon changes in the pacing rate and provide a physiological mechanism for SERCA gene therapy failure.

BP 34.6 Thu 15:30 ZEU 118

Synchronization-based reconstruction of electromechanical wave dynamics in elastic excitable media — Jan Lebert[1,2,3] and •Jan Christoph[1,2,3] — [1]University Medical Center Göttingen, Germany — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [3]German Center for Cardiovascular Research, Partnersite Göttingen, Germany

Reconstructing electrical excitation wave dynamics within the heart muscle remains a major scientific challenge. Recently, it was shown using high-resolution 4D ultrasound that it is possible to identify mechanical filament-like phase singularities within the contracting, fibrillating heart wall, suggesting that the tissue mechanics reflect three-dimensional electrical scroll wave dynamics.

Here, we present a mechano-electrical data assimilation approach

with which it is possible to reconstruct electrical excitation wave dynamics, including electrical vortex filaments, within the volume of deformable excitable media. By observing the spatio-temporal deformation patterns, which occur in response to the electrical excitation, the mechanical data is assimilated in a numerical replication of the observed elastic excitable system, and within this replication the data drives the intrinsic excitable dynamics, which then co-evolve and correspond to a reconstruction of the original dynamics. We provide a numerical proof-of-principle and demonstrate the performance of the approach by recovering even complicated three-dimensional scroll wave patterns.

BP 35: Bioimaging and Biospectroscopy II

Time: Thursday 15:00–17:30 Location: HÜL 386

BP 35.1 Thu 15:00 HÜL 386

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

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

BP 35.2 Thu 15:15 HÜL 386

Confocal single molecule localisation microscopy for super-resolved fluorescence lifetime imaging — •Jan Christoph Thiele, Eugenia Butkevich, Oleksii Nevskyi, and Jörg Enderlein — Third Institute of Physics - Biophysics, Georg August University, Göttingen, Germany

Localisation based super-resolution microscopy techniques like dSTORM, PALM and PAINT usually rely on wide field or TIRF illumination and wide field detection. This allows for simultaneous acquisition of the whole field of view but comes with the limitations of a camera based detection. Instead, we use a confocal setup with a pulsed excitation, single photon detection and a fast laser scanner. We evaluate different dyes and conditions to achieve slow blinking kinetics and a high number of photons per switching event. Individual switching events could be localised utilising our confocal scanning approach and the corresponding super-resolved image could be reconstructed. The huge advantage of a single photon detection is that each localisation contains information about the fluorescence lifetime. This enables us to combine dSTORM with metal induced energy transfer (MIET), a distance dependant modulation of the lifetime of a fluorophore by a thin metal film. MIET enables axial localising single fluorophores with a precision below 5 nm. Our goal is to achieve a high, isotropic 3D-localisation accuracy by combining the high lateral precision of dSTORM with the high axial precision of MIET.

BP 35.3 Thu 15:30 HÜL 386

Super-resolution structured illumination microscopy of MreB dynamics and cell wall synthesis in B. subtilis — •Julian Roth, Johanna Mehl, and Alexander Rohrbach — Albert-Ludwigs-Universität, Freiburg

Total internal reflection fluorescent structured illumination microscopy (TIRF-SIM) is a unique approach combining high acquisition speeds with a two-fold increased lateral resolution at very high contrast. Our TIRF-SIM implementation enables simultaneous dual-color super-resolution imaging of dynamic, low fluorescent samples at several Hertz. The design is based on mechanical beam steering and phase shifting devices as well as a Michelson interferometer, thus avoiding diffractive elements. The fast TIRF-SIM setup is employed to gain a clearer view on the dynamics of cell wall synthesis machinery proteins in Bacillus subtilis, as we still lack fundamental knowledge of how bacteria build, expand and maintain their cell wall. The cytoskeletal proteins MreB, RodA and PbpH are essential components of the bacterial cell-shape generation system. By imaging these proteins with TIRF-M and TIRF-SIM, directional movement and non-continuous motion patterns could be analyzed in enhanced details. Based on a multi-motor transport model, a mechanistic Brownian dynamics simulation was developed that was able to reproduce measured transport quantities like velocity and number of transport pauses and direction reversals. These new insights support the model of MreB being transported by several motors, where PbpH and RodA are likely candidates for synthesis motors based on their measured and simulated motion patterns.

Invited Talk BP 35.4 Thu 15:45 HÜL 386

Super-resolution microscopy with DNA molecules — •Ralf Jungmann — LMU Munich — MPI of Biochemistry

Super-resolution fluorescence microscopy is a powerful tool for biological research. We use the transient binding of short fluorescently labeled oligonucleotides (DNA-PAINT) for easy-to-implement multiplexed super-resolution imaging that technically achieves sub-5-nm spatial resolution.

To translate this resolution to cellular imaging, we introduce Slow Off-rate Modified Aptamers (SOMAmers) as efficient and quantitative labeling reagents. We demonstrate the achievable image resolution and specificity by labeling and imaging of transmembrane as well as intracellular targets in fixed and live cell-specimen.

Apart from ever increasing spatial resolution, efficient multiplexing strategies for the simultaneous detection of hundreds of molecular species are still elusive. We introduce a new approach to multiplexed super-resolution microscopy by designing the blinking behavior of targets with engineered binding frequency and duration. We assay this kinetic barcoding approach in silico and in vitro using DNA origami structures, show the applicability for multiplexed RNA and protein detection in cells and finally experimentally demonstrate 124-plex super-resolution imaging within minutes.

15 min. coffee break

BP 35.5 Thu 16:30 HÜL 386

Phase-Contrast X-Ray Tomography of Marmoset Cochlea — •Jannis Justus Schaeper[1], Marius Reichardt[1], Marina Eckermann[1], Jasper Frohn[1], Christoph Kampshoff[2], Tobias Moser[3], and Tim Salditt[1] — [1]Institute for X-Ray Physics, Göttingen University — [2]Max-Planck-Institute for Experimental Medicine, Göttingen — [3]InnerEarLab, University Medical Center, Göttingen

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

We present optimized 3D imaging of excised small-animal cochleae by phase-contrast x-ray tomography using highly brilliant synchrotron radiation, and show how this technique can complement classical histology and light sheet microscopy in a correlative imaging approach. Shape, volumes and densities of individual neurons can be assessed.

In view of age-related hearing loss we particularly aim at quantitatively evaluating the number of spiral ganglion neurones and hair cells in different age groups of marmoset models. We show how high contrast for soft tissue [1] can be achieved, in particular using our endstation GINIX at DESY [2]. Due to high contrast and little noise, automated segmentation becomes possible. The CT-images are compared to lightsheet microscopy data to infer structural changes induced by the clearing process. [1] M. Töpperwien et al., Sci. Rep. 8, 4922 (2018), [2] T. Salditt et al., J Synchrotron Radiat. 22 (2015), 867-878

BP 35.6 Thu 16:45 HÜL 386

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

Tissues display a complex spatial structure and their mechanical properties remain largely unexplored on the nanometer scale. Here we present a multisensory interface that makes nanomechanical tissue properties accessible to human perception and cognition. With a haptic interface, we translate the 3D force fields measured with an atomic force microscope (AFM) on the nanometer scale into forces perceivable to humans. This allows human users to explore haptically the specimen's surface shape as well as its local nanomechanical properties while simultaneously employing multiple senses. We developed a generic hysteresis model that uses the force-vs.-distance data collected with the AFM to predict the force (output) of the haptic device for an arbitrary indentation trajectory (input). This allows the user to perceive the specimen's local elastic response as well as different types of dissipative processes including viscoelasticity, elasto-capillary effects, adhesion hysteresis, and hysteresis due to capillary forces. The first samples studied include native (unfixed) hydrated tendon and living cancerous epithelial breast cells in culture medium.

BP 35.7 Thu 17:00 HÜL 386

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

Every year, more than 200 million people are infected with malaria. The protozoon is transmitted into the human body by a mosquito bite. In the blood stream, malaria parasites invade red blood cells (RBC), mature to rings and trophozoites, multiply to schizonts and then burst out of the cells, ready to invade further ones. The digestion of haemoglobin by all Plasmodium species results in the accumulation of a metabolic byproduct and in morphological changes of the RBC, alterating topology and mechanics, which are typically characterized with bright-field microscopy (BF).

To explore correlations of the Plasmodium-induced molecular, topographical and mechanical changes, we investigated infected RBC with atomic force microscopy (AFM), phase contrast and total internal reflection fluorescence (TIRF) microscopy. By combining these imaging methods, we could correlate the morphological changes of RBC with the Plasmodium falciparum developmental stages.

BP 35.8 Thu 17:15 HÜL 386

Thermal non-equilibrium drives concentration, salt and pH gradients — •Thomas Matreux, Dieter Braun, and Christof B. Mast — Systems Biophysics, Ludwig-Maximilians-Universität, München, Deutschland

The first steps in the emergence of life on Earth occurred on rocks and their constituent phases with a feedstock of simple molecules. Our aim is to combine this scenario with thermal non-equilibrium and bring together geomaterials, chemistry and microfluidics in a realistic environment.

The reaction chambers are sandwiched between highly heat conducting sapphire plates ensuring complete thermal control including possible thermal gradients. Microfluidic structures are made from FEP, which lets us focus on the interactions between the molecules. Ions leached from prebiotically plausible mineral samples are selectively accumulated by thermal gradients and permit enzymatic activity. Thermal non-equilibrium boundary conditions drive concentration gradients, enabling chemical reactions and generating and controlling pH gradients in a plausible prebiotic scenario. Local gradients driven by heat fluxes will offer unique opportunities to enable molecular selection and evolution at the origins of life.

BP 36: Cytoskeletal Filaments I

Time: Thursday 15:00–17:30 Location: SCH A251

BP 36.1 Thu 15:00 SCH A251

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

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

BP 36.2 Thu 15:15 SCH A251

Hidden Dynamics of the Red Blood Cell Cytoskeleton — •Julia Jäger[1,2], Michael Lanzer[3], and Ulrich S Schwarz[1,2] — [1]Institut für Theoretische Physik, Universität Heidelberg — [2]Bioquant, Universität Heidelberg — [3]Parasitologie, Universitätsklinikum Heidelberg

The spectrin-actin cytoskeleton of the red blood cell (RBC) is usually considered to be relatively static. Recent studies on malaria infections however have started to change this picture. Malaria parasites invade red blood cells in order to hide from the immune system and to digest hemoglobin. During the time course of the 48 hours until exit, they completely remodel the host cell envelope. This includes dramatic changes of the cytoskeleton, which most likely exploit dynamical processes that have gone unnoticed before. To better understand the dynamics of the cytoskeleton of healthy RBCs, we perform stochastic particle-based computer simulations, which in particular include the polymerization and depolarization of the junctional actin filaments. We then examine different potential mechanisms with which the parasite could exploit these dynamics of the RBC-cytoskeleton to remodel the host cell.

BP 36.3 Thu 15:30 SCH A251

What it takes to become a MAP — •Hauke Drechsler[1], Yong Xu[1], Veikko F. Geyer[1], Yixin Zhang[1], and Stefan Diez[1,2] — [1]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [2]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

The microtubule-binding domains of microtubule-associated proteins (MAPs) are structurally divergent, but often depend on electrostatic interactions with the negatively charged microtubule surface - suggesting that a MAP may primarily be defined by the surface exposure of positive charges rather than by a certain structural fold. Consistently, positively charged artificial objects are able to bind to microtubules and to diffuse along their lattice. Natural MAPs, however, exhibit a more sophisticated functionality beyond lattice-diffusion. Hence, we asked whether basic electrostatic interactions also support advanced MAP functionality. To test this, we studied simple positively charged peptides for the occurrence of typical MAP-like behavior. We found that a multivalent peptide construct featuring four lysine-alanine heptarepeats (starPEG-(KA7)4) shows advanced, biologically relevant MAP-like behavior: starPEG-(KA7)4 binds microtubules in the low nanomolar range, diffuses along their lattice, and tracks depolymer-

izing microtubule ends. Further, it promotes microtubule nucleation and growth, mediates depolymerization coupled pulling at plus ends, and bundles microtubules without significantly interfering with other proteins on the microtubule. Our results show that positive charges and multivalency are sufficient to mimic advanced MAP-like behavior.

Invited Talk BP 36.4 Thu 15:45 SCH A251

Mechanical properties of intermediate filaments at high strains — Johanna Forsting, Julia Kraxner, Charlotta Lorenz, Anna Schepers, and •Sarah Köster — Institute for X-Ray Physics, University of Göttingen

Mechanical properties of eukaryotic cells are to a great part determined by the cytoskeleton, a composite biopolymer network composed of three filament systems – intermediate filaments, F-actin and microtubules – along with cross-linkers and molecular motors. While actin and tubulin are conserved between cell types and organisms, intermediate filament proteins are expressed in a cell type dependent manner. It has been shown previously that the presence of filaments in a cell has an influence on cell mechanics. Here we unravel the role of the mechanical properties of the individual filaments, in particular at high strains. The molecular architecture of intermediate filaments displays several particularities, such as a strictly hierarchical build-up and multipe alpha-helical domains arranged in parallel. This architecture gives rise to intriguing mechanical properties, such as high flexibility and extreme extensibility. We employ optical traps to obtain precise force-strain data of vimentin and keratin intermediate filaments and model our data by Monte Carlo simulations. We are thus able to show differences between different types of intermediate filaments, as well as a dependence on the ionic anvironment and pH, thus revealing a strong influence of charge interactions.

15 min. coffee break

BP 36.5 Thu 16:30 SCH A251

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

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

BP 36.6 Thu 16:45 SCH A251

Influence of Phosphorylation on Vimentin Mechanics — •Julia Kraxner[1], Julia Menzel[2], Henning Urlaub[3], Blanche Schwappach[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, University of Göttingen — [2]Department of Molecular Biology, University Medical Center Göttingen — [3]Bioanalytical Mass Spectrometry, Max Planck Institute for Biophysical Chemistry, Göttingen

The mechanical properties of biological cells are determined by the cytoskeleton. This composite biopolymer network consists of microtubules and microfilaments, which are conserved throughout all cell types, and different types of intermediate filaments (IFs), which are expressed in a cell-type specific manner. The adaption to specific mechanical requirements may be further achieved by post-translational modifications of the proteins. In this context, phosphorylation which adds negative charges to the modified site, plays an important role. Regarding IFs, phosphorylation heavily affects disassembly of the filaments and provides binding sites for proteins like 14-3-3 which is a regulator for signaling proteins. Here, we study partially phosphorylated single vimentin IFs by analyzing stress-strain curves recorded with an optical tweezer setup which combines microfluidics and fluorescence microscopy. Furthermore, we investigate the influence of bound 14-3-3 on the mechanics and the contribution of single phosphorylation sites by phosphomimetics. Our results show that additional charges within the filament soften the vimentin filaments and the binding of 14-3-3 weakens the filaments even more.

BP 36.7 Thu 17:00 SCH A251

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

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

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

BP 36.8 Thu 17:15 SCH A251

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

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

BP 37: Systems Biology, Evolution and Neural Networks I

Time: Thursday 15:00–17:30 Location: ZEU 250

Invited Talk BP 37.1 Thu 15:00 ZEU 250

Growth, death, and adaptation of bacterial cells: a quantitative analysis — •Ulrich Gerland — TUM, Munich, Germany

Bacteria such as *Escherichia Coli* serve as model systems to study basic principles of evolving living systems. For physicists seeking a quantitative understanding of such systems there are essentially two complementary approaches: One can consider a functionally defined subsystem and seek to understand how its function emerges from the

interplay between the constituent molecules. If an entire cell is taken as a functional unit (arguably the smallest unit of life), this bottom-up approach is currently intractable. Alternatively, one can analyze the behavior of a functional unit, and extract quantitative phenomenological laws that reflect either fundamental trade-offs or evolved strategies. Importantly, this approach is applicable also to entire cells. It can form both the starting point and the guiding principle for a systematic top-down analysis of living systems. I will illustrate this increasingly popular approach with our own work (partially unpublished) on the growth, death, and interdependence between growth and death of *Escherichia Coli* cells. In particular, I will also discuss a trade-off in the apparent survival strategy of these bacteria and its evolutionary implications.

BP 37.2 Thu 15:30 ZEU 250

Ruggedness and accessibilioty in tradeoff induced landscapes — •Suman Das and Joachim Krug — University of Cologne, Cologne, Germany

Evolutionary fitness landscapes depend on environmental parameters. Contrary to the widespread attention given to fitness landscapes at fixed environments, the effect of environmental changes on gene-gene interactions has not been studied systematically. We study the case of environment dependent landscapes where the fitness effects of mutations exhibit adaptational tradeoffs, i.e mutations which are beneficial in one parameter regime become deleterious in another. We find that such landscapes have predictable properties that are largely independent of the precise details of individual parameter values in the system. In particular, we find that high ruggedness and high accessibility of fitness maxima coexist in these systems, making them distinct from the commonly studied random landscape models. We discuss the relevance of such landscapes in the context of antibiotic resistance.

BP 37.3 Thu 15:45 ZEU 250

Sequence selection of oligonucleotides under a ligation chain reaction — •Patrick Kudella and Dieter Braun — Systems Biophysics, Ludwig-Maximilians-Universität München

Replication of information on oligonucleotides such as RNA or DNA is essential for the emergence of life. Previous studies focus on the replication of single sequences, but we believe it is the key to monitor selection dynamics and replication starting in an already completely random pool of sequences.

We expect a nonlinear ligation dynamic had set in, once polymerization was able to create oligomers long enough for hybridization and thus capable of structure formation and templated ligation. We study if certain sequences could have been selected at this onset of replication that potentially lead to interesting non-linear and frequency-dependent behavior.

By using adenine-thymine-only 12mers long random-sequence strands as starting material, the sequence space for the first ligation stage creating 24mers can still be completely sampled. We obtained more than 12 million individual strands by Next Generation Sequencing (NGS), showing a significant selection of sequences undergoing this elongation dynamic. Utilizing a self-written LabView code we can study starting sequence pool biases, short- and long- range correlation in sequence space, base-fraction evolution as a function of product length as well as the driving selection mechanics as a function of product length. In addition, we show temperature, concentration and sequence-space dependent dynamics of this system by PAGE.

BP 37.4 Thu 16:00 ZEU 250

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

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

15 min. coffee break

BP 37.5 Thu 16:30 ZEU 250

Collective dynamics shape drug resistance evolution in dense cellular populations — •Jona Kayser[1,2], Carl Schreck[3], and Oskar Hallatschek[3] — [1]Max-Planck-Institute for the Science of Light, Erlangen — [2]Zentrum für Physik und Medizin, Erlangen — [3]University of California, Berkeley

The principle factor limiting curative cancer treatment is the evolution of drug resistance. Recent work has yielded substantial progress in our understanding of the molecular and biochemical mechanisms of resistance while studies of well-mixed microbial cultures have shed light on the ensuing evolutionary dynamics in disperse populations. Yet, how the mechanical interactions between cells in dense populations, including solid tutors, shape evolutionary trajectories is not well understood.

Here, using a genetically tailored model system of neoplastic growth, based on microbial colonies, I show that the physical cell-cell interaction inherent to dense cellular populations can induce collective phenomena that reshape evolutionary outcomes and may boost drug resistance evolution. In addition, I present new results advocating for an intricate interplay between such an emergent mechano-cooperation and multi-step adaptation. The uncovered mechanisms lay the foundation for a new conceptual framework of intratumoral evolutionary dynamic as an emergent phenomenon, which might crucially inform novel treatment strategies, such as adaptive therapy.

BP 37.6 Thu 16:45 ZEU 250

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

Phylogenetic studies have provided strong evidence that gene transfer happens frequently and acts across species. However, the rate at which gene transfer occurs and its short-term effect on genome dynamics are poorly understood. To address the effect of intra- and interspecies gene transfer on genome dynamics we developed an evolution experiment and analysis method to detect horizontal gene transfer. To investigate mechanistic contributions to gene transfer probability, we ensured minimal selection by not allowing for population dynamics. We were able to detect a remarkably high gene transfer rate of 0.4 $\%h^{-1}$ across subspecies of *Bacillus subtilis*. This rate was lower by 125 times when gene transfer was probed between *B. subtilis* and *Bacillus atrophaeus*. Interestingly, the average sequence divergence of integrated segments is comparable between both donors with a mean of 6.7 %. In both experiments, gene transfer increased the number of mutations depending on replacement quantity. The fact that the fraction of replaced genome increases linearly throughout the 40 h of DNA uptake suggests that transfer of genes is not yet saturated. In future long term evolutionary experiments, it will be interesting to relate the rate of gene transfer across donor and recipient with the pattern of sequence divergence to better understand what sets species apart.

BP 37.7 Thu 17:00 ZEU 250

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

Many essential biological behaviors originate from an entanglement of biological (cellular) and physical processes. This is a challenge not only for traditional biology and physics methodology, but also for synthetic biology, where such interactions severely limit the ability to engineer desired behavior with artificial gene regulatory networks. We show how to achieve control of phenotypic structure in bacterial microcolonies by simultaneously exploiting internal gene expression and metabolism, as well as physical coordination through signal diffusion and growth,

which leads to self-generated nutrient gradients and a heterogeneous population consisting of both dividing and dormant cells. In microfluidic experiments and a mathematical model, we show that gene circuits which sense and control growth can create a spatio-temporal feedback loop via nutrient transport and generate sustained growth oscillations, while a phenotype-specific lysis circuit can selectively eliminate dormant cells. Our results demonstrate how to understand and control multicellular substrates as complex active physical systems.

BP 37.8 Thu 17:15 ZEU 250

Gene Expression Dynamics Determine Toxin Driven Bacterial Competition — •Alexandra Götz, Anna Weiss, Benedikt von Bronk, Andreas Mader, and Madeleine Opitz — Ludwig-Maximilians-Universität, München, Germany

Microbial community composition is greatly influenced by stochastic and deterministic bacterial interactions on the single cell level, determining stability and fate of mixed bacterial populations in a given habitat. Here, we study bacterial competition that is driven by production and release of the toxic bacteriocin ColicinE2 of Escherichia coli. In this model system, a complex regulatory network controls the expression of the toxin from the ColicinE2 operon. Using fluorescence time-lapse microscopy, we investigated how the regulatory system controls the time-point and amount of toxin released into the environment and disentangled the components responsible for toxin expression dynamics and release. Investigating several mutant strains, we determined how different regulatory modules affect gene expression noise. In a next step, we investigated the impact of noise and toxin expression dynamics on the competition of the toxin-producing bacterium with a bacterium sensitive towards the toxin. Finally, theoretical simulations allowed us to analyze the role of toxin release times and toxin amounts with regard to the bacterial competition over a broad parameter range.

BP 38: Focus: Biological Cells in Microfluidics II

Microfluidic devices have a great potential to enable precise label-free analysis and manipulation of heterogeneous cell suspensions based on the intrinsic properties of the cell. This focus session will discuss recent advances in the behavior of biological cells and cell-mimicking systems in microfluidic flow, and represent a forum of theoretical and experimental contributions.

Time: Friday 9:30–12:00 Location: HÜL 386

Invited Talk BP 38.1 Fri 9:30 HÜL 386

Physical phenotyping of cells in microfluidic systems — •Jochen Guck — Max-Planck-Institut für die Physik des Lichts & Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

While most current biological research focuses on molecular, biochemical aspects of cell processes, we are interested in the physical properties of cells, their importance for biological function, and ultimately transfer of insights to medical application. One major roadblock has been a paucity of appropriate tools for the convenient quantification of such properties. Recently, we have introduced real-time deformability cytometry (RT-DC) to address this need. RT-DC permits the continuous physical single-cell characterization of large populations (> 100.000 cells) with analysis rates of 1,000 cells/s - approaching that of conventional fluorescence-based flow cytometers. Using RT-DC we can sensitively detect physiological and pathological changes in cell function by image-based parameters such as size, shape, deformability, and any other information contained in an image. Combined with machine learning, conventional fluorescence detection and sorting, this constitutes a novel discovery machine specifically well suited to identify and characterize cell populations and states invisible to marker-based techniques. Physical phenotyping adds a new functional, marker-free and unbiased dimension to flow cytometry with diverse applications in biology, biotechnology and medicine.

BP 38.2 Fri 10:00 HÜL 386

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

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

BP 38.3 Fri 10:15 HÜL 386

Hydrogel-based cell mimics and applications — •Salvatore Girardo[1], Ruchi Goswami[1], Nicole Träber[2,3], Anna Taubenberger[2], Katrin Wagner[2], and Jochen Guck[1] — [1]MPL,Erlangen,Germany — [2]Biotec,Dresden,Germany — [3]IPF,Dresden,Germany

In recent decades it has become increasingly obvious that cell mechanical properties can be used to monitor physiological and pathological changes in cells. It has been reported that mechanical properties measured by using different techniques on the same cell type span a wide range of values, making hard the comparison of the obtained results. Therefore, a mechanical standard is needed to validate and calibrate mechanical measurements. Furthermore, quantification of stresses exerted and experienced by cells at the cell-scale level in in vivo and in vitro systems is fundamental to improve the understanding of the role of mechanics in biology and medicine. This quantification is still a challenge due to the lack of the availability of appropriate measurement tools. All these aspects can be addressed by using elastic, compressible and homogeneous spheres whose shape, size, mechanical properties and functionalization with specific adhesion sites are well established before use. Here we illustrate the production, characterization and functionalization of standardized microgel beads covering all these features. We demonstrate that these beads can be used as mechanical standards, as cell-scale stress sensors able to sense forces through their deformation and as building blocks of novel 3D scaffolds to investigate mechanosensing.

BP 38.4 Fri 10:30 HÜL 386

Sensorimotor processing and navigation in confined microswimmers — Samuel Bentley, Vasileios Anagnostidis, Fabrice Gielen, and •Kirsty Y. Wan — Living Systems Institute, Exeter, United Kingdom, EX4 4QD

All living organisms are environmentally intelligent. This is the fundamental distinction between life, and other forms of matter. Even unicellular organisms are capable of complex behaviours, for they can sense as well as respond to changes in the environment. Here, we study spontaneous and constrained motor actions in algal microswimmers, using motility as a dynamic read-out of behaviour and physiology. Previous studies have focussed on locomotion transients over short timescales ranging from milliseconds to minutes. We present a novel microfluidic platform which allowed us for the first time to monitor and analyse algal cell motility over hours, and even developmental timescales. We focus on two species, a biflagellate which exhibits a form of run-and-tumble, and an octoflagellate which which exhibits a tripartite behavioural repertoire termed run-stop-shock. Excitability and stochastic transitions in swimming gait are projected onto a low-

dimensional state space. We reveal how flagellar mechanosensitivity mediates repetitive boundary interactions, and discuss the discovery of a light-dependent quiescent regime. Finally, we conduct pharmacological perturbations within these microenvironments, to shed new light on the physiological origins of excitable flagellar dynamics.

BP 38.5 Fri 10:45 HÜL 386

DNA-mediated programmable functionalization and symmetry break in microfluidic droplets — •Kevin Jahnke[1,2] and Kerstin Göpfrich[1,2] — [1]Biophysical Engineering Group, Max Planck Institute for Medical Research, Jahnstraße 29, 69120 Heidelberg, Germany — [2]Department of Physics and Astronomy, Heidelberg University, 69120 Heidelberg, Germany

Droplet-based microfluidics has emerged as a powerful tool in synthetic biology. For many applications, chemical functionalization of the droplets is a key process. Therefore, we developed a straight-forward and broadly applicable approach to functionalize the inner periphery of microfluidic droplets with diverse reactive groups and components. This method relies on cholesterol-tagged DNA that self-assembles at the droplet periphery [Jahnke et al., Adv. Funct. Mat. 2019]. The cholesterol-tagged DNA serves as an attachment handle for the recruitment of complementary DNA, which can carry diverse functional groups. We demonstrate that the attachment is thermo-responsive and exemplify the versatility of our approach. Further, we employ our DNA-linker system to engineer light-activated directional contractility of a minimal actomyosin network inside microfluidic cell-sized compartments. Ultimately, symmetry breaking is achieved using the DNA link between the actin network and the compartment periphery.

We envision that droplet functionalization via DNA handles will help to tailor interfaces for diverse applications – featuring programmable assembly, unique addressability, and stimuli-responsiveness – hence increasing the complexity of synthetic cellular systems.

30 min. coffee break

BP 38.6 Fri 11:30 HÜL 386

Bayesian parameter estimation and model selection for biophysical models of leukocyte cell extensions during leukocyte rolling — •Mats Leif Moskopp[1], Philipp Rosendahl[2,3], Jochen Guck[2,4], Andreas Deussen[1], and Peter Dieterich[1] — [1]Institut für Physiologie, TU Dresden, Dresden, Germany — [2]Biotechnology Center, TU Dresden, Dresden, Germany — [3]Zellmechanik Dresden GmbH, Dresden, Germany — [4]MPL & MPZ-PM, Erlangen, Germany

The leukocyte adhesion cascade describes the extravasation of leukocytes from the blood stream into tissue. We focus on the initial process of leukocyte rolling, which is driven by shear stress and (passive) restoring forces in leukocyte cell extensions (microvilli, tethers and slings). We investigate the biomechanical properties of cell extensions based on experimental data combined with mathematical modelling and Bayesian inference. High speed (2000 fps) video sequences of rolling leukocytes (THP-1) were used to obtain cell positions as a function of time over a periode of about 10 s. Bayesian inference allows for model selection and parameter estimation of visco-elastic models (Maxwell, Kelvin-Voigt, Standard linear solid) for the fast deceleration of cell extensions during leukocyte rolling. This new technique identified differences in the biomechanical stress responses of cell extensions according to isoforms of selectins. These findings correlate to distinct rolling dynamics on P- and E-selectin isoforms regarding overall velocity and fast deceleration events. Further, this approach allows to quantify model parameters. This was tested using Glutaraldehyde (tissue fixation) and Cytochalasin D (inhibitor of actin polymerization).

BP 38.7 Fri 11:45 HÜL 386

Synthetic cells: De novo assembly with microfluidics and DNA nanotechnology — Yannik Dreher[1,2], Julius Fichtler[1,2], Kevin Jahnke[1,2], and •Kerstin Göpfrich[1,2] — [1]Biophysical Engineering Group, Max Planck Institute for Medical Research, Jahnstraße 29, 69120 Heidelberg, Germany — [2]Department of Physics and Astronomy, Heidelberg University, 69120 Heidelberg, Germany

Bottom-up synthetic biology has been successful at isolating components from cells and reconstituting subcellular functions in vitro. Progress towards a fully functional synthetic cell, however, requires strategies to recombine and arrange a multitude of components in space and time. Here, we merge two precision technologies, microfluidics and DNA nanotechnology, to position and manipulate various components in synthetic cells [K. Göpfrich *et al., Trends Biotechnol.*, 2018; Jahnke *et al., Adv. Funct. Mater.*, 2019]. After encapsulation, we actuate DNA nanostructures in microfluidic or lipid-based compartments [K. Göpfrich *et al., ACS Synth. Biol.*, 2019] to assemble dynamic systems with structural reconfigurability. By the integration of plasmonic probes we achieve real-time optical feedback to monitor the dynamics upon external stimulation. Moreover, we demonstrate the division of lipid vesicles relying on physical mechanisms and show that it can be regulated by metabolic activity. These unique tools, bridging the micro- and nanoscale, enrich the complexity and diversity of functional synthetic cellular systems.

BP 39: Cytoskeletal Filaments II

Time: Friday 9:30–12:00 Location: SCH A251

BP 39.1 Fri 9:30 SCH A251

Mechanosensitive Self-Assembly of Myosin II Minifilaments — •Justin Grewe[1], Kai Weissenbruch[2], Martin Bastmeyer[2], and Ulrich S. Schwarz[1] — [1]Ruprecht Karl University Heidelberg, Germany — [2]Karlsruhe Institute for Technology, Germany

Self-assembly and force generation are two central processes in biological systems that usually are considered in separation. However, the signals that activate non-muscle myosin II molecular motors simultaneously lead to self-assembly into myosin II minifilaments as well as progression of the motor heads through the crossbridge cycle.

We investigate theoretically the possible effects of coupling these two processes. Our assembly model, which builds upon a consensus architecture of the minifilament, predicts a critical aggregation concentration at which the assembly kinetics slow down dramatically. The combined model predicts that increasing actin filament concentration and force both lead to a decrease in the critical aggregation concentration in addition to force decelerated myosin turnover. We benchmark our model, in particular the turnover, against in-vivo fluorescence recovery after photobleaching experiments we performed in different experimental conditions and find reasonable agreement with the model.

We suggest that due to these findings, myosin II minifilaments in a filamentous context couple self-assembly with force generation and by this effect might be in a critical state that reacts faster to varying conditions than in solution.

BP 39.2 Fri 9:45 SCH A251

Development of microtentacles in suspended cells upon weakening of the actin cortex — •Lucina Kainka[1,2], Reza Shaebani[2], Ludger Santen[2], and Franziska Lautenschläger[1,2] — [1]INM - Leibniz Institute for New Materials, Campus D2 2, 66123 Saarbrücken, Germany — [2]Saarland University, Physics Department, Campus E2 6, 66123 Saarbrücken, Germany

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

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

Further experiments on the dynamics of McTNs, especially during retraction after drug wash-out, give a better insight in the role of individual cytoskeletal elements.

BP 39.3 Fri 10:00 SCH A251

Balance of forces and torques in a mean-field approximation in mitotic spindles — •Arian Ivec[1], Iva Tolić[2], and Nenad

Pavin[1] — [1]Department of Physics, Faculty of Science, University of Zagreb, Croatia — [2]Ruder Bošković Institute, Zagreb, Croatia

The mitotic spindle is a self-organized micro-machine composed of microtubules and associated proteins, which divides genetic material between its two nascent daughter cells. Forces exist in the spindle throughout mitosis and are crucial for spindle functioning in each phase. In metaphase, the mitotic spindle has a recognizable shape with a characteristic arrangement of microtubules. Microtubules extend from opposite spindle poles and interact with the chromosomes and with each other. Though a significant progress in understanding the mechanics of the spindle has been achieved, the question of force balance in the spindle is still open. We explore the force balance of the entire spindle by introducing a mean-field approach, in which discrete microtubule bundles in a certain region, together with forces and torques exerted by these bundles, are approximated by an averaged bundle. The model provides predictions for forces and torques in the spindle, and consequently it predicts the shape of the entire spindle, including the shapes of inner and outer bundles, which is compared with shapes observed in our experiments. Based on this information, we provide a mechanical explanation for the shapes of inner and outer bundles, including major differences between them. This approach provides comprehensive insight into forces and torques acting in the entire spindle, which are crucial for proper cell division.

BP 39.4 Fri 10:15 SCH A251

The kinesin-14, Ncd, drives the helical motion of microtubules around each other — •Laura Meissner[1], Aniruddha Mitra[2], Felix Ruhnow[3], and Stefan Diez[4] — [1]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [2]Department of Physics and LaserLaB Amsterdam, Vrije Universiteit Amsterdam, Amsterdam, Netherlands — [3]School of Biosciences, University of Melbourne, Parkville, VIC 3010, Australia — [4]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

Within the mitotic spindle, several kinesin motors crosslink and slide microtubules. Some kinesins, including kinesin-5 and kinesin-14, have been shown to exhibit sideways components in their step cycles, but the impact of the resulting off-axis power strokes on motility and force generation in the spindle has not been studied so far. Here, we investigate kinesin-14, Ncd, driven sliding of crosslinked, fluorescently-labeled microtubules with a novel three-dimensional in vitro motility assay. We find that free microtubules, sliding in an antiparallel orientation on microtubules suspended between nanofabricated ridges, not only rotate around their own axis but also move around the suspended microtubules with right-handed helical trajectories. In contrast, microtubules crosslinked in parallel orientation are static with neither longitudinal nor helical motion. We argue that the capability of microtubule-crosslinking kinesins to cause helical motion of microtubules around each other allows for flexible filament organization, roadblock circumvention and torque generation in the mitotic spindle.

BP 39.5 Fri 10:30 SCH A251

Anillin Propels Myosin-Independent Constriction of Actin Rings — Ondřej Kučera[1], Daniel Janda[1], Valerie Siahaan[1], Sietske H. Dijkstra[1], Eva Zatecka[1], Stefan Diez[2,3], •Marcus Braun[1], and Zdenek Lansky[1] — [1]Institute of Biotechnology of the Czech Academy of Sciences, BIOCEV, Prague West, Czechia — [2]B CUBE - Center for Molecular Bioengineering, Technische Universität Dresden, 01307 Dresden, Germany — [3]Cluster of Excellence Physics of Life, Technische Universität Dresden, 01062 Dresden, Germany

Constriction of the cytokinetic ring, a circular structure of actin filaments, is an essential step of cell division. In a generally accepted view, the constriction is driven by relative sliding of actin filaments propelled by myosin motors. However, in multiple organisms, the ring constriction is myosin independent. How actin rings constrict in the absence of motor activity remains unclear. Here, we demonstrate that actin contractility can be propelled by anillin, a diffusible non-motor actin crosslinker, colocalising with the cytokinetic ring. We in vitro observed the formation and constriction of rings comprising multiple actin filaments bundled by anillin. Rings constricted due to anillin-driven maximisation of overlaps between the filaments. Actin disassembly promoted constriction. Optical trapping demonstrated that anillin molecules, crosslinking bundles of several actin filaments, collectively, generate forces of tens of pico-Newtons. We propose that diffusible non-motor actin crosslinkers, generating forces complementary to the activity of molecular motors, may contribute to the contractility of diverse actin structures, including the cytokinetic ring.

45 min. coffee break

BP 39.6 Fri 11:30 SCH A251

Active Model C: mean-field theory of cytoskeletal pattern formation — •Ivan Maryshev[1], Alexander Morozov[2], Davide Marenduzzo[2], and Erwin Frey[1] — [1]Ludwig-Maximilians-Universität München, Germany — [2]The University of Edinburgh, Edinburgh, EH9 3FD, UK.

The self-organization of mixtures of biological polymers and molecular motors provides a fascinating manifestation of active matter. Microtubules re-oriented by the molecular motors can form far-from-equilibrium cell-scale structures. The link between individual microscopic interactions of filaments and their macroscopic dynamics is poorly understood. Here we formulate a theoretical approach based on a Boltzmann-like kinetic equation, to describe pattern formation in two-dimensional mixtures of microtubules and molecular motors. We consider motors that can push apart antiparallel microtubules and cluster parallel ones. Using our kinetic approach, we derive the equations governing the collective behavior of microtubules by rigorously coarse-graining microscopic motor-induced interactions. Through numerical simulations, we show that this model generically creates either stable stripes with the antiparallel arrangement of filaments inside them or an ever-evolving pattern formed by self-extend dynamic bands. Finally, we consider our model with phenomenological coefficients and besides the chaotic bands, also observe the formation of patterns with topological defects, including foams and asters. By the analogy with passive Model C in Hohenberg-Halperin classification, we call our model Active Model C.

BP 39.7 Fri 11:45 SCH A251

Buckling instability and active oscillations in a pair of clamped elastic filaments — •Andrej Vilfan[1,2], Laura Collesano[1], and Ramin Golestanian[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]J. Stefan Institute, Ljubljana, Slovenia

A pair of microtubules that are fixed at the proximal end and connected via dynein motors at the distal end can serve as a minimal synthetic system aimed at re-creating active oscillations resembling those of biological cilia. Here, we study theoretically the static shapes and the active dynamics of two connected filaments, modeled as flexible beams. We first determine the shape of a pair of elastic rods of different lengths with clamped ends (i.e., with coinciding endpoints and tangent vectors). Starting from equal lengths, the system first undergoes a transition similar to Euler buckling, however at a different critical load, and then assumes a planar shape. After a secondary bifurcation, the shape becomes non-planar with spontaneously broken chiral symmetry. At an even higher length ratio, it changes to planar again. To study the active system, we replace the passively clamped end with molecular motors exerting a tangential force with a given density in the overlap zone. The dynamical system can have a stable fixed point, with either bent or straight filaments, or limit cycle oscillations reminiscent of ciliary beating.

BP 40: Systems Biology, Evolution and Neural Networks II

Time: Friday 9:30–12:00 Location: ZEU 250

BP 40.1 Fri 9:30 ZEU 250

Towards topological quantum computing in the brain — •Chrsitian Kerskens — Institute of Neuroscience, Trinity College Dublin

In recent years, the mathematical formalism of quantum theory has been adopted to formalise models of cognition. However, the success of quantum cognition over classical approaches opens up the following questions; Is the computing power of the brain sufficient to simulate

quantum computation? And if yes, why would nature use so much computational power to simulate quantum computing resulting in a low reliability through non-commutative behaviour and human error? We believe that the brain doesn't simulate quantum computing. Instead, we propose that consciousness and cognition is based on topological quantum computing (TQC), which may be, if at all, the only way of quantum computing reliable enough in the wet and hot environment of the brain . The proposal relies on the experimental findings that the two main ingredients to realise TQC, topological defects and topological phase, may exist in the conscious brain. While the existence and important roles of topological defects are well established, we will focus on questions around the topological phase. Especially, we will discuss why our recent results which showed long-range quantum entanglement in the conscious brain can be interpreted as a topological phase. Further, we will discuss how the experimental results can shed light on the underlying mechanisms which provide the topological-like phase.

BP 40.2 Fri 9:45 ZEU 250

Multiscale activity in circadian clocks — •Pablo Rojas[1], Jenny A. Plath[2], Julia Gestrich[2], Bharath Ananthasubramaniam[3], Hanspeter Herzel[3], Monika Stengl[2], and Martin E. Garcia[1] — [1]Theoretical Physics, University of Kassel, Kassel, Germany — [2]Animal Physiology, University of Kassel, Kassel, Germany — [3]Institute for Theoretical Biology, Humboldt University of Berlin and Charité Universitätsmedizin, Berlin, Germany

The circadian clock orchestrate daily rhythms in physiology, metabolism and behavior. A group of neurons in the brain (the clock) is responsible for this ~24h rhythm. Single neurons in the clock show rhythms with periods ranging from milliseconds (action potential firing) to ~24 hours (circadian expression of clock genes). How cells interact and achieve synchronization in the clock is still a central question. To address this fundamental problem, we performed long term in-vivo electrophysiology (loose-patch clamp) recordings in the cockroach circadian clock. We developed and applied a method, based on wavelets, to detect and analyze electrical events of different timescales, an reduce the complexity of the datasets. We also provide tools for screening and detecting signatures of synchronization and network interaction episodes ranging from minutes to hours, promisingly closing the gap between the fastest and slowest timescales [1]. Our result over experimental datasets are combined with mathematical modeling, in order to describe internal configuration in the clock network.

[1] Rojas, P. et al, Network Neuroscience 2019

BP 40.3 Fri 10:00 ZEU 250

Dynamics and computation with anti-leaky integrate-and-fire neurons — •Paul Manz, Sven Goedeke, and Raoul-Martin Memmesheimer — Universität Bonn

Networks in the brain consist of different types of neurons. Here we investigate the influence of neuron diversity on the dynamics, phase space structure, and computational capabilities of spiking neural networks. We find that already a single neuron of a different type can qualitatively change the network dynamics and that mixed networks may combine the computational capabilities of ones with a single-neuron type. We study inhibitory networks of concave leaky (LIF) and convex "antileaky" (XIF) integrate-and-fire neurons that generalize irregularly spiking nonchaotic LIF neuron networks. Endowed with simple conductance-based synapses for XIF neurons, our networks can generate a balanced state of irregular asynchronous spiking as well. We determine the voltage probability distributions and self-consistent firing rates assuming Poisson input with finite-size spike impacts. Further, we compute the full spectrum of Lyapunov exponents (LEs) and the covariant Lyapunov vectors (CLVs) specifying the corresponding perturbation directions. We find that there is approximately one positive LE for each XIF neuron. This indicates in particular that a single XIF neuron renders the network dynamics chaotic. A simple mean-field approach, which can be justified by properties of the CLVs, explains the finding. As an application, we propose a spike-based computing scheme where our networks serve as computational reservoirs and their different stability properties yield different computational capabilities.

BP 40.4 Fri 10:15 ZEU 250

Dynamics, Statistics and Coding in Random Rate and Binary Networks — •Tobias Kühn[1,2,3], Christian Keup[2,3], David Dahmen[2], and Moritz Helias[2,3] — [1]Laboratoire de Physique Théorique de l'ENS, Paris, France — [2]INM-6, Forschungszentrum Jülich, Germany — [3]Department of Physics, RWTH Aachen, Germany

Cortical neurons communicate with spikes, discrete events in time. Functional network models often employ rate units that are continuously coupled by analog signals. Is there a benefit of discrete signaling? By a unified mean-field theory for large random networks of rate and binary units, we show that both models can be matched to have identical statistics up to second order. Their stimulus processing properties, however, are radically different: contrary to rate networks [Sompolinsky et al. 1988], the chaos transition in binary networks [van Vreeswijk & Sompolinsky 1998] strongly depends on network size, and we discover a chaotic submanifold in binary networks that does not exist in rate models. Its dimensionality increases with time after stimulus onset and reaches a fixed point that depends on the synaptic coupling strength. Low dimensional stimuli are transiently expanded into higher-dimensional representations that live within the manifold. We find that classification performance typically peaks within a single neuronal time constant, after which performance degrades due to variability in the manifold. During this transient, resilience to noise by far exceeds that of rate models with matched statistics, which are always regular. Our theory mechanistically explains all these observations.

BP 40.5 Fri 10:30 ZEU 250

Long-ranged signalling gradients generated by short-ranged molecular interactions — •Johanna Dickmann[1,2], Jochen Rink[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Embryonic development, regeneration, and tissue renewal require tissue organisation as can be provided by signalling molecules forming concentration profiles in space, i.e. signalling gradients. Planarian flatworms are a great model for tissue organisation as they constantly turn over their entire body and are able to regenerate from arbitrary amputation fragments. At a body length of up to 2 cm, they are orders of magnitudes larger than tissue organised during embryonic development in other species, yet, they employ signalling gradients for tissue organisation. In this project we investigate how such long-ranged signalling gradients can be formed. We chose the Wnt signalling gradient organising the main body axis of the worm as a model system. Building a discrete 1D model we account for signalling molecule levels in the extracellular space and signalling levels inside the cells. We consider diffusion and degradation of signalling molecules as suggested to explain signalling gradient formation during development. Motivated by observations in the worm, we add positive feedback. Thus, all cells become sources of signalling molecules. The directionality of the profile is organised by a signal-independent input from one side. The suggested mechanism can explain the formation of signalling gradients with a longer length scale compared to the diffusion/degradation mechanism.

BP 40.6 Fri 10:45 ZEU 250

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

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

30 min. coffee break

BP 40.7 Fri 11:30 ZEU 250

Testing developmental reaction-transport models by physical perturbations — •Moritz Kreysing — Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

From Alan Turing we know that rates of biochemical reactions (in units of seconds) need to be coupled to physical processes to account for the generation of spatial structure (in units of meters) in biology. Suggested morphogenetic driving forces include: passive or active diffusion, directed motor-driven fluxes, and the enigma of cytoplasmic streaming. Since Turing, a great deal of causal insight into the biochemical basis of cellular organization and morphogenesis has been attained by genetic perturbations. In stark contrast to this, the functional role of physical transport in morphogenesis and homeostasis remains very poorly understood. Specifically, we lack the ability to test the functional role of these physical processes inside cells by appropriate perturbations, i.e.: how would one change direction, velocity or temporal persistence of flows within the cytoplasm of a developing embryo? This is clearly not possible by genetics. As a result of this methodological shortcoming, there is hardly one accepted proof of a reaction-transport system in biology. It is now time for experimental biophysics to catch up with molecular biologists and to test great quantitative models of patterning and morphogenesis. I will discuss challenges to test especially reaction-transport systems, while emphasizing chances to interactively guide early organism development via suitable physical perturbations.

Reference: M. Kreysing, Developmental Cell 51, 135-144 (2019)

BP 40.8 Fri 11:45 ZEU 250

Mitochondrial dynamics facilitates precise sensing of metabolic states — •Felix Jonathan Meigel[1], Philipp Mergenthaler[2], and Steffen Rulands[1,3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Charite - Universitätsmedizin Berlin, Department of Experimental Neurology, Berlin, Germany — [3]Center for Systems Biology Dresden, Dresden, Germany

Cellular behaviour relies on robustly sensing and reacting to fluctuating environmental signals. In recent years, cellular organelles such as mitochondria were recognized as signaling hubs on which different environmental cues are integrated. While the formation of dynamic protein complexes on the outer mitochondrial membrane triggers cell death, the reversible aggregation of these complexes is embedded into a fusion and fission dynamics of the mitochondria themselves. Here, giving the example of the metabolic regulation cell death, we show how the interplay of mitochondrial and protein dynamics facilitates sensitive and specific sensing of fluctuating metabolite levels. By identifying collective degrees of freedom that resemble localised modes in Josephson junction arrays, we demonstrate that such multiscale dynamics form a kinetic low-pass filter that is able to distinguish between fluctuations and biologically informative signals. Our work shows paradigmatically how biological function relies on the integration of non-equilibrium processes on different spatial scales.

BP 41: Active Matter V (joint session DY/BP/CPP)

Time: Friday 10:00–11:30 Location: ZEU 160

BP 41.1 Fri 10:00 ZEU 160

A particle-field approach bridges phase separation and collective motion in active matter — •Robert Grossmann[1,2], Igor Aranson[3], and Fernando Peruani[2] — [1]Institute of Physics and Astronomy, University of Potsdam, Potsdam, Germany — [2]Laboratoire J.A. Dieudonné, Université Côte d'Azur, Nice, France — [3]Department of Chemistry, Pennsylvania State University, University Park (PA), United States of America

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

BP 41.2 Fri 10:15 ZEU 160

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

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

BP 41.3 Fri 10:30 ZEU 160

Active Brownian particles show motility-induced spatially periodic patterns — •Samuel Grimm[1], Andreas Fischer[2], Thomas Speck[2], and Walter Zimmermann[1] — [1]Theoretische Physik I, Universität Bayreuth, 95440 Bayreuth, Germany — [2]Physics Institute, University of Mainz, 55099 Mainz, Germany

We suggest and investigate a model for active Brownian particles, that shows motility induced pattern formation. We complement a model of motility induced phase separation (MIPS) [J. Chem. Phys. 142, 224149 (2015)] by the dynamics of auto-inducer molecules. This results in a prototype model for spatially periodic patterns under conservation constraints, here the conservation of Brownian particles. By increasing the chemotactic sensitivity of active Brownian particles a transition from MIPS to motility induced periodic patterns takes place. They are found in a wide parameter range. Besides the phase diagrams for the onset of spatially periodic patterns also their nonlinear behavior beyond onset is investigated for selected parameter ranges.

BP 41.4 Fri 10:45 ZEU 160

The role of advection in the diffusioosmosis of an active micropump — •Gonçalo Antunes[1,2], Paolo Malgaretti[1,2], Jens Harting[3,4], and Siegfried Dietrich[1,2] — [1]MPI-IS, Stuttgart, Germany — [2]U. Stuttgart, Stuttgart, Germany — [3]HI-ERN, Forschungszentrum Jülich, Nürnberg, Germany — [4]TU/e, Eindhoven, The Netherlands

Diffusioosmosis can be exploited to fabricate active colloids that swim in a fluid/solute mixture through a self-generated inhomogeneous concentration of solute [1]. Using the same mechanism, an active channel can be fabricated such as to pump fluid in a way that is tunable via the geometry and chemistry of the channel.

In this talk, we study the flow inside an active hourglass-shaped channel. Our Lattice Boltzmann simulations are combined with a finite-difference solver for the advection-diffusion equation that determines the solute dynamics [2]. We find that even when the channel is fore-aft symmetric, advection can lead to the pumping of fluid, in analogy to the steady motion of isotropic colloids [3,4]. Furthermore, sustained oscillations are found where the magnitude of the flow oscillates with a tunable frequency. Our findings are thus relevant for

those who wish to exploit surface-driven flows at small scales.

[1] J. L. Anderson, Ann. Rev. Fluid Mech. **21** 61-99 (1989) [2] T. Peter, P. Malgaretti, N. Rivas, A. Scagliarini, J. Harting, S. Dietrich, arXiv:1911.06324 (2019) [3] S. Michelin, E. Lauga, and D. Bartolo, Phys. Fluids **25** 061701 (2013) [4] P. de Buyl, A. S. Mikhailov, and R. Kapral, EPL **103** 60009 (2013)

BP 41.5 Fri 11:00 ZEU 160

Dynamical states in underdamped active matter — •Dominic Arold and Michael Schmiedeberg — Institut für Theoretische Physik I, Universität Erlangen-Nürnberg, Staudtstraße 7, 91058 Erlangen, Germany

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

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

BP 41.6 Fri 11:15 ZEU 160

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

We present a predictive local field theory for the dynamics of interacting spherical active Brownian particles in two spatial dimensions. Alongside the general theory, which includes configurational order parameters and derivatives up to infinite order, we present reduced models that are easier to apply. We show that our theory contains popular models such as Active Model B + as special cases and that it provides explicit expressions for the coefficients occurring in these models. As further outcomes, the theory yields analytical expressions for the density-dependent mean swimming speed and the spinodal corresponding to motility-induced phase separation of the particles. The analytical predictions for the spinodal are found to be in very good agreement with the results of Brownian dynamics simulations. Furthermore, the critical point predicted by our analytical results agrees excellently with recent computational results from the literature.
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BP 42: Closing Talk (joint session BP/DY/CPP)

Time: Friday 12:30–13:15 Location: HSZ 02

Invited Talk BP 42.1 Fri 12:30 HSZ 02

Physics of active droplets — •Frank Jülicher — Max Planck Institute for the Physics of Complex Systems, Dresden

Phase separation provides a general physical mechanism for the spatial organization of cells and for the compartmentalization of chemical processes. Proteins together with other molecules can condense to form liquid-like droplets that provide localized chemical environments and that can serve as micro-reactors for biochemical reactions without an enclosing membrane. The cell cytoplasm can thus be viewed as an emulsion, where phase-separated compartments organize biochemical processes in space. Droplets that carry chemical activity are active systems that maintained away from thermodynamic equilibrium by chemical energy input. I will discuss the physics of such active droplets and active emulsions and show that they exhibit unusual properties and behaviors. Examples are the arrest of coarsening and the suppression of Ostwald ripening, spontaneous droplet division and droplet positioning by concentration gradients. The physics of active droplets could play important roles in fundamental cellular processes of many organisms and could have emerged early in the evolution of life.