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Fachverband Biologische Physik (BP)

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Overview of Invited Talks and Sessions

(Lecture halls H4, H10, H11, and H1; Poster B2)

Plenary Talks of BP

PRV II	Mon	13:15–13:45	H1	**Ultimate Rayleigh-Bénard and Taylor-Couette turbulence** — •Detlef Lohse
PLV II	Mon	14:00–14:45	H1	**Self-propelled topological defects in biological systems** — •Julia M Yeomans
PLV IV	Tue	8:30– 9:15	H1	**Impact of Turbulence on Cloud Microphysics** — •Eberhard Bodenschatz
PLV VII	Wed	8:30– 9:15	H1	**Mechanics of Single Protein Molecules** — •Matthias Rief
PLV XIV	Fri	8:30– 9:15	H1	**Soft Matter: Topological constraints do matter** — •Kurt Kremer

Invited Talks

BP 1.1	Mon	9:30–10:00	H4	**Structural dynamics of active membrane transporters as seen by single-molecule techniques** — •Thorben Cordes
BP 2.5	Mon	10:30–11:00	H10	**Lessons learned from complex mimics of biological membranes** — •Georg Pabst
BP 3.7	Mon	11:30–12:00	H11	**Cryo-Electron Tomography: Reconstruction Methods and Applications** — •Achilleas Frangakis
BP 5.1	Mon	15:00–15:30	H11	**Gene transfer between bacteria: from single molecules to genome dynamics** — •Berenike Maier
BP 8.7	Tue	11:30–12:00	H10	**Force generation by actin, microtubules and motors** — •Rhoda Hawkins
BP 9.1	Tue	9:30–10:00	H11	**Biomolecular structure determination from single molecule X-ray scattering with three photons per image** — •Helmut Grubmueller, Benjamin von Ardenne
BP 13.7	Wed	11:15–11:45	H4	**Non-equilibrium dynamics in biological matter** — •Christoph F Schmidt
BP 14.5	Wed	10:30–11:00	H10	**Physical determinants of phagocytic uptake and transport** — •Holger Kress
BP 15.1	Wed	9:30–10:00	H11	**Statistical physics of correlated neuronal variability** — •Moritz Helias
BP 17.4	Wed	15:45–16:15	H4	**Chaos in self-propelled droplets** — •Annette Zippelius, Reiner Kree
BP 18.7	Wed	16:30–17:00	H10	**Physics of epithelial folding** — •Guillaume Salbreux
BP 19.1	Wed	15:00–15:30	H11	**Self-organized wave-like beating of actin bundles** — Marie Pochitaloff, Mathieu Richard, Takagi Yasuharu, Wenxiang Cao, Enrique De La cruz, Jim Sellers, Jean-François Joanny, Frank Jülicher, Laurent Blanchoin, •Pascal Martin
BP 24.1	Thu	9:30–10:00	H11	**Active motion in living systems: from molecules to assemblies of organisms** — •Ben Fabry
BP 26.1	Thu	15:00–15:30	H4	**Understanding molecular machines by single-molecule FRET** — •Thorsten Hugel
BP 27.4	Thu	15:45–16:15	H10	**3D scaffolds as cell-instructive biomaterials** — •Christine Selhuber-Unkel
BP 28.7	Thu	16:30–17:00	H11	**Spontaneous buckling of active matter** — •Karsten Kruse

BP 31.1	Fri	9:30–10:00	H10	**Mechano-chemical self-organization determines search pattern in migratory cells** — •Milos Galic
BP 33.1	Fri	12:30–13:15	H1	**Pattern formation in active cytoskeletal systems** — •Andreas R. Bausch

Invited talks of the joint Symposium SKM Dissertation-Prize 2019

See SYSD for the full program of the symposium.

SYSD 1.1	Mon	9:30– 9:50	H2	**Synchronization and Waves in Confined Complex Active Media** — •Jan Frederik Totz
SYSD 1.2	Mon	9:50–10:10	H2	**Spin scattering of topologically protected electrons at defects** — •Philipp Rüssmann
SYSD 1.3	Mon	10:10–10:30	H2	**Beyond the molecular movie: Revealing the microscopic processes behind photo-induced phase transitions** — •Chris W. Nicholson
SYSD 1.4	Mon	10:30–10:50	H2	**Thermodynamic bounds on current fluctuations** — •Patrick Pietzonka
SYSD 1.5	Mon	10:50–11:10	H2	**Lightwave-driven quasiparticle acceleration** — •Fabian Langer
SYSD 1.6	Mon	11:10–11:30	H2	**Ultrafast plasmon-driven point-projection electron microscopy** — •Jan Vogelsang
SYSD 1.7	Mon	11:30–11:50	H2	**Helimagnets, sand patterns and fingerprints linked by topology** — •Peggy Schönherr

Invited talks of the joint Symposium Patterns in Nature: Origins, Universality, Functions

See SYPN for the full program of the symposium.

SYPN 1.1	Mon	15:00–15:30	H1	**Engineering spatial-temporal organization of bacterial suspensions** — •Igor Aronson
SYPN 1.2	Mon	15:30–16:00	H1	**Collective behaviour and pattern formation in phoretic active matter** — •Ramin Golestanian
SYPN 1.3	Mon	16:00–16:30	H1	**Control and selection of spatio-temporal patterns in complex systems** — •Svetlana Gurevich
SYPN 1.4	Mon	16:45–17:15	H1	**Self-organization of Active Surfaces** — •Frank Jülicher
SYPN 1.5	Mon	17:15–17:45	H1	**Front instabilities can reverse desertification** — •Ehud Meron

Invited talks of the joint Symposium Czech Republic as Guest of Honor

See SYCZ for the full program of the symposium.

SYCZ 1.1	Thu	9:30–10:00	H4	**Crystal symmetries and transport phenomena in antiferromagnets** — •Tomas Jungwirth
SYCZ 1.2	Thu	10:00–10:30	H4	**Terahertz subcycle charge and spin control** — •Rupert Huber
SYCZ 1.3	Thu	10:30–11:00	H4	**1D molecular system on surfaces** — •Pavel Jelinek
SYCZ 1.4	Thu	11:15–11:45	H4	**Tunneling microscopy on insulators provides access to out-of-equilibrium charge states** — •Jascha Repp
SYCZ 1.5	Thu	11:45–12:15	H4	**Occam's razor and complex networks from brain to climate** — •Jaroslav Hlinka
SYCZ 1.6	Thu	12:15–12:45	H4	**Long range temporal correlations in complex systems** — •Holger Kantz

Invited talks of the joint Symposium Physics of Self-Organization in DNA Nanostructures

See SYDN for the full program of the symposium.

SYDN 1.1	Thu	9:30–10:00	H1	**Functional DNA Nanostructures and Their Applications** — •Itamar Willner
SYDN 1.2	Thu	10:00–10:30	H1	**Gaining control of DNA-based nanodevices** — •Francesco Ricci
SYDN 1.3	Thu	10:30–11:00	H1	**Self-assembly and optical properties of single molecule polymers on DNA origami** — •Kurt Gothelf
SYDN 1.4	Thu	11:15–11:45	H1	**DNA origami route to dynamic plasmonics** — •Laura Liu
SYDN 1.5	Thu	11:45–12:15	H1	**DNA templated metal nanostructures** — •Ralf Seidel

Sessions

BP 1.1–1.11	Mon	9:30–13:00	H4	**Protein structure and dynamics**
BP 2.1–2.9	Mon	9:30–12:30	H10	**Membranes and vesicles I (joint session BP/CPP)**
BP 3.1–3.10	Mon	9:30–12:45	H11	**Bioimaging and biospectroscopy I**
BP 4.1–4.5	Mon	15:00–16:15	H10	**Membranes and vesicles II (joint session BP/CPP)**
BP 5.1–5.6	Mon	15:00–16:45	H11	**Systems biology & gene expression and signaling**
BP 6.1–6.83	Mon	17:30–19:30	Poster B2	**Poster I**
BP 7.1–7.10	Tue	9:30–12:30	H4	**Bioimaging and biospectroscopy II**
BP 8.1–8.10	Tue	9:30–12:45	H10	**Cytoskeletal filaments**
BP 9.1–9.12	Tue	9:30–13:00	H11	**Computational biophysics**
BP 10.1–10.4	Tue	9:30–10:30	H14	**Crystallization, nucleation and self-assembly (joint session CPP/BP)**
BP 11.1–11.2	Tue	11:30–12:30	H17	**Evolutionary game theory (joint session SOE/BP)**
BP 12.1–12.80	Tue	14:00–16:00	Poster B2	**Poster II**
BP 13.1–13.12	Wed	9:30–13:00	H4	**Active matter I (joint session BP/CPP/DY)**
BP 14.1–14.12	Wed	9:30–13:00	H10	**Cell mechanics I**
BP 15.1–15.11	Wed	9:30–13:00	H11	**Focus session: Collective Dynamics in Neural Networks**
BP 16.1–16.5	Wed	9:30–12:00	H17	**Dynamics of multilayer networks I (joint session SOE/DY/BP)**
BP 17.1–17.9	Wed	15:00–17:30	H4	**Statistical physics of biological systems I (joint session BP/DY)**
BP 18.1–18.8	Wed	15:00–17:15	H10	**Cell mechanics II**
BP 19.1–19.7	Wed	15:00–17:00	H11	**Focus session: Physics of cilia: Dynamics of synchronized oscillators**
BP 20.1–20.5	Wed	15:00–16:45	H17	**Dynamics of multilayer networks II (joint session SOE/DY/BP)**
BP 21.1–21.9	Wed	15:45–18:30	H13	**Biopolymers, biomaterials and bioinspired functional materials (joint session CPP/BP)**
BP 22	Wed	18:00–19:00	H4	**Annual general meeting of the BP division (BP Mitgliederversammlung)**
BP 23.1–23.12	Thu	9:30–12:45	H10	**Biomaterials and biopolymers I (joint session BP/CPP)**
BP 24.1–24.12	Thu	9:30–13:00	H11	**Cell adhesion and migration, multicellular systems I**
BP 25.1–25.3	Thu	12:15–13:00	H13	**Physics of self-organization in DNA nanostructures (joint session CPP/BP)**
BP 26.1–26.3	Thu	15:00–16:00	H4	**Single molecules biophysics**
BP 27.1–27.7	Thu	15:00–17:00	H10	**Biomaterials and biopolymers II (joint session BP/CPP)**
BP 28.1–28.9	Thu	15:00–17:30	H11	**Statistical physics of biological systems II (joint session BP/DY)**
BP 29.1–29.8	Thu	15:00–18:45	H17	**PhD Focus session: Theory of stochastic processes with applications in biology (joint session SOE/BP/DY/AKjDPG)**
BP 30.1–30.3	Thu	16:15–17:00	H4	**Cell mechanics III**
BP 31.1–31.9	Fri	9:30–12:00	H10	**Cell adhesion and migration, multicellular systems II**
BP 32.1–32.10	Fri	9:30–12:00	H11	**Active matter II (joint session BP/CPP/DY)**
BP 33.1–33.1	Fri	12:30–13:15	H1	**Closing talk (joint session BP/CPP/DY)**

Annual General Meeting of the Biological Physics Division

Wednesday 3.4.2019 18:00–19:00 H4

- Report of the current speaker team
- Award of the EPL poster prizes of the Biological Physics Division
- Election of the next BP spokespersons
- Miscellaneous

BP 1: Protein structure and dynamics

Time: Monday 9:30–13:00 Location: H4

Invited Talk BP 1.1 Mon 9:30 H4

Structural dynamics of active membrane transporters as seen by single-molecule techniques — •Thorben Cordes — Physical and Synthetic Biology, LMU Munich, Germany — Molecular Microscopy Research Group, University of Groningen, The Netherlands

Membrane transporters are vital to any living system and are involved in the translocation of a wide variety of different substrates. Despite their importance, all proposed molecular models for transport are based on indirect evidence due to the inability of classical biophysical and biochemical techniques to visualize dynamic structural changes. We recently started to use single-molecule fluorescence microscopy to characterize conformational states and changes in active membrane transporters in vitro to directly observe how different steps in transport are coordinated.[1-4] In my contribution I will first introduce our methodological approach to visualize structural dynamics[5] and accurate distances in biomacromolecules[6] using single-molecule spectroscopy and microscopy. Secondly, I will provide an overview of our mechanistic contributions to the field of primary[1,2,4] and secondary active transporters[3]. These involve various prokaryotic transporters, i.e., ABC importer-related periplasmic binding proteins[1,2], the ABC exporter McjD[4] and the sodium-symporter BetP[3].

[1] Gouridis et al., NSMB 22 (2015) 57-64. [2] van der Velde et al., Nature Communications 7:10144 (2016). [3] Jazi et al., Biochemistry 56 (2017) 2031-2041. [4] Husada et al., EMBO Journal (2018) e100056. [5] Lerner et al., Science 359 (2018) eaan1133. [6] Hellenkamp et al., Nature Methods 15 (2018) 669-676.

BP 1.2 Mon 10:00 H4

A Coarse-Grained Network Description of Protein Tertiary Structure — •Nora Sophie Martin[1,2] and Sebastian Edmund Ahnert[1,2] — [1]Theory of Condensed Matter Group, Cavendish Laboratory, University of Cambridge, Cambridge, UK — [2]Sainsbury Laboratory, University of Cambridge, Cambridge, UK

Due to the complexity of protein tertiary structure, many methods of describing, classifying and comparing solved structures have been proposed. Network-based descriptions, known as protein structure networks, amino acid networks or protein contact maps, have been used successfully. There is some regularity and redundancy in protein structure networks: two segments of the polypeptide chain, which are close in the native structure, give rise to a group of edges in the contact network. We identify these groups of edges to coarse-grain and simplify protein structure networks. First, the network is compressed: a shorter encoding of a protein structure network is found by sorting network edges into groups. Then, a minimal network is constructed by choosing all nodes of the full network, but only one edge per group. In this contribution, we will present the construction of these coarse-grained networks and how they can be used to compare protein structures.

BP 1.3 Mon 10:15 H4

Imaging single proteins with Low Energy Electron Holography — •Hannah Ochner[1], Sven Szilagyi[1], Sabine Abb[1], Stephan Rauschenbach[1,2], and Klaus Kern[1,3] — [1]Max-Planck-Institut für Festkörperforschung, Stuttgart — [2]Chemistry Research Laboratory, Department of Chemistry, University of Oxford — [3]École Polytechnique Fédérale de Lausanne

Recently, Low Energy Electron Holography (LEEH) has been shown to be able to image proteins at the single molecule level (without averaging), while avoiding radiation damage [1]. LEEH [2] is a lens-free imaging method in which the sample is radiated by coherent low energy electrons (50-200eV) [3] to form holograms that in principle contain full 3D information of the object. Basic Kirchhoff-Fresnel propagation-based numerical reconstruction of the holograms yields the shapes of the investigated proteins, as well as some internal contrast that already hints at 3D information. Thus, this technique can serve as a complementary method for protein structure determination, especially for types of proteins that are hard to access using other methods such as Cryo-EM or X-ray crystallography. We present the current state of the experiment and the reconstruction process along with future plans to enhance resolution and to improve the reconstruction towards including 3D information.

[1] PNAS 114, 1474-1479 (2017)
[2] Phy. Rev. Lett, 1990, 65(10), 1204-1206.
[3] Phys. Scr., 1988, 38, 260

BP 1.4 Mon 10:30 H4

Single Amyloid Fibrils Studied in a Thermophoretic Trap — •Martin Fränzl[1], Tobias Thalheim[1], Juliane Adler[2], Daniel Huster[2], and Frank Cichos[1] — [1]Peter Debye Institute for Soft Matter Physics, Molecular Nanophotonics Group, Universität Leipzig, Linnéstr. 5, 04103 Leipzig, Germany — [2]Institute for Medical Physics and Biophysics, Universität Leipzig, Härtelstr. 16-18, 04107 Leipzig, Germany

The aggregation of soluble proteins into highly ordered, insoluble amyloid fibrils is characteristic for a range of neurodegenerative disorders. While many different techniques have been applied to the investigation of fibril formation, almost all of them address the average properties of the ensemble. Here, we present a method that removes the ensemble average observing single fibrils freely dispersed in solution enabling to detect events commonly hidden in the ensemble average. The trapping scheme is based on the thermophoretic drift of nano-objects in temperature gradients allowing to probe the dynamics of a single fibril at various stages of its growth, e.g., the time evolution of the diffusion coefficients. It is shown that the rotational diffusion coefficient provides a unique measure to follow the growth of single fibrils with a precision below the optical resolution. Fibril growth of a few 10 nm can be identified providing a promising platform for studies of molecular interactions and in particular of protein and macromolecular aggregation processes at the single fibril level.

BP 1.5 Mon 10:45 H4

Compression of Single DNA Molecules in a Thermophoretic Trap — •Tobias Thalheim and Frank Cichos — Peter Debye Institute for Soft Matter Physics, Leipzig University, 04103 Leipzig, Germany

The Brownian motion of single DNA molecules, which are suspended in liquid, can be counter-acted by inhomogeneous temperature gradients which are generated by an optically heated metal structure of a thermophoretic trap. The trap [1] relying on thermophoresis, also known as Soret effect, consists of a focused laser beam which rotates on the ring-like metal nano-structure in a continuous fashion thereby generating the inhomogeneous temperature profile which, in turn, induces thermophoretic drift velocities preventing the free fluctuations of the DNA strand. Drift velocities in outer regions of the trap are due to the inhomogeneity of the temperature landscape larger than those closer to the trapping center. An elongated soft molecule like DNA therefore experiences different drift velocities at different parts of the molecule in the trap leading to a compression of the DNA strand which is reflected in a decreased radius of gyration. The influence of the trap on the conformation dynamics of the DNA molecule will be studied with a model-free statistical tool which is called principal-components analysis applied as introduced by Cohen and Moerner [2].

References

[1] M. Braun, A. P. Bregulla, K. Günther, M. Mertig, and F. Cichos, Nano Lett 15, 5499–5505 (2015)
[2] A. E. Cohen, and W. E. Moerner, PNAS 104, 12622–12627 (2007)

30 minutes break.

BP 1.6 Mon 11:30 H4

LOVely aureochromes: Time-resolved small-angle X-ray scattering reveals the global structure recovery time of the multidomain photoreceptor — •Saskia Bannister, Elena Herman, Thomas Hellweg, and Tilman Kottke — Bielefeld University, Germany

Aureochromes (AUREO) function as blue-light-regulated transcription factors in algae.[1] Their basic region/leucine zipper (bZIP) effector domain binds DNA with a specific sequence while a light-, oxygen-, or voltage-sensitive (LOV) domain acts as the C-terminal sensor. In the dark, LOV binds flavin non-covalently while upon illumination an adduct is formed. Due to their unusual domain arrangement AUREOs are versatile candidates for new synthetic optogenetic tools. We therefore characterized a full-length AUREO1c variant (38 kDa) and found that its quantum yield of adduct formation is exceptionally low. Furthermore, we applied time-resolved small-angle X-ray scat-

tering (SAXS) on an inhouse setup to investigate the recovery of the overall structure of AUREO1c in the dark. Additionally, the recovery kinetics of the flavin was determined by UV/vis spectroscopy under similar conditions. These studies revealed a discrepancy between the lifetime of the flavin adduct and the global structural recovery time of the multidomain photoreceptor. We therefore conclude that an additional spectrally silent intermediate exists that significantly prolongs the lifetime of the signalling state.

[1] Takahashi et al. (2007), *PNAS 104*, 19625-19630.

BP 1.7 Mon 11:45 H4

Protein-ligand interaction and hierarchical complex dynamics of Hsp90 — •Steffen Wolf[1], Benedikt Sohmen[2], Björn Hellenkamp[2], Thorsten Hugel[2], and Gerhard Stock[1] — [1]Biomolecular Dynamics, Institute of Physics, Albert Ludwigs University Freiburg, Germany — [2]Institute of Physical Chemistry, livMatS and CIBSS, University of Freiburg, Germany

Ligand binding to proteins and subsequent functional control by the appearing structural changes is at the heart of regulation of protein function. As these processes take place on timescales from μs (ligand binding) to hours (ligand off-binding), accessing them via molecular dynamics simulations is challenging, and requires state-of-art unbiased simulations. Here, we report on extensive unbiased all-atom molecular dynamics simulations with the full 1300 amino acid Hsp90 dimer on the order of 25 μs simulated time, and compare these results to recent single molecule FRET experiments. We show how external energy input in the form of ATP puts the protein under strain, and forces the protein into an energetically disfavored active folding confirmation. Interestingly, only few amino acids appears to be responsible to mediate this conformational shift between nucleotide binding pocket and the full protein dimer. Hydrolysis of ATP to ADP+P_i removes this strain from the protein, causing a relaxed, inactive confirmation. The transition of structural information from the nucleotide binding site to the full dimer structure follows hierarchical dynamics, from initial nucleotide/amino acid contact loss on a ns time scale to complex structure changes on the order of $0.1 - 1$ μs.

BP 1.8 Mon 12:00 H4

Dynamical Coring of Markov State Models — •Anna Weber, Daniel Nagel, Benjamin Lickert, and Gerhard Stock — Albert Ludwigs University, 79104 Freiburg

The construction of suitable metastable conformational states is fundamental for the description of protein dynamics through Markov state models. These microstates can be generated via density-based clustering algorithms as, e.g., presented by Sittel et al. [J. Chem. Theory Comput. 38, 152 (2017)], resulting in clusters that are cut at the energy barriers. However, the lack of sampling in the transition region combined with the inevitable projection from high dimension onto a low dimensional space, typically leads to a misclassification of points in the transition region. This often causes intrastate fluctuations to be misinterpreted as interstate transitions, causing artificially short life times of the microstates and spoiling calculations of MSM transition rates.

Dynamical coring represents an effective and simple remedy for those problems by requiring the trajectory to spend a minimum time in the new state for a transition to be counted. Adopting molecular dynamics simulations of a well-established biomolecular system (villin headpiece), we demonstrate that coring immensely improves the Markovianity and metastability of the microstates. Providing high structural and temporal resolution, the combination of density-based clustering and dynamical coring is particularly well suited to describe the complex structural dynamics of unfolded biomolecules.

BP 1.9 Mon 12:15 H4

MD Simulation Studies of Protein Dynamics in Molecule-Shaped Confinement — •Timothy Wohlfromm and Michael Vogel — TU Darmstadt, Institut für Festkörperphysik, Hochschulstr. 6, 64289, Darmstadt, Germany

We report on findings regarding dynamics of the elastin-like polypeptide $(VPGVG)_{50}$ and its surrounding hydration shell in confinement. An understanding of confinement effects on protein dynamics is of utmost importance to improve our still limited knowledge about protein functions in the crowded interior of cells. To isolate pure geometrical effects of the confinement on protein dynamics, we generated the pores consisting of the same type of molecules as the solvent, in our case water, but restrained in position by harmonic potentials of varying restoring forces to simulate confining surfaces with differing rigidity. Moreover, we use a pore shape which is consistent with the protein shape such that the thickness of the hydration layer is well defined. Varying the thickness of hydration layers we find that the minimal hydration level for the confined protein to show bulk behaviour is 1 g/g, defined as ratio of water mass to protein mass. We observe in spatially resolved analyses that the correlation times of water vary by more than one order of magnitude across the confinement depending on the rigidity of the pore wall. We find a correlation between the slowdown of water molecules in vicinity of the protein surface and the protein dynamics. This effect is not caused by the reduced center of mass motion of the protein in confinement, but related to internal flexibility. These results shed new light on protein-solvent couplings.

BP 1.10 Mon 12:30 H4

Drug-induced changes in protein secondary structure and its relation to major globular rearrangements and activation of integrin alphaIIb beta3 — •Una Janke[1,2], Martin Kulke[1], Walter Langel[1], and Mihaela Delcea[1,2] — [1]Institute for Biochemistry, University of Greifswald, Felix-Hausdorff-Straße 4, 17489 Greifswald, Germany — [2]ZIK HIKE, University of Greifswald, Fleischmannstraße 42, 17489 Greifswald, Germany

The heterodimeric platelet receptor integrin αIIbβ3 is involved in hemostasis and clot formation. αIIbβ3 exists in three different conformations: the bent (resting) state; the intermediate extended state; and the ligand-occupied active state. The dramatic rearrangements of the overall structure due to αIIbβ3 activation, is possibly related to changes in the secondary structure of the protein. Here, we use a combination of biophysical methods and molecular dynamics simulations (MDS) to investigate whether clinically relevant drugs induce changes in protein structure and lead to its activation in a membrane environment (e.g. liposomes). By QCM and CD spectroscopy we show Mn2+-induced binding of the active-conformation specific antibody PAC-1. However, no major secondary structural changes of αIIbβ3 were found. We also show that treatment with drugs (e.g. quinine) causes activation of αIIbβ3 without any significant changes in secondary structure. MDS studies confirmed the idea of a hinge motion in the extracellular part of the integrin. The combination of biophysical tools and MDS can be applied to study other transmembrane proteins in a membrane environment.

BP 1.11 Mon 12:45 H4

Quantum Mechanics of Proteins in Water: The role of Plasmon-like Solute-Solvent Interactions — •Martin Stöhr and Alexandre Tkatchenko — Physics and Materials Science Research Unit, University of Luxembourg, Luxembourg

van der Waals dispersion interactions form a major component of both intra-protein and protein-water interactions. As such, they play an essential role for the spontaneous folding of proteins in aqueous environments. van der Waals forces arise from long-range electron correlation and are thus inherently quantum-mechanical and many-body in nature. Nevertheless, they are typically only treated in a phenomenological manner via pairwise potentials. Here, we employ an explicit quantum-mechanical framework based on the many-body dispersion formalism, which allows us to highlight the importance of the many-body character of dispersion interactions for protein energetics and protein-water interactions. As such, our study provides unexplored insights into the fundamental quantum-mechanics of proteins in water. In contrast to commonly used pairwise approaches, many-body dispersion effects significantly affect relative stabilities during protein folding in the gas-phase. Embedding in an aqueous environment leads to a quenching of such effects and stabilizes native conformations. Remarkably, this quenching arises from a high degree of delocalization and collectivity of protein-water dispersion interactions, which hints at an unexpected persistence of electron correlation through aqueous environments. Our findings are exemplified on several prototypical proteins, emphasizing their broad validity in the biomolecular context.

BP 2: Membranes and vesicles I (joint session BP/CPP)

Time: Monday 9:30–12:30 Location: H10

BP 2.1 Mon 9:30 H10

Soft Thermal Treatment Stabilizes Vacuum-deposited Phospholipid Layers for Sensor Applications — Sebastian Molina[1], Marcelo Cisternas[1], Maria J. Retamal[2], Nicolas Moraga[1], Hugo Zelada[1], •Jonas Fortmann[1,3], Tomas P. Corrales[4], Patrick Huber[5], Marco Soto-Arriaza[2], 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]TU Clausthal, Germany — [4]Department of Physics, UTFSM, Valparaiso, Chile — [5]TUHH, Hamburg, Germany

Artificial membranes allow one to study of the behavior of biological membranes, which are the base of the cell membrane structure. The cell membrane is composed of different lipids and proteins that change their behavior when they are stimulated physically and/or chemically. Besides traditional methods we use a solvent free, dry method for phospholipid deposition in high vacuum onto residue-free silicon substrates. The cleanness of the substrate and the precise thickness of the DPPC layer on the substrate is controlled in-situ using Very High Resolution Ellipsometry. In this work we show the enhancement of phospholipid bilayer self-assembling and stability due to a soft thermal treatment. The behavior of the artificial membranes is studied in air and immersed in aqueous medium, which mimics the natural environment of the biological membrane. Acknowledgements: FONDECYT Nos. 3160803 (MJR), 1180939 (UGV) 1171047 (MSA) and 11160664 (TPC), CONICYT Fellowship (MC) and CONICYT-PIA ACT 1409.

BP 2.2 Mon 9:45 H10

Prolonged Phospholipid Bilayer Stability due to Hydration on Porous Silicon: Pore Diameter and Porosity Optimization — Nicolas Moraga[1], Marcelo Cisternas[1], Diego Diaz[1], Rodrigo Catalan[1], Maria J. Retamal[2], Tomas P. Corrales[3], Mark Busch[4], Patrick Huber[4], Marco Soto-Arriaza[2], 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 — [4]TUHH, Hamburg, Germany

Study of artificial membranes has become an important way to gain insight into the physical behavior of cell membranes. In this work, porous silicon substrates (pSi) were prepared with different pore diameters and porosities. The substrates were characterized with Field Emission Electron Microscopy. The phospholipid (DPPC) was deposited in high vacuum from the gas phase on the pSi. Film thickness was controlled in-situ using Very High Resolution Ellipsometry (VHRE). Samples were hydrated in air with ultrapure water to assemble the bilayer. Phase transitions were measured with VHRE and Stray Light Intensity during temperature cycles. AFM was used to study morphological changes of bilayers as a function of temperature. Our results show that specific pore diameters and porosities of nanoporous substrates prolong phospholipid bilayer stability due to hydration with water stored in the pores. Acknowledgement: FONDECYT Nos. 3160803 (MJR), 1180939 (UGV), 1171047 (MSA) and 11160664 (TPC), CONICYT Fellowship (MC) and CONICYT-PIA ACT 1409.

BP 2.3 Mon 10:00 H10

Mechanisms of Interactions between Lipid Membranes in the Presence of Biological Cosolutes — •Amanuel Wolde-Kidan[1], Quoc Dat Pham[2], Alexander Schlaich[3], Emma Sparr[2], and Roland Netz[4] — [1]Freie Universität, Berlin, Germany — [2]Lund University, Lund, Sweden — [3]Laboratoire Interdisciplinaire de Physique, Grenoble, France — [4]Max Planck Institute of Colloids and Interfaces, Potsdam, Germany

Lipid membranes form the diffusional barrier of eukaryotic cells and determine processes when cells come into close contact, for example during cell fusion or vesicle formation. We analyze the effects of three cosolutes on membrane interactions, which are all abundantly found in biological systems, namely urea, TMAO and sodium chloride. The effect of the polar solutes urea and TMAO on protein stability has been studied extensively, but their influence on lipid bilayers has only recently started to be investigated. Using atomistic molecular dynamics simulations and theoretical modeling we analyze different mechanisms of lipid-solute and lipid-lipid interactions. By means of solution thermodynamics we model the effect of the cosolutes on the hydration repulsion between lipid bilayers. Results from our simulations compare well to experimental calorimetric measurements. We find that the osmotic pressure due to the added solute has the most important influence on the hydration repulsion. Furthermore, we find that the interaction mechanism of sodium chloride with lipid bilayers is dominated by the ion-membrane potentials of mean force. Other factors such as the dielectric response seem to be of less importance.

BP 2.4 Mon 10:15 H10

Glycolipids as zippers between phospholipid membranes — •Victoria Latza[1], Bruno Demé[2], and Emanuel Schneck[1] — [1]Max-Planck Institut für Kolloid und Grenzflächenforschung, Potsdam, Germany — [2]Institut Laue-Langevin, Grenoble, France

Essential mechanisms in biological cells, such as molecular transport and cell division, involve the spatiotemporal reorganization of membranes in terms of membrane adhesion or vesicle release. These processes are largely determined by membrane-membrane interactions and thus highly sensitive to the membranes* surface chemistry. It is known that certain membrane-bound saccharide motifs, such as the LewisX trisaccharide, promote membrane adhesion. These cases, however, have been viewed as exceptions. Here, with the help of small-angle x-ray scattering, we investigate the interaction between membranes composed of ternary lipid mixtures of (i) uncharged phospholipids as matrix, (ii) negatively charged phospholipids to induce electrostatic repulsion, and (iii) glycolipids featuring various mono- and oligosaccharide headgroups. We find that a large fraction of saccharide types are able to induce membrane adhesion through the formation of weak inter-membrane bonds. These bonds are resistant to electrostatic repulsion at levels that lead to the complete unbinding of pure phospholipid membranes. Our results strongly indicate that glycolipid-induced membrane-binding is not an exceptional feature of few saccharide types but a highly abundant phenomenon of great relevance for membrane biophysics.

Invited Talk BP 2.5 Mon 10:30 H10

Lessons learned from complex mimics of biological membranes — •Georg Pabst — University of Graz, Institute of Molecular Biociences, NAWI Graz, 8010 Graz, Austria

Lipid-only mimics of biological membranes serve as valuable platforms for studying the functional role of membrane lipids under chemically and experimentally well-defined conditions. Of recent, we have focused on complex mimics of mammalian and bacterial plasma membranes with either lateral or transbilayer inhomogeneities. In particular, we have developed protocols for fabricating and analyzing asymmetric lipid vesicles, which are sufficiently stable and which are amenable for biophysical studies using diverse techniques. We have specialized on small-angle X-ray/neutron scattering combined with complimentary techniques to address leaflet specific structure and transbilayer coupling mechanisms. Complementary, we are currently developing tools for reliable estimates for intrinsic lipid curvatures, which are known to play a pivotal role in coupling to protein function. I will present recent research highlights resulting from these efforts and discuss some applications to membrane-active drugs, such as antimicrobial peptides, or the partitioning of transmembrane proteins function.

30 minutes break.

BP 2.6 Mon 11:30 H10

The interaction of viral fusion peptides with model lipid membranes at high hydrostatic pressure — Göran Surmeier[1], Michael Paulus[1], Susanne Dogan[1], Yury Forov[1], Mirko Elbers[1], Simon Egger[2] und •Julia Nase[1] — [1]Fakultät Physik/DELTA, TU Dortmund, 44221 Dortmund — [2]Physikalische Chemie, TU Dortmund, 44221 Dortmund

When a virus enters a host cell, the insertion of viral fusion peptides (FPs) into the target membrane catalyzes the membrane fusion reaction. We investigated the interaction of different FPs with model membranes in X-ray reflectivity measurements at the interface between monoolein/water mixtures and a silicon substrate. In addition, the bulk and interfacial structures were investigated with small angle X-ray scattering in transmission and in grazing incidence. Monoole-

in/water mixtures have a very rich pressure-dependent phase diagram. Notably, the inverse bicontinuous cubic phases exhibit structural analogies to the hemifusion intermediates. We found that pressurization triggers formation of ordered lamellar monoolein multilayers close to the interface even in a pressure range where the bulk material is in the cubic phase. Previous studies demonstrated the effect of FPs on the pressure-dependent phase boundaries [1]. We resolved the vertical membrane structure of some multilayers and monitored the penetration of FPs into the membrane. Experiments were performed in a custom-made high hydrostatic pressure cell [2] at beamlines ID31 of the ESRF and BL9 of DELTA. [1] A. Levin et al, J Phys Chem B 121 (2017) [2] F.J. Wirkert et al, J. Synchr. Radiat. 21 (2014)

BP 2.7 Mon 11:45 H10

Lipid membrane fusion in proteoliposomes and multilamellar stacks studied by X-ray scattering — •Kilian Frank[1], Karlo Komorowski[1], Veronica Chappa[2], Max Scheu[1], Marcus Müller[2], and Tim Salditt[1] — [1]Georg-August-Universität, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen — [2]Georg-August-Universität, Institute for Theoretical Physics, Friedrich-Hund-Platz 1, 37077 Göttingen

Intermediate structures of membrane fusion, e.g. during release of neurotransmitter at the synapse, are difficult to resolve at the molecular level, especially in the close-to-physiological regime with SNARE fusion proteins. To provide structural information, we combine two X-ray scattering approaches: First, SAXS on proteoliposomes (PL) with reconstituted SNAREs serves to identify changes in PL size and radial density profile upon fusion in a hydrated environment. We present a simulation framework based on 3D-FFT to estimate how well size and shape changes (homogeneous swelling of an ensemble, thermal fluctuations, and strong equilibrium defomations) are detected in PL-SAXS. Second, GISAXS on solid-supported multilamellar membrane stacks at controlled humidity and salt concentration allows to characterize the energy of fusion stalk formation, prior to crystallization to a stalk phase with rhombohedral symmetry. Here we find that CaCl2, in contrast to other salts, facilitates stalk phase formation, also cooperatively in fusiogenic lipid mixtures. By combining both methods, we lay the foundation for a quantitative X-ray analysis of the membrane fusion process with natural proteins or artificial peptides.

BP 2.8 Mon 12:00 H10

Structural changes in biomimetic myelin membranes induced by Myelin Basic Protein — •Benjamin Krugmann[1,2], Andreas Stadler[1], Aurel Radulescu[2], Alexandros Koutsioumpas[2], and Stephan Förster[1,2] — [1]Forschungszentrum Jülich JCNS-1, 52428 Jülich, Germany — [2]Forschungszentrum Jülich JCNS-MLZ, 85748 Garching, Germany

The myelin sheath plays an important role in nerve signal conduction. It acts as an insulating layer which enables fast signal transport by reducing conduction losses. In demyelinating diseases like multiple sclerosis, this membrane is damaged, which leads to severe problems in nerve conduction. In literature different values for the lipid composition of healthy and modified membranes have been found. Based on these results, we investigate the membrane structure for the respective compositions. As next step we add Myelin Basic Protein (MBP) to the membrane and investigate the induced structural change. Small angle neutron scattering (SANS) and cryo-transmission electron microscopy data show the structure of vesicles with healthy and modified membrane composition and the strong structure change induced by MBP. Neutron Reflectometry (NR) data indicates that MBP interacts differently with healthy and modified myelin membranes.

BP 2.9 Mon 12:15 H10

Influenza A matrix protein (M1) multimerization is the main driving force for membrane bending and tubulation. — •Ismail Dahmani — Cell Membrane Biophysics Group / Universität Potsdam Karl-Liebknecht-Str. 24-25, Haus 25, B/1.04 14476 Potsdam-Golm Deutschland

The matrix protein of the Influenza A virus (M1) forms a shell underlying the viral lipid envelope and controls the geometry of the virus capsid. In infected cells, M1 orchestrates the process of new virion formation by binding to the inner leaflet of the plasma membrane (PM), which finally results in bending of the lipid bilayer and virus release . The exact role of M1 polymerization in inducing membrane deformation and budding is not clear. Here, to model virus egress through the PM, we analyzed M1 binding to giant unilamellar vesicles (GUVs). Our results show that M1 and a construct consisting of its Nterminal domain (NM1) bind to negatively charged lipids causing unidirectional deformation by imposing an inward curvature and membrane tabulation . Detergent-mediated solubilization of the lipid bilayer after M1 binding leaves the three-dimensional organization of the protein intact, indicating that M1 forms a very stable network adjacent and independent from the lipid membrane. Our data also indicate that the C-terminal domain of M1 is not needed for the establishment of protein-protein interactions and membrane deformation. Finally in acidic conditions (pH=5) M1 irreversibly loses its ability to multimerize and induce curvature, thus confirming that M1 multimerization is the molecular mechanism responsible for membrane deformation.

BP 3: Bioimaging and biospectroscopy I

Time: Monday 9:30–12:45 Location: H11

BP 3.1 Mon 9:30 H11

Microviscosity of bacterial biofilm matrix characterized by quantitative fluorescence microscopy — •Valentin Dunsing, Tobias Irmscher, Stefanie Barbirz, and Salvatore Chiantia — Universität Potsdam, Institut für Biochemie u. Biologie, Potsdam, DE

Bacterial biofilms are surface-adherent communities of bacteria surrounded by an extracellular polymeric substance (EPS), which protects bacteria from antibiotics and pathogens. In this context, it remains unclear to which extent the EPS matrix imposes a physical barrier, e.g. to the transport of bacteriophages. To address this question, we have reconstituted the EPS of the bacterium *Pantoea stewartii* and investigated the diffusion properties of fluorescent particles using fluorescence correlation spectroscopy and single particle tracking. This approach allows to study the EPS spatial organization under various physicochemical conditions. We show that small probes diffuse freely in the EPS with diffusion coefficients similar to those measured in water. In contrast, large probes are drastically slowed down, showing anomalous subdiffusion. The degree of confinement increases with EPS concentration. At physiological concentrations, beads of the size of bacteriophages are up to 100-fold slowed down compared to the dynamics in aqueous solution. To overcome this physical barrier, bacteriophages are equipped with EPS degrading enzymes. We show that upon EPS degradation, strongly confined diffusion rapidly turns to free diffusion. Thus, our approach allows the investigation of dynamic changes of the biofilm microviscosity and shows that the EPS imposes a probe-size dependent diffusion barrier under physiological conditions.

BP 3.2 Mon 9:45 H11

Time resolved fluorescence spectroscopy of European Robin Cryptochrome 4. — •Anitta Rose Thomas[1], Jingjing Xu[2,3], Henrik Mouritsen[2,3], and Christoph Lienau[1] — [1]Institut for Physics,Carl Von Ossietzky University Oldenburg — [2]Institute of Biology and Environmental Sciences,Carl Von Ossietzky University Oldenburg — [3]Research Center for Neurosensory Sciences,Carl Von Ossietzky University Oldenburg

Cryptochrome proteins are special candidates for sensing the direction of the earth magnetic field due to the radical pair mechanism. While it is known that blue light absorption by the chromophore Flavin Adenine Dinucleotide(FAD), non- covalently bound to Cryptochrome, is initiating radical pair formation, it is challenging to probe the crucial chromophore-protein binding by all-optical means. Here, we study binding between FAD and European Robin Cryptochrome 4, the most likely candidate for avian magnetoreception, using time resolved fluorescence anisotropy measurement with 100 ps time resolution. The measurements show that the binding of FAD inside the Cryptochrome protein cage essentially locks the alignment of the optically excited transition dipole and effectively suppresses its rotational relaxation. The results give partial access to the electron transfer of the photo excited FAD chromophore which is faster than 100 ps.

BP 3.3 Mon 10:00 H11

Non-equilibrium dynamics of endoplasmic reticulum structures — •Konstantin Speckner, Lorenz Stadler, and Matthias Weiss — Experimental Physics 1, University of Bayreuth, Germany

Intracellular transport frequently shows anomalous characteristics, i.e. a sublinear increase of the mean-square displacement in time. Using single-particle tracking we have studied the subdiffusion of cellular organelle structures, with a particular emphasis on the impact of non-equilibrium driving forces imposed by cytoskeletal elements. In particular, we have analyzed the dynamics of tubular junctions in the endoplasmic reticulum (ER) network [1] and of ER membrane domains (ER exit sites, ERES) [2]. Our results demonstrate that both, ER junctions and ERES show a distinct subdiffusion with an anti-correlation of successive steps, reminiscent of fractional Brownian motion. Disrupting the microtubule cytoskeleton significantly altered the subdiffusive characteristics of both entities, highlighting that even subdiffusion in living cells is an actively driven process. While the motion pattern of ER junctions was seen to be directly dependent on the presence of microtubules, ERES were only indirectly affected. Our experimental data indicate that ER junctions move like monomer units of (semi)flexible polymers with the overall dynamics of the ER network being governed by fractons. ERES rather are mobile domains that perform a quasi-one-dimensional random walk on the shivering backbone of ER tubules.

[1] K. Speckner et al., Phys. Rev. E 98, 012406 (2018).
[2] L. Stadler et al., Biophys. J. 115(8), 1552 (2018).

BP 3.4 Mon 10:15 H11

Photoinduced processes of free bilins in solution: Femtosecond transient absorption spectroscopy on phycocyanobilin — •Maximilian Theiss[1], Tilman Lamparter[2], Maria Andrea Mroginski[3], Jörg Matysik[4], Chen Song[4], Wolfgang Gärtner[4], and Rolf Diller[1] — [1]TU Kaiserslautern, D-67663 Kaiserslautern — [2]KIT, D-76131 Karlsruhe — [3]TU Berlin, D-10623 Berlin — [4]Universität Leipzig, D-04103 Leipzig

Bilins are linear tetrapyrroles with rich photochemistry in solution (1,2). When bound to proteins they serve as chromophore in plant-phytochromes, bacterial sensor proteins and optogenetic systems (3). In the bound form protein-chromophore interaction restricts the potentially possible degrees of freedom (4). For a better understanding of the underlying mechanisms we study the primary photochemistry of the free bilin phycocyanobilin (PCB), employing fs transient absorption in the UV/Vis and mid-IR spectral region, complemented by quantum chemical calculations, static fluorescence and NMR measurements. In particular, PCB consists of different ground state species and shows photoinduced conformational changes (5) as well as alteration of protonation state. Additionally, broad IR continuum absorption bands in the transient absorption spectra indicate an ultrafast proton release reaction.

(1) Falk. (2012) The chemistry of linear oligopyrroles and bile pigments. SSBM. (2) Carreira-Blanco et al. (2016) PCCP 18:7148. (3) Gasser et al. (2014) PNAS 111.24:8803. (4) Singer et al. (2016) CPC 17:1288. (5) Dietzek et al. (2011) CPL 515:163.

BP 3.5 Mon 10:30 H11

High throughput real-time measurements and image analysis of suspended cells and particles — •Daniel Geiger, Tobias Neckernuss, Jonas Pfeil, and Othmar Marti — Institute of Experimental Physics, University of Ulm, Germany

Imaging of cells has proven to be a viable tool to determine properties like type or pathogenicity. Recent advances in microfluidics and lab-on-a-chip devices are based on the availability of detection systems to observe single cells with very high throughput. High-speed cameras in such applications have several drawbacks. The large amount of data needs buffering, which in turn requires offline data evaluation. Furthermore, data evaluation by standard computer architectures introduces unpredictable latency between measurement and data analysis. Hence, applications such as sorting are hardly possible by a system built of conventional camera and data processing.

We present a novel device that is based on an advanced imaging system combined with a field programmable gate array (FPGA) for control and data analysis. Due to specially developed algorithms the FPGA is able to analyze the data in real time with a fixed latency. Therefore, applications based on image analysis that require a fixed and reliable latency are feasible. Our measurement system is able to analyze up to eight regions of interest, each running at 5000 frames per second, simultaneously.

BP 3.6 Mon 10:45 H11

Light induced phycobiliprotein dynamics in *Halomicronema hongdechloris* adapted to far red light — •Franz-Josef Schmitt and Züleyha Yenice Campbell — Technische Universität Berlin, Sekr. PC 14, Straße des 17. Juni 135, 10623 Berlin

The phototrophic cyanobacterium *Halomicronema hongdechloris* contains chlorophyll *a* and *f* in photosystem II when it is grown under far red light conditions (> 720 nm). In former studies we had shown that the phycobiliproteins (PBS) exhibit effcient excitation energy transfer (EET) to Chl *a* and Chl *f* within 200 ps if *H. hongdechloris* grown under far red light is illuminated with 630 nm. After adaption to far red light the PBS are localized in separated clusters of the cell. Short illumination with blue light (405 nm) leads to a mobilization of the PBS on the time scales of seconds. The PBS quickly appear completely decoupled from the photosystem II (PS II) for several seconds and subsequently recouple to the PS II with recovery of the EET from PBS to PS II within seconds.

We assume that production of reactive oxygen species (ROS) leads to mobilization and recoupling of the PBP antenna complexes after the cells had been adapted to far red light conditions. In parallel high content of carotenoids is found in *H. hongdechloris* grown under far red light. We present a quantitative analysis of the PBP mobility in dependence of the applied light intensity and wavelength.

30 minutes break.

Invited Talk BP 3.7 Mon 11:30 H11

Cryo-Electron Tomography: Reconstruction Methods and Applications — •Achilleas Frangakis — Goethe Universitaet Frankfurt, Frankfurt, Germany

Correction of the contrast transfer function (CTF) of the microscope is a necessary step, in order to achieve high resolution from averaged electron microscopic images. Thereby, the CTF is first estimated and subsequently the electron micrograph is corrected, so that the negative oscillations of the CTF are equalized. Typically, the CTF correction is performed in 2D and the tilt-induced focus gradient is taken into account. Most often, the sample-thickness-induced focus gradient is ignored. Theoretical considerations, as well as implementation suggestions, for a 3D CTF correction that considers both gradients have been proposed before, although an implementation achieving a resolution improvement has been lacking, primarily due to computational reasons. Here, we present a comprehensive solution for a 3D CTF correction based on the Jensen-Kornberg scheme, which performs a slice-by-slice correction of the CTF within the tomographic reconstruction. We show that the computational requirements are comparable to those of 2D CTF correction. Using the examples of mitochondrial ribosomes and tobacco mosaic virus we demonstrate the improvement of the reconstruction quality with the 3D CTF correction, and the resolution gain on sub-tomogram averaging. More interestingly, for tomographic applications, the quality of the individual sub-tomograms before averaging increases significantly. We find that 3D CTF correction always produces equal or better results than 2D CTF correction.

BP 3.8 Mon 12:00 H11

Nanoscale dipole dynamics of protein membranes by Broadband Dielectric Microscopy — •G. Gramse[1,3], A. Schönhals[2], and F. Kienberger[3] — [1]JKU, Biophysics Institute, Linz, Austria — [2]BAM, Berlin, Germany — [3]Keysight Laboratories, Linz, Austria

The response of biological matter to electric fields is an intrinsic property in Biophysics which can be used to identify and characterize complex biological structures and sub-structures. At the same time, many physiological processes down to the cellular and sub-cellular level are based on electric and electrostatic interactions. Therefore quantitative investigation of dielectric properties at the nanoscale has gained major interest in recent years [1,2]. While dipoles at decreasing spatial scales within the biological structures relax with increasing frequencies, until now researchers could not address the frequency dependency of the dielectric permittivity and lacked a fundamental dimension for the understanding of many physical processes. We combined instrumentation for high frequency electrical characterization with the SPM and precise FEM based quantification procedures. The technique can be used to locally characterize biological micro-and nanoscale objects and allows for the first time quantitative nanoscale dielectric spectroscopy of bio-membranes in a broad frequency window from 3 kHz -10 GHz

covering almost six orders of magnitude [3]. This allowed us to investigate the effect of surface water on the dipole dynamics in bR-membrane patches. The technique can be operated in dry and liquid environment. [1] Gramse G et al. 2013 Biophysical Journal 104 (p1257-62) [2] Biagi MC et al. 2016 ACS Nano 10, 1 [3] G. Gramse et al. Under Review

BP 3.9 Mon 12:15 H11

Machine learning approaches for optical microscopy in scattering media — •Johannes Seelig — caesar, MPG, Bonn

Light scattering hinders optical microscopy in many applications. For example in biological tissue such as the brain, only a small fraction of the entire sample can typically be accessed with diffraction limited resolution. Improved computational methods in machine learning open up novel opportunities to overcome these limitations. We will discuss the combination of approaches from adaptive optics, optical microscopy, and machine learning to improve optical imaging in various weakly and strongly scattering samples.

BP 3.10 Mon 12:30 H11

A multisensory interface for exploring nanomechanical tissue properties with human senses — •Robert Magerle[1], Stephen Barrass[2], Andreas Otto[1], Mónica Tamara Heredia Muñoz[1], Martin Dehnert[1], Thomas Baumann[1], and Alexandra Bendixen[1] — [1]TU Chemnitz, Chemnitz, Germany — [2]sonification.com, Canberra, Australia

With an atomic force microscope (AFM), the shape of a surface and its local mechanical properties can be measured in great detail on the nanometer scale. Understanding this complex and multidimensional data, however, is still in its infancy. Biological tissues in particular display a very complex spatial structure, and their mechanical properties remain largely unexplored on the nanometer scale. In the case of such complex data, analytical methods based on statistical data reduction have reached their limits. Here we present a new approach that fundamentally changes data analysis by making this complex data accessible to human perception and cognition. With a haptic interface, the force fields measured with an AFM are translated into forces perceivable to humans. Simultaneously, the surface shape and its local mechanical properties are visually and acoustically presented. This allows human users to interactively explore the forces measured on the nanometer scale, while simultaneously employing multiple senses. Humans are remarkably adept at discovering patterns within complex structures as well as deviations from these patterns. If we succeed in using this human ability for exploring nanomechanical tissue properties, this would offer the opportunity to discover new biomechanical phenomena.

BP 4: Membranes and vesicles II (joint session BP/CPP)

Time: Monday 15:00–16:15 Location: H10

BP 4.1 Mon 15:00 H10

Screening of small molecules with bilayer-modifying properties using coarse-grained simulations — •Alessia Centi, Kurt Kremer, and Tristan Bereau — Max Planck Institute for Polymer Research, Mainz, Germany

Small molecules, including alcohols and anesthetics, can alter the lateral organization of plasma membranes by preferentially partitioning between domains, thereby affecting lipid bilayer properties and stability. Although lipid segregation is key to many biological processes, precise understanding of the physical and chemical properties governing membrane phase behaviour is still lacking. Gaining more fundamental insight into the underlying mechanism is pivotal for developing enhanced drugs that can act through targeted domain phase separation.

In this work, we employ coarse-grained simulations based on the MARTINI force field [1] as a screening tool to identify compounds which can affect phase separation in model membranes. Hence, our approach based on a combination of molecular dynamics simulations and potential of mean force calculations, provides a rapid and affordable platform for gaining a better understanding of the driving forces of lipid domain stabilisation/destabilisation.

[1] S. J. Marrink, et al. Journal of Physical Chemistry vol. 111 p. 7812-7824, 2007.

BP 4.2 Mon 15:15 H10

Drug-membrane permeability across chemical space — •Roberto Menichetti, Kiran H. Kanekal, and Tristan Bereau — Max Planck Institute for Polymer Research, Mainz, Germany

Unraveling the link between the chemical structure of a small drug-like molecule and its rate of passive permeation across a lipid membrane is of fundamental importance for pharmaceutical application. However, the elucidation of a structure-permeability relationship in terms of few molecular descriptors has been so far hampered by the overwhelming number of possible compounds. In this work, we reduce a priori the size of chemical space by relying on physics-based coarse-grained models, and perform high-throughput coarse-grained simulations (HTCG) to cover a subset of chemical space both efficiently and broadly. This comprehensive exploration allows us to derive a smooth surface relating the permeability of a compound to two simple molecular properties—the bulk partitioning free energy and acid dissociation constant. By projecting HTCG predictions back to atomistic resolution, we provide an estimate of the permeability coefficient for more than 500,000 small molecules in the range $30-160$ Da. Our large scale analysis establishes a clear connection between specific functional groups and the resulting permeability, enabling for the first time inverse molecular design. This study further highlights that favoring the incorporation of certain groups will reduce the range of accessible permeabilities, thus affecting bioavailability.

[1] R. Menichetti, K. H. Kanekal, and T. Bereau, arXiv preprint arXiv:1805.10158 (2018).

BP 4.3 Mon 15:30 H10

X-Ray Reflectivity Investigation of Structure and Kinetics of Photoswitchable Lipid Monolayers — •Jonas Erik Warias[1], Svenja Carolin Hövelmann[1], Franziska Reise[2], Andrea Sartori[1], Rajendra Prasad Giri[1], Chen Shen[3], Thisbe Lindhorst[2], Olaf Magnus Magnussen[1], and Bridget Mary Murphy[1,4] — [1]Institut für Experimentelle und Angewandte Physik, University of Kiel, Germany — [2]Otto Diels-Institut für Organische Chemie, University of Kiel, Germany — [3]Deutsches Elektronen Synchrotron, Hamburg, Germany — [4]Ruprecht Heansel Laboratory, University of Kiel, Germany

The mechanical and dynamic properties of phospholipid membranes are of importance for biological functions, such as switching of embedded proteins and cell transportation. In order to investigate these properties we study model systems in which amphiphilic photoswitchable molecules are integrated into Langmuir films of phospholipids. We have modified glycolipids to contain an azobenzene photoswitch between the chain and the head group and successfully embedded those in a monolayer of dipalmitoylphosphatidylcholine (DPPC). This allows us to reversibly change the azobenzene-glycolipid orientation between trans- and cis-conformation by illumination with UV and blue light. We have followed the structural changes in this model membrane and the switching kinetics of the system with Langmuir isotherms and in situ X-ray reflectivity at the LISA diffractometer P08, PETRA III. Strong changes in membrane conformation upon switching have been observed and an additional phase transition has been discovered.

BP 4.4 Mon 15:45 H10

On the propagation of acoustic waves along the membrane based on the thermodynamic state of the interface — •Kevin Kang and Matthias Schneider — Technische Universität Dortmund

Biological membranes form hydrated, quasi-2D elastic interfaces, and it has been proposed that acoustic waves propagating along the membrane play a fundamental role in biological communication. Here we investigate whether thermodynamic principles can be applied on interfaces to study mechanical signaling along membranes. Using fluorescent probes embedded on an lipid monolayer assembled at the air-water interface, we excite the monolayer and measure the acoustic waves propagating along the membrane using FRET. We find that stimulation near the phase transition region of the state diagram (liquid-expanded/liquid condensed) can generate all-or-none type pulse, and the threshold behavior and the pulse shape show similarity with the

nervous impulse. Altering the environment (pH, Ca2+, temperature, etc.) changes the material properties of the membrane (e.g. lateral compressibility), and the observed pulse characteristics (velocity, amplitude, period, etc.) generally agree with those expected from the compressibility profile. Furthermore, these characteristics also appear consistent with pulses seen in various excitable systems (squid axons, algae, etc.) under varying environmental conditions (e.g. increase in conduction velocity with increase in temperature). These results altogether show that the signaling properties along the interface can be derived from its state diagram and the thermodynamic properties, and they support a physical basis of communication in living systems.

BP 4.5 Mon 16:00 H10

Stochastic dynamics of nanoparticle and virus uptake — •Felix Frey, Falko Ziebert und Ulrich Schwarz — Institute for Theoretical Physics and BioQuant-Center, Heidelberg University, Germany

Biological cells constantly transport material and information across their plasma membrane. In particular cells routinely take up particles of diverse shapes and sizes between 10-300 nm, especially viruses, which often come in either spherical or cylindrical shapes. In general, particle uptake requires that the gain in adhesion energy overcomes the cost of plasma membrane bending. We first show by using a simple deterministic model that cylindrical particles are taken up faster than spherical particles for the same radius and volume. We then investigate stochastic effects, which might be relevant because of the small system size. We find that now spherical particles can be taken up faster because the mean first passage time is affected by multiplicative noise for the sphere rather than additive noise as in the case of the cylinder. Our findings suggest that stochasticity is equally important as geometry during particle uptake.

BP 5: Systems biology & gene expression and signaling

Time: Monday 15:00–16:45 Location: H11

Invited Talk BP 5.1 Mon 15:00 H11

Gene transfer between bacteria: from single molecules to genome dynamics — •Berenike Maier — University of Cologne

Horizontal gene transfer (HGT) plays an important role in bacterial genome evolution. Gene transfer between bacteria of different species but also between bacteria and eukaryotes has been reported. A particularly widespread mechanism of gene transfer is transformation which enables bacteria to import and inheritably integrate external DNA. The first part of the presentation will focus on the import of DNA through the cell envelope, a key step to transformation. The proteins forming the DNA uptake machine have been identified. Yet, the biophysical mechanism of the motor pulling DNA from the environment into the bacterial cell remains poorly understood. We used single molecule approaches for studying the molecular mechanism of DNA uptake. Our results are in remarkable agreement with a translocation ratchet model, whereby a periplasmic chaperone rectifies DNA diffusion through the membrane by reversible binding. In the second part, the I will address the question how gene transfer between different bacterial subspecies affects genome dynamics and bacterial fitness. Using laboratory evolution, we show that despite considerable sequence divergence, large portions of the genome are rapidly transferred.

BP 5.2 Mon 15:30 H11

Why E. coli dies exponentially during carbon starvation — •Severin Schink[1,2], Elena Biselli[2], Constantin Ammar[2], Yu-Fang Chang[1], Markus Basan[2], and Ulrich Gerland[1] — [1]Harvard Medical School, Department of Systems Biology, 200 Longwood Ave, Boston 02115 MA, USA — [2]Technical University of Munich, Physics Department, James-Franck-Str 1, 85748 Garching, Germany

While growth of bacteria is well understood and studied, its counterpart death is not. We use the mathematical simplicity of the decay of viability during carbon starvation, a simple exponential function, to uncover how E. coli survives nutrient limitation. We find that survival crucially depends on cannibalistic biomass recycling, where bacteria survive by metabolizing biomass of perished cells. The interdependence of survival and death leads to a negative feedback loop: increased cell death results in more available nutrients, which in turn reduces cell death. As a result, the state of the cells becomes naturally balanced, so that the death rate remains invariant for several days and viability decreases exponentially. This finding permits quantitative insights into how environments and genetic elements affect bacterial survival, as exemplified by a study of the cost of a wasteful enzyme and the benefit of the stress response sigma factor rpoS.

BP 5.3 Mon 15:45 H11

Suppressive antibiotic interactions result from jamming in the translation cycle — •Bor Kavčič[1], Gašper Tkačik[1], and Tobias Bollenbach[2] — [1]IST Austria, Klosterneuburg, Austria — [2]University of Cologne, Cologne, Germany

Translation - synthesis of proteins by ribosomes - is regulated by translation factors and perturbed by certain antibiotics (translation inhibitors). When antibiotics are combined, they interact diversely: the combined effects range from synergistic (combined effect is stronger) to suppressive (one of the drugs loses potency). Such drug interactions are difficult to predict and their underlying mechanisms remain unknown. We systematically measured all pairwise interactions for a set of translation inhibitors. A theoretical model based on ribosomal growth laws explained some of the interactions, but was unable to explain suppression. To further elucidate the origin of these drug interactions, we mimicked antibiotic effects on translation by externally controlling the concentration of one or several key translation factors, which revealed how antibiotic action depends on the translation bottlenecks. Furthermore, if the transition rates are modified, ribosomes can get stuck in traffic jams, leading to a decrease in translation efficiency. We interpret these experiments using a stochastic model of translation based on the TASEP. Our analysis suggests that traffic jams of ribosomes in the translation cycle are at the heart of suppressive interactions between antibiotics that target initiation and translocation.

BP 5.4 Mon 16:00 H11

Towards synthetic cells using peptide-based reaction compartments — Kilian Vogele[1], Thomas Frank[1], Lukas Gasser[1], Marisa A. Goetzfried[1], Mathias W. Hackl[2], Stephan A. Sieber[2], Friedrich C. Simmel[1], and •Tobias Pirzer[1] — [1]Physics of Synthetic Biological Systems - E14, Physics-Department and ZNN, Technische Universität München, 85748 Garching, Germany — [2]Department of Chemistry, Center for Integrated Protein Science Munich (CIPSM), Technische Universität München, Lichtenbergstraße 4, 85748 Garching, Germany

Membrane compartmentalization and growth are central aspects of living cells, and are thus encoded in every cell's genome. For the creation of artificial cellular systems, genetic information and production of membrane building blocks will need to be coupled in a similar manner. However, natural biochemical reaction networks and membrane building blocks are notoriously difficult to implement in vitro.

In this work we utilized amphiphilic elastin-like peptides (ELP) to create self-assembled vesicular structures of about 200 nm diameter. In order to genetically encode the growth of these vesicles, we encapsulate a cell-free transcription-translation system together with the DNA template inside the peptide vesicles. We show in vesiculo production of a functioning fluorescent RNA aptamer and a fluorescent protein. Furthermore, we implement in situ expression of the membrane peptide itself and finally demonstrate autonomous vesicle growth due to the incorporation of this ELP into the membrane.

BP 5.5 Mon 16:15 H11

Membrane diffusion imposes a cell size-dependent polarity switch — •Lars Hubatsch[1,2], Florent Peglion[2], Jacob Reich[2], Nelio TL Rodrigues[2], Nisha Hirani[2], Rukshala Illukkumbura[2], and Nathan W Goehring[2,3] — [1]MPI for the Physics of Complex Systems — [2]The Francis Crick Institute — [3]MRC LMCB, University College London

Reaction - diffusion networks have been established as a ubiquitous way of patterning living systems, bridging between length scales, from single cells to large tissues. Cell polarity, as one of the most fundamental patterns in biology, has been the subject of detailed biological

studies, enabling quantitative modelling of the underlying patterning networks. Here, we investigate how cell polarity patterns are influenced by cell size. Many classical types of reaction-diffusion systems exhibit intrinsic length scales, giving rise to a minimum system size below which a pattern returns to uniformity. We show theoretically that such a size threshold is a common feature of current models for polarity. Next, using kinetic parameters measured by single-molecule techniques we quantitatively predict the cell size below which polarity should become unstable in our experimental system, the early C. elegans embryo. Using different mechanical and genetic perturbations in conjunction with 3D live-imaging we show that this size threshold exists in vivo. Cell size-dependent polarity thresholds may explain the commonly observed link between cell size and asymmetric division potential in stem cell lineages.

BP 5.6 Mon 16:30 H11

Modelling the Single Photon Response in Rods — •Charlotte J. Beelen[1], Karl-Wilhelm Koch[1], and Daniele Dell'Orco[2] — [1]Dept. Neuroscience, Biochemistry, University of Oldenburg — [2]Department of Neurosciences, Biomedicine and Movement Sciences, Sect. of Biological Chemistry, University of Verona

Rod cells mediate vision in dim light. After the activation of the pigment molecule rhodopsin, a complex signal transduction cascade leads to an electrical signal, which can then be transmitted further through the retina. This phototransduction cascade can be modelled using differential equations for the relevant molecular species, mainly with mass-action kinetics. It has been tested for a broad range of stimulus conditions in deterministic simulations [1,2].
The phototransduction cascade exhibits a reproducible response to single photons, thus operating at the physical sensing limit. These single photon responses show astonishingly little variability [3]. To investigate the uniformness of the single photon response and find out which reactions are essential for its reproducibility, we perform stochastic simulations of single photon responses. The effect of multiple phosphorylation sites of rhodopsin is studied, as well as single photon responses in different knockout conditions.
[1] D. Dell'Orco et al, Mol. BioSyst. **5** 1232-1246 (2009)
[2] B.M. Invergo et al, Mol. BioSyst. **10** 1481-1489 (2014)
[3] R.D. Hamer et al, J. Gen. Physiol. **122** 419-444 (2003)

BP 6: Poster I

Topics: Active matter (6.1 - 6.9); Biomaterials and biopolymers (6.10 - 6.19); Cell adhesion and migration and multicellular systems (6.20 - 6.33); Cell mechanics (6.34 - 6.51); Cytoskeletal filaments (6.52 - 6.67); Statistical physics of biological systems (6.68 - 6.83)

Time: Monday 17:30–19:30 Location: Poster B2

BP 6.1 Mon 17:30 Poster B2

Nano-stir bars for perturbing biofluid microdroplets in a microfluidic channel — •Mithun Thampi, Pierre-Yves Gires, and Matthias Weiss — Experimental Physics I, University of Bayreuth, Germany

Studying reactions in the cytoplasm of living cells or in biofluid droplets, e.g. produced in microfluidic channels for lab-on-chip applications, is key for elucidating the dynamics of living matter. However, due to their small dimensions, a controlled and gentle stirring of the interior of biofluid droplets, e.g. for speeding up diffusion-limited reactions, has remained challenging. Here we report on an approach to synthesizing few micrometers long magnetic nano-stir bars (NSBs) for perturbing biofluid microdroplets. NSBs were produced by aligning Fe_3O_4 nanoparticles via magnetic fields and adding a biocompatible silica coating, followed by magnetic sedimentation to extract the required length range from the polydisperse bulk solution. Scanning electron microscopy confirmed the successful production and isolation of NSBs. Incorporating NSBs into aqueous biofluid microdroplets, produced at PDMS-based microfluidic junctions within a hydrophobic carrier fluid, and addressing them with alternating magnetic fields resulted in a rotational motion of NSBs with angular frequencies in the range 0.01-10 Hz. The resulting gentle mixing of the droplets' interior was monitored via fluorescence microscopy.

BP 6.2 Mon 17:30 Poster B2

A phase field crystal approach to active systems with inertia — •Dominic Arold and Michael Schmiedeberg — Institut für Theoretische Physik 1, Friedrich-Alexander-Universität Erlangen-Nürnberg, Staudtstrasse 7, 91058 Erlangen, Germany

A phase field crystal approach for active systems consisting of particles with inertia is investigated. In our model the direction of the inertia given by the velocity can be different from the direction of the self-propulsion due to the activity. The implementation of the inertia is motivated by the derivation of an phase field crystal model of underdamped passive particle from a dynamical density functional theory [1], while the activity is modelled as in a phase field crystal model of active systems without inertia [2,3]. In the overdamped regime the results of the latter model can be reproduced including the formation of stable resting or migrating crystals. In the opposite underdamped regime where inertial effects become relevant the migrating crystalline order is destroyed due to the high self-propulsion strength and a chaotic behaviour is observed instead.

[1] A. J. Archer, J. Chem. Phys. **130**, 014509 (2009).
[2] A. Menzel and H. Löwen, Phys. Rev. Lett. **110**, 055702 (2013).
[3] A. Menzel, T. Ohta and H. Löwen, Phys. Rev. E **89**, 022301 (2014).

BP 6.3 Mon 17:30 Poster B2

The Role of Loops in Transport Networks — •Leonie Bastin, Mirna Kramar, and Karen Alim — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Transport networks play an important role in living organisms and man-made structures. Treelike networks are found to be the most efficient transport networks. However, in biology, many networks grow into loop containing structures. It is still an open question, why loops are favored by some organisms. We investigate the effect of loops on the transport efficiency in a network, using the model organism *Physarum polycephalum*, which grows as a highly interconnected tubular network. Selforganized contractions drive the fluid flow in these networks. For our studies, we developed a method to incorporate fluorescent beads into *P. polycephalum*'s streaming cytoplasm and use particle tracking for flow visualization. We prepare both treelike and loop-containing networks and compare measured flow velocities. Our findings suggest that loops increase the transport homogeneity in *P. polycephalum*. In contrast, the foraging fronts of the organism lead to hierarchically organized networks.

BP 6.4 Mon 17:30 Poster B2

Microscopic active systems learning in noisy environments — •Santiago Muiños-Landin and Frank Cichos — University of Leipzig. Peter Debye Institut for Experimental Physics

Optimal behavior at the microscopic scale is a particularly challenging achievement. In addition to the intrinsic stochasticity of the motion observed in microscopic swimmers, the information that can be collected by active agents to optimize their behavior at this regime is usually sparse and noisy. However biological systems manage to face such challenge through different strategies depending on the propulsion and the sensing mechanisms coupled in robust enough sensory-motor processes. These achievements have been also recently observed in an artifical context, where following learning strategies, synthetic swimmers can also optimize their behavior in simple navigation tasks and also a significant influence of noise in the optimality of a strategy has been reported. Here we present a platform to study in detail such influence of noise in the dynamics and the behavior of a self-thermophoretic swimmer. Exploring the possibility of taking advantage of such fluctuations in single tasks but also considering collective behavior.

BP 6.5 Mon 17:30 Poster B2

Feedback Control of Active Microswimmers to Imitate Phototaxis — •Alexander Fischer and Frank Cichos — Universität

Leipzig

Collective motion created by the interaction of autonomous individuals plays a major role in flocks of birds, bacterial growth or the motion of robotic swarms. Sensing and reacting to signals is a fundamental issue of life. Microswimmers, which are artificial objects that mimic the active motion of biological systems, do not have such sensing and response features built in yet, but may gain them through an external control of their propulsion. Here we explore an information exchange between artificial microswimmers by computer-controlled feedback processes. We have created a setup where multiple active microswimmers can react to their position in space or their distance to other microswimmers. Our system consists of autonomous agents performing directed motion in a plane and their orientation is subject to noise. The speed of the agent slows down in those regions where it measures a higher concentration of messengers. Thus, the probability of presence of the agent is higher in regions with higher concentration. According to Volpe et al. [1], a change between segregation and aggregation of the agents in the high messenger concentration regions can be achieved by introducing a delayed response to the messenger concentration.

[1] M. Mijalkov, A. McDaniel, J. Wehr, G. Volpe, Phys. Rev. X 6, 011008 (2016)

BP 6.6 Mon 17:30 Poster B2

Capillary condensation forces between inclusions in an active bath — •Milos Knezevic and Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstraße 36, 10623 Berlin, Germany

We present a systematic study of capillary condensation forces between objects immersed in an active bath of microswimmers. We study two types of active baths, consisting of either Active Brownian particles (no hydrodynamic interactions) or spherical squirmers (with hydrodynamic interactions). Inclusions of various shapes and sizes are considered. We find that forces between inclusions can be either attractive or repulsive, depending on the density and motility of microswimmers, and the geometric properties of inclusions. We explore ways of controlling these forces, which is relevant for self-assembly.

BP 6.7 Mon 17:30 Poster B2

Thermoviscous flows at reduced heating impact — •Matthias Loidolt, Matthaeus Mittasch, Archit Bhatnagar, Anatol Fritsch, and Moritz Kreysing — MPI of Cell Biology, Dresden

Recently it was demonstrated that thermoviscous flows can be used to move the cytoplasm of cells and developing embryos (1). These flows are induced by laser scanning of a temperature spot through the cytoplasm, and reach velocities that are comparable with flow velocities happing during early stages of embryogenesis. As a side effect, this laser scanning introduces weak temperature gradients, that are on the order of 1-2 kelvins when time-averaged. While this is sufficient to avoid side effects in heterothermic animals, some mammalian cells might require even more stable temperature conditions. Here, we present that exploiting symmetry relations during laser scanning, we can still generate significant flow fields, while greatly reducing time-averaged temperature gradients. Specifically we find that scan paths that visit every point in the sample equally often can still be used to cause localized flows. At the same time the resulting temperature distributions are near homogenous across the region of interest and can therefore be much better compensated for by ambient cooling.

(1): Mittasch et al., " Non-invasive perturbations of intracellular flow reveal physical principles of cell organization", Nature Cell Biology 1 (2018)

BP 6.8 Mon 17:30 Poster B2

Taming the Factor: Upstream dynamics of Circular Dorsal Ruffle (CDR) regulation — •Malte Ohmstede and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

CDRs are actin based, ring-shaped undulations of the dorsal membrane in, among others, fibroblast cells. CDRs are involved in macropinocytosis, a process in cell proliferation and are also a gateway for various pathogens to enter the cell. Stimulation of CDRs is achieved by various growth factors, e.g. Platelet Derived Growth Factor (PDGF), stimulating their corresponding receptor tyrosine kinase (RTK). The RTKs then trigger a signalling cascade resulting in the formation of CDRs and ultimately macropinocytosis, collapsing CDRs into large vesicles which are then transported to the nucleus. Delivery of growth factors in vitro can be done either passively by relying on growth factors of unknown low concentrations contained in FBS or by explicitly adding known concentrations to the medium. Depending on PDGF concentration, a clear difference in CDR shape is observed. Larger concentrations result in CDRs spanning over most of the lammelipodium, whereas low concentrations yield small rings. Upon stimulation of the entire lammelipodium, most RTKs are consumed, resulting in a recovery time needed for the cell to re-express the receptors before being able to be stimulated again. Using a combination of microfluidics and microcontact printing, it is possible to observe medium switching at precise times and without imaging interruption. Thus, cell reaction and recovery times can be precisely measured.

BP 6.9 Mon 17:30 Poster B2

MT-kinesin bundle and cross-linked network formation — •Amna Abdalla Mohammed Khalid[1], Fanomezana Moutse Ranaivoson[2], Anne Houdusse[2], and Christoph F. Schmidt[1,3] — [1]Drittes Physikalisches Institut - Biophysik, Fakultät für Physik, Georg-August-Universität, Göttingen, Germany. — [2]Structural Motility Group, Institut Curie, Paris, France — [3]Department of Physics, Duke University, Durham, USA

The mitotic kinesin-like protein 2 (MKLP2), is an N-terminal kinesin of the kinesin 6 family. MKLP2 plays critical roles in mitosis, in particular for the metaphase to anaphase transition and for cytokinesis. This kinesin motor is likely to have a diverging mechanism due to several inserts near the motor domain and the neck-linker which make the motor domain $\sim 60\%$ larger than that of other kinesins. Its neck-linker is four times longer than that found in other kinesins. We studied dimeric truncated MKLP2 in vitro motility experiments. It is an active motor, although we have not found any processive motility yet in single-molecule assays. A conspicuous feature of this kinesin is its high microtubule (MT) bundling activity. MKLP2 has the ability to form 2D and 3D strongly bundled cross-linked MT networks that evolve and coarsen slowly in time over many hours. We hypothesize that these bundled networks are occurring as a collective dynamic phenomenon based on weak and reversible interactions between the motors and the microtubules.

BP 6.10 Mon 17:30 Poster B2

Hofmeister series for RNA and metal cations: Binding affinities and kinetics and thermodynamics from all-atom molecular dynamics simulation — Sergio Cruz-León and •Nadine Schwierz — Department of Theoretical Biophysics, Max Planck Institute of Biophysics, Max-von-Laue-Str. 3, 60438 Frankfurt, Germany.

RNA folding and function is crucially governed by metal cations. In addition to valence and concentration, the ion type is decisive in processes like folding, or interaction with other molecules. In spite of its biological importance, unraveling the molecular mechanism of ion-specific effects from experiments is challenging due to their limited spatial and temporal resolution. To fill this gap, we combine all-atom molecular dynamics simulation and advanced sampling techniques, to gain insight into the microscopic interactions between an RNA dinucleotide and metal cations. Our results show ordering of the ions according to binding affinities and exchange kinetics. Particularly, direct and reversed Hofmeister series are found to hold true for the interaction with backbone and nucleobase, respectively. We further include the microscopic level of understanding into Poisson-Boltzmann theory to calculate ion competition constants for monovalent ions which agree well with recent experiments. This detailed description of metal cation-RNA interactions provides the molecular origin of ion-specific effects for cations and RNA, being a tool to boost the modeling of complex RNA-cation phenomena.

BP 6.11 Mon 17:30 Poster B2

Differential uptake of graphene quantum dots into human cell lines — •Jennifer Kurth[1], Stefan Fasbender[1], Marina Ludescher[2], Hans Neubauer[2], and Thomas Heinzel[1] — [1]Condensed Matter Physics Laboratory, Heinrich-Heine-University Düsseldorf — [2]Department of Obstetrics and Gynecology, University Hospital Dusseldorf

Fluorescent graphene quantum dots (GQDs) are prepared by the established recipe of Qu et al. [1], using citric acid as carbon source and diethylentriamine as reduction agent. The breast cancer cell lines MCF-7 and MDA-MB-231 and the non-tumorigenic cell line MCF-10A are exposed for up to 48 h to GQDs at a concentration of 500 ug/ml. Flow cytometry and fluorescence spectroscopy are used to analyse the time dependent uptake of the GQDs into the cells. The number of in-

corporated GQDs is estimated to be in the range of 10 and 50 million per cell for MCF-7 and MDA-MB-231 cells and around 0.5 million for MCF-10A cells. [1] Qu et al., Light: Science & Applications, 2015, 4, e364

BP 6.12 Mon 17:30 Poster B2

Investigating the morphology and nanomechanical properties of snake scale microstructures — •Loïc Musy[1], Iaroslav Gaponenko[1], Raul Gonzalez[2], and Patrycja Paruch[1] — [1]DQMP, University of Geneva, Switzerland — [2]Vivarium de Meyrin, Geneva, Switzerland

Epithelial microstructures in living organisms can inspire biomimetic approaches to materials development, and provide a fascinating window into the evolutionary interplay between environmental constraints and phylogenetic relations.

Here, we study the morphology and mechanical properties of snake scale microstructures, at a macroscopic level using scanning electron microscopy and stress-strain measurements, and at the much less studied nanoscale level via a range of scanning probe microscopy techniques. Investigating sheds from over 20 snake species in 6 different families provided by the Meyrin Vivarium, in each case we fully characterise ventral, dorsal and side scale morphology, and local as well as macroscale response to normal and lateral forces. We find relatively homogenous pattering of the microstructures on ventral scales, possibly as a result of an optimisation for sliding motion, while dorsal scale microstructure patterns vary widely from species to species.

At the nanoscale, we identify very local regions in the microstrucure, particularly on the ventral scales, that dominate the mechanical response of the system.

BP 6.13 Mon 17:30 Poster B2

Probing the Escalation of DNA-Polymerization in Thermal Traps — •Christina Felicitas Dirscherl and Dieter Braun — Systems Biophysics, LMU Munich, Germany

Starting conditions with highly diluted monomers and the 'tyranny of the shortest' are the main problems for de novo strand formation of DNA/RNA on early earth. A possible scenario that could have overcome these issues are thermogravitational traps. We demonstrated that theses traps can accumulate solutions of single molecules at least 35-fold within 30 hours despite their high diffusivity, and that both monomers and activation chemistry molecules (carbodiimide EDC [1]) can be co-accumulated. We could prove that EDC - which is a replacement for the prebiotically plausible cyanoimidazole - polymerizes RNA as well as DNA bases, however only up to 8-mers. Also concentrations of the longer strands decrease exponentially. In thermogravitational traps the accumulation of DNA strands is exponentially length dependent ([2]). Therefore, the trapping procedure is expected to significantly increase the probability that longer strands are linked together. If additionally two complementary monomers are present in the system self-templated ligation can take place which can lead to an escalation of strand formation ([3]).

[1] M. Jauker, H. Griesser and C. Richert, Angew Chem Int Ed 2015 Nov 23; 54(48): 14564-9

[2] C. B. Mast, S. Schink, U. Gerland and D. Braun, PNAS 110(20), 8030-5 (2013)

[3] T. A. Lincoln and G. F. Joyce, Science 323.5918 (2009): 1229-1232

BP 6.14 Mon 17:30 Poster B2

Movement of DNA within microporous materials in an electric field — •Natascha Heinsohn, Robert Niedl, and Carsten Beta — Universität Potsdam, Potsdam Golm, Deutschland

We performed experiments with DNA fragments in different microfibre materials to investigate the molecular interaction of biopolymers under electrical force. For our experimental set up we prepared printed electrodes with conductive ink to apply a constant electric field within the fibre network. We could observe differences in mobility of DNA fragments in organic and inorganic fibre materials. Our main focus of interest is to indentify and understand these observations in dependence on DNA properties like length and structure together with fibre properties and applied electrical force. This will influence our development of low-cost and disposable devices for point-of-care diagnostics.

BP 6.15 Mon 17:30 Poster B2

A selection mechanism to emerge the first functional sequences — •Alexandra Kühnlein[1], Hannes Mutschler[2], Dieter Braun[1], and Christof Mast[1] — [1]Systems Biophysics, Ludwig-Maximilian University Munich — [2]MPI of Biochemistry,Martinsried

Life has managed to transfer sequence information on Earth for about 4 billion years despite the high complexity and short lifetime of oligonucleotides and maintained the information against degradation and dilution. To achieve this, life must have had mechanisms for the selection and replication of complex sequences. Contrary to today's biology however, the mechanism must have been simple and driven by physical non-equilibria. A local thermal gradient across a microfluidic pore can overcome the tyranny of the shortest by autonomously driving length selection and accumulation of DNA, thereby fostering more complex sequences. This can lead to hybridization and the formation of hydrogels. We use the sequence dependence and specificity of Watson-Crick base pairing and hydrogel formation to find a physical selection mechanism for DNA sequences. Hybridization and hydrogel formation can break the symmetry in sequence space and select mutually interacting and thus potentially functional sequences. Experimentally, we start with a pool of random ssDNA libraries and quantify the bias of hydrogelation by high throughput sequencing. With increasing selection pressure and modifying the initial library, we will narrow down the pool of functional sequences and see possible replicating function emerge.

BP 6.16 Mon 17:30 Poster B2

Effects of increased electrostatic repulsion between head groups of cardiolipin monolayers — Renko Kensbock, •Heiko Ahrens, and Christiane A. Helm — Institute of Physics, University of Greifswald, Germany

Cardiolipin is an anionic lipid, consisting of four hydrophobic alkyl chains and a hydrophilic head, which carries up to two charges. We investigate tetramyristoyl cardiolipin (TMCL) monolayers at the air-water interface with isotherms, grazing incidence diffraction and model calculations. TMCL undergoes a fluid (LE) to gel (LC) phase transition at a transition surface pressure π_c(T). By tuning the subphase composition, the surface charge density is varied. We verify the linear temperature dependence of π_c(T). With increasing surface charge density, the tilt of the alkyl chains in the LC phase increases. Furthermore, we find a correlation between the slope ($d\pi_c/dT$) and the tilt of the alkyl chains in the gel phase. We compare the obtained TMCL monolayer results with other lipids from literature.

BP 6.17 Mon 17:30 Poster B2

Tailor-made single electrode device to study human stem cell derived neurons — •Jeremy Teuber — Center for Hybrid Nanostructures

Studying the electrophysiological properties of cells is a basic requirement for understanding the nature of electrical impulses between single neurons. We have designed and fabricated tailor-made single electrode devices on silicon wafers for electrophysiological measurements of individual cells. The bilayer electrode system on a silicon wafer was prepared by UV laser photolithography and chemical vapor deposition. Here, the electrode consists of a conducting gold layer where the electrical supply lines are covered with an insulating layer of silicon dioxide. Alignment and material deposition of the custom-made device were examined by light microscopy as well as scanning electron microscopy. Stable and robust bonding of the individual material layers ensures that the device endures a cleaning procedure with trypsin and EDTA to enable multiple usability of the device. A 3D-printed ring glued with PDMS to the wafer is used to form a defined volume, in which the neurons are confined during the cultivation forming neural networks on the electrode. In detail, human stem cells are stimulated by using glutamate or patch clamping and the generation of the action potential is measured by the substrate electrode. The devices are further optimized with respect to geometry and materials to obtain increased signal-to-noise ratios. This device offers the opportunity to gain deep understanding of the characteristics of stem cells derived neurons.

BP 6.18 Mon 17:30 Poster B2

C. Elegans Nematodes Deform like Elastic Rods. — •Octavio Albarran[1], Peter Weist[1], Eugenia Butkevich[1], Renata Garces[1], and Christoph Schmidt[1,2] — [1]Drittes Physikalisches Institut - Biophysik Friedrich-Hund-Platz 1 37077 Goettingen — [2]Department of Physics, Duke University, Durham, NC 27708, USA.

To perform undulatory locomotion, C. elegans nematodes generate forces with their body-wall muscles acting on the surrounding environment and against their own body deformation resistance. The

knowledge of the body rigidity is crucial to understand the dynamic functions of the worm.

It has been hypothesized that the worm kinematics can be understood in terms of viscoleastic beam theory. However, to date, mechanical studies in the large deformation regime, typical of native undulatory locomotion, are lacking. We here present a micro-needle-based experiment imposing large strains. Living worms were kept straight by clamping their extremities onto agar plates. We laterally displaced the centers of worms with a glass cantilever of known spring constant. To separate passive responses from muscle activity, we varied the contraction relaxation state of the muscles using pharmacological interference. We directly probed the beam theory through the analysis of the loading curves. Interestingly, we found that linear constitutive relations (without viscous effects) are sufficient to explain the experimental data. We provide a synthesis of the typical range of magnitudes of effective elastic modulus for different muscles states of the worms.

BP 6.19 Mon 17:30 Poster B2

Adsorption of Bovine Serum Albumin on Glass Surfaces observed by X-ray Reflectometry — •Annemarie Pfnür[1], Michail Goldes[1], Sarah Höhn[2], Aldo Roberto Boccaccini[2], and Tobias Unruh[1] — [1]Institute of Crystallography and Structural Physics, Friedrich-Alexander-Universität Erlangen- Nürnberg (FAU), Staudtstr. 3, 91058 Erlangen, Germany — [2]Department of Materials Science and Engineering, Institute for Biomaterials, Friedrich-Alexander-Universität Erlangen- Nürnberg (FAU), Cauerstr. 6, 91058 Erlangen, Germany

Bioactive glass (e.g. 45S5) is used since more than 30 years in bone and dental implants. In contact with liquids soluble silica, calcium phosphate, and sodium ions are released from the surface and a crystalline hydroxyapatite layer on the glass surface is formed which can bond to bone tissue. A basic understanding of the medical compatibility on a molecular level has, however, not been achieved yet.

Thus, we present first X-Ray Reflectivity (XRR) data on protein adsorption on glasses which is intended to mimic the very first step of glass interaction with body fluid and cells after implantation. We were able to detect protein monolayers and determine the thickness and roughness of the protein layer on the angstrom scale. Furthermore, we are sensitive to aging effects of the glass surface, e.g. glass corrosion, which occur when the glass is immersed in water or buffer. The results from bio glass is compared to soda lime and borosilicate glass.

BP 6.20 Mon 17:30 Poster B2

Towards a more realistic model of adhesion clusters under force — •Andrea Bräutigam, Gerhard Gompper, and Benedikt Sabass — Theoretical Soft Matter and Biophysics, Institute of Complex Systems and Institute of Advanced Simulation, Forschungszentrum Jülich, Germany

Adhesion domains play a crucial role in many cellular processes such as cell migration or communication with surrounding tissue. These usually localized contacts to the extracellular environment are composed of organized aggregates of proteins that form a dynamic cluster sensitive to internal and external signals. Especially under the influence of force, adhesion domains show a rich behavior affecting cluster size, constitution and lifetime. Although the complex system of adhesion sites and their response to force are not fully understood, they apparently have high importance for cellular integrity and mechanical sensing.

Here we present a minimal model for an adhesion cluster of parallel bonds under force. The state of the cluster evolves stochastically through (un)binding events and conformational changes of single bonds until the system eventually ruptures. In our analysis, cluster dynamics is described by an absorbing Markov Process. We derive a mean field approximation which reduces the complexity of the system significantly and allows further studies. In addition, statistically correct trajectories of adhesion clusters with different sizes are generated *in silico*. The approximative system and simulation results show good agreement and provide insight into force-dependent characteristics, such as cluster size and lifetime.

BP 6.21 Mon 17:30 Poster B2

Dynamic patterns of the plant growth regulator auxin — •Joao Ramos and Karen Alim — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Auxin is a plant hormone that promotes growth by altering the mechanical properties of the cell wall, ubiquitously acting throughout plant development. Specific morphologies are tied to patterns of auxin concentration and flow emerging from carrier mediated cell-cell auxin transport. In particular, efflux carrier proteins of the PIN family are the main players in directing auxin flow. Recent data suggest that PIN polarity and mechanical stress may be causally linked. In order to explore the interplay between auxin-mediated cell wall loosening, growth and mechanically-regulated PIN polarity, we have developed a mechanical vertex model coupled to a compartment model for auxin transport. We apply our model to the developmental process of lateral root formation (LRF), which offers empirical accessibility as well as a wide range of developmental patterns accompanied by a wide variety of impactful mechanical cues. Here, we can explain auxin flows down-the-gradient of auxin concentration, present in fountain-like patterns during LRF, by the competition between stress or stiffness gradients and PIN expression. During early LRF, we can explain auxin accumulation and founder cell swelling through differential turgor pressure. Independent of a specific developmental process, we show that mechanical relaxation of cell geometry amplifies mechanically-mediated PIN polarity.

BP 6.22 Mon 17:30 Poster B2

Robust increase in supply by vessel dilation in globally coupled microvasculature — •Felix J. Meigel[1], Peter Cha[2], Michael P. Brenner[2], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, 37077 Göttingen, Germany — [2]Harvard University, Cambridge, MA, U.S.A.

Neuronal activity induces changes in blood flow by locally dilating vessels in the brain microvasculature. How can the local dilation of a single vessel increase flow-based metabolite supply given that flows are globally coupled within microvasculature? Solving the supply dynamics for a microvasculature excerpt, we find one parameter regime to dominate. This regime allows for robust increase in supply independent of the exact position in the network, which we explain analytically. We show how the local coupling of supply in vessels promotes spatial clustering in increased supply by dilation.

BP 6.23 Mon 17:30 Poster B2

Functionalized lipid bilayers as a platform to study cell adhesion — •Anastasia Svetlova, Vanessa Maybeck, Jana Ellieroth, Frano Milos, and Andreas Offenhäusser — Institute of Bioelectronics (ICS-8), Forschungszentrum Juelich, Wilhelm-Johnen Straße, 52425 Juelich, Germany

Artificial lipid bilayer is the closest possible model for the cell membrane. Despite that, current methods of lipid bilayer assembly and functionalization do not provide a satisfactory mimic of cell-cell contact due to the inability to recreate an asymmetrical multicomponent system. In the current work, a method to produce an integrated solid-supported lipid bilayer combining natural extracts from cell membranes and artificially made lipid vesicles is proposed. This simple method allows delivery of transmembrane proteins and components of the extracellular matrix into the substrate. Physical properties such as lateral diffusion coefficient of lipids in the bilayer can be controlled by adjusting the ratio of components in the substrate. Biocompatibility of the composite natural/artificial lipid bilayers is evaluated by their interactions with the cardiomyocyte-like HL-1 cell line. Compared to fully artificial mixes, composite bilayers allow cells to adhere and develop a morphologically more normal cytoskeleton.

BP 6.24 Mon 17:30 Poster B2

Foraging behaviour of *Physarum polycephalum* — •Lisa Schick, Mirna Kramer, 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 6.25 Mon 17:30 Poster B2

Roughness and wettability assessment of substrates with regard to cell adhesion — •Paul Lühe, Issam Assi, Christian Völkner, Regina Lange, Ingo Barke, and Sylvia Speller — Institute of Physics, University of Rostock, 18051 Rostock

Cell adhesion and spreading on surfaces are crucial properties for medical applications, e.g. for biocompatibility of human implants. Important parameters frequently considered in this context are wettability and roughness, both being dependent on geometric and chemical details of the surface, including the history of preparation and treatment. Common techniques for surface conditioning are rinsing and ozone cleaning. In this study we assess the effect of treatment and exposure time in ambient conditions on roughness and wettability of glass with and without transparent Au layers and PDMS surfaces by means of contact angle measurement and atomic force microscopy. The results are discussed in view of expected cell adhesion and spreading properties.

BP 6.26 Mon 17:30 Poster B2

To stick or not to stick - interfacial forces and biological mechanisms regulating microalgae adhesion — •Alexandros Fragkopoulos, Christian Kreis, Anaelle Chretien, Alice Grangier, Christine Linne, and Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization, D-37077 Göttingen, Germany

For many microorganisms, attaching to a substrate is of paramount importance since it allows for cells to stay at nutrient-rich environments or form biofilms. In particular, a population of microbes that grows in porous environments is in constant interactions with interfaces. Here we present a study on the adhesion and surface colonization of *C. reinhardtii*, a unicellular biflagellated microalga. Using micropipette force spectroscopy experiments, we can measure the adhesion force on a single-cell level [1]. We show that its flagella-mediated adhesion to surfaces can be switched on and off by controlling the light conditions [2]. We exploit this behavior to study the cells on a population level by analyzing the Langmuir-type adsorption-desorption dynamics of cells on solid interfaces as they switch between the planktonic (freely swimming) and the surface-associated state. Using tailored model substrates, we reveal the intermolecular forces governing the adhesion of Chlamydomonas to surfaces. Finally, we use both methods to study the effect of the cell mating type, growth medium, and life stage on the adhesion.

[1] M. Backholm, O. Bäumchen, *Nat. Protoc.*, in press (2018)
[2] C.T. Kreis et al., *Nat. Phys.*, **14**, 45 (2018).

BP 6.27 Mon 17:30 Poster B2

Fluid flow control on morphological changes — •Noah Ziethen and Karen Alim — Max Planck Institute for Dynamics and Self-Organization, Göttingen, 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. One particular way of adaptation is the simplification of the network by erosion of specific vessels (pruning). Interestingly, pruning controlled by local flow shear rate is equivalent to global optimization towards minimal dissipation at a fixed network volume.

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 vessel junctions in *P. polycephalum*. We extract the vessel diameters evolution and the corresponding flow field using particle image velocimetry (PIV). We determine the flow profiles for different vessel thicknesses which show surprisingly good agreement with Poiseuille flow. The flow profiles are used to calculate the local shear rate acting on the tube walls. Additionally, we measured the flow rate, the maximum and the variation of the flow velocity. All these above-mentioned quantities are then correlated with the event of pruning.

BP 6.28 Mon 17:30 Poster B2

Memory capacity of a flow network — •Komal Bhattacharyya and Karen Alim — Max Planck Institute for Dynamics and Self-Organization, Göttingen, 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. And most inspiringly, *Physarum* was observed to adapt its networks tube radii network-wide in response to stimuli, reaching a steady-state as a long term response to the applied stimuli, keeping 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 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 pin-point to the information storing and processing capabilities of adaptive flow networks in general and *Physarum* networks specifically.

BP 6.29 Mon 17:30 Poster B2

Application of 3D Lithography — •Jana Kredl[1], Christian Denker[1], Cornelius Fendler[2], Julia Bethune[4], Nina Meyer[1], Tobias Tubandt[1], Finn-F. Lietzow[1], Neha Jha[1], Chris Badenhorst[3], Alena Rong[5], Jakob Walowski[1], Mark Doerr[3], Raghvendra Plankar[4], Mihaela Delcea[5], Uwe T. Bornscheuer[3], Robert Blick[2], Swadhin Mandal[6], and Markus Münzenberg[1] — [1]Institute of Physics, University Greifswald, Germany — [2]Institute of Nanostructure- and Solid State Physics, University Hamburg, Germany — [3]Institute of Biochemistry, University Greifswald, Germany — [4]Institute of Immunology and Transfusion Medicine, University Medicine Greifswald, Germany — [5]Centre for Innovation Competence - Humoral Immune Reactions in Cardiovascular Diseases, University Greifswald, Germany — [6]Indian Institute of Science Education and Research Kolkata, India

3D 2-Photon-Lithography, originally developed for 3D photonic crystals, opens a wide range of new possible applications in many fields, e.g. life sciences, micro-optics and mechanics [1]. We will present our recent applications of 3D 2-Photon-Lithography and show 3D evaporation masks for in-situ device fabrication using different deposition angles, infra-red laser light focusing lenses directly fabricated on optical fibers, tunnel structures for guiding growth of neurons, pillars for investigation of cell mechanics and master-mold fabrication for Polydimethylsiloxane (PDMS) micro-fluidic channels.

[1] J. K. Hohmann et al., Adv. Optical Mater. 3 (2015) 1488

BP 6.30 Mon 17:30 Poster B2

Influence of extracellular vimentin on cell migration — •Divyendu Goud Thalla[1] and Franziska Lautenschläger[1,2] — [1]Cytoskeletal Fibers, INM-Leibniz-Institut für Neue Materialien gGmbH, Saarbrücken,Germany — [2]Experimental Physics, Saarland University, Saarbrücken, Germany

Vimentin is a cytoskeletal protein of the family of intermediate filaments which plays a role in cell migration, adhesion and signaling. Apart from its presence in the cytoplasm, it is also found in the extracellular spaces around cells. Secreted vimentin controls inflammation by reducing the neutrophil infiltration, helps in bacterial elimination and consequently triggers the oxidative metabolites in activated macrophages.It promotes axonal growth in astrocytes by activating IGF1 receptors in the same signaling pathway as IGF1. The IGF1/IGF1-R pathway plays a significant role in general cellular functions such as cell migration, proliferation, adhesion and invasion. In this study, we demonstrate the functional similarities of extracellular vimentin and IGF1 in context with these cellular functions. Using a MTT proliferation assay, we show that extracellular vimentin increases the proliferation rate in MCF-7 cells. Furthermore, we carried out wound healing assays suggesting that extracellular vimentin promotes MCF-7 cell migration. In future, we plan to investigate the role of extracellular vimentin in adhesion and invasion to show if it has a similar role in these cellular functions. Consequently, it might be useful for altering and stimulating these cellular functions which would open up the possibility for treating various disease conditions.

BP 6.31 Mon 17:30 Poster B2

The nanomorphology of osteoblasts with regard to adhesion parameters investigated by Scanning Ion Conductance Microscopy — •Christian Völkner[1], Regina Lange[1], Martina Grüning[2], Ingo Barke[1], Barbara Nebe[2], and Sylvia Speller[1] — [1]University of Rostock, Institute of Physics, 18051 Rostock —

[2]University Medical Center Rostock, Dept. of Cell Biology, 18057 Rostock

Our aim is to elucidate the behavior of osteoblasts (MG-63) and mechanisms of cell adhesion on material surfaces. This we address by investigating the nanomorphology of the cells on various substrate surfaces by means of Scanning Ion Conductance Microscopy (SICM). The cell membrane surfaces exhibit protrusions with leave-like shapes. We attribute these features to so called ruffles [1]. They were found to be very mobile on the cell surface, dominating the signal of membrane height fluctuations. Latter may be developed as a parameter to monitor cell activity. We also focus on the rim of the cells, which exhibits heights between 100 nm up to micrometers with respect to the underlying substrate surface with its own physico-chemical characteristic. This implies large gaps between the cell and the substrate in the periphery, indicating locally varying adhesion clefts.

[1] Chhabra et al., Nature Cell Biol. 9, 1110 (2007)

BP 6.32 Mon 17:30 Poster B2

Influence of substrate elasticity and geometry on cell migration — •Stefanie Haberlandt and Florian Rehfeldt — Georg-August-University Goettingen, Third Institute of Physics - Biophysics, Friedrich-Hund-Platz 1, 37077 Goettingen, Germany

Cell migration plays an important role in many processes which are vital for the development and homeostasis of multi-cellular organisms. It is also a crucial aspect in the development of several diseases such as cancer. Since the various tissues in our body differ significantly with respect to mechanical properties, biochemical composition, and topography, a systematic investigation of how these micro-environments impact migration is essential. This will lead to a better understanding of e.g. invasive cancer cells during tumor metastasis. Here, we experimentally observe and analyze unconfined 2D migration of NIH-3T3 fibroblasts and hMSCs on collagen-I coated polyacrylamide (PA) gels of different Young's moduli E. Using a micro-patterning approach we also created distinctly confined areas on the elastic gels to analyze the impact of geometry on migration. Since patterning on soft gels is challenging, we compared different approaches and present data from migration analysis that depends on cell type, Young's modulus E, and geometry.

BP 6.33 Mon 17:30 Poster B2

Scaling Emergency Response of *Physarum polycephalum*: On the verge of death — •Jonghyun Lee, Adrian Fessel, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

Physarum polycephalum is a unique unicellular organism that displays a wide array of behavioural patterns and structures. Some of these behaviours, such as learning or having a memory, were previously thought to be associated with more evolved organisms. We explore the capabilities of this organism further, by fragmenting it into microscopic particles called microplasmodia.

Normally, microplasmodia fuse together to form one giant network, previously described as a percolation transition [1]. However, under starvation, these microplasmodia do not reconstitute as one body, but as multiple mesoplasmodia, referred to as satellites, that move away from their original spot [2]. We investigated how the initial conditions influence the outcome of the growth pattern, via maximum search area hypothesis based on optimal foraging theory.

We found that the initial distribution of microplasmodia is the main factor of satellite formation, and the scaling relationship can be derived to describe the number and the size of these fragments. We further refine the model by accounting for collisions and probabilities of fusion during satellite formation, which agrees well with experimental results. Therefore, our unicellular organism on the verge of death maximizes its search area.

[1] Fessel, A. et al. (2012), Physical Review Letters 109, 078103. [2] Lee, J. et al. (2018), Journal of Physics D: Applied Physics 51, 244002

BP 6.34 Mon 17:30 Poster B2

Comparison of mechanical properties of cells using different cantilevers as probe tips for atomic force microscopy — •Florian Frederick Stuckmann, Hsiao-Ching Tsai, and Mathias Getzlaff — Institut für Angewandte Physik, Heinrich-Heine-Universität, Düsseldorf, Deutschland

The elasticity is one of the most important characteristics of the cell. To determine concerning deviations caused by pathologies, atomic force microscopy with a precise cantilever represents a powerful tool.

This scientific work analyzed mechanical properties of fibroblasts. Using a spherical or a pyramidal cantilever the cell elasticity of the fibroblasts can be determined. After the application of the AFM-Mode 'Force-Mapping' and the following data process, values of the Young Modulus of the fibroblasts can be obtained, which are illustrated in a map. Hence, the elasticity of typical areas such as the cell perimeter or above the nucleus can be quantified.

As a consequence of the tip shape, performance differences between the two cantilever types can be observed when working with biological samples. Because elasticity values cannot be determined at every point in case of the pyramidal cantilever, the sharp tip seems to damage the cell membrane.

BP 6.35 Mon 17:30 Poster B2

Epithelial-Mesenchymal Transition (EMT)-induced changes of cortical contractility and stiffness in breast epithelial cells — •Kamran Hosseini and Elisabeth Fischer-Friedrich — Biotechnology center of TU Dresden (Biotec), Dresden, Germany

Cancer cells have been reported to show a softer phenotype. At the same time, it has been speculated that invasive cancer cells are particularly contractile. Epithelial mesenchymal transition (EMT) has been previously identified as a key process in cancer progression and metastasis, suggesting that EMT reduces cell stiffness and enhances cell contractility. To test this hypothesis, we probed breast epithelial cells mechanically before and after chemically induced epithelial mesenchymal transition (EMT). We uniaxially compressed isolated suspended cells in a parallel plate confinement assay using an atomic force microscope in conjunction with a wedged cantilever. In this way, we measured cortical contractility and cortical stiffness. We find that cell stiffness is decreasing jointly with cortical contractility through EMT in suspended cells.

BP 6.36 Mon 17:30 Poster B2

Correlation of force generation and actin structure in blood platelets — •Anna Zelena[1], Dimitri Probst[2], Johannes Blumberg[2], Ulrich S. Schwarz[2], and Sarah Köster[1] — [1]Institute for X-ray Physics, Georg-August-University Göttingen, Göttingen, Germany — [2]Institute for Theoretical Physics, Heidelberg University, Heidelberg, Germany

Human blood platelets are non-nucleated fragments of larger cells (*megacaryocytes*), which are important for blood clotting. The hemostatic function of platelets is directly linked to their mechanics and cytoskeletal morphology. However, the exact mechanism of spreading and contraction remains elusive. In our study, we focus on the investigation of single blood platelets *in vitro* by traction force microscopy (TFM) and direct imaging using an SiR actin probe. By analysis of bead displacements inside the polyacrylamid (PAA) gels, which serve as substrates for the platelets, we are able to correlate the force generation with the actin reoganization in a time resolved manner. The force maps we obtain show a hot spot distribution, typically in spindle-like, triangular or circular shape, that we correlate with actin structures inside spreading blood platelets. In addition, we investigate the actin structures of platelets on PAA gels with different elasticity in the physiological range (1-100 kPa) and their behavior in presence of micropatterned fibrinogen surfaces.

BP 6.37 Mon 17:30 Poster B2

Numerical Investigation of Cell Deformation during Bioprinting Processes — •Sebastian Müller and Stephan Gekle — University of Bayreuth

Cell viability and functionality during bioprinting processes strongly depend on the deformations that cells experience during printing. These, in turn, result from the mechanical stresses caused by the surrounding fluid motion.

Using the multiple-relaxation-time Lattice Boltzmann Method implemented in the software package ESPResSo, which we extended with shear thinning viscosity models and a neo-Hookean cell model, we investigate the deformation of cells during the printing process qualitatively in dependence of the shear thinning properties and the printing parameters.

BP 6.38 Mon 17:30 Poster B2

Acoustic wave irradiation of cancer cells — •Lena Fastenrath[1], Maja Strugacevac[1], Tobias Löffler[1], Constanze Wiek[2], Julia Kristin[2], Jörg Schipper[2], and Mathias Getzlaff[1] — [1]Heinrich-Heine-Universität Düsseldorf, Institute of Applied Physics, Universitätsstr. 1, 40225 Düsseldorf, Germany — [2]Düsseldorf University Hospital, Department of Otorhinolaryngology,

Moorenstrasse 5, 40225 Düsseldorf, Germany

Our group is developing new, alternative, cell-selective treatment strategies for squamous cell carcinoma cells of the head-neck area. This therapy is based on the different mechanical properties of oral keratinocytes and cancer cells.

Squamous cell carcinoma cells were exposed in vitro to sound waves exhibiting frequencies between 0.5 kHz and 10.0 kHz. For those frequencies that have lead to the strongest cell reaction we varied input voltage and the distance between the cells and the sound probe.

The reaction and the change of areal extent of the cells were observed under a fluorescence confocal laser scanning microscope. Our latest results will be presented and discussed.

BP 6.39 Mon 17:30 Poster B2

Size-dependent forces during phagosomal transport — Simon Wieland[1,2], •David Gitschier[1,2], Magdalena Haaf[1], Solange Hoffbauer[1], and Holger Kress[1] — [1]Biological Physics Group, Department of Physics, University of Bayreuth, Germany — [2]Joint first authors

The intracellular transport of organelles plays an important role for a large variety of cellular processes, such as exocytosis and endocytosis. It is well established that the transport of organelles is biochemically regulated. However recently, it was shown that also the size of the organelles has a strong influence on the transport. In macrophages it was found that large phagosomes are transported very persistently towards the nucleus whereas small phagosomes show a highly irregular Motion[1]. To unravel the molecular causes of this behavior, we investigated the intracellular transport forces of phagosomes as a function of their size by using magnetic tweezers. We found that transport forces increase monotonically for organelle sizes up to four micrometers. The scaling of the transport forces with the organelle sizes together with an identification of the types and numbers of involved motors can lead to a more fundamental understanding of intracellular transport and the cooperation of molecular motors.

[1] S. Keller, K. Berghoff, H. Kress, Phagosomal transport depends strongly on phagosome size. Scientific Reports, 7 (2017), 17068

BP 6.40 Mon 17:30 Poster B2

CAOS - How to Stretch Adherent Cells — •Tobias Neckernuss, Daniel Geiger, Jonas Pfeil, and Othmar Marti — Institute of Experimental Physics, Ulm University

We demonstrate a new method to stretch adherent cells with light. This has the advantage that no interaction with a probe is necessary to determine the mechanical properties of cells. Additionally not only point like forces can be applied, but the cell is stretched over its whole membrane surface. We show measurements on 3T3 cells as cultured and compare them to measurements taken on 3T3 cells treated with latrunculin. The deformation data is fitted to viscoelastic models consisting of networks of springs and dashpods. With the Akaike singular information criterion the best models are selected. Results confirm that the new technique works well an delivers results in agreement with literature. Additionally, by investigation of the behavior of individual parameters conclusions about different parts of the cytoskeleton can be drawn. In addition, the new technique proved to be more sensitive and precise than the well established technique of passive microrheology.

BP 6.41 Mon 17:30 Poster B2

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

Phagocytosis can be initiated by the binding of an immunoglobulin G (IgG)-opsonized particle to Fcγ-receptors in the cell membrane. While the molecular components of the underlying signaling cascades are well known, it is unclear how fast and how far the corresponding signals propagate in the cell. To address these issues, we investigate the spatial spreading of phagocytic signaling 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 polystyrene beads opsonized with IgG to single macrophages. The use of holographic optical tweezers allows us to precisely control the bead-to-bead distance during the attachment. The subsequent uptake into one joint or in two separate phagosomes is distinguished by analyzing the intracellular particle trajectories after the uptake.

For medium-sized phagosomes with a diameter of two micrometers, we found that the probability for joint uptake is very high for small distances and very low for large distances, with a transition between these regimes at distances of several hundreds of nanometers. Further studies with larger and smaller target beads will allow us to determine whether this resolution limit is constant or whether it scales with the target size, which will provide quantitative insights into the spatial spreading of signaling during phagocytosis.

BP 6.42 Mon 17:30 Poster B2

Traction Force Microscopy during Phagocytosis — •Wolfgang Gross and Holger Kress — Biological Physics Group, Department of Physics, University of Bayreuth, Bayreuth, Germany

In the process of phagocytosis, cells internalize objects like bacteria and dead cells that have a size of several micrometers, thus being a main function of innate immunity. After the detection of foreign particles, the membrane starts to wrap around the phagocytic target. This so-called phagocytic cup is mechanically supported by the polymerization of actin filaments in combination with myosin motors. Even though the main molecular players have been identified already, there is only few quantitative data describing the dynamics of the major regulators.

To investigate the uptake dynamics we use immunoglobulin G (IgG) coated polystyrene particles with a diameter of 10 micrometers as a model system. Using a combination of traction force microscopy (TFM) and holographic optical tweezers, we are able to measure cellular forces during phagocytosis in a spatially and temporally resolved manner. As a substrate, we use soft polyacrylamide films with a thickness of a few tens of micrometres which we coat with fibronectin to mediate cell adhesion. TFM allowed us to quantify the forces, which J774 macrophages exert during adhesion and phagocytic uptake. Preliminary data show the distribution of contractile forces in the direct vicinity of the phagocytic target. We anticipate our results to pave the way for a more quantitative understanding of phagocytosis and thus, enable the development of new models for this process.

BP 6.43 Mon 17:30 Poster B2

Rayleigh-Plateau-like instability of an active cylindrical cell membrane — •Katharina Gräßel, Christian Bächer, and Stephan Gekle — Universität Bayreuth, Bayreuth, Deutschland

A free liquid jet undergoes a pearling instability, named after Rayleigh and Plateau, that is triggered by the surface tension of the fluid. To account for a biological membrane consisting of the cell cortex underlying a lipid bilayer, the classical model of the Rayleigh-Plateau instability is extended to include bending elasticity of the bilayer as well as anisotropic surface tension, modelling contractile active stresses in the cortex. These extensions lead to alteration of the wavelength of the instability and are confirmed by Lattice-Boltzmann simulations.

BP 6.44 Mon 17:30 Poster B2

First evidence of cellular uptake of environmentally relevant microplastic particles — •Anja Ramsperger[1,2,4], Bangalore Vinay Kumar[1,4], Wolfgang Gross[2,4], Holger Schmalz[3,4], Holger Kress[2,4], and Christian Laforsch[1,4] — [1]Animal Ecology I and BayCEER — [2]Biological Physics Group — [3]Macromolecular Chemistry II and BPI — [4]University of Bayreuth, Germany

Research efforts on microplastic (MP) pollution is strongly increasing during the last 15 years. Plastic introduced to the environment undergoes processes of degradation and disintegrates to MP. Furthermore, microbes attach to MP surfaces and, together with biomolecules, form an ecocorona that can enhance the ingestion of MP by organisms. Once ingested there is evidence that MP can harm organisms for example by translocating into tissue causing e.g. inflammatory responses. The processes involved in the translocation of MP into tissue are not known and to our knowledge a process for cellular uptake of environmentally relevant MP was not described to date. Therefore, we investigated the cellular uptake of MP and show that MP from environmental media gets internalized by murine macrophages significantly more often than control MP. To unravel which surface properties might trigger internalization into cells, we are currently analyzing the composition of the ecocorona on MP by using SEM and micro-Raman spectroscopy. A quantification and characterization of the internalization of environmentally relevant MP by cells will likely be an important step for understanding the potential subsequent translocation into tissue and inflammatory responses which can harm the whole organism.

BP 6.45 Mon 17:30 Poster B2

Cross-talk between cell shape and state during cell fate transitions — •Wolfram Pönisch[1], Irene Aspalter[1], Agathe

Chaigne[1], 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

The development of an organism is characterized by a series of cellular fate transitions where cells acquire increasingly specialized phenotypes. Such fate transitions are often accompanied by cellular shape changes and there are strong indications of a coupling between cell shape and fate. Here, we present a pipeline to quantify and analyze cell shapes as cells undergo fate transitions. We will present how the morphometric features of cell shapes can be quantified and how the high dimensional dataset can be analyzed with the help of dimensional reduction methods such as PCA and tSNE. To identify clusters of cells and classify cells based on those clusters, we use a variety of machine learning algorithms. To apply our analysis pipeline, we study 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: While cells possess a spherical shape before exiting naïve pluripotency, they spread on a substrate after exiting. Furthermore, cell shape change appears to be essential for the associated fate change.

BP 6.46 Mon 17:30 Poster B2

Rheology of hydrogels based on chemically modified hyaluronic acid — •Martin Schilling and Florian Rehfeldt — Third Institute of Physics - Biophysics, Georg-August-University, Göttingen, Germany

Many aspects of cell behavior are influenced by the mechanical properties of their microenvironment. To mimic the various elastic Young's moduli E of different in vivo environments of cells, it is necessary to design and mechanically characterize hydrogels for cell culture that are biocompatible and allow for a tunable elasticity.

Hyaluronic acid (HA), a polysaccharide consisting of disaccharide units, was chosen as base for the hydrogel system as it is biocompatible and not toxic for cells, thus allowing for 3D encapsulation.

Native HA hydrogels exhibit a visco-elasticity at the lower end of the physiologically relevant stiffness range. Here, we show that by chemical modification and subsequent covalent cross-linking, we can cover the required range from 0.1 kPa to 100 kPa. Additionally, altering the degree of modification of HA allows distinct and independent tuning of Young's modulus and biochemical recognition of HA by cells. Mixtures of both high and low modified HA are examined to combine both properties. The gelation kinetics of the resulting hydrogels are investigated by rheology using oscillatory shear tests both in the low and high strain (LAOS) regime.

BP 6.47 Mon 17:30 Poster B2

Traction force microscopy of HAELVI cells on silicone gel substrate — •Susan Tavakoli[1], Kay-E. Gottschalk[1], Manfred Frick[2], Kathrin Diem[2], Eric Dufresne[3], and Kathryn Anne Rosowski[3] — [1]Institute for Experimental Physics, Ulm University, Germany — [2]Institute of General Physiology, Ulm University, Germany — [3]Soft and living Materials, ETH Zürich, Switzerland

Cells interact with their environment in different ways, chemically and mechanically. Through various interactions, cells exert forces on their substrate or adjacent cells. Quantifying these forces under different environmental changes have been the subject of many studies. The method of measuring these forces - known as Traction Force Microscopy, calculates the forces based on the deformation made by cell on a highly flexible substrate that is measurable by tracking the displacement of fluorescent beads attached to the surface. We make the substrates from a biocompatible polymer gel known as Polydimethylsiloxane (PDSM) that has a very low stiffness and its transparency facilitates microscopy. Briefly, a glass coverslip is covered with a uniform layer of the gel using spin-coating technique then a layer of fluorescent beads covers the surface of the gel. We use a matlab code that calculates the forces using the geometry and mechanical characteristics of the gel and the beads displacements to quantify traction forces of HAELVI cells under normal condition as well as treatment with Blebbistatin. Our aim will be to combine this method with a stretcher device, simulating the breathing function to study lung epithelial cells.

BP 6.48 Mon 17:30 Poster B2

The effect of reactive oxygen species on the molecular and mechanical phenotype of C6 glioma cells — •Yesaswini Komaragiri[1], Doreen Biedenweg[2], Ricardo H. Pires[1], and Oliver Otto[1] — [1]ZIK-HIKE, Universität Greifswald, Greifswald, Germany — [2]Universitätsmedizin Greifswald, Greifswald, Germany

Reactive oxygen species (ROS) are one of the main sources of oxidative stress which are associated with important alterations in cell physiology. Mechanical properties have long been established as a label-free biomarker but their interplay with alternating levels of ROS has not been fully investigated. This study focusses on understanding the impact of oxidative stress on the mechanical properties of immortalized rat brain C6 glioma cells. In an in vitro assay, mitochondrial superoxide was generated by exposing cells to varying concentrations of hydrogen peroxide. Using real-time fluorescence deformability cytometry, we link for the first time the molecular phenotype of ROS using MitoSOX-red as a fluorescent marker to changes in the mechanical phenotype as a label-free biomarker. We show that for micro-molar concentrations of H2O2, the elastic Young's modulus of the cells increases, which is in contrast to previous studies focusing on concentrations in the millimolar range.

BP 6.49 Mon 17:30 Poster B2

A muscle cell seen as active matter: Heterogeneities and dynamic instabilities in sarcomere contraction of cardiomyocytes — •Daniel Härtter[1], Wolfram-Hubertus Zimmermann[2], and Christoph F. Schmidt[1,3] — [1]Drittes Physikalisches Institut - Biophysik, Georg-August-Universität Göttingen — [2]Institut für Pharmakologie, Universitätsmedizin, Georg-August-Universität Göttingen — [3]Department of Physics, Duke University, USA

Cardiac muscle contraction involves highly coordinated dynamics, from the level of the myosin motors on the length-scale of nanometers to that of the whole organ. Many features of muscle contraction, however, emerge on the mesoscopic length scale of (half-)sarcomeres, the basic contractile unit of muscles consisting of mechanically coupled molecular motors. Basic theories of collective molecular motor dynamics predict emergent phenomena such as dynamic instabilities and spontaneous oscillatory motion due to non-monotonic force-velocity relations. On the next level of the hierarchy, when half-sarcomeres are coupled in series and in parallel, even richer emergent dynamics are expected. So far, inter-sarcomere dynamics have not been studied systematically. We have imaged sarcomere dynamics in individual stem-cell-derived cardiomyocytes with endogenous fluorescent labeling of z-bands introduced by CRISPR/Cas9, and have observed that mechanical competition leads to sarcomere de-coherence and complex dynamic heterogeneity. We have modelled the phenomena with a dynamic myofibril model of multiple heterogeneous elements with non-monotonic force-velocity relations from a complex systems / active matter perspective.

BP 6.50 Mon 17:30 Poster B2

Myosin-dependent mechanosensory adaptation in Drosophila — •Chonglin Guan[1], Kengo Nishi[1], Christian Kreis[2], Oliver Bäumchen[2], Martin Göpfert[3], and Christoph F. Schmidt[1,4] — [1]Drittes Physikalisches Institut - Biophysik, Fakultät für Physik, Georg-August-Universität Göttingen, 37077 Göttingen — [2]Max-Planck-Institut für Dynamik und Selbstorganisation, 37018 Göttingen — [3]Abteilung Zelluläre Neurobiologie, Schwann-Schleiden-Forschungszentrum, Georg-August-Universität Göttingen, 37077 Göttingen — [4]Department of Physics, Duke University, Durham, NC 27708, USA

Mechanosensory receptor cells detect and convert a diverse range of physical forces such as sound, vibration and stretch into biological (electrical) signals. The fruit fly Drosophila melanogaster possesses specialized organs, chordotonal organs (ChO), to "hear" external sound, feel airflow and keep track of body motions (propiosensing). Mechanoelectrical transduction in these organs is typically controlled by active, force-generating processes (adaptation motors). The nature of those force generators, however, is not known. We have combined electrophysiological analysis with mechanical stimulation, and have correlated mechanical properties and active manipulation with neuronal activity. We show that non-muscle myosin II activity in ChOs of Drosophila larvae is responsible for both mechanosensoy adaptation and neuronal responsiveness. Mechanical experiments suggest that elasticity and pretension in the ChO's depend on the activities of myosin motors.

BP 6.51 Mon 17:30 Poster B2

Passive and active response of bacteria under mechanical compression — •Renata Garces[1], Samantha Miller[2], and C.F. Schmidt[1,3] — [1]DPI, University of Goettingen — [2]The Institute of Medical Sciences, University of Aberdeen — [3]Department of Physics,

Duke University

The ability to maintain a positive turgor pressure, by means of higher osmolarity of the cell interior than the exterior, is a requirement for proper metabolism in walled microbial cells. Turgor pressure is sensitive to changes in external osmotic conditions, and is drastically increased upon osmotic downshock, together with cell volume. Bacteria prevent lysis caused by excessive osmotic pressure through mechanosensitive (MS) channels: membrane proteins that release solutes (ions) in response to mechanical stress. The exact mechanism of channel gating in the natural setting, however, has been elusive due to the lack of experimental methods appropriate for the small dimensions of prokaryotes. We here present experimental data on the gating of MS channels of E. coli subjected to compressive force under iso-osmotic conditions. We indent living cells with micron-sized beads attached to the cantilever of an atomic force microscope (AFM) and characterize the mechanical response. We show that turgor pressure can be monitored through the measured response and quantify its value and fluctuations for individual single cells before and after MS channel gating.

BP 6.52 Mon 17:30 Poster B2

Near Real Time Analysis of Stress Fiber Formation in Stem Cells — •Lara Hauke[1], Carina Wollnik[1], Benjamin Eltzner[2], Stefan Huckemann[2], and Florian Rehfeldt[1] — [1]Third Institute of Physics, Biophysics, Georg-August-University Göttingen — [2]Institute of Mathematical Stochastic, Georg-August-University Göttingen

Human mesenchymal stem cells (hMSC) can be directed to differentiate into various lineages by different matrix elasticities. While changes in lineage specific protein expression occur over a period of days to weeks, significantly different structures of stress fibers are observable within the first 24 hours of plating [1] quantified by an order parameter S. With our massively parallel live-cell imaging set-up we record cells under physiological conditions (37 °C, 5 %CO2) over a period of 24-48 hours to obtain a statistically sufficiently large data set. We aim for a full representation of filament processes over time and space allowing for statistical analysis. This unbiased classification will be represented by persistence in space and time and potential cross-talk with other cytoskeletal components. For this we developed the FilamentSensor [2,3] a freely available tool for near real-time image analysis of stress fibers. We present experimental data where we can distinguish the development of hMSCs on 1 kPa, 10 kPa and 30 kPa elastic substrates with 99 % confidence and are working on single filament tracking and better analysis of orientation fields.

References: [1]A. Zemel, et al., Nat. Phys., 2010. [2]www.filamentsensor.de [3]B. Eltzner, et al., PLoS One, 2015.

BP 6.53 Mon 17:30 Poster B2

Recovery behavior of stretched single vimentin filaments — •Julia Kraxner, Johanna Block, and Sarah Köster — Institut für Röntgenphysik, Georg-August-Universität Göttingen

Varying mechanical properties of different cell types are determined by the cytoskeleton. The cytoskeleton consists of microtubules and microfilaments, which are conserved throughout all metazoan cell types, and different types of intermediate filaments (IFs), expressed in a cell-type specific manner. Therefore, IFs are believed to have an important impact in determining the mechanical properties of different cell types. Using optical tweezers, combined with microfluidics and fluorescence microscopy, we directly probe the stress-strain behavior of single IFs. Regarding the force-strain curves, stretching a single filament shows three regimes: the elastic stretching of α-helices, a plateau region and a stiffening at high forces. One interpretation of this behavior is that within this plateau regime the α-helices in the rod-domain of the vimentin monomers uncoil to β-sheet like structures. This process is called α-β-transition and it is suggested to be reversible even though the energy barrier between these two states is quite high. Here, we investigate the filament recovery after this α-β-transition of untreated and chemically fixed vimentin filaments.

BP 6.54 Mon 17:30 Poster B2

Influence of Ions on the Assembly of Vimentin Intermediate Filament — •Manuela Denz and Sarah Köster — Institut für Röntgenphysik, Georg-August-Universität Göttingen

Intermediate filaments (IFs) are part of the cytoskeleton, together with microfilaments (MFs), microtubules (MTs), molecular motors and cross-linkers. In contrast to MFs and MTs, IFs vary between different cell types. Despite the many different types, all IFs 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 and as the monomers are highly charged, ions can trigger the assembly. Therefore, it is of high interest to study the influence of different ions on the assembly. In this study we focused on the IF protein vimentin. As a buffer system, MOPS (3-(N-morpholino)propanesulfonic acid) was chosen. We used two methods for our study: (i) small angle x-ray scattering (SAXS), a technique that probes primarily the lateral assembly of vimentin monomers into so-called unit-length filaments. (ii) Additionally, we employed atomic force microscopy, with which we directly imaged individual filaments. We tested the influence of several different ions with varying valence, sizes and concentrations on assembly. Our study helps to understand the molecular charge interactions between vimentin monomers or higher order assemblies. The variation in filament thickness, compactness or homogeneity that is observed in different ionic environments may eventually play a role in cells, where differently built filaments locally define different mechanical properties of the cytoskeleton.

BP 6.55 Mon 17:30 Poster B2

Ion Depending Stress-strain Behavior and Interaction of Intermediate Filaments — Anna Schepers, •Charlotta Lorenz, Johanna Block, Julia Kraxner, and Sarah Köster — Institute for X-Ray Physics, Georg-August-Universität, Göttingen, Germany

The cytoskeleton, consisting of microtubules, actin filaments and intermediate filaments (IFs), is essential for the survival of the cell. Only intermediate filaments are expressed in a cell-type specific manner. Therefore, they are ideal candidates to tune the stability and mechanics of a cell to the environment and requirements. In cells, IFs usually form networks which have been thoroughly studied in vitro by rheology. The properties of single filaments, but also the network structure itself, influence the results derived from rheology. To decouple these two effects, we measure the interaction of two single vimentin IFs with optical trapping in combination with microfluidics and fluorescence microscopy. The interactions between IFs depends on the concentration and ionic strength of surrounding ions. We study how these ions influence the interactions and the stress-strain behavior of single filaments. Thus, we also quantify the effect of ion addition to single vimentin and keratin IFs. We suggest that the cooperativity between monomers within the IF is enhanced upon ion addition, which can be modeled theoretically. Results from a Monte-Carlo simulation support our model qualitatively.

BP 6.56 Mon 17:30 Poster B2

DNA Damage and its Influence on the Mechanical Properties of the Nucleus — •Nora Olszok[1], Alia Dos Santos[2], Christopher Toseland[2], and Florian Rehfeldt[1] — [1]University of Göttingen - Third Institute of Physics - Biophysics — [2]University of Kent

In response to DNA damage actin is imported into the nucleus, nuclear actin strands are formed and the chromatin structure is remodeled [C. P. Caridi et al. *Nature* (2018); C. Andrin at al. *eLife* (2015); M. J. Kruhlak et al. *The Journal of Cell Biology* (2006)]. This change in the nuclear "cytoskeleton" might change the mechanical properties of the nucleus. We investigated such potential changes with a combined study using fluorescent microscopy and atomic force microscopy (AFM). Following systematically induced DNA damage by cisplatinum we measured the mechanical properties of isolated nuclei and nuclei in whole adhered cells. Here, we collected force maps of the nucleus and its surroundings and extracted an effective Young's modulus. Complementary we use fluorescence microscopy to assess the amount of DNA damage (by staining for phosphorylation of the histone H2A.X.) that can be quite heterogeneous within a cell population treated with cisplatinum. These measurements were complemented with similar experiments on elastic polyacrylamide (PA) gels to acoount for the diverse *in vivo* micro-environments cells encounter.

In summary, we see a clear impact of DNA damage on nuclear mechanics, that might help to elucidate further the underlying mechanisms of cellular damage remedy.

BP 6.57 Mon 17:30 Poster B2

Automated tracing algorithm for scanning electron microscopy images of the actin cortex — •Moritz Schu[1,2], Daniel Flormann[2], and Franziska Lautenschläger[2] — [1]Saarland University — [2]INM-Leibniz Institute for New Materials

The actin cortex is a thin layer of actin, myosin, and actin-binding proteins that supports the membrane of animal cells. It defines cell shape

and plays a fundamental role in cell motility. Several researchers have already imaged the actin cortex using scanning electron microscopy (SEM) after removing the membrane with detergents. In their works the SEM images have been compared mostly qualitatively. Quantitative fibre image analysis tools already exist, but are not well adapted for SEM images of the actin cortex. This leaves only the possibility for manual image analysis that is prone to bias and cumbersome. Therefore, we developed an automated vectorial fibre tracing algorithm based on the Hessian of Gaussian convolution, that is applicable to SEM images and allows extraction of useful parameters such as mesh hole size and relative angle distribution. The algorithm has been tested on SEM images of the actin cortex of retinal pigmented epithelial cells (RPE-1) and is likely applicable to a wide range of image types. This method is well suited to highlight differences between cell types or conditions and is adaptable to any fibre system.

BP 6.58 Mon 17:30 Poster B2

Failure of Biological Networks with Dynamic Crosslinks — •Mareike Berger, David Brückner, and Chase Broedersz — Ludwig-Maximilians-Universität, Munich

The cytoskeleton is a complex network of crosslinked biopolymers, which is crucial for cellular rigidity and cell motility. By remodeling on different time scales, it allows the cell to both withstand stress and adapt to external forces. Rheological experiments with reconstituted crosslinked actin filament networks have revealed a complex, time-dependent stress response that depends sensitively on the properties of the crosslinks. In a simple model of a dynamically crosslinked network, we investigate the rheology and rupture behavior of such transient networks. We find that in a network with fixed crosslinks, the rupture stress is determined by a characteristic stress distribution in the network, where highly stressed crosslinks in the vicinity of defects that exceed their maximum extension threshold cause the failure of the network. In contrast, a network with dynamic crosslinks exhibits an entirely different, system-size dependent rupture mechanism. This model therefore reveals two distinct rupture mechanisms that could provide a conceptual framework for the rupture dynamics of experimental systems.

BP 6.59 Mon 17:30 Poster B2

Influence of Intermediate Filaments on Microtubule Dynamics and Organisation — •Laura Schaedel, Charlotta Lorenz, Susanne Bauch, and Sarah Köster — Institut für Röntgenphysik, Universität Göttingen

The cytoskeletal networks are involved in fundamental cellular functions such as the control of cell shape and mechanics. They are composed of different types of biopolymers that have substantially distinct mechanical, structural and biochemical properties. These contrasting characteristics make the study of the interactions between the cytoskeletal subsets interesting, as cells are likely to regulate and combine them in a coordinated manner in order to efficiently carry out diverse processes. Here, we study the direct interaction between two major components of the cytoskeleton - vimentin filaments, one of the most abundant members of the intermediate filament family, and microtubules - in a reconstituted in vitro setup. We build different vimentin network architectures and characterise their impact on microtubule dynamics and mechanics. With our minimalist approach, we aim at better understanding the fundamental properties of vimentin-microtubule composite network architectures and self-organisation.

BP 6.60 Mon 17:30 Poster B2

Active contraction of biopolymer networks in elastic confinement — •Johannes Flommersfeld — Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilans-Universität München, Germany

Mechanical properties of cells are largely determined by their cytoskeleton, a complex network consisting of biopolymers and molecular crosslinks. The interaction of actin filaments and the molecular motor myosin plays a central role in cell biology, since it gives rise to various forms of cell movement including muscle contractions and cell division. In vivo such actin myosin networks are usually confined by an elastic cell membrane. Recent studies of confined active fluids have revealed a strong dependence of the systems properties on the parameters of the confining walls, which is in stark contrast to passive systems. Since actin-myosin assemblies are intrinsically active, these findings raise the question if the properties of the boundaries influence the behavior of such networks. To investigate this question, we present a simple model of contractile networks, with which we can investigate how the boundaries steer the dynamics and the final state of an actively contracting network.

BP 6.61 Mon 17:30 Poster B2

Dynamic properties of actin cortex depend on the adhesion state of cells. — •Kevin Kaub[1,2], Emmanuel Terriac[1], and Franziska Lautenschläger[1,2] — [1]INM, Saarbrücken, Germany — [2]Saarland University, Saarbrücken, Germany

The actin cortex plays an important role in mechanical stability and migration. In recent years new information on the structural and the dynamical properties of the actin cortex have been obtained but their interplay and their link to mechanical properties is still poorly understood. For adhered cells it has been shown that there are two essential processes that constitute the dynamics of the cortex. These processes are linked to the polymerisation mechanisms of actin filaments: one, fast, is induced by Arp2/3, while the other, slower, is induced by formins. Furthermore it has been established that these processes contribute to the overall dynamics in different proportions. Finally, the activity of the molecular motor myosin II is another factor to take into account in order to link the structure and the mechanical properties. In the case of suspended cells, there have been conflicting reports on the role of myosin activity in regards to the stiffness.

It is our goal to understand this contradiction. To that aim, we analyzed the dynamical properties of the actin cortex by the use of FRAP (Fluorescence recovery after photobleaching). We further assessed the influence of myosin, Arp2/3 and formin inhibition in different states of adhesion. Our results shows that the dynamical properties of the actin cortex are adhesion-state specific.

BP 6.62 Mon 17:30 Poster B2

Vimentin intermediate filaments rings deform nucleus during the first steps of adhesion — •Emmanuel Terriac[1], Susanne Schütz[2], and Franziska Lautenschläger[1,2] — [1]Leibniz Institute for New Materials, Saarbrücken, Germany — [2]Faculty NT, Saarbrücken, Germany

The role of vimentin intermediate filament in different cellular processes, such as cell migration or cellular mechanics has been increasingly studied during the last decade.

Here, we show an unreported phenotype during the first hours of adhesion: filamentous vimentin is found in close vicinity of the cell nucleus and occasionaly, nuclei-deforming vimentin rings could be observed. We show that the accumulation of filamentous vimentin is decreasing over time as a function of the adhesion affinity of the cell for the substrate. Most structures are dissolved within the first 6 hours after depositing the cells over the surface which may be the reason of why these structures are not widely reported yet.

We propose that upon forced detachment of cells by conventional techniques such as trypsinization, cells are not able to control the depolymerization of vimentin while this step is controlled during mitosis. Due to the entanglement of the nucleus within the vimentin fibers the nucleus is deformed during spreading, potentially caused by the stretching of the entire vimentin network. This deformation is released once vimentin filaments get slowly dissolved and recycled during full adhesion. The implication of the strong applied forces on the nucleus via this mechanism remains to be investigated in future.

BP 6.63 Mon 17:30 Poster B2

Formation of Microtentacles — •Lucina Kainka[1,2], Emmanuel Terriac[1,2], Ludger Santen[2], and Franziska Lautenschläger[1,2] — [1]NM - Leibniz Institut for New Materials, Saarbrücken, Germany — [2]Saarland University, Saarbrücken, Germany

Microtentacles (McTNs) are tubulin based membrane protrusions appearing in circulating tumor cells and playing a significant role in tumor cells reattachment efficiency. A weakened actin cortex enables microtubule to form protrusions with a diameter of less than 1 μm and a length of tens of μm. Using cytoskeletal drugs which are targeting the actin cortex integrity and its contractility, we induce McTNs even in non-cancerous RPE1 cells. We investigate the presence of microtubules and actin as well as vimentin, which has been hypothesized to stabilize McTNs [1], under those conditions. We further establish a statistic over the number and lengths of McTNs depending on different drug concentrations applied. Experiments on the dynamics of McTNs, especially during retraction after drug wash-out, give a better insight in the role of individual cytoskeletal elements. Understanding the mechanisms of the formation of McTNs may help the development of new cancer therapies targeting CTCs in the microvasculature.

[1] R.A. Whipple, E.M. Balzer, E.H. Cho, M.A. Matrone, J.R. Yoon,

S.S. Martin, Vimentin Filaments Support Extension of Tubulin-Based Microtentacles in Detached Breast Tumor

BP 6.64 Mon 17:30 Poster B2

The Influence of Force on the Self-Assembly of Myosin II Minifilaments — •Justin Grewe[1,2], Kai Weissenbruch[3], Martin Bastmeyer[3], and Ulrich S. Schwarz[1,2] — [1]BioQuant, Heidelberg, Germany — [2]Institute for Theoretical Physics, Heidelberg, Germany — [3]Karlsruhe Institute of Technology, Germany

Force generation and self-assembly are two central processes in biological systems that usually are considered in separation. However, the signals that activate non-muscle myosin II simultaneously lead to self-assembly into myosin II minifilaments as well as progression of the motor heads through the crossbridge cycle. Here 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 slows down dramatically. We validate our model by comparing fluorescence recovery after photobleaching simulated with our model against experimental results. Our model also predicts that increasing actin filament concentration and force both lead to a decrease in the critical aggregation concentration. We suggest that due to these effects, myosin II minifilaments in the cell might be in a supercritical state that can react faster to changing conditions than in solution.

BP 6.65 Mon 17:30 Poster B2

A dynamic model for the cytoskeleton of malaria-infected RBCs — •Julia Jäger[1,2], Michael Lanzer[3], and Ulrich S Schwarz[1,2] — [1]Institut für Theo- retische Physik, Universität Heidelberg — [2]Bioquant, Universität Heidelberg — [3]Parasitologie, UniversitätsKlinikum Heidelberg

Once inside the body, malaria parasites invade red blood cells (RBCs) in order to hide from the immune system and to digest hemoglobin. Over the course of 48 hours the parasite completely remodels the red blood cell, so that the cell becomes round and stiff, and eventually breaks open. The main point of attack by the malaria parasite is the spectrin-actin network underlying the membrane. It has been shown that the parasite removes some of the actin junctional points and uses this actin to build up its own filament system inside the RBC. We develop a particle-based reaction-diffusion model, which captures this remodeling process and examine possible mechanisms by which the parasite could induce the actin mining. In the long run, such a model might help to identify possible ways to interfere with the parasite lifecycle.

BP 6.66 Mon 17:30 Poster B2

Multi-scale microrheology using fluctuating semiflexible filaments as stealth probes — •Kengo Nishi[1], Fred MacKintosh[2], and Christoph Schmidt[1,3] — [1]University of Goettingen, Goettingen, Germany — [2]Rice University, Houston, USA — [3]Duke University, Durham, USA

Microrheology is commonly performed using micron-sized beads embedded in the (soft)medium to be studied. Inserting beads can be problematic in confined or hard to access places and can cause artefacts. Here, we introduce the use of single-walled carbon nanotubes (SWNTs), which are model semi-flexible polymers with non-photobleaching fluorescence, as stealth probes. We embedded SWNTs in viscoelastic media and analyzed thermally driven shape fluctuations. We show that the bending dynamics of SWNTs embedded in soft media can be used to probe the viscoelastic properties of such media at multiple scales, corresponding to the wavelengths of the modes analyzed. We found that the viscoelastic moduli of polymer solutions measured by SWNTs are in excellent agreement with those by measured by conventional micro/macrorheology, which validates the method.

BP 6.67 Mon 17:30 Poster B2

Super-resolution microscopy of the bacterial cell wall synthesis machinery — •Julian Roth and Alexander Rohrbach — Albert-Ludwigs-Universität, Freiburg, Deutschland

We constructed a total-internal-reflection fluoresecence structured illumination microscope (TIRF-SIM) with 10Hz frame rate, which enables us to gain a better view on the cell wall synthesis of the bacterium Bacillus subtilis, since it is still unclear how bacteria build, maintain and expand their cell wall. The actin-like, cytoskeletal protein MreB is an essential component of the bacterial cell-shape generation system. MreB filaments are thought to mechanically couple several synthesis motors that putatively synthesize the cell wall, whereas the filaments* traces mirror the trajectories of the motors. The cell wall synthesis machinery proteins, RodA and PbPH, are closely associated with MreB : PbPH is hypothesized to be the synthesis motor driving the MreB filaments, while there are indicators that RodA provides the motor with new cell wall material. By imaging these proteins with TIRF-SIM under different chemical and mechanical conditions, we are able to extract new information via trajectories providing propagation velocities as well as interaction processes and correlated population behavior at high resolution. This information is utilized to set-up an improved mechanistic model supported by simulations investigating the coupled work of possessive motors.

BP 6.68 Mon 17:30 Poster B2

Time series irreversibility and entropy production in biological systems — •Samuel Salinas Almaguer and Matthias Weiss — Experimental Physics I, University of Bayreuth, Germany

Quantifying whether a noisy signal, e.g. some fluorescence time series, originated from a non-equilibrium process is a big challenge. Differentiating between the forward time series and its inverse at least allows for identifying whether detailed balance is broken, i.e. if there is a preferred flux direction in phase space. Following previous reports, we have explored with numerical and experimental data to which extent an autoregressive model can detect broken detailed balance. We also used the approach to assign lower bounds to the system's entropy production via the Kullback-Leibler divergence.

BP 6.69 Mon 17:30 Poster B2

External forces on the cell membrane — •Kristian Blom and Aljaz Godec — Max-Planck-Institute for Biophysical Chemistry, Mathematical Biophysics Group, Göttingen, Germany

Cell adhesion is the process by which neighboring cells attach to each other through specialized adhesion molecules on the cell surface. The formation of receptor-ligand bond clusters between two cell surfaces is essential for cellular regulation, intercellular communication, immune response, tissue formation, and cell signaling.

While most of our current understanding about adhesion dynamics derives from the theory of non-interacting receptor-ligand bonds, recent experiments have revealed striking collective properties of adhesion clusters arising from a coupling of nearby individual adhesion bonds through deformations of the fluctuating membrane. However, how exactly this coupling affects the dynamics of cluster formation and dissolution remains an elusive problem.

In order to arrive at a deeper understanding of adhesion cluster dynamics under an external force we incorporated both the coupling of adhesion bonds due to membrane fluctuations as well as an external force into a theory of adhesion cluster stability. We obtained rigorous results for the depinning time statistics, i.e. the time to the state in which all N adhesion bonds become detached. The interplay between the pulling force and the inter-bond coupling yields non-trivial effects on the depinning time.

BP 6.70 Mon 17:30 Poster B2

Thermodynamics of Active Droplets — •Jan Kirschbaum and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Biological cells need to organize their material in space and time. One organization principle is phase separation leading to membraneless compartments. Phase separation implies that large droplets grow at the expense of small ones. To counteract this instability cells can use non-equilibrium processes driven by the consumption of ATP. One example are active droplets, where the droplet material is created by driven chemical reactions.

We study active droplets by developing a thermodynamically consistent model combining phase separation with chemical reactions based on linear non-equilibrium thermodynamics. In the limiting case of first order reactions, hexagonal patterns are typical. Using a mathematical analogy with equilibrium systems with long range interactions we determine numerically how these patterns depend on the parameters of phase separation and chemical reactions. This analysis shows that the analytical predictions work better than expected. Our results show how cells can use chemical reactions to control the size of active droplets.

BP 6.71 Mon 17:30 Poster B2

Mechanisms of Permeation in Potassium Channels —

•Maximilian Vossel[1,2] and Bert de Groot[2] — [1]Mathematical Biophysics Group, Max-Planck-Institute for Biophysical Chemistry (Göttingen) — [2]Computational Biomolecular Dynamics Group, Max-Planck-Institute for Biophysical Chemistry (Göttingen)

K^+ channels are proteins that facilitate the passive permeation of K^+ ions through the cell membrane. They conduct at rates close to the diffusion limit while selecting against Na^+ ions by more than a thousandfold. It has been confirmed that the channels' narrowest constriction – the selectivity filter – forces the K^+ ions to move in single file and is thereby responsible for both high current and high fidelity in rejecting Na^+.

In this work, we aim for a deeper understanding of the permeation mechanism by comparing computational models of different members of the K^+ channel family against each other. Using data from (recently published) non–equilibrium steady state molecular dynamics simulations of permeating K^+ channels we built discrete models of the permeation mechanism on a reduced phase space.

We could show that the 'direct knock-on' mechanism, where K^+ ions are in immediate adjacency to each other, is a robust process of permeation. Although exhibiting small, measurable variations, it is conserved in its main theme through all studied channels and force fields. Exploiting local detailed balance we estimated a lower bound for the voltage drop across the selectivity filter, finding values which are in very good agreement with those expected from the literature.

BP 6.72 Mon 17:30 Poster B2

Non-equilibrium dynamics of isostatic spring networks — •Benedikt Remlein, Federico Gnesotto, and Chase Broedersz — Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität München, D-80333 München, Germany

Mechanical systems exhibit rich critical behavior in the vicinity of the isostatic point. Inspired by living matter such as cytoskeletal networks and tissue, we here consider marginal assemblies driven out of equilibrium by internal activity. To date it remains unclear how the critical nature of such systems affects their non-equilibrium dynamics. We elucidate the role of the isostatic threshold in active diluted spring networks: heterogeneously distributed active noise sources drive the system into a non-equilibrium steady state. The non-equilibrium dynamics between pairs of network nodes are quantified by the characteristic cycling frequency ω – a measure of the circulation of the associated phase space currents. We reveal critical scaling of the cycling frequencies and intuitively understand their local behavior employing a mean-field approach. Overall, our work serves as a bridge connecting the well-established theory of mechanical stability to the novel field of non-equilibrium statistical mechanics.

BP 6.73 Mon 17:30 Poster B2

Theory for active transport by DNA-relaying — •Christian Hanauer and Chase Broedersz — Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität, D-80333 München

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 cargoes, 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. To understand the DNA-relay mechanism, we develop an analytical 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 6.74 Mon 17:30 Poster B2

Interacting active droplets — •Ajinkya Kulkarni and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen

Liquid-liquid phase separation plays an important role in organizing material inside biological cells. Examples are membrane-less organelles, which can be described as liquid droplets. In equilibrium systems, droplets coarsen over time, so their size and count is not controlled. This instability could be counteracted by active processes inside cells. For instance, in active droplets, driven chemical reactions create diffusive fluxes, which affect the droplet dynamics. Consequently, multiple active droplets can co-exist.

We study how active droplets interact by numerically solving a modified Cahn-Hilliard equation and comparing the results with analytical predictions. We start by considering a single active droplet in an externally imposed chemical gradient. The results can be used to understand how two droplets interact. Our goal is to understand emulsions of many droplets, which will elucidate how cells could use driven chemical reactions to control droplets.

BP 6.75 Mon 17:30 Poster B2

Investigation of Spatial Dynamics of an Evolutionary Food Web Model on Random Geometric Graphs — •Johannes Reinhard, Tobias Rogge, and Barbara Drossel — TU Darmstadt, Germany

We examine an evolutionary food web model without population dynamics. Each species is characterized by a few traits based on its body mass, and the network context (predation, competition) determines species survival. We study a meta-network of patches coupled by migration on a random geometric graph (RGG). To this purpose we use an algorithm, based on the transition rates of the network, to divide the RGG into several modules allowing us to analyse the dynamics in and between modules. In addition to the investigation of species dispersal in dependence on the lifetime of the species our main focus is on the study of species area relationships (SARs, i.e., increase of species richness with increase of sampling area). There are two ways to determine the SAR: by looking at nested areas, as previously done, or by looking at nonoverlapping areas, such as the modules. This allows us to understand the results of a large-scale meta study that found a different scaling behaviour depending on which of the two methods was used.

BP 6.76 Mon 17:30 Poster B2

Artificial intelligence in biological physics. — •Norbert Sadler — Wasserburger Str. 25a ; 85540 Haar

Through the application of artificial intelligence to complex biological systems the machine learning and deep mind method can be verified in the areas of synthetic genetics and the Crispl-Cas technique.

The algorithms of artificial intelligence are based on methods of statistical physics and the basic matrix of the Exceptional E8-Group.

Informations:www.artificial-intelligence-in-science.com

BP 6.77 Mon 17:30 Poster B2

Sequence selection of oligonucleotides under a ligation chain reaction — •Patrick Kudella[1] and Dieter Braun[2] — [1]Patrick.Kudella@physik.uni-muenchen.de — [2]Dieter.Braun@lmu.de

The replication of information on RNA or DNA is central for the emergence of life (Szostak, 1990). Previously, the replication of one sequence has often been in the focus, but we think it is essential to monitor the replication and selection dynamics out of a completly random pool of sequences.

We focus on the transition from template-free polymerization to templated ligation. Once polymerization could create oligomers long enough to hybridize, we expect a nonlinear ligation dynamic to set in. We study whether sequences were selected at this onset of replication and if interesting non-linear and frequency-dependent behavior can be found (Toyabe, 2018).

We find, that for short strands, the ligation is dominated by the weak hybridization dynamics (ssDNA linked by Watson-Crick-basepairing (Crick, 1970)). By using adenine-thymine-only 12mer random sequences as starting material, the sequence space for the first ligation stage that creates 24mer can still be completely sampled. We could obtain more than 12 million individual strands using Next Generation Sequencing (NGS), showing a significant selection of sequences undergoing this elongation dynamics. We analyze the sequences with self-written LabView code and show how spiking with defined sequences changes the sequence selection dynamics of the replicated and remaining sequence pool.

BP 6.78 Mon 17:30 Poster B2

Chlorophyll f in the cyanobacterium H. Hongdechloris — •Züleyha Yenice Campbell, Franz-Josef Schmitt, and Thomas Friedrich — Technische Universität Berlin, Institut für Chemie, Fachgebiet Bioenergetik

In this work the excitation energy transfer (EET) processes in the antenna system of the phototrophic cyanobacterium Halomicronema hongdechloris that contains chlorophyll a and f in photosystem II with

red light (720-730 nm) induced accumulation of Chl f was investigated by UV-Vis absorption spectroscopy, time integrated fluorescence spectroscopy and Decay associated spectra (DAS).

BP 6.79 Mon 17:30 Poster B2

Quantifying non-equilibrium nuclear shape fluctuations — •Heidi Somsel[1], Federico Gnesotto[3], Chase P. Broedersz[3], and Christoph F. Schmidt[1,2] — [1]Drittes Physikalisches Institut - Biophysik, Fakultät für Physik, Georg-August-Universität Göttingen, 37077 Göttingen — [2]Department of Physics, Duke University, Durham, NC 27708, USA — [3]rnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität, München, Germany

Cells actively generate forces that lead to rapid fluctuations, slow shape changes, locomotion, and more. The cell nucleus also shows shape changes and fluctuations. The main driver of active dynamics in cells is the cytoskeleton, via actin and myosin. We focus on the nuclear envelope to analyze nuclear non-equilibrium dynamics . We use fluorescent labeling of the nuclear lamina to visualize the fluctuations of this membrane. The fluctuations are analyzed using Broken Detailed Balance analysis (BDB), a technique to reveal and quantify non-equilibrium dynamics in steady-state systems. BDB is non-invasive, meaning that it does not require chemical or mechanical perturbations, which are difficult to perform in the cell nucleus.

BP 6.80 Mon 17:30 Poster B2

Gel formation of self-interacting DNA strands — •Giacomo Bartolucci — MPI PKS Dresden, Germany

Aqueous DNA solutions can exhibit a variety of condensed phases, depending on their nucleotide sequence and control parameters such as temperature and DNA concentration. It has been shown that DNA strands composed of self-complementary strand segments can form hydrogel phases. Inspired by these findings, we introduce a simple lattice model accounting for different configurations of DNA strands, namely single stranded DNA and a folded hairpin-like configuration. Our model is used to predict the phase diagrams of the solution as a function of temperature and total DNA concentration. We find that the region corresponding to gel formation is bounded by an upper and lower limiting temperature where gels dissolve. This behavior is due to the fact that at low temperature all DNA strands are folded in hairpins while at high temperature entropy spreads out open strands. Additionally, we discuss how this phase diagram is affected by the number of self-complementary strand segments. Our model serves as a starting point to understand the constituting principles underlying self-assembling bio materials based on DNA.

BP 6.81 Mon 17:30 Poster B2

Statistical Physics of Binary Decisions in *Physarum polycephalum* — •Tanja Huxoll and Hans-Günther Döbereiner — Universität Bremen, Institut für Biophysik

Physarum polycephalum is a unicellular giant amoeba that has been proposed as a model organism for basal cognition. Previous work by others demonstrated that *Physarum* makes optimal decision in choosing the best possible food source and exhibits complex behaviour such as speed-accuracy trade-offs. Here, we explore the binary decision process in *Physarum*. We are interested in the partition of the slime mould between different environments measured by the occupation probability of either side. Our experimental set up consists of two different environments, which differ only in KCl concentrations. KCl acts as an attractor or repellent depending on its concentration. *Physarum* is placed at the centre and the foraging behaviour is observed over time. We propose a simple statistical two state model to describe the probabilities of the area occupation for each environment $P_s(c) = \frac{1}{1+\exp(kc)}$ with $k = 1/A \ \mathrm{d}A/\mathrm{d}c$ and P_s the occupation of the KCl side. We present our experimental results described by this model and we show that k is a measure of the percentage loss of the occupied KCl area with increasing repellent concentration.

BP 6.82 Mon 17:30 Poster B2

Probing mesoscopic dynamics in the developing *Drosophila* embryo using fluorescent carbon nanotubes — •Constantin Kohl[1], Zhiyi Lv[2], Jörg Grosshans[2], and Christoph F. Schmidt[1,3] — [1]Drittes Physikalisches Institut, Georg-August-Universität, 37077 Göttingen, Germany — [2]Institut für Entwicklungsbiochemie, Universitätsmedizin Göttingen, 37077 Göttingen, Germany — [3]Department of Physics, Duke University, Durham, NC 27708, USA

Semiconducting near-infrared (NIR) fluorescent carbon nanotubes (CNTs) are promising markers for *in vivo* studies. In this project, we use NIR fluorescent CNTs as markers for *in vivo* studies in *Drosophila* embryos. The photostable and intermittency-free NIR fluorescence of CNTs allows us to capture high frequency information of individual CNT trajectories in the whole developing organism over multiple cell cycles. We have built a setup, allowing for simultaneously imaging of CNT NIR fluorescence and nuclear His-GFP fluorescence. This enables us to capture intracellular dynamics on multiple time scales. We have combined the high frequency CNT NIR signals with the corresponding low frequency nuclear His-GFP signals. We have computed correlations of individual CNT trajectories in different fly types and in different cell cycle phases to characterize particular dynamics. Furthermore, we use NIR fluorescent CNTs in conjunction with particle image velocimetry (PIV) to capture the dynamics of the cytoplasmic flow in the developing *Drosophila* embryos.

BP 6.83 Mon 17:30 Poster B2

DNA Denaturation Induced by Local Salt Fluctuations in a Microfluidic Water Cycle — •Alan Ianeselli and Dieter Braun — Systems Biophysics, Ludwig Maximilian University Munich (Germany)

The evaporation of aqueous solutions can separate pure water from a salt-rich stock. Here, we used a thermal gradient to power a water cycle in a microfluidic chamber filled with water, salts and DNA, under conditions that mimic the Early Earth. The condensation of water vapor led to the formation of water droplets with a low salt content, which then precipitated and diluted the solution locally. The continuous evaporation, condensation and precipitation resulted in local dilution of solutes at the air-water interface. Since salts play a major role in the stability of nucleic acids, we found that the temporary low salt conditions lowered the melting temperature of dsDNA and slowed down the re-annealing process, leading to persistent strand separation at moderate temperatures. This can be important for many prebiotic replication reactions for RNA or DNA that do not tolerate elevated temperatures. The oscillatory dilution mechanism described here provides a route to overcome the strand separation problem and demonstrates microscale implementations of the hydrological cycle for the molecular evolution.

BP 7: Bioimaging and biospectroscopy II

Time: Tuesday 9:30–12:30 Location: H4

BP 7.1 Tue 9:30 H4

Strong cytoskeleton activity on millisecond timescales upon particle binding revealed by ROCS microscopy — Felix Jünger and •Alexander Rohrbach — Laboratory for Bio- and Nano-Photonics, Department of Microsystems Engineering, University of Freiburg, Germany

Cells change their shape within seconds, cellular protrusions even on subsecond timescales enabling various responses to stimuli of approaching particles. Typical responses are governed by a complex reorganization of the actin cortex, where single filaments and molecules act on even faster timescales. These dynamics have remained mostly invisible due to a superposition of slow and fast motions, but also due to a lack of adequate imaging technology. Whereas fluorescence techniques require too long integration times, novel coherent techniques such as ROCS microscopy can achieve sufficiently high spatiotemporal resolution. ROCS uses rotating back-scattered laser light from cellular structures and generates high-contrast images with 100 Hz and 150nm resolution, without fluorescence or bleaching. Here, we present an extension of ROCS microscopy that exploits the principles of dynamic light scattering for precise localization, visualization and quantification of the cytoskeleton activity of mouse macrophages. The local structural reorganization processes, encoded by dynamic speckle patterns, occur upon distinct mechanical stimuli, such as soft contacts with optically trapped beads. We find that a substantial amount of the near-membrane cytoskeleton activity takes place on millisecond timescales, which is much faster than reported ever before.

BP 7.2 Tue 9:45 H4

Imaging nanoscale aggregation of proteins ex vivo using the contrast in Förster resonance energy transfer obtained from 2D polarization fluorescence imaging (2D POLIM) — •Daniela Täuber[1], Adrian T. Press[2], Petra Martinac[2], Kay-Jovanna Benecke[2], Michael Bauer[2], Juanzi Shi[3], and Ivan G. Scheblykin[3] — [1]Biopolarisation, Leibniz-IPHT & Friedrich-Schiller-University Jena, Germany — [2]Anesthesiology and Intensive Care Medicine & Center for Sepsis Control and Care, Jena University Hospital — [3]Single Molecule Spectroscopy, Lund University, Sweden

Förster resonance energy transfer (FRET) is a well-established nanoruler suited to discriminate small aggregates of fluorescent molecules from just high concentration. Contrary to spectrally resolved two-color-FRET, polarization resolved fluorescence microscopy allows to determine homo-FRET between similar fluorophores. Conventional fluorescence anisotropy is restricted to isotropic samples, otherwise, the results depend on the choice of the lab frame. 2D POLIM was recently applied to study early protein aggregation of GFP-labeled human α-synuclein in models of Parkinson's disease ex vivo.[1] We used 2D POLIM to study f-actin aggregation in healthy and pathologic liver tissue, which is related to liver damage in systemic infection. A qualitative analysis showed variations of the FRET parameter, which can be compared to the pathologic condition of the sample. – [1] Camacho et al. 2D Polarization Imaging as a Low-Cost Fluorescence Method to Detect α-Synuclein Aggregation Ex Vivo in Models of Parkinson's Disease. Commun. Biol. 2018, 1, 157.

BP 7.3 Tue 10:00 H4

Photo-induced force microscopy (PiFM) and IR & Raman-spectroscopy on multicore magnetic nanoparticles (MCNPs) — •Nila Krishnakumar[1,2,3], Anika Strecker[1,3,4], Philip Biehl[2,5], Felix H. Schacher[2,5], Anne-Dorothea Müller[6], Anuradha Ramoji[1,7], Ute Neugebauer[1,2,5,7], Heidemarie Schmidt[1,2], and Daniela Täuber[1,2] — [1]Leibniz-IPHT, Jena, Germany — [2]Friedrich-Schiller-University Jena — [3]Abbe Center of Photonics, Jena — [4]Ernst-Abbe University of Applied Science, Jena — [5]Jena Center for Soft Matter — [6]Anfatec Instruments GmbH, Oelsnitz, Germany — [7]Center for Sepsis Control and Care, Jena University Hospital

MCNPs are promising candidates for theranostics of cancer and infectious diseases. PiFM is a new spectroscopy/imaging method which combines excitation in the mid infrared by quantum cascade lasers with detection using a conductive AFM tip. PiFM and IR & Raman-spectroscopy shall be used for detecting such MCNPs, and the results of the three spectroscopy/imaging methods compared.

BP 7.4 Tue 10:15 H4

3D depth profiling the interaction between an AFM tip and hydrated, native collagen fibrils in sheep tendon — •Martin Dehnert[1], Diana Voigt[1], Anke Bernstein[2], and Robert Magerle[1] — [1]Fakultät für Naturwissenschaften, TU Chemnitz, Germany — [2]Department Chirurgie, Universitätsklinikum Freiburg, Germany

Imaging with atomic force microscopy (AFM) the structure and the viscoelastic properties of hydrated, native tissue on the nanometer scale is challenging since the AFM tip interacts with a soft, compliant, partially fluid, and adhesive specimen. Furthermore, the tissue's water content needs to be maintained during AFM imaging. Here we study collagen fibrils in hydrated, native sheep tendon with AFM-based measurements of force–distance (FD) curves and amplitude–phase–distance (APD) curves. From this data, we reconstruct three-dimensional (3D) depth profiles of the tip–sample interaction. This allows for distinguishing the viscoelastic response of individual collagen fibrils within the tendon from the attractive capillary forces between the AFM tip and the viscous interfibrillar matrix. The 3D depth profiles reveal a large diversity in nanomechanical properties among individual collagen fibrils in both their viscoelastic response and the attractive tip–sample interaction. Furthermore, we obtain information about the local mechanical response of the interfibrillar matrix. We expect that this comprehensive nanomechanical characterization will contribute to a better understanding of tendon biomechanics on the nanometer scale.

BP 7.5 Tue 10:30 H4

Imaging biological samples with AFM using stiff qPlus sensors — •Korbinian Pürckhauer[1], Alfred J. Weymouth[1], Katharina Pfeffer[1], Estefania Mulvihill[2], Lars Kullmann[1], Michael P. Krahn[1,3], Daniel J. Müller[2], and Franz J. Giessibl[1] — [1]University of Regensburg, Regensburg, Germany — [2]ETH Zürich, Basel, Switzerland — [3]University Hospital of Münster, Münster, Germany

High-resolution imaging of soft biological samples with atomic force microscopy (AFM) is challenging because they need to be imaged with very low forces to prevent deformation. Typically, AFM of those samples is performed with soft silicon cantilevers ($\sim$ 0.1-10 N/m) and optical detection in a liquid environment. In this work we demonstrate the advantages of using stiffer sensors ($\sim$ 1 kN/m) which were used to obtain unprecedented spacial resolution of molecules in vacuum at low temperatures [1]. In liquid environments, the high stiffness of the qPlus sensor allows us to use small amplitudes in a non-contact mode and obtain high quality factors. The samples are immersed in aqueous solution in a liquid cell and we use qPlus sensors with long tips, only submerging the tip apex. Atomic resolution of muscovite mica was achieved in various solutions. To prove that we can non-destructively image soft biological samples with stiff sensors, we show molecular resolution images of a lipid bilayer and preliminary results on DNA Origami [2].

[1] Gross et al., Science 325, 1110 (2009). [2] Pürckhauer et al., Sci. Rep. 8, 9330 (2018).

BP 7.6 Tue 10:45 H4

Single particle tracking in 2+1 Dimensions using interferometric scattering Microscopy — •Philipp Kellner[1], Francesco Reina[2], Christoffer Lagerholm[2], and Christian Eggeling[1,2] — [1]Institute of Applied Optics and Biophysics, Philosophenweg 7, 07743 Jena — [2]Weatherall Institute of Molecular Medicine University of Oxford, Headley Way, Oxford

Directly recording Tracks of moving particles is essential for various parts of physics. In modern biophysics measuring the diffusion of lipids and proteins on biological membrane model systems is an example. Those measurements reveal not only information about the moving particle itself but also about heterogenities in the surrounding structures. Such observations require high spatial and temporal resolution. Novel interferometric scattering Microscopy (iScat) provides localization precision in the nm-range and time-resolution down to several microseconds. This talk will present the basic principles of iScat-Microscopy and underline its usability for biological questions. Further, optical improvement of the setup and the possiblity of detec-

tion using small labels in biological model membrane systems will be highlighted.

30 minutes break.

BP 7.7 Tue 11:30 H4

Quantitative 3d histology of Alzheimer's disease by holotomography — •Marina Eckermann[1], Mareike Töpperwien[1], Jasper Frohn[1], Thany Bui[1], Anna-Lena Robisch[1], Franziska Van der Meer[2], Christine Stadelmann-Nessler[2], and Tim Salditt[1] — [1]Institute for X-ray Physics, Göttingen University, Göttingen, Germany — [2]Institute for Neuropathology, University Medical Center, Göttingen, Germany

Towards quantitative 3d virtual histology of the human brain, we have recently achieved significant progress in reconstructing the neuronal architecture of human cerebella [1], combining propagation-based x-ray phase contrast imaging using laboratory μCT and synchrotron radiation [2]. In this way, we aim at a multi-scale workflow, to automatically identify nanometric pathological alterations from ccm-sized tissue blocks. In [3], nano- and μCT was used to image Aβ plaques in heavy metal stained murine tissue. In the present work, we investigate structural alterations from Alzheimer's disease (AD) in unstained, paraffin-embedded human hippocampus, hence based on native electron density variations. In control tissue data, we predominantly find intact neurons, characterized by a clear difference in electron density between the cytosol and the nucleus. Furthermore, affected neurons appear overall shrinky, with a perishing nucleus and increased density. Beyond that, we also observe diffuse objects of increased density in specific locations (analysis ongoing work).
[1] Töpperwien et al., PNAS 115, 27 (2018). **[2]** Töpperwien et al., Sci. Rep. 7, 42847 (2017). **[3]** Massimi et al., NeuroImage 184 (2019).

BP 7.8 Tue 11:45 H4

Nanoscale X-ray computed tomography for the 3D structural characterization of electrospun fibers — Adriana T González[1], Cristine S de Oliveira[1], Tobias Kürbitz[2,3], Christian E H Schmelzer[3], Ralf B Wehrspohn[1,3], and •Juliana Martins de S e Silva[1,3] — [1]Institute of Physics, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany — [2]Anhalt University of Applied Science, Köthen, Germany — [3]Fraunhofer Institute for Microstructure of Materials and Systems IMWS, Halle (Saale), Germany

Electrospinning is a well-established method for the production of fibrous non-woven biomaterials which are used in tissue engineering as biomimetic three-dimensional (3D) scaffolds to assist cell growth. The properties of these non-woven biomaterials, including their porous network, the size, and interconnectivity of the electrospun fibers are critical parameters for their successful application as scaffolds. As the conventional methods for characterizing these fibers have deficiencies, such as the use of toxic substances and incomplete visualization of the porous structure, here we explored phase-contrast nanoscale X-ray computed tomography (nano-CT) as an alternative method to image and characterize the 3D structure of electrospun gelatin-based fiber matrices. The 3D datasets obtained gave a visual insight into the morphology of the fibers. We observed changes in fiber thickness upon chemical cross-linking, resulting in declines of porosity of 23 % and of the surface area of 39 %. We show that phase-contrast nano-CT is a promising method for the fast, non-destructive and high-resolution 3D imaging and quantitative characterization of electrospun nanofibers.

BP 7.9 Tue 12:00 H4

Ratiometric fluorescence imaging and marker-free motion tracking of Langendorff-perfused beating rabbit hearts — •Vineesh Kappadan[1,2], Johannes Schröder-Schetelig[1,2], Ulrich Parlitz[1,2,3], Stefan Luther[1,2,3,4,5], and Jan Christoph[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for Nonlinear Dynamics, Georg-August-Universität, Göttingen, Germany — [3]German Center for Cardiovascular Research (DZHK e.V.), partner site Göttingen, Germany — [4]Institute of Pharmacology and Toxicology, University Medical Center Göttingen, Göttingen, Germany — [5]Department of Physics and Department of Bioengineering, Northeastern University, Boston, USA

Optical mapping based on fluorescence imaging is used for visualizing membrane voltage and Ca^{2+} concentration of isolated, Langendorff-perfused intact hearts. Despite recent progress in imaging of isolated beating hearts, accurate measurements of quantities such as the duration of action potentials are still challenging due to residual motion artifacts present in the fluorescence signal. Motion artifacts can be significantly reduced by the electromechanical uncoupler Blebbistatin, which may, however, affect properties like the action potential duration (APD). We show that marker free motion tracking combined with ratiometric fluorescence imaging techniques can be used to more reliably measure the APD from Langendorff-perfused, beating rabbit hearts and we use this technique to investigate the effects of Blebbistatin on the APD and restitution properties of the heart.

BP 7.10 Tue 12:15 H4

Label-free detection of individual nanosystems in liquids — •Larissa Kohler — Karlsruhe Institute of Technology

The label-free detection of nanosystems provides the opportunity to understand biomolecular dynamics and interactions without undesired modifications of the system. To achieve the high sensitivity required for studying individual solved nanosystem, we use signal enhancement in a fiber-based Fabry-Perot cavity with high finesse ($F \approx 10^5$), which is integrated in a microfluidic channel. The presence and dynamics of an individual nanoobject in the tight focus of the cavity mode ($w_0 \approx 1\,\mu m$) can be detected due to its induced frequency shift and decrease of amplitude of the signal. In this talk I will show results on the time-resolved measurement of the Brownian motion of individual silica nanoparticles and report the progress towards sensing of individual biomolecular nanosystems.

BP 8: Cytoskeletal filaments

Time: Tuesday 9:30–12:45 Location: H10

BP 8.1 Tue 9:30 H10

The influence of vimentin on actin dynamics — •Zahra Mostajeran[1], Emmanuel Terriac[1], and Franziska Lautenschläger[1,2] — [1]INM-Leibniz Institute for New Materials, Saarbrücken, Germany — [2]Saarland University, Saarbrücken, Germany

The cytoskeleton is a network of polymers which extends inside the cytoplasm to form and maintain the cell shape. It is composed of three main types of filaments: microtubules (MTs), actin filaments, and intermediate filaments (IFs). Vimentin belongs to the family of IFs and is involved in fixing organelles in the cytoplasm and regulating the direction of cell migration. It forms non-polar filaments and has therefore no known molecular motor directly interacting on it. Vimentin is linked via plectin protein cross-linker to MTs and actin filaments as well as to itself. Vimentin has been shown to colocalize to actin stress fibers (SFs). These are bundles of actin filaments assembled by the molecular motors and crosslinker proteins. Actin SFs play a key role in cell contractility and cell migration. We investigate the effect of vimentin in processes like cell migration and traction forces which are known to be initiated by forces generated by actin filaments and the molecular motor myosin. To understand how vimentin IFs are involved in these processes, we study the dynamics of the actin SFs on cells with different amounts of vimentin. We also consider the role of plectin on our results. We demonstrate that actin SFs are less dynamic in vimentin depleted cells compared to vimentin wild-type cells. We could further show that the dynamics of actin SFs is not influenced by plectin, suggesting a role of vimentin itself on actin SF dynamics.

BP 8.2 Tue 9:45 H10

Cytoskeletal organization within polar cells and interactions between different components — •Carsten Baltes[1,2], Emmanuel Terriac[1], and Franziska Lautenschläger[1,2] — [1]Leibniz-Institut für neue Materialen — [2]Universität des Saarlandes

The cytoskeleton is composed of three main parts: actin filaments, microtubules and intermediate, like for in this study, vimentin. The organization of the cytoskeleton and shape of cells are linked. Here we investigate the effect of imposing shape on the cytoskeletal organization. We further disturb particular cytoskeletal parts in this setup

to test their interactions between different filaments. To acquire those defined shapes we used micropatterns of fibronectin achieved with the Primo device (Alvéole Paris). We focused on two circular shapes, full circles as example for a symmetric shapes and 3/4 circle (which resemble the shape of PacMan) to enforce polarity to the cell. Using withaferin A, blebbistatin and rho-associated-protein kinase (ROCK) inhibitor Y27632, we selectively disturbed vimentin organization and myosin II activity. We observed effects on the distribution of the cytoskeletal elements. We further found different behavior between cells treated with blebbistatin and Y27632, leading to the hypothesis that ROCK may be essential in the structure and dynamic of the vimentin network. Our results help to understand the cytoskeletal architecture in cells and the link between the different networks. Our method might be useful for further investigations in the cytoskeletal interplay.

BP 8.3 Tue 10:00 H10

Studying Cytoskeletal Processes, including T-cell activation, at the single-molecule level with optical tweezers and correlated fluorescence microscopy (OT-CFM) — •Ann Mukhortava, Aida Llauró Portell, Roleand van Wijk, Andrea Candelli, and Gerrit Sitters — LUMICKS, Amsterdam, Netherlands

Microtubules, actin and intermediate filaments are highly dynamic cytoskeletal structures that interact with various motor proteins and regulatory factors and thus play fundamental roles in many essential biological processes. A lot of these, including cell division, signaling, and migration, involve mechano-chemical and -biological pathways. Force spectroscopy on a single-molecule and single-cell level permits exploring and manipulating these complex interactions to help understand their nature better. OT-CFM which we commercialized as the C-Trap^{TM} integrates optical tweezers, confocal/STED microscopy, and an advanced microfluidics system in a truly correlated manner. It enables live, simultaneous and correlative visualization and manipulation of molecular interactions with sub-picoNewton (pN) force resolution and microsecond temporal resolution. Here, we present our experiments on visualizing and quantifying the elastic properties of filaments, the motility of cytoskeletal molecular motors and the force-triggered activation of T-cells using the C-Trap^{TM} system. These experiments show that 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 8.4 Tue 10:15 H10

Effect of the molecular architecture on vimentin intermediate filament mechanics — •Anna Schepers, Charlotta Lorenz, Johanna Block, Julia Kraxner, and Sarah Köster — Institute for X-Ray Physics, Georg-August-University Göttingen, Germany

Intermediate filaments (IFs), together with microfilaments (MFs) and microtubulues (MTs), give cells specific and unique mechanical properties in shape of the cytoskeleton. While MFs and MTs are conserved between cell types, IFs are expressed in a cell type specific manner. To understand the mechanisms within IFs that determine the mechanical response to stresses, single IFs are investigated in vitro using a setup that combines optical tweezers, fluorescence microscopy and microfluidics. By changing the environment (pH, buffer, ion valency and ion concentration) different force-strain behaviours of single vimentin IFs are observed in stretching experiments. The IFs show a remarkable dependency on the buffer pH and presence of cations while the cation valency and buffer seem to be neglectable. With these results, we can link the molecular architecture and, in parts, the primary protein structure of vimentin IFs to their mechanical response.

BP 8.5 Tue 10:30 H10

Stress-Strain Behavior of Keratin and Vimentin IFs — •Charlotta Lorenz, Johanna Block, Anna Schepers, Julia Kraxner, and Sarah Köster — Institute for X-Ray Physics, Georg-August-Universität, Göttingen, Germany

The cytoskeleton is vital for cell motility, cell division and mechanical stability of the cell. These tasks are distributed among three different protein classes, microfilaments (MFs), microtubules (MTs) and intermediate filaments (IFs). Unlike MFs and MTs, IFs are expressed in a cell-type specific manner giving the cell a tool to adapt to different mechanical requirements. So far, the mechanical properties of different IFs on a single filament level have not been probed. Therefore, we study the stress-strain behavior of two IFs, vimentin and keratin filaments, by optical trapping in combination with fluorescence microscopy and microfluidics. In comparison to keratin IFs, vimentin IFs are stiffer and exhibit a strong loading-rate depending behavior, which predestines vimentin to act as a cellular "safety belt". Monte-Carlo simulations based on theoretical modelling allow the decoupling of different IF-type depending parameters like the monomer interaction and the number of monomers per cross-section of the IF. The obtained parameter distributions show that more energy is required to extend vimentin IFs than keratin IFs. This behavior can possibly be explained by a compaction step of vimentin during IF assembly which is not observed for keratin IFs.

BP 8.6 Tue 10:45 H10

Germanium nanospheres as high precision optical tweezers probes — •Swathi Sudhakar and Erik Schaeffer — Cellular Nanoscience, Center for Plant Molecular Biology, Eberhard Karls University of Tuebingen, Tuebingen, Germany.

Force spectroscopy on single biological molecular machines is often performed using optical tweezers. Commonly microspheres composed of silica or polystyrene are trapped in a highly focused laser beam and are used as handles to measure the mechanics of motor proteins such as kinesin. The ultimate precision of such experiments is limited by thermal fluctuations and, among others, the size of the microsphere. Thus, ideally, microspheres should be as small as possible. However, since trapping forces scale with the particle volume, maximum trapping forces quickly approach motor-generated forces creating a lower practical size limit of about 200 nm for polystyrene microspheres when studying kinesin motors. Here, we have developed germanium nanospheres with diameters ranging from 30-200 nm. With a high refractive index of 4.4, their trapping efficiency and maximum force per power is more than 10-fold improved compared to equal-sized silica spheres. Using 70-nm-diameter germanium nanospheres, we measured the stepping behavior of kinesin-1. With an improved precision, we could measure intermediate steps of kinesin. In the long-term, the development and application of novel high-precision probes will provide new insight into the working mechanism of molecular machines.

30 minutes break.

Invited Talk BP 8.7 Tue 11:30 H10

Force generation by actin, microtubules and motors — •Rhoda Hawkins — University of Sheffield, UK

When driven out of equilibrium by the consumption of biochemical energy, cytoskeletal protein filaments alone and in combination with molecular motors are able to generate sufficient forces to deform and move cells as well as to transport cargo within a cell. I will present some of my group's work theoretical work on force generation mechanisms using both analytical calculations and simulations in combination with experimental data.

First I will discuss our work on polymerising branched actin, comparing in vitro data with simulations and analytical calculations. Then I will present stochastic simulations of polymerising branched actin exerting force to deform a model membrane in the context of phagocytosis, which is a process by which immune cells engulf pathogens.

In the second part of the talk I will present analytical calculations and simulations of molecular motors moving along cytoskeleton filaments transporting a cargo. I will compare our results with experimental data of molecular motors on microtubules in vitro and in vivo in axons. In particular I will discuss the differences between processive and non-processive motors and the effects of multiple motors and multiple filaments. Finally, I will discuss the effects of competing molecular motors pulling a cargo in different directions for a deformable cargo and relate this to experimental data on cell nucleus deformation.

BP 8.8 Tue 12:00 H10

Contractile actin flow in Xenopus egg extract droplets — •Jianguo Zhao, Kengo Nishi, and Christoph F. Schmidt — Drittes Physikalisches Institut - Bio-physik, Fakultät für Physik, Georg-August-Universität Göttingen

The actin cytoskeleton of eukaryotic cells is a highly dynamic viscoelastic active material. A typical cell maintains a cortex lining that supports the cell membrane, a polymer network consisting of actin, myosin motors and a plethora of regulatory proteins. Actin turns over between polymeric and monomeric forms on a time scale of minutes. Myosin motors generate active contractile stresses that can induce large-scale actin flow, which is essential for the transport of cytoplasmic components, locomotion as well as shape changes of cells. How exactly so many interacting biochemical processes result in static or dynamic steady states is unclear. Using water-in-oil droplet containing cyto-

plasmic extract of Xenopus laevis eggs as a model system for an active cytoskeleton, we could produce radially convergent continuous flows of polymerized actin that persist over time scales much longer than the turn-over time of a single actin filament. We mapped the spatiotemporal distribution of this contractile persistent actin flow. Interestingly, we found that macromolecular cargo present in the extract gets transported into the center of the droplet and compacted into a jammed state. We demonstrated this by tracking embedded IR fluorescent single-walled carbon nanotubes as mechanical probes.

BP 8.9 Tue 12:15 H10

The structure and mechanics of the cellular cortex before, during and after adhesion — •Daniel Flormann[1], Emmanuel Terriac[1], and Franziska Lautenschläger[1,2] — [1]Leibniz Institut für neue Materialien — [2]Universität des Saarlandes

The cellular cortex plays an important role in biological processes such as cell migration and division. This thin (roughly 200nm) network beneath the cell membrane is mainly composed of actin, associated motors and linkers. It is highly dynamic and the main contributor to the so-called cortical tension. This tension drives the mechanical properties of cells as well as its shapes. During cell adhesion this cortex is altered. In order to test if such alterations of the actin cortex during adhesion influence cellular mechanics, we compared the mechanical properties of RPE1 cells in adhered and suspended state by atomic force microscopy. This results were then correlated to the local structure of the actomyosin network using electron microscopy. We found indeed differences in the mechanical responses and structures depending on the state of adhesion. Altering the activity of the motor protein myosinII allowed us to change the mechanical properties of the cells in both states and changes of the structure could also be observed. Hence, we describe here a quantitative correlation between the structure of the actin cortex and the mechanical properties of cells both in the frame of adhesion state or by chemical alteration. These results may be promising in understanding the mechanical plasticity of cells in processes like embryogenesis or metastasis.

BP 8.10 Tue 12:30 H10

Experimental Characterization and Theoretic Modeling of Circular Dorsal Ruffles — Julia Lange[1], Malte Ohmstede[1], •Merthe Schwachenwald[1,2], Christof Taxis[2], and Hans-Günther Döbereiner[1] — [1]Institut für Biophysik, Universität Bremen — [2]Fachbereich Biologie, Phillips-Universität Marburg

Circular Dorsal Ruffles (CDRs) are dynamic actin structures propagating on the dorsal cell side. Three factors influence CDR dynamics: Stimulation with growth factors, protein composition, and boundary conditions of cells. In our set-up the latter is ensured by using microcontact printed substrates to receive an even cell shape. The influence of different proteins and growth factor stimulation on CDR dynamics is controlled by microfluidics and examined with light microscopy. We will use optogenetics to control protein expression linking a light sensitive protein to a peptide degron and connect both to an actin regulator. This leads to a degradation of the construct, when exposing it to blue light. Optogenetic manipulation allows a more refined control of protein concentration than with traditional biochemical means. CDR dynamics under changing biochemical conditions is compared with theory through two-dimensional simulations of propagating wave fronts. We aim to verify a bistable model and augment it to include the effects of fluctuations in an active cytosol. We found CDR characteristics to cluster with their number. Moreover, we observe clear long-distance interaction of CDRs. We examine the effects of Jasplakinolide (Actin inhibitor), Wiskostatin (N-WASP inhibitor), and Wortmannin (PI3K inhibitor) on wave characteristics.

BP 9: Computational biophysics

Time: Tuesday 9:30–13:00 Location: H11

Invited Talk BP 9.1 Tue 9:30 H11

Biomolecular structure determination from single molecule X-ray scattering with three photons per image — •Helmut Grubmueller and Benjamin von Ardenne — Department of Theoretical and Computational Biophysics, Max Planck Institute for Biophysical Chemistry, Am Fassberg 11, 37077 Göttingen, Germany

Scattering experiments with femtosecond high-intensity free-electron laser pulses provide a new route to time resolved macromolecular structure determination. While currently limited to nano-crystals or virus particles, the ultimate goal is scattering on single biomolecules. The main challenge in these experiments is the extremely low signal-to-noise ratio due to the very low expected photon count per scattering image, often well below 100. We describe a correlation-based approach and show that three coherently scattered photons per image suffice for structure determination. Using synthetic scattering data of a small protein, we demonstrate near-atomic resolution of 3.3 A using 3.3×10^{10} coherently scattered photons from 3.3×10^9 images, which is within experimental reach. Our correlation approach is robust to additional noise from incoherent scattering.

BP 9.2 Tue 10:00 H11

Thermodynamics and conformations of homopolymeric polypeptides — •Arne Böker, Paul Käthner, and Wolfgang Paul — Martin-Luther-Universität Halle-Wittenberg

Although the number of structures in the PDB is continuously growing, the topic of protein folding still requires great attention and is being treated with a variety of methods. Especially the reasons for proteins to aggregate as amyloids are far from being understood. While aggregation is a collective feature of multiple molecules, the starting point must be a single chain, so understanding single molecule structure is a prerequisite for understanding aggregation. The stability of motifs such as β-sheets may give us insight into the formation and stability of aggregates.

For these reasons, we simulate different polypeptides (polyalanines/polyA, polyglutamines/polyQ and polyserines/polyS with 8 to 23 monomers) and investigate their thermodynamics and structure formation. We use a four-bead representation called PRIME20 (Cheon et al., 2010) together with a flat histogram Monte Carlo method (Liang et al., 2007) which provides full thermodynamic information over a broad temperature range.

We find that polyS and polyQ, disordered under physiological conditions, can fold into distinct ground states where polyS forms a helix similar to polyA while polyQ prefers a hairpin. β-type intermediates occur during folding of all our peptides. We also investigate the influence of end-attached spectroscopy dyes and solubility-enhancing residues and find significant deviations in the folded structures.

BP 9.3 Tue 10:15 H11

A framework for spatially embedded biological network growth — •Torsten Paul[1], Felix Repp[2], and Philip Kollmannsberger[1] — [1]Center for Computational and Theoretical Biology, University of Würzburg, Germany — [2]Department of Neurophysiology, University of Würzburg, Germany

Spatial biological networks are important for signaling, transportation and stability, and are found on many scales, from osteocytes and neuronal connections up to vasculature or roots. By combining image analysis of such multicellular networks with graph theory, they can be compared quantitatively to different random or regular networks. The biological interpretation of the results so far was limited, as we lack an appropriate model linking local cell behavior and tissue organization during growth to the resulting global network architecture. Here, we introduce a new 3D parallel simulation framework that aims to fill this gap. We model spatial network growth as a biased correlated random walk where growth direction and branching probability depend on the local environment, e.g. soluble cues, tissue anisotropy, or other cells. This is implemented by representing the environment as a multi-layer image from which gradients, structure tensors and other influencing parameters are calculated. Our generally applicable framework will help to better understand how biological network patterns depend on the growth rules under different environmental conditions, and to identify the biological cause of deviations from healthy network function.

BP 9.4 Tue 10:30 H11

Coarse-Grained Molecular Dynamics reveals the optimal folding pathways of self-entangled proteins — •Claudio Perego[1] and Raffaello Potestio[2] — [1]Polymer Theory Department, Max Planck Institute for Polymer Research, Mainz, Germany

— [2]Physics Department, University of Trento, Trento, Italy

Among the known protein motifs, several structures exhibit a self-entangled backbone topology. Understanding how polypeptides can efficiently and reproducibly attain such topologies is a crucial biophysical challenge, which might shed new light on our general knowledge about protein folding. In this work we present a molecular dynamics method for finding the possible folding pathways of self-entangled proteins. The technique is based on a Coarse-Grained, minimalistic representation of the polypeptide chain, driven by a structure-based angular potential. The relative magnitude of these interaction potentials is optimized by means of an evolutionary strategy, aimed at maximizing the folding probability within the first stages of the dynamics. By means of this approach we construct a simple protein model that is capable of attaining the self-entangled structure in a reproducible and efficient way. At the same time the optimization process mimics the action of evolutionary pressure, that might have selected a specific folding pathway among all the possible routes. Applying this methodology to relevant test cases we retrieve indications on the optimal pathways chosen by self-entangled proteins to attain their native topology, and useful guidelines for simulations employing more detailed molecular models.

BP 9.5 Tue 10:45 H11

QM/MM free energy maps and nonadiabatic simulations for a photochemical reaction in DNA: cyclobutane thymine dimer — •Jesus I. Mendieta Moreno[1,2], Daniel G. Trabada[2], Jesus Mendieta[3], Paulino Gomez-Puertas[3], and Jose Ortega[2] — [1]FZU of the CAS, Prague, Czequia — [2]UAM, Madrid, Spain — [3]CBMSO, Madrid, Spain

The absorption of ultraviolet radiation by DNA may result in harmful genetic lesions that affect DNA replication and transcription, ultimately causing mutations, cancer, and/or cell death. We analyze the most abundant photochemical reaction in DNA, the cyclobutane thymine dimer, using hybrid quantum mechanics/molecular mechanics (QM/MM) techniques and QM/MM nonadiabatic molecular dynamics. We find that, due to its double helix structure, DNA presents a free energy barrier between nonreactive and reactive conformations leading to the photolesion. Moreover, our nonadiabatic simulations show that most of the photoexcited reactive conformations return to standard B-DNA conformations after an ultrafast nonradiative decay to the ground state. This work highlights the importance of dynamical effects (free energy, excited-state dynamics) for the study of photochemical reactions in biological systems.

Jesús I. Mendieta-Moreno et al, Quantum Mechanics/Molecular Mechanics Free Energy Maps and Nonadiabatic Simulations for a Photochemical Reaction in DNA: Cyclobutane Thymine Dimer. J. Phys. Chem. Lett. 2016 7, 4391-4397.

15 minutes break.

BP 9.6 Tue 11:15 H11

Fine- grained simulation of the microenvironment of vascularized tumors — •Thierry Fredrich[1], Edoardo Milotti[2], Roberto Chignola[3], and Heiko Rieger[1] — [1]Center for Biophysics & Theoretical Physics, Saarland University, D-66123 Saarbrücken — [2]Physics Department, Triest University, I-34127 Triest — [3]Department of Biotechnology, I-37134 Verona

The road to the understanding of cancer is long and we are just at the beginning, however the life science community provides more and more insight into the underlying processes causing the, not always, deadly modifications of organs, tissue, vasculature, cells, etc. We combined a lattice-free simulation of tumor cells (*VBL*) with a lattice based blood vessel dynamic simulation (*tumorcode*) to mimic vascularized solid tumors at tissue scale. We reproduced in vivo measurements of pH and partial oxygen pressure (P_{O2}) obtained by Jain et. al. and observe the formation of different ecological niches at very early stages of tumor growth which could be a source of tumor heterogeneity.
I will present the two models and their combination, and discuss first results.

BP 9.7 Tue 11:30 H11

The physics of brain folding — •Lucas da Costa Campos[1,2], Svenja Caspers[2,3,4], and Jens Elgeti[2] — [1]Institute of Neuroscience and Medicine (INM-1), Forschungszentrum Jülich, Jülich, Germany — [2]Institute for Complex Systems (ICS-2), Forschungszentrum Jülich, Jülich, Germany — [3]Institute for Anatomy I, Medical Faculty, Heinrich-Heine University Düsseldorf, Germany — [4]JARA-BRAIN, Jülich-Aachen Research Alliance, Jülich, Germany

Humans possess the most folded brain among the primates. In humans, misfolding of the brain is strongly correlated with several maladies. Folding itself, however, is a physical process. One proposed mechanism is that of differential growth. Like a bimetallic strip, the outer gray matter expands more during development than the inner white matter. This leads to residual stress, and consequentially, to buckling.

We explore this hypothesis using an incompressible Neo-Hookean finite element model. Our system consists of two layers with distinct thicknesses, representing gray matter and white matter, where only the gray matter grows.

Brain folding is further complicated by spatial inhomogeneities in the cortex and its growth. We model these by sinusoidal profiles of cortical thickness or growth rate. In both cases, competition between distinct length scales proves crucial for the formation of sulci-like structures. We quantify the resulting patterns by measuring the curvature and thickness along the layers interface in the buckled system and analyze their correlations.

BP 9.8 Tue 11:45 H11

Numerical simulations to extract cell viscosity from microfluidic experiments — •Lucas D. Wittwer[1,2], Sebastian Aland[2], and Jochen Guck[1] — [1]BIOTEC, Center for Molecular and Cellular Bioengineering, TU Dresden, Germany — [2]Faculty of Informatics / Mathematics, University of Applied Science Dresden, Germany

The mechanical properties of biological cells are promising biomarkers to differentiate for example cell phenotypes, cell states or between healthy and unhealthy cells with applications ranging from research facilities to medical laboratories. Real-time deformability cytometry (RT-DC) allows probing the mechanical characteristics of ˜1000 cells/s by imaging the cells when flowing through a microfluidic channel. The observed deformation can be used to infer the mechanical properties. So far, the expected deformation has been analysed theoretically and numerically assuming the cell to be a homogeneous elastic material. Here, we extend the mathematical framework to include the viscosity of the cell based on a fluid-structure interaction (FSI) simulation. In this talk, we present the extended numerical model, compare it with experimental results and illustrate the new possibilities to infer viscosity from real-time measurements in RT-DC.

BP 9.9 Tue 12:00 H11

A polarizable MARTINI model for monovalent ions in aqueous solution — Julian Michalowsky[1], Johannes Zeman[1], Christian Holm[1], and •Jens Smiatek[1,2] — [1]Institute for Computational Physics, University of Stuttgart, Germany — [2]Helmholtz-Institute Münster: Ionics in Energy Storage (HIMS - IEK 12), Forschungszentrum Jülich, Germany

We present a new polarizable coarse-grained MARTINI force field for monovalent ions, called refIon, which is developed mainly for the accurate reproduction of electrostatic properties in aqueous electrolyte solutions. The ion model relies on full long-range Coulomb interactions and introduces satellite charges around the central interaction site in order to model molecular polarization effects. All force field parameters are matched to reproduce the mass density and the static dielectric permittivity of aqueous NaCl solutions up to moderate salt concentrations.. Our model is validated with regard to analytic solutions for the ion distribution around highly charged rod-like polyelectrolytes in combination with atomistic simulations and experimental results concerning structural properties of lipid bilayers in presence of distinct salt concentrations. Further results regarding the coordination numbers of counterions around distinct polyelectrolytes also highlight the applicability of our approach. The introduction of our force field allows us to eliminate heuristic scaling factors, as reported for previous MARTINI ion models in terms of effective salt concentrations, and in consequence provides a better agreement between simulation and experimental results.

BP 9.10 Tue 12:15 H11

Decompostion of the proton transfer dynamics in the Zundel cation — •Florian N. Brünig and Roland R. Netz — Institut für Theoretische Physik, Freie Universität Berlin

Although extensively studied in experiment and theory, the dynamics of excess protons in water and in particular the proton transfer between molecules remain elusive. The direct intermediate of the proton trans-

fer in water is indisputably the $H_2O_5^+$ or Zundel cation, which has recently been studied experimentally by infrared spectroscopy. The experiments have been interpreted in terms of a low-barrier double-well potential for the excess proton caused by the two adjacent water molecules. We investigate the proton transfer mode by ab-initio simulations of a single Zundel cation and decomposition techniques. We compare calculated spectra with analytic theory that predicts a low frequency spectral tail due to barrier-crossing events. The fast exchange dynamics produces a high-frequency spectral contribution that can be interpreted using a one-dimensional generalized Langevin equation.

BP 9.11 Tue 12:30 H11

Optimized all-atom force fields for Mg^{2+} based on water exchange properties — •Kara K. Grotz and Nadine Schwierz — Department of Theoretical Biophysics, Max Planck Insitute of Biophysics, Frankfurt am Main, Germany

Magnesium cations are essential in many vital processes. Binding of a Mg^{2+} ion to the functional group on a biomolecule involves the removal of one water molecule from the first hydration shell. With the current force fields, this initial step takes about a microsecond. Hence, the description of binding events in a statistically meaningful way or the exploration of different binding sites of complex nucleic acids is beyond reach of Molecular Dynamics simulations. Here, we develop two improved Mg^{2+} force fields in combination with TIP3P water as required for many biomolecular simulations. For both models, we reproduce the experimental solvation free energy, the number of water molecules in the first hydration shell, their mean distance to the $^{2+}$ cation, and the diffusion coefficient. Modifying the Lorentz-Berthelot combination rules and using Kirkwood-Buff theory allows us to simultaneously reproduce the experimental activity derivatives. In addition, our first parameter set captures experimentally determined water exchange rates while the second parameter set enables us to accelerate the rate. Thereby, the second parameter set allows us to speed up simulations of binding events without changing thermodynamic properties.

BP 9.12 Tue 12:45 H11

Influence of DNA rotation and solvent on the electronic transport properties of diamondoid-functionalized electrodes — •Frank C. Maier, Maofeng Dou, and Maria Fyta — Institute for Computational Physics, Stuttgart, Germany

Diamondoid-functionalized gold electrodes have the potential to identify single DNA nucleotides by measuring the electronic tunneling current across the electrodes. The diamondoid functionalization can prolong the measurement time and enhance the nucleotide specificity in the current signals by forming hydrogen bonds with single nucleotides. In this study, we assess the influence of a solvent environment and the dynamics of a DNA molecule within the electrodes on their transport properties. For this, we assume a water solvent within the electrodes and evaluate the chance in the conductance. In order to account for the DNA dynamics, we allow the single DNA nucleotides to rotate within the electrode gap and monitor the changes in the corresponding transport properties. Our results are based on quantum-mechanical simulations implementing the density functional theory, together with the non-equilibrium Green's function scheme, as well as Quantum-Mechanics/Molecular mechanics simulations. In the end we discuss the relevance of our results in view of DNA sequencing with nanopores, in which our diamondoid-functionalized electrodes are embedded.

BP 10: Crystallization, nucleation and self-assembly (joint session CPP/BP)

Time: Tuesday 9:30–10:30 Location: H14

BP 10.1 Tue 9:30 H14

Investigation of the Short-Time Diffusive Dynamics During Salt-Induced Protein Crystallization Using Neutron Spectroscopy — •Christian Beck[1,2], Marco Grimaldo[1], Felix Roosen-Runge[3], Fajun Zhang[2], Frank Schreiber[2], and Tilo Seydel[1] — [1]Institut Laue Langevin, Grenoble, France — [2]University of Tübingen, Germany — [3]Lund University, Lund, Sweden

Protein crystals are needed to obtain high-resolution protein structures, and therefore understanding different processes/pathways leading to their formation is of fundamental biophysical and medical interest. Previous studies investigating the kinetics of crystallization *in situ* using static methods (SAXS and microscopy) provided evidence for non-classical crystallization pathways in the presence of multivalent salts [1,2]. Using dissolved β-lactoglobulin proteins as a model system, we studied the $ZnCl_2$-induced crystallization. Here, we employ quasi-elastic neutron backscattering (NBS) and neutron spin-echo (NSE) spectroscopy to access the kinetics of the nanosecond diffusive dynamics of proteins during crystallization on a nanometer length scale. NBS provides information on the changes of the center-of-mass diffusion, internal diffusive dynamics and on the fraction of immobile proteins associated with the crystals. Accessing coherent scattering with NSE, we probe different scattering vectors q to disentangle the different diffusive contributions of proteins in crystals or aggregates, and in the liquid phase, respectively.

[1] A. Sauter *et al.* ACS Cryst. Growth Des. 14 (2014) 6357
[2] A. Sauter *et al.* Faraday Discuss. 179 (2015) 41

BP 10.2 Tue 9:45 H14

Protein crystallization near liquid-liquid phase separation — Klim Petrov, Jan Hansen, •Florian Platten, and Stefan U. Egelhaaf — Heinrich Heine University Duesseldorf

The crystallization of protein (lysozyme) solutions is studied as a function of protein and salt concentration at ambient conditions. In addition to tetragonal crystals at low salt concentrations (far away from phase separation), needle-like and kinetically roughened crystals occur in the vicinity of the binodal. The crystallization induction time and the growth rate are inferred from optical microscopy and linked to the solubility and protein-protein interactions. Based on these data, the different states of the protein solution are linked to different driving forces for crystallization.

BP 10.3 Tue 10:00 H14

Does liquid-liquid phase separation enhance protein crystallization? — •Ralph Maier[1], Andrea Sauter[1], Georg Zocher[1], Stefano Da Vela[1], Olga Matsarskaia[1], Ralf Schweins[3], Michael Sztucki[4], Fajun Zhang[1], Thilo Stehle[1,2], and Frank Schreiber[1] — [1]Universität Tübingen, Germany — [2]Vanderbilt University School of Medicine, Nashville, USA — [3]ILL, Grenoble, France — [4]ESRF, Grenoble, France

Solutions of the protein human serum albumin (HSA) exhibiting a reentrant phase behavior with a metastable liquid-liquid phase separation (LLPS) inside the condensed regime in the presence of trivalent salts [1] were studied, focussing on the effects of the metastable dense liquid phase on the crystallization pathways. Optical microscopy and small angle X-ray and neutron scattering were used to follow protein crystallization and to explore the role of metastable LLPS. No evidence of nucleation inside the dense liquid phase was observed. On the contrary, heterogeneous nucleation at the walls of the glass container dominates. This suggests that the existence of a metastable LLPS is not a sufficient condition for a two-step nucleation. The unstable or metastable dense liquid phases serve as a reservoir for crystal growth. Furthermore, the crystallographic analysis of the resulting crystals shows that crystals with different morphology grown under different conditions share the same structure and the metal ions create two bridging contacts within the unit cell which stabilize the unit cell.

[1] Matsarskaia *et al.*, *J. Phys. Chem. B*, **120**, 7731 (2016)

BP 10.4 Tue 10:15 H14

Using x-ray scattering to understand the formation of unexpected structures in organic thin films — Jenny Lebert[1], Eva M. Kratzer[1,2], Axel Bourdick[3], Mihael Coric[1], Stephan Gekle[3], and •Eva M. Herzig[1,2] — [1]Herzig Group, MSE Technische Universität München, Lichtenbergstr. 2a, 85748 Garching, Germany — [2]Dynamik und Strukturbildung - Herzig Group, Universität Bayreuth, Universitätsstr. 30, 95447 Bayreuth, Germany — [3]Biofluid Simulation and Modeling, Universität Bayreuth, Universitätsstr. 30, 95447 Bayreuth, Germany

The morphology plays an important role for the performance of organic, semi-conducting thin films. Understanding the self-assembly processes that occur during the drying of the photoactive films, will allow us to make progress in controlled nanomorphology tuning. We

have therefore developed tools to investigate thin film formation processes using synchrotron radiation to resolve structure and structural developments [1,2]. We have now investigated an in-situ polymerization method for polythiophene to examine how much we can influence the morphology during film formation with such an approach. GI-WAXS measurements, molecular dynamics simulations, and spectroscopic analysis suggest the presence of polythiophene in a novel and stable crystal structure with an enhanced intermolecular interaction [3]. [1] S. Pröller et al. Rev. Sci. Instrum. 2017, 88(6): 066101. [2] S. Pröller et al. Adv. Energy Mater. 2016, 6(1): 1501580. [3] J. Lebert et al. ACS Omega 2018, 6: 6388-6394.

BP 11: Evolutionary game theory (joint session SOE/BP)

Time: Tuesday 11:30–12:30 Location: H17

BP 11.1 Tue 11:30 H17

Evolutionary dynamics of multiple games — •Vandana Revathi Venkateswaran and Chaitanya S. Gokhale — Department of Evolutionary Theory, Max Planck Institute for Evolutionary Biology, August-Thienemann-Str. 2, 24306 Plön

Phenomena from bacterial population dynamics to evolution of social behaviour are being successfully described using evolutionary game theory. However, it has typically focused on a single game describing the interactions between individuals. Organisms are simultaneously involved in many intraspecies and interspecies interactions. Therefore, one should move from single games to multiple games. However, the interactions in nature involve many players. Shifting from two player games to multiple multiplayer games yield different interesting dynamics and help us get closer to naturalistic settings. A complete picture of multiple game dynamics (MGD), where multiple players are involved, was lacking. We present a complete and general method to study multiple games with many strategies and players, all at once. We provide a concise replicator equation, and analyse its resulting dynamics. We show that if the individual games involved have more than two strategies, then the combined dynamics cannot be understood by looking only at individual games. Moreover, in the case of finite populations, we formulate and calculate a basic and useful stochastic property, fixation probability. Our results reveal that even as interactions become increasingly complex, their properties can be captured by relatively simple concepts of evolutionary game(s) theory.

BP 11.2 Tue 12:00 H17

Control of biodiversity in evolutionary dynamics: extension to higher dimensions — •Jens Christian Claussen — Department of Mathematics, Aston University, Birmingham B4 7ET, U.K.

Cyclic dominance, as observed in biology and socio-economic systems, has frequently been investigated in its role towards stabilization of diversity of strategies [PRL 100, 058104], and it has been shown that the introduction of a parameter in the payoff matrix can lead to a stabilization of the symmetric state of coexistence. Recently, we had introduced a feedback control method which utilizes a feedback term derived from a conserved property of motion of the case of a neutral oscillation. This mechanism was discussed, analyzed and numerically demonstrated explicitly for the cyclic rock-paper-scissors game. Here, we discuss the generalization to cyclic dominance of M strategies and their implications. First, it is observed that the straightforward generalization leads again to payoff functions with polynomial degrees up to third order, multiplied by the feedback term which in this case is of order M, resulting in characteristic polynomials of order 2(M + 2), compared to order 4 without control, prohibiting closed eigenvalue expressions even for the fixed point stability. To circumvent this, alternative feedback functions are introduced which allow for lower orders. Finally, we discuss the applicability of this approach.

BP 12: Poster II

Topics: Bioimaging and biospectroscopy (12.1 - 12.24); Computational biophysics (12.25 - 12.33); Membranes and vesicles (12.34 - 12.46); Neurosciences (12.47 - 12.49); Focus session: Collective dynamics in neural networks (12.50 - 12.56); Focus session: Physics of Cilia: Dynamics of synchronized oscillators across scales (12.57 - 12.58); Protein structure and dynamics (12.59 - 12.61); Single molecule biophysics (12.62 - 12.75); Systems biology & Gene expression and signaling (12.76 - 12.80)

Time: Tuesday 14:00–16:00 Location: Poster B2

BP 12.1 Tue 14:00 Poster B2

High-statistics SAXS of desmin-expressing cells — •Chiara Cassini[1], Manfred Burghammer[2], Harald Herrman[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 performed scanning small angle X-ray scattering (SAXS) experiments 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 Si_3N_4 windows and measured in freeze-dried state. Each window contained tens to hundreds of cells. In the past, each cell scan took minutes to hours. Recently, we were able to employ a special fast scanning mode that allowed us to image an entire window within a single scan in about 8 hours only. This approach ensured the collection of a statistically significant pool of data in a reasonable time span. However, the data analysis became more challenging: the selection of the different regions of interest needed to be automated. This was achieved by segmenting the dark field image of a scan with Bradley's and Otsu's thresholding; it was subsequently possible to compare local structure-related parameters of the three cell lines in a statistically relevant way.

BP 12.2 Tue 14:00 Poster B2

Studying molecular interactions under flow — •Eleonora Perego and Sarah Köster — Institute for X-Rays physics, University of Göttingen

In recent years the investigation of assembly and aggregation of proteins attracted attention in the scientific community. These processes are the basis of important cellular mechanisms, thus it is important to gain a complete knowledge of the interactions between molecules. Here, we focus on studying the ordered assembly of intermediate filament proteins (IFs), a cytoskeletal component. Although in human more than 70 types of IFs exist, the assembly pathway is common to all of them. The assembly starts with the lateral association of small rod-shaped monomers forming a so called unit length filament (ULF), that is the starting point for the elongation step. We combine photon counting histogram (PCH) to study this process with high spatial resolution, with microfluidics to achieve high temporal precision. We use a multi-layer microfluidics device that prevents the protein from come in contact with the channel walls. This type of device also provides a controlled mixing of assembly buffer and protein solution. Employing PCH on these devices enables us to precisely measure the labelling stoichiometry of the assembling protein, helping us to understand the first steps of vimentin assembly. Our results show that the combination of microfluidics and single molecule fluorescence provides a suitable approach for studying the aggregation of biomolecules in real time, which

is important for understanding cellular behaviour.

BP 12.3 Tue 14:00 Poster B2

Quantification of DNA by Combined X-ray Scanning Nanodiffraction and Holography — •Andrew Wittmeier, Mareike Töpperwien, Tim Salditt, and Sarah Köster — Uni Göttingen. Institute for X-ray Physics. Göttingen, Germany.

Imaging nanostructures within a cell presents several challenges. Although traditional optical imaging techniques, such as visible light phase contrast or fluorescence microscopy, are widely used, they cannot access the necessary length scales of subcellular structures such as nuclear DNA. Techniques such as electron microscopy can image the necessary length scales but at the invasive expense of slicing the cells. These two challenges are overcome by x-rays: with their short wavelengths and high penetration depths, they are capable of imaging nanostructures in whole cells. Measurements can be performed on both living and lyophilized cells but, when compared to living cells, the electron density contrast between the sample and environment is higher when the cells are lyophilized. Here, we preform both x-ray scanning nanodiffraction and holography measurements on lyophilized 3T3 fibroblasts. The presented analysis supplies information concerning the morphology, aggregation state and projected electron density of nuclear material within distinguishable regions of the nucleus. The relationship between the number of scattered photons (nanodiffraction) of a distinguished region and its corresponding electron density (holography) is investigated.

BP 12.4 Tue 14:00 Poster B2

Photo-induced force microscopy (PiFM) - a promising new spectroscopic imaging technique for chemical information of biomaterials — •Anika Strecker[1,2,3], Nila Krishnakumar[1,3,4], Anuradha Ramoji[1,5], Ute Neugebauer[1,4,5], Anne-Dorothea Müller[6], Heidemarie Schmidt[1,4], and Daniela Täuber[1,4] — [1]Leibniz-IPHT, Jena, Germany — [2]Ernst-Abbe University of Applied Science, Jena — [3]Abbe Center of Photonics, Jena — [4]Friedrich-Schiller-University Jena — [5]Center for Sepsis Control and Care, Jena University Hospital — [6]Anfatec Instruments GmbH, Oelsnitz, Germany

Staining-free imaging methods are advantageous for revealing chemical information of biomedical materials. PiFM is a promising new spectroscopic imaging method, which combines excitation in the mid infrared by quantum cascade lasers with detection using a conductive AFM tip, thereby, enabling nanoscale lateral resolution. Here we present PiFM and discuss advantages and disadvantages compared to established IR- and Raman spectroscopy imaging methods.

BP 12.5 Tue 14:00 Poster B2

Metal Induced Energy Transfer reveals nanostructure of an focal adhesion complex — •Fabian Port, Lydia Rebehn, and Kay-E. Gottschalk — Institute of Experimental Physics, Ulm University, Germany

Cell adhesion to the extracellular matrix does not only function as an anchor, it also enables cells to sense their environment [1]. The focal adhesion complex, which is responsible for these adhesions, is a complex structure consisting of a multitude of different proteins. Despite this important role its structure remains difficult to resolve [2]. Knowing the exact position of these proteins in the focal adhesion complex is necessary to understand the sensing mechanisms of the cell. For a detailed analysis of the focal adhesions, a method to measure small distances in cells is needed. A technique which meets this challenge is Metal Induced Energy Transfer (MIET) [3]. Here we show a first analysis of the distance between various focal adhesion proteins and the underlying surface in different cell lines and demonstrate the usefulness of MIET for analyzing molecular structures close to the basal membrane with nm accuracy in life cells.

[1] Geiger, B., Spatz, J. P., & Bershadsky, A. D., Nature Reviews. Molecular Cell Biology, 10(1), 21-33 (2009)

[2] 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)

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BP 12.6 Tue 14:00 Poster B2

Tunable nanoplasmonic substrates for biosensory applications — •Peter Kolb and Kay-E. Gottschalk — Institute for Experimental Physics, Ulm University, Germany

Arrays of metallic nanoparticles show specific electromagnetic resonances which are strongly dependent on their geometry. Coupling between closely spaced plasmonic particles leads to a strong resonance dependence on the inter-particle distance. By combining gold nanoparticles with a soft PDMS substrate, resonances can be mechanically tuned [1] or used to detect substrate strain [2]. As gold and PDMS are both biocompatible they are frequently used in biological applications.

Utilizing electron beam lithography, electron beam evaporation, and lift-off procedures, we produce gold nanodisc arrays on soft PDMS substrates. We investigate the optical properties of these substrates by simulation and experimentation, with further testing of suitability for biosensing applications.

References:

[1] Liu, Wenjie, et al., Mechanically tunable sub-10 nm metal gap by stretching PDMS substrate. Nanotechnology 28.7 (2017): 075301.

[2] Gao, Li, et al., Optics and nonlinear buckling mechanics in large-area, highly stretchable arrays of plasmonic nanostructures. ACS nano 9.6 (2015): 5968-5975.

BP 12.7 Tue 14:00 Poster B2

Fluorescent nanodiamonds as a nanoscopic magnetic field detector — •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 can not only be used for bioimaging but also find an application as part of various biosensors. A nanodiamond sensor can be smaller than 50 nm in diameter and read-out optically without contact, also in biological samples. As they are biocompatible and non cytotoxic, they can be used for many experiments *in vivo*.

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 12.8 Tue 14:00 Poster B2

Developing a fast microrheological sensor device with live tracking — •Jonas Pfeil, Daniel Geiger, Tobias Neckernuss, and Othmar Marti — Institute of Experimental Physics, Ulm University, Ulm, Germany

Passive microrheology (PMR) based on tracking of incorporated coated polystyrene beads is an established technique to measure physical properties of biological tissue. PMR works by imaging the beads at very high frame rates in the kHz range and observe the brownian motion with sub-pixel resolution. From this motion the rheological properties of the tissue are computed. Some of the issues are the high speed imaging requirements and the needed tracking to calculate the information. We present a new device consisting of an image sensor and a field programmable gate array (FPGA) to lower the bandwidth requirements of the sensor and to track the beads in real time. This drastically reduces the storage requirements and bandwidth needed for the measurement, allowing very long duration, continuous measurements with cost efficient hardware.

BP 12.9 Tue 14:00 Poster B2

Cyclic olefin copolymer microfluidic devices for SAXS studies on protein assembly — •Gerrit Brehm and Sarah Köster — Universität Göttingen, Institut für Röntgenphysik

Protein assembly is essential in cellular mechanics and, in particular, the mechanical properties of assembled proteins in higher-ordered structures. The mechanical properties of bundles and networks, for example, are directly encoded by the specific hierarchical architecture of protein structures. Therefore, understanding the assembly pathway of proteins is essential in determining their biological function.

Combining the high spatial resolution of small angle X-ray scattering (SAXS) with the precise, controllable sample environment inside microfluidic devices enables investigation of such processes, as they take place on nanometer and micrometer length scales and occur on

sub-second to second times scales. We present a straightforward fabrication method for X-ray compatible microfluidic devices made solely from cyclic olefin copolymers. Furthermore, no gluing between interfaces is necessary, rendering the production very reliable.

As a biophysical application we investigate the early time points of the assembly of vimentin intermediate filament proteins into higher-order structures. We benchmark the performance of the devices against other devices including more commonly used Kapton windows and obtain data of equal quality using SAXS. This weakly scattering protein system leads to high quality data in the new devices, thus opening up the way for numerous future applications.

BP 12.10 Tue 14:00 Poster B2

X-ray diffraction studies on bovine red blood cells in microfluidic devices — •Jan-Philipp Burchert[1], Gerrit Brehm[1], Rita Graceffa[1], Manfred Burghammer[2], and Sarah Köster[1] — [1]Institut für Röntgenphysik, Universität Göttingen, Germany — [2]European Synchrotron Radiation Facility, Grenoble, France

Red blood cells (RBCs) belong to the major cellular components of blood. They possess a very flexible but stable cytoskeleton below their membrane that is based on an actin-spectrin network. This cortex structure allows them to deform under shear stress and to pass through blood vessels with diameters smaller than their own size. In contrast to other cells, erythrocytes possess no cell organelles. Consequently, their cytoplasm is made up from water and proteins only. One important protein is hemoglobin which is, due to its high volume fraction, proposed to play a role in cell volume regulation. It is suggested that shear forces alter the equilibrium between aggregated and single hemoglobin inside the cell resulting in a change of cytoplasmic properties close to the cell membrane. Thereby, membrane proteins such as pumps and channels might be influenced. In our experiments, bovine RBCs flow through a microfluidic capillary device that simulates shear forces of different magnitudes. Moreover, different osmotic conditions are taken into consideration. To examine the aggregation state of hemoglobin for these experiments, small angle X-ray scattering (SAXS) is applied at different positions within the device. The resulting scattering images are related to the concentration and velocity fields simulated by finite element simulations.

BP 12.11 Tue 14:00 Poster B2

Imaging of folded proteins deposited via soft-landing native electrospray ion beam deposition — •Sven Szilagyi[1], Hannah Ochner[1], Lukas Krumbein[1], Joseph Gault[2], Albert Konijnenberg[3], Esther Martin[3,4,5], Justin Benesch[2], Frank Sobott[3,4,5], Carol Robinson[2], Sabine Abb[1], Stephan Rauschenbach[1,2], and Klaus Kern[1,6] — [1]Max-Planck-Institut für Festkörperforschung, Stuttgart — [2]Department of Chemistry, University of Oxford — [3]Department of Chemistry, University of Antwerp — [4]Astbury Centre, University of Leeds — [5]School of Molecular and Cellular Biology, University of Leeds — [6]École Polytechnique Fédérale de Lausanne

Imaging techniques provide valuable information on the structure of proteins. Gaining reliable data strongly depends on the sample preparation technique, such as shock-freezing and staining of proteins or drop casting of samples. Here, we present the soft landing electrospray ion beam deposition (ES-IBD) as an alternative sample preparation approach in (ultra) high vacuum for imaging of protein samples. To this end, native electrospray ionization brings the proteins into the gas phase while preserving their folded state [1]. In this poster, we present successfully deposited proteins of different size which were imaged using different techniques, such as TEM, AFM, STM and Low Energy Electron Holography (LEEH) [2]. We further discuss the substrate influence on the folded state of the proteins from metal surfaces to free-standing graphene. [1] Nat. Meth., 5(11), 2008, 927-933. [2] PNAS, 114(7), 2017, 1474-1479.

BP 12.12 Tue 14:00 Poster B2

Force microscopy studies of mechanically loaded albumin films — •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, 18051 Rostock — [2]Biomechanics and Implant Technology Research Laboratory, University Medical Center Rostock, 18057 Rostock

In humans articulating joints such as hip or knee contain synovial fluid for sufficient lubrication. Major components are polysaccharides, lipids and proteins such as albumin. During walking oscillating pressure is applied leading to structural changes of the proteins. Under dynamic pressure the proteins might be partially unfolded or even formation of amyloid may occur. Such degraded protein possibly contributes to lubrication. Typical tip-sample pressures in atomic force microscopy are in the same regime as macroscopic joints. Our research question is whether a parameter can be derived from force spectra and be established as a measure for protein degradation. In an initial stage we use albumin as a model protein. This approach requires substantial energy transfer from an oscillating cantilever tip to the protein. In this work we present first results of topographic and spectroscopic analysis of mechanical-loaded albumin films on surfaces.

BP 12.13 Tue 14:00 Poster B2

Towards Label Free Imaging of Action Potentials by Deep Learning — •Stephan Rinner[1], Alberto Trentino[1], Heike Url[2], Bernhard Wolfrum[2], and Friedemann Reinhard[1] — [1]Walter Schottky Institut and Physik-Department, Technische Universität München, Am Coulombwall 4, 85748 Garching, Germany — [2]Munich School of Bioengineering, Technische Universität München, Boltzmannstrasse 11, 85748 Garching, Germany

Imaging of action potential signals in cells thus far requires fluorescence labels. Interestingly, it is plausible that action potentials could also induce small intrinsic changes in the optical properties of a cell. We aim to develop a label-free imaging method by searching for such signatures, capitalizing on the emergence of powerful cameras and image recognition schemes over the past years. On this poster, I will present our efforts to resolve such signals using high resolution polarized light microscopy of heart cells. I will introduce the key features of our setup, namely high-powered LED illumination, a high framerate slow-motion camera and an incubation system for keeping cells alive. Furthermore, the poster will summarize data processing methods to identify patterns in small fluctuations, such as different filtering methods. If successful, this experiment will provide a new method to observe action potentials in a label-free and non-invasive manner.

BP 12.14 Tue 14:00 Poster B2

Targeted near infrared sensing and imaging with GFP-nanobody nanotube hybrids — Florian Mann, Jörg Grosshans, Felipe Opazo, and •Sebastian Kruss — Göttingen University, Göttingen, Germany

Fluorescent nanomaterials have many advantages in terms of their photophysics but it is difficult to target them to specific locations in living systems. In contrast, the green fluorescent protein (GFP) can be genetically targeted to proteins in cells or animals. Therefore, GFP can be seen not only as a fluorophore but as a universal target/handle. Moreover, many transgenic organisms or transfected cells are available. We wanted to combine the advantage of GFP targeting and fluorescent nanomaterials. Therefore, we conjugated a GFP nanobody to near infrared (nIR) fluorescent single-walled carbon nanotubes (SWCNTs). SWCNTs fluoresce in the nIR tissue transparency window (900 nm -1700 nm) and do not bleach. The GFP nanobody serves as recognition unit for GFP and the SWCNT serves as superior nIR fluorophore. These hybrids were then used in biological experiments to demonstrate the versatility of this approach. First, we demonstrated that it is possible to label single GFP-tagged kinesin motors in living drosophila embryos and track their directional movement during embryogenesis. Second, we labeled the cytoskeleton in mammalian cells in the nIR. Finally, we targeted cell surface receptors and used the SWCNTs fluorescence for sensing and to detect the neurotransmitter dopamine. In summary, we show that GFP nanobody conjugated SWCNTs show great potential for targeted nIR imaging, sensing and labeling.

BP 12.15 Tue 14:00 Poster B2

Nanomorphology of living sinus nodal cells — •Max Ulbrich[1], Mirco Wendt[1], Julia J. Jung[2], Christian Völkner[1], Regina Lange[1], Heiko Lemke[2], Christian Rimmbach[2], Robert David[2], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, University of Rostock, 18051 Rostock — [2]Reference and Translation Center for Cardiac Stem Cell Therapy, University Medical Center Rostock, 18057 Rostock

Cardiomyocytes exhibit electro-mechanical activity and may therefore be envisioned as sensor or actuator cells. Sinus nodal cells form the pacemaker of the heart and exhibit autonomous activity while working myocardial cells follow their pace. In our studies, we use scanning ion conductance microscopy (SICM) [1] to observe the live-cell morphology and surface dynamics of individual sinus nodal cardiomyocytes derived by forward programming of pluripotent stem cells [2]. Here, we focus on the question whether the sinus nodal cell subtype exhibits

characteristic features on its surface which can help to conclude on their origin as well as functionality.

[1] C-C Chen et al., Annu. Rev. Anal. Chem. 5, 207 (2012)
[2] J.J. Jung et al., Stem Cell Rep. 2, 592 (2014)

BP 12.16 Tue 14:00 Poster B2

Myofiber orientation in a whole mouse heart — •Marius Reichardt and Tim Salditt — Institut für Röntgenphysik, Göttingen, Deutschland

Heart contractility is one of the most important physiological functions and relies on an intricate, hierarchical molecular- and cytoarchitecture. With recent advances in high-resolution imaging techniques, most notably computed tomography (CT) and magnetic resonance imaging (MRI), the cardiac cytoarchitecture and muscle fiber arrangement can now be resolved in three-dimensions with micrometer resolution. The resolution offered by such conventional means, i.e. ultrasound, diffusion-tensor MRI or clinical CT, is however still not sufficient to resolve the full fiber network down to the level of a single muscle fiber. We performed experiments on an entire mouse heart at a liquid-metal jet μCT laboratory setup with an effective pixel size of 5.5x5.5 μm^2. Based on the reconstructed 3D electron density the fiber orientation, degree of filament alignment and thickness of single muscle bundles in the whole heart could be determined by applying an algorithm based on the 3D Fourier transform of sub-volumes of the reconstruction. The results will be very useful for structural and dynamical models of cardiac tissue as electromechanical finite element models in order to increase the precision and the way they represent the geometry of the heart. This information may also be used in the future to differentiate healthy and pathological heart tissue in clinical computed tomography as we could already show for neuronal tissue.

BP 12.17 Tue 14:00 Poster B2

Surface relief scanning beyond the diffraction limit with optically trapped probes — •Matthias Allkemper, Lars Friedrich, and Alexander Rohrbach — Laboratory for Bio- and Nano-Photonics, Department of Microsystems Engineering - IMTEK, University of Freiburg, Germany

Optical traps play an increasing role in the bio-nano-sciences due to their ability to flexibly apply forces on tiny structures in fluid environments. Combined with particle tracking techniques they allow sensing miniscule forces exerted on these structures. Similar to atomic force microscopy (AFM), but much more sensitive, an optically trapped probe can be scanned across a structured surface to measure the height profile from the displacements of the probe. Here we demonstrate that by a combination of a time-shared twin-optical trap and nanometer-precise three-dimensional interferometric particle tracking reliable height-profiling and surface imaging is possible with a spatial resolution below the diffraction limit. The technique exploits the high energy thermal position fluctuations of the trapped probe, leading to a sampling of the surface 5000 times softer than in AFM. The measured height and force profiles from test structures and helicobacter cells illustrate the potential to uncover specific properties of hard and soft surfaces. We present a novel approach to minimize sticking events between surface and probe, by driving the trapped sphere in tapping mode.

BP 12.18 Tue 14:00 Poster B2

Perceptual evaluation studies of a multisensory interface for exploring nanomechanical tissue properties — •Mónica Tamara Heredia Muñoz[1], Andreas Otto[1], Matthias Löw[1], Sophie Neumann[1], Stephen Barrass[2], Martin Dehnert[1], Thomas Baumann[1], Alexandra Bendixen[1], and Robert Magerle[1] — [1]TU Chemnitz, Chemnitz, Germany — [2]sonification.com, Canberra, Australia

Biological tissues display a very complex spatial structure and their mechanical properties remain largely unexplored on the nanometer scale. We are building an interface that allows humans to explore the spatially complex data of nanomechanical force fields interactively and with multiple senses simultaneously (visual, auditory, and haptic). From a technological viewpoint, the multisensory display has to translate the user's hand motion fluently and quasi in real time into a haptic, visual, and auditory presentation of the data. Avoiding a perceivable delay between the different display channels is essential, since humans are very sensitive to asynchronies between the senses and to delays between perception and action. Of equally high importance as the technical challenge is the question of how particular nanomechanical properties—such as different types of adhesive and repulsive forces—can be translated to the human senses and represented so that they can be efficiently explored. Here we report on our implementation of the multisensory interface, its multisensory information design, and perceptional evaluation studies.

BP 12.19 Tue 14:00 Poster B2

Analysis of Organic Molecules in the THz Regime using Whispering-Gallery Mode Resonators — •Felix Lammermann, Maria Th. Schlecht, Stefan Malzer, and Heiko B. Weber — Lehrstuhl für Angewandte Physik, FAU Erlangen-Nürnberg, Germany

Distinguishing small amounts of organic or biomolecules like single- and double-stranded DNA in aqueous solutions in a fast and non-destructive way is of great interest for bioanalysis [1]. For this task, we present a measurement scheme based on whispering-gallery mode resonators (WGMR) and continous-wave THz-radiation in the frequency range from 80 GHz to >1 THz. The evanescent field of a PTFE THz-waveguide couples to a WGMR made of PE (disk $\varnothing$ 10 mm). A hole in this disk allows to insert a cannula filled with the fluid to be examined.

This local disturbance of the refractive index of the disk severely shifts the resonance frequencies of the WGMR such that the organic molecules can be identified. In a first step, the frequency shifts of short-chained alcohols and organic materials with a high refractive index like glycerine were investigated. We were able to distinguish 1- and 2-propanol which only differ by the position of the $-$OH group. We verified our results with finite element method simulations. To differentiate various sucrose concentrations of aqueous solutions the sensitivity of our setup had to be improved. Thus, the transmission through larger volumes of the corresponding fluid was measured to determine its specific absorption frequencies. Studying the resonance shifts of the resonator close to those should severely increase our selectivity.

[1] Weisenstein, DOI: 10.1109/IRMMW-THz.2018.8510052 (2018)

BP 12.20 Tue 14:00 Poster B2

Open-source 3D-printed Digital Inline Holographic Microscope for microscopic cell analysis — Stephan Amann[1,2], Max von Witzleben[1], and •Stefan Breuer[1] — [1]Institute of Applied Physics, Technische Universität Darmstadt, Schlossgartenstraße 7, 64289 Darmstadt, Germany — [2]Department of Physics, Norwegian University of Science and Technology, Høgskoleringen 5, NO-7491 Trondheim, Norway

Digital inline holographic microscopy (DIHM) is a promising cellular object imaging modality. We demonstrate two cost-efficient DIHM experiments set-ups comprising of standard LED and semiconductor laser light sources and a Raspberry Pi Camera for image acquisition. The DIHM is 3D-printed yielding a highly compact and portable microscope. Imaging of cellular micro objects including tobacco cells and human red blood cells is performed by the use of open-source reconstruction software. Spatial resolutions of 3.96 micrometer and 1.98 micrometer are achieved. The developed DIHM is cost-efficient (<$200), compact and portable and constitutes a highly flexible tool to be used in science and education that can be tailored flexibly to the researchers demand.

BP 12.21 Tue 14:00 Poster B2

Nanomechanical sub-surface mapping of cells by atomic force microscopy — •Lukas Stühn, Anna Fritschen, and Christian Dietz — Physik der Oberflächen, Materialwissenschaften, TU-Darmstadt, Alarich-Weiss-Str. 16, 64287 Darmstadt

We aim to visualize nanomechanical properties of the cell's interior with the atomic force microscope. Compared to optical methods, the atomic force microscope can sense the mechanical properties of cells with high spatial and depth precision. In combination with fluorescence microscopy methods cell processes can be specifically investigated. We demonstrate how the atomic force microscope can be utilized to produce nanomechanical maps of human breast cancer epithelial cells.

To this end, we exploit conventional force-distance techniques or dynamic approaches where we force the cantilever to oscillate in several cantilever eigenmodes (flexural/torsional) simultaneously and record the cantilever motion as function of the tip-sample indentation at each pixel. Thus, tip-sample interactions in different spatial directions can be reconstructed and mapped in various sample depths.

We can mechanically distinguish several components of the cell's interior. The nucleus and cytoskeleton are clearly visible. Within the nucleus, nucleoli appear as mechanically stiffer, small round objects.

In cross-sections drawn through the three-dimensional maps, the stiff cytoskeleton that mechanically stabilizes the cell becomes apparent in the proximity of the membrane. Strikingly, the soft gel-like cytosol within the cell can be detected beneath this stiff enclosure.

BP 12.22 Tue 14:00 Poster B2

Probing mitochondrial dynamics and heterogeneity during cell state switching using multiplexed, environment-sensitive fluorescent dyes — •Sufi O. Raja[1,2], Gandhi Sivaraman[1], Christoph F. Schmidt[2], and Akash Gulyani[1] — [1]Technology for Advancement of Science, Institute for Stem Cell Biology & Regenerative Medicine, Bellary Road, Bangalore-560065, India — [2]Drittes Physikalisches Institut - Biophysik, Fakultät für Physik, Georg-August-Universität Göttingen, 37077 Göttingen

Mitochondria are known as power house of the cell also play significant role in regulating cellular metabolism, calcium and ROS signaling as well as in programmed cell death. Despite decades on research, precise and real-time information on mitochondrial dynamics and functionality, is still limiting.To better visualize the functional dynamics of mitochondrion, we have developed red-emitting, multi-functional, novel mitochondrial probes that are sensitive to local environment, specifically parameters like micro-viscosity, pH, ROS, etc. The developed dyes have low toxicity and very high photo-stability, allowing their use in long term imaging. These dyes have yielded new insights into mitochondrial dynamics in embryonic stem cells as well as during onset of differentiation. In a different example, we have also used our new dyes to probe mitochondrial heterogeneity within primary *activated* cells. These results would be placed in the context of our larger efforts to build new ways of probing *cellular dynamics* with a focus on physico-chemical changes in the intra-cellular compartments.

BP 12.23 Tue 14:00 Poster B2

In-line DNA optical mapping in nanochannels for biomedical applications — •Franziska Esmek — Center for Hybrid Nanostructures

On-chip DNA optical mapping allows studying intact individual molecules with higher throughput than conventional sequencing techniques. In optical mapping, typically a "fluorescent barcode-like" pattern is first created, then the DNA molecules are elongated and the fluorescent signal is read out to get information about the genomic structure for biomedical applications. We explore a technique to selectively label the DNA molecules with organic fluorophores as well as by competitive binding at specific locations of interest. The DNA molecules are then stretched in nanofluidic devices made by nanoimprint lithography in a two-minute process. The signal is read out in real time in a home made confocal set up. We perform in-line detection of DNA molecules as they pass through the nanochannels with a focused laser as point excitation and a photon counter, without using a camera. In this configuration, the molecules are detected as step-like peaks in time scans, allowing for real time read-out, with high throughput. Peak analysis (as intensity and duration) gives information about the molecule length, as well as its sequence-dependent barcode. Here there is no limitation with the length of the molecules, or the resolution due to the thermal drift and molecule movement.

BP 12.24 Tue 14:00 Poster B2

Modern data workflow management providing new insights into biomedical data — Henrik tom Wörden[1,2], •Alexander Schlemmer[1,3], Daniel Hornung[1], Timm Fitschen[1,2], Ulrich Parlitz[1,2,3], and Stefan Luther[1,2,3,4,5] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Institute for Nonlinear Dynamics, Georg-August-Universität, Göttingen, Germany — [3]German Center for Cardiovascular Research (DZHK), partner site Göttingen, Germany — [4]Institute of Pharmacology and Toxicology, University Medical Center Göttingen, Göttingen, Germany — [5]Department of Physics and Department of Bioengineering, Northeastern University, Boston, USA

The progress in measurement and imaging technologies, such as multichannel EEG, 4D ultrasound imaging or real-time MRI, results in unprecedented amounts of high-resolution, multi-modal data. The processing, analysis, and interpretation of this complex data is a major scientific challenge and a significant bottleneck. Links and interdependencies can exist between all kinds of data on multiple levels, possibly spanning single experiments, experiment series or even larger collaborative projects. Although analysis procedures in biomedical sciences are often advanced, limits in data management may constrain their application. Using data from cardiac research we show how a modern data workflow management allows for a more effective and versatile interface to the data. The workflow also supports the connection of experimental data to simulation data and analysis results, ensuring a high flexibility of data access and reusability for the researcher.

BP 12.25 Tue 14:00 Poster B2

Computational optimization of compound selectivity to different membrane environments — Bernadette Mohr and •Tristan Bereau — Max Planck Institute for Polymer Research

Current virtual screening approaches reduce the computational cost by using simplified representations and approximations, statistical mechanical effects are excluded. We investigate one way to include the effects determining the selectivity of a molecule to a specific target into virtual screening by using physics-based models. Coarse-grained simulations are introduced as a preliminary step to allow the effective screening of a large number of molecules. As a test case, the physical and chemical properties of the fluorescent dye 10-N-nonyl acridine orange are modified to increase its binding affinity to Cardiolipin. In eukaryotes, Cardiolipin is almost exclusively found in the inner mitochondrial membrane. Mitochondria are the location of important metabolic pathways and are linked to diseases and apoptosis. Therefore, targeting a lipid specific to mitochondria is of great interest. In the coarse-grained representation, the bead types at selected positions of the acridine orange molecule are changed and the difference in binding affinity between the original and modified structures are determined by free energy calculations. The present results from the coarse-grained simulations indicate that hydrogen bonding has the desired effect. As a next step, the information lost in the coarse-graining process is to be reintroduced to a small subset of the screened molecules by repeating the free energy calculations in atomistic detail.

BP 12.26 Tue 14:00 Poster B2

Applying microwaves on a cellular level — •Simon Streit and Stephan Gekle — Theoretische Physik VI, Universität Bayreuth, Germany

The influence of microwaves in the range of MHz and GHz on the human body and particular cellular components are still not fully understood. For new treatment methods in the medical field like hyperthermia, absorption characteristics need to be understood on the cellular level. Therefore we present our cell model which uses prior work on the specific absorption rate (SAR) of a cell membrane to calculate SAR values for different common cell sizes and frequencies. In addition we take a look into the absorption behaviour of short DNA pieces by means of molecular dynamic simulations and dipole correlation calculations for spectral analysis.

BP 12.27 Tue 14:00 Poster B2

Simulation of visco-elastic behavior of cells in a microfluidic device — •Ralf Schuster, Tobias Neckernuss, Daniel Geiger, Jonas Pfeil, Kay Gottschalk, and Othmar Marti — Institute of Experimental Physics, Ulm University, D-89081 Ulm

Variations of structure and shape of cells play an important physiological role. For instance, tumor and normal cells can be distinguished by elasticity, indicated by the amount of deformation under given stress. The mechanical characterization of a certain cell type is meaningful to obtain (patho-) physiological insight. Simulations help to understand, verify and improve the analysis of deformation based cell characterization such as CAOS (1) or flow based cytometry (2). We aim to provide a simulation-based database for the mechanical deformation of cells in microfluidic channels. The variation of parameters of the viscoelastic models for the cells results in a library of possible cell deformation classes. The cell develops characteristic shapes, while moving through a microfluidic channel with varying width. We compare the cell*s deformation with measurements. We achieve efficient computations using a 2D-rotational symmetric model, based on Fluid-Structure-Interaction with a hyper-elastic material. Distortions of the mesh, due to strong deformations of the cell, often lead to computational instabilities. This challenge was mastered and our model is able to describe the deformation of the cell along the entire channel.

(1) Neckernuss (2018): Stretching adherent cells with light. Dissertation. (2) Otto et al., Real-time deformability cytometry: on-the-fly cell mechanical phenotyping, Nat. Methods, 2015

BP 12.28 Tue 14:00 Poster B2

Optimization of the Ligase Cycling Reaction (LCR) via Rule-Based Modeling — •Lara Becker, Niels Schlichting, Johannes Falk, Johannes Kabisch, and Barbara Drossel — TU Darmstadt,

Germany

Synthetic biologists are working to find a way for efficient and robust implementation of complex genetic circuits into living systems. One approach to this is the employment of computer-aided design tools and the exploitation of automatization procedures, e.g. for DNA assembly. The Ligase Cycling Reaction (LCR) is a powerful method for automated and modularized assembly of DNA. Our goal is to further optimize the LCR based on insights from computer simulation models that mimic, in a simplified fashion, the main steps of the LCR.

To this end, we built a rule-based model of the LCR in Kappa (κ) - a language for modeling systems of interacting agents. The dynamics of the LCR is stochastically simulated in κ, and we explore how changing parameters, concentrations, and timing affects the efficiency. This is done in close collaboration with synthetic biologists from our team who perform assays in the wet lab to validate our findings and predictions, which in turn causes the modelers to include additional features that appear to be relevant in the experiments.

BP 12.29 Tue 14:00 Poster B2

Binding properties of SIM/SUMO complexes — •Alexander Kötter and Andreas Heuer — Institut für Physikalische Chemie, WWU Münster

The interaction between the small ubiquitin related modifier (SUMO) and different sumo interacting motifs (SIMs) has been the subject of a number of studies in the past few years(e.g., [1]). We investigate complexes formed by the SUMO protein and SIMs by means of atomistic molecular dynamics simulations. We calculate the standard binding free energies for a number of SIMs and find that their relative order agrees well with experiments[1]. We quantify the importance of acidic residues in the neighborhood of the SIMs for the binding and measure the contribution of single residues in the SIM to the interaction energy. Furthermore we find, that, in general, two binding modes exists for the considered SIMs. Their relative importance however varies strongly. [1] Xu et al. Nat. Comm. 5

BP 12.30 Tue 14:00 Poster B2

Fundamentals of domain formation in lipid bilayers: Analyzing atomistic molecular dynamics simulations — •Fabian Keller and Andreas Heuer — Westfälische Wilhelms-Universität, Münster, Germany

The complex interplay of the myriad of different lipid species as well as membrane proteins that are found in plasma membranes and the resulting unique properties still remain elusive and not well understood. A cell's ability to tune phase behavior clearly is crucial for sustaining vital functionality.

Efforts have been made simulating lipid bilayers with a close-to native lipid composition to shed light on this behavior. [1] Nevertheless the underlying mechanisms remain unidentified.

In this work we approach the problem from a fundamental point of view, analyzing the interaction enthalpies of different lipid species as well as of one candidate of a transmembrane domain to get a better understanding of the driving forces of domain formation. These results can directly be used to expand a recent lattice model of lipid bilayers. [2]

[1] H. I. Ingólfsson,. et al. JACS, 136, (2014)
[2] D. Hakobyan, A. Heuer, J. Chem. Phys. 146, (2017)

BP 12.31 Tue 14:00 Poster B2

Generalized Markov State Modeling of Electric Field Induced Conformational Changes in the HIV-1 V3 Loop Peptide — Bernhard Reuter[1,2], •Daungruthai Jarukanont[2], Sina Zendehroud[2], and Martin E. Garcia[2] — [1]Zuse Institute Berlin (ZIB), Berlin, Germany — [2]University of Kassel, Kassel, Germany

Conformational changes regulate the physiological functionality of proteins. The influence of environmental conditions on the function and, therefore, on the conformation of proteins is being studied very intensively. In this work, we investigate the influence of a static external electric field on the secondary and tertiary structure formation of the V3 loop of the HIV-1 envelope glycoprotein gp120. Based on extensive molecular dynamics (MD) simulations, the conformational dynamics of the system were modeled applying a recently developed generalized Markov state modeling method termed Generalized Perron Cluster Cluster Analysis (G-PCCA) from [Reuter et al. (2018). JCTC, 14(7), 3579-3594. https://doi.org/10.1021/acs.jctc.8b00079]. G-PCCA enables the unsupervised and automatic coarse graining of both reversible and nonreversible molecular kinetics. Using G-PCCA the dominant conformational dynamics of the system were learned for different strengths of the electric field.

BP 12.32 Tue 14:00 Poster B2

Computer simulations of SAS-6 assembly on surfaces — •Dennis Wörthmüller[1,2] and Ulrich Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg — [2]Bioquant, Heidelberg

The scaffold protein SAS-6 self-assembles into a 9-fold ring that forms the structural basis for centrioles and thus is essential for many important cellular processes, including cell division and the genesis of cilia and flagella. Recently the self-assembly of SAS-6 has been studied by high-speed AFM on mica surfaces (Nievergelt et al., Nature Nanotechnology 13:696-701, 2018). Motivated by this experimental study, we have developed a 2D Brownian dynamics simulation model to identify possible assembly pathways, including malformed structures. Our main finding is that strong fluctuations, which are suppressed by the interaction with the surface, lead to malformed structures. Fluctuations also result in a distribution of ring sizes that favors 8-rings over 10-rings.

BP 12.33 Tue 14:00 Poster B2

Range Expansions in a Stochastic Metapopulation Model — •David Muramatsu[1], Erwin Frey[1], and Marianne Bauer[2] — [1]Ludwig-Maximilians-Universitaet Muenchen, Germany — [2]Princeton University, USA

In range expansions, the colonization of a territory by an invading species, the front between invaded and new territory roughens due to stochastic fluctuations. To investigate the growth laws describing the front width of a given system, large sized systems have to be considered, since finite size effects may otherwise obscure the dynamics that govern the interface. Naive implementations of exact simulation algorithms like the Gillespie algorithm scale unfavorably in the system size such that the simulation of ensembles of large systems with complex interactions quickly becomes unfeasible. We address this problem by implementing a parallelized version of the Gillespie algorithm, which scales linearly in the system size, suited for lattice based systems that display local fast dynamics while having a low rate of particle exchange between lattice sites. We employ this algorithm to determine the growth law governing the front width of a system which has been inaccessible to previously used simulation methods.

BP 12.34 Tue 14:00 Poster B2

Fast discrete Cell Volume Tracking for Blood Flow Simulations using the Lattice Boltzmann Method — •Moritz Lehmann, Sebastian Müller, and Stephan Gekle — University of Bayreuth, Germany

The Lattice Boltzmann Method (LBM) is often used to simulate the movement of red blood cells through blood vessels via the immersed boundary method. However, the basic model does not include the different fluid viscosities of the inside of cells and the blood plasma, which also affect cell deformation. For taking into account multiple viscosity domains, we present a fast tracking algorithm that can determine whether any lattice point of LBM is located inside or outside an arbitrarily enclosed cell volume and we investigate how a viscosity change affects cell deformation.

BP 12.35 Tue 14:00 Poster B2

DMPC/cholesterol membranes at high hydrostatic pressure — •Göran Surmeier, Michael Paulus, Christian Sternemann, Susanne Dogan, Mike Moron, Marc Moron, and Julia Nase — Fakultät Physik/DELTA, TU Dortmund, 44221 Dortmund, Germany

Phospholipid bilayers, which are the basic component of cell membranes, form various liquid-crystalline and gel-like phases depending on temperature, pressure, and their composition. A typical constituent that regulates the structure of cell membranes is cholesterol. Due to its rigid sterol rings, it affects the mobility and order of lipid tail groups. We conducted a small angle X-ray scattering (SAXS) and X-ray reflectivity (XRR) study on the structure of 1,2-dimyristoyl-sn-glycero-3-phosphocholine (DMPC) model membranes containing cholesterol at high hydrostatic pressures. We were able to extract a detailed pressure- and cholesterol content-dependent phase diagram of multilamellar DMPC vesicles in the gel-like regime at 20 °C from SAXS. Additionally, XRR was used to obtain more in-depth information about the vertical membrane structure of solid-supported DMPC/cholesterol multilayers in an aqueous buffer solution. Combining both techniques enables to distinguish substrate-, pressure- and composition-induced

effects. We observed that cholesterol strongly affects the compressibility of the membranes. At high concentrations, the spacing changes linearly over the whole pressure range, indicating that configurational changes are suppressed. Experiments were performed at beamlines BL9 at DELTA (Dortmund, Germany) and ID31 at the ESRF (Grenoble, France).

BP 12.36 Tue 14:00 Poster B2

Effect of reactive oxygen and nitrogen species on lipid monolayers — •Florian Gellert, Heiko Ahrens, Renko Kensbock, and Christiane A. Helm — Institute of Physics, University of Greifswald, 17489 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. Self-assembling- and phase transition behaviour of monolayers in a Langmuir-Blodgett trough are studied by isotherms. Domain formation is studied by video-speed Brewster angle microscopy. The reactive species are formed either by a low temperature plasma jet (kINPen) or are dissolved in the subphase at low concentrations. Thus, we address the question whether the ROS/ RNS attacks the unsaturated alkyl chains or the head group of the lipid.

BP 12.37 Tue 14:00 Poster B2

A Biomimetic Model to Probe Adhesion Induced Lipid Membrane Properties — •Philipp Pauli and Cornelia Monzel — Experimental Medical Physics, Heinrich-Heine University Düsseldorf, 40225 Düsseldorf, Germany

Adhesion plays an important role in the biological functions of cells influencing signalling, cell migration, or the building of tissue. The basis of adhesion are the short range attractive forces induced by biological molecules like cadherins or integrins. Using giant unilamellar vesicles (GUV), it is possible to mimic the envelope of a cell - namely the plasma membrane - and to decipher physical mechanisms underlying cell adhesion. As biomimetic model system, GUVs lack the complex structures of cells and enable quantification of designated membrane properties.

Utilizing the biotin-neutravidin binding between a substrate and a vesicle, we investigate the adhesion strength relative to a variable number of adhesive bonds by calculating the contact angle between the surface and the vesicle. The contact angle information is measured via microinterferometry. Moreover, using a ternary mixture of lipids, we study the effect of adhesion on the formation of liquid domains using fluorescence microscopy. Thus, a model system is developed to probe how variable adhesive linker densities affect lipid organization in the membrane.

BP 12.38 Tue 14:00 Poster B2

Complexity of micelle formation as studied by a minimum particle-based model — •Simon Raschke and Andreas Heuer — Institute of Physical Chemistry, WWU Münster, Correnstr. 28/30 48149 Münster, Germany

The formation of self assembled structures such as micelles has been intensively studied and is well understood. The ability of a solution of amphiphilic molecules to develop micelles is depending on the concentration and characterized by the critical micelle concentration (cmc), above which micelle formation does occur. We developed a minimalistic coarse grained model for amphiphilic molecules in the continuum and simulated the time evolution via dynamic Monte Carlo simulations in the canonical (NVT) ensemble. This approach enables long timescales and allows studying of related processes. The model is also capable of simulating the frame-guided assembly process [1], which makes vesicle formation into a predefined frame possible and reliable below cmc. Equilibration in the cmc domain turns out to happen on very long timescales and the cluster formation is highly non trivial. We discuss the influences of local energies, curvature, frame-guides and disorder and their connection to the processes of cluster formation.

[1] Y. Dong, D. Liu, Angewandte Chemie International Edition 2014, 10, 53.

BP 12.39 Tue 14:00 Poster B2

The impact of antifoam agents on lipid membranes at the air-water-interface — •Mike Moron, Michael Paulus, Julia Nase, Susanne Dogan, and Metin Tolan — Fakultät Physik/DELTA, TU Dortmund, 44221 Dortmund, Germany

The control of foam by means of antifoam agents is of great importance in a number of industrial and medical applications. For example, the oral medication of simethicone is prescribed in the case of surfactant intoxication and also in order to dispose patients for coloscopy. While the macroscopic behavior of liquid systems containing antifoam agents and lipids is well described, the behavior of antifoam agents on the molecular scale is not completely understood.

We present surface pressure-dependent in-situ X-ray reflectometry (XRR) experiments and a Brewster-angle microscopy (BAM) study on Langmuir monolayers consisting of different lipids and antifoam agents. Both, the XRR and BAM measurements were performed at the liquid-air interface.

A stearic acid monolayer served as a model for a foam lamella and the impact of an industrial used antifoam agent was analysed. Furthermore, a dipalmitoylphosphatidylcholine (DPPC) monolayer was prepared to mimic a cell membrane and the impact of the medical antifoam agent simethicone was studied. The measurements showed a strong effect on the lipid layers structure for low surface pressures of the lipid films. For high surface pressures the antifoam agents had little to nearly no effect on the lipid films.

BP 12.40 Tue 14:00 Poster B2

3D-Printed Microfluidic Chip to Study Protein Organization in a Lipid Bilayer — •Sevde Puzda, Ralf Seemann, and Jean-Baptiste Fleury — Saarland University, Saarbruecken, Germany

We developed a layout for a 3D microfluidic chip whose master can be fabricated by state of the art 3D-Printing. The microfluidic chip allows to form, in a quasi-automatic manner, a free-standing lipid bilayer. The bilayer is produced by contacting two water droplets in an oil phase, where lipids molecules have been dispensed. Interestingly, this method does not require any microfluidic pumps (volume, or pressure). The bilayer formation is demonstrated by electrophysiological measurements and optical investigations with a normal view direction onto the bilayer. Proteins are reconstitute in this bilayer, and their dynamical self-organization properties are study in-situ.

BP 12.41 Tue 14:00 Poster B2

Small-angle X-ray Scattering on Photo-switchable Lipid Membranes — •Martina Ober[1], Patrick Urban[1], Stefanie Pritzl[1], David Konrad[2], Dirk Trauner[2,3], Theobald Lohmüller[1,3], and Bert Nickel[1,3] — [1]Department of Physics, and Center for Nano Science, Ludwig-Maximilians-Universität, Munich, Germany — [2]Department of Chemistry and Center of Integrated Protein Science, Ludwig-Maximilians-University, Munich, Germany — [3]Nanosystems Initiative Munich, Germany

Light-switchable lipids which are prepared by incorporation of a photosensitive azobenzene into a phosphatidylcholine (Azo-PC) enabled a novel approach to study and control the properties of membranes. Azo-PC undergoes a reversible photo-isomerisation of cis- and trans-state on irradiation with UV, respectively visible light, which is well understood on the molecular level. The photo-isomerisation induces a configurational change in the lipid which further affects the overall structure of an Azo-PC membrane. Here, we use small-angle x-ray scattering (SAXS) to perform structure analysis and phase behaviour studies of Azo-PC membranes in a physiological environment. Our research will help to extend the molecular control of photo-switchable lipids to a control of photo-switchable membranes in order to investigate membrane perforation, drug release, and membrane enzyme activity.

BP 12.42 Tue 14:00 Poster B2

Mechanical parameters of phospholipid multi-layers from off-specular x-ray scattering — •Max Scheu, Tim Salditt, Kilian Frank, and Karlo Komorowski — Institut für Röntgenphysik, Göttingen

The structural analysis of phospholipid bilayers which exert a prominent role in different biological systems is of increasing importance for understanding processes such as membrane adhesion or fusion. In order to determine the continuum mechanical parameters namely compression and bending modulus of solid-supported phospholipid multilayers different specular and off-specular x-ray scattering experiments were conducted. Via comparison to smectic elastic theory the results give insight to membrane dynamics as well as to potential pre-critical phenomena prior to the so-called stalk phase transition. We used a model with three free parameters, derived from membrane displacement correlation functions in the kinematic approximation of the scattering function, to describe stratified interfaces of membranes with correlated roughness. This model was used to simulate complete recip-

rocal space maps and extract the bending rigidity and the compression modulus from experimental data. In particular the structural changes of lamellar phases of different phospholipids, promoted by change in relative humidity or ionic environment, are evaluated by measurement and modeling in direct vicinity of bragg peaks. These findings may help to ascertain further insight on interaction potentials of membranes as well as transmembrane cellular medication uptake.

BP 12.43 Tue 14:00 Poster B2

Study of the Structure and Kinetic of Photoswitchable Lipid Monolayers Influenced by Different Sugar Groups — •Svenja Carolin Hövelmann[1], Jonas Erik Warias[1], Alexander Hebel[1], Franziska Reise[3], Thisbe Lindhorst[3], Olaf Magnus Magnussen[1], and Bridget Mary Murphy[1,2] — [1]Institut für Experimentelle und Angewandte Physik, University of Kiel, Germany — [2]Ruprecht Haensel Laboratory, University of Kiel, Germany — [3]Otto Diels-Institut für Organische Chemie, University of Kiel, Germany

The phospholipid membranes with their mechanical and dynamical properties have an important role in biological functions. To study these properties we us a model system of a Langmuir film of amphiphilic phospholipids with embedded photoswitchable molecules. These molecules are glycolipids containing an azobenzene photoswitch between the chain and the head group and are embedded in a monolayer of dipalmitoylphosphatidylcholine (DPPC). In order to investigate the influence of a different number of sugar groups attached to the molecules multiple molecules are prepared. Langmuir isotherms and X-ray reflectivity are used to study the structural differences between the molecules and the structural changes when illuminated as the orientation of the azobenzene-glycolipid switches reversibly between trans- and cis-conformation by illumination of UV and blue light. Differences between the molecules in terms of their switching behaviour and membrane conformations can be observed.

BP 12.44 Tue 14:00 Poster B2

Protein-radical interaction: structure analysis using atomic force microscopy — •Sanjai Karanth[1,2], Una Janke[1,2], and Mihaela Delcea[1,2] — [1]Institute of Biochemistry, University of Greifswald, Greifswald, Germany — [2]ZIK HIKE, University of Greifswald, Greifswald, Germany

Reactive nitrosative species (RNS) such as nitric oxide (NO.) released in the body attack the thiol groups of proteins altering their function (e.g. protein activation upon ligand binding)[1]. Here, we investigate in a biomimetic system the interaction of RNS with integrin alpha IIb beta 3 (αIIbβ3)- a transmembrane protein present on blood platelets and responsible for thrombotic activity. αIIbβ3 protein was reconstituted into nanodiscs which generate planar lipid bilayers which stabilize the protein. Using atomic force microscopy (AFM) imaging, we were able to distinguish the different states of protein (i.e. open/active and closed/bent state). Radical attack on the nanodiscs was performed and structural analysis was carried out using AFM imaging and single molecule force spectroscopy (SMFS). Nanodiscs prove to be a reliable membrane system to study biophysical properties of transmembrane proteins.

[1] Mor-Cohen, R. (2016). Disulfide bonds as regulators of integrin function in thrombosis and hemostasis. Antioxidants & redox signaling, 24(1), 16-31.

BP 12.45 Tue 14:00 Poster B2

Limiting shapes of confined lipid vesicles — •Bor Kavčič[1], Ai Sakashita[2,3], Hiroshi Noguchi[3], and Primož Ziherl[4,5] — [1]IST Austria, Klosterneuburg, Austria — [2]Ochanomizu University, Tokyo, Japan — [3]University of Tokyo, Tokyo, Japan — [4]University of Ljubljana, Ljubljana, Slovenia — [5]Jožef Stefan Institute, Ljubljana, Slovenia

We theoretically study the shapes of lipid vesicles confined to a spherical cavity, elaborating a framework based on the so-called limiting shapes constructed from geometrically simple structural elements such as double-membrane walls and edges. Partly inspired by numerical results, the proposed non-compartmentalized and compartmentalized limiting shapes are arranged in the bilayer-couple phase diagram which is then compared to its free-vesicle counterpart. We also compute the area-difference-elasticity phase diagram of the limiting shapes and we use it to interpret shape transitions experimentally observed in vesicles confined within another vesicle. The limiting-shape framework may be generalized to theoretically investigate the structure of certain cell organelles such as the mitochondrion.

BP 12.46 Tue 14:00 Poster B2

Influencing liposome structure by terpenoids: a TEM analysis — •Bernhard Kaltschmidt, Inga Ennen, Daniela Ramermann, and Andreas Hütten — Thin Films & Physics of Nanostructures, University of Bielefeld, Bielefeld, Germany

Today, multiresistant bacteria are more and more common in hospitals.Therefore the development of novel treatments is mandatory. Terpenoids are plant substances with antimicrobial activity. A new approach is to use the antibacterial properties of terpenoids as therapeutics. Since most terpenoids are insoluble in water, here we dissolved them in EtOH and used liposomes as carriers. Liposomes are nanoscale spherical vesicles, which were produced with an extruder and then analysed by Cryo transmission electron microscopy (Cryo-TEM). Different approaches were tested to determine the best imaging parameters. As terpenoids 1,8 cineol, campher, menthol and thymol of pharmaceutical grade were used. Cryo-TEM revealed a gradient of multi-lamellar liposomes to unilamellar liposomes. The highest antibacterial activity could be shown by thymol.

BP 12.47 Tue 14:00 Poster B2

Subsampling impact on the inferred properties of cortical networks — •Mehrdad Hasanpour[1,2], Paolo Massorbio[3], and Anna Levina[1,2] — [1]University of Tübingen, Germany — [2]MPI for Biological Cybernetics, Germany — [3]University of Genova, Genova, Italy

Uncovering the topological properties of the brain network is essential for understanding brain function. Typically network structure is inferred from observations of a tiny fraction of the system, resulting in a severe subsampling of the whole network. How this inevitable subsampling influences the inferred network properties, such as the widely used small-world index, remains mostly unknown. The small-world index is defined as a clustering coefficient divided by diameter. For random, small-word, and scale-free networks we demonstrate analytically and numerically that the subsampling preserves the clustering coefficient. However, the diameter is strongly influenced by the subsampling, biasing the inference of small-worldness in subsampled networks. Our primary goal is to understand how to correct for such bias rigorously. Brain networks have a highly complex structure that is not captured by simple random networks we consider in theoretical studies. For a more realistic comparison, we investigate functional networks extracted from the High-Density Multi-Electrode Array recordings from cortical cultures using transfer entropy. The extracted network contains 4096 nodes, allowing for a further subsampling. We demonstrate that already the thresholding procedure used for extraction of the binary network is strongly influenced by subsampling.

BP 12.48 Tue 14:00 Poster B2

Influence of nanostructured polymer surfaces on neuronal development — •Frano Milos[1], Andreea Belu[1], Dirk Mayer[1], Maria Rosa Antognazza[2], Vanessa Maybeck[1], and Andreas Offenhäusser[1] — [1]Institute of Complex Systems ICS-8, Forschungszentrum Jülich GmbH, Jülich, Germany — [2]Center for Nano Science and Technology @Polimi, Istituto Italiano di Tecnologia, Milano, Italy

The complexity of the extracellular matrix consists of micro- and nanoscale structures that influence neuronal development, differentiation, and neuritogenesis through contact guidance. Therefore, the ability to manipulate neuronal growth has great implications for both neuronal repair and the potential design of implantable biomedical devices. We employ precisely designed nanostructured polymers to investigate the effects of surface topography on growth and guidance of primary cortical neurons using time-lapse fluorescent microscopy. Recently, we demonstrated that nanoscale pillars accelerate axon establishment and change the periodicity of the axon growth dynamics resulting in longer axons aligned to the underlying topography. These results demonstrate that axon growth can be modulated and guided by the dimensions of physical cues on the surface. Axon growth cones sense their environment through complex signaling pathways that modulate cytoskeletal dynamics and induce growth in a specific direction. Therefore, we aim to investigate F-actin dynamics and mechanosensing in relation to surface topography during different stages of development to elucidate the mechanisms underlying the topography-induced responses.

BP 12.49 Tue 14:00 Poster B2

Spike Termination in Networks of Bistable Neurons — •Muhammet Uzuntarla[1], Joaquin J. Torres[2], Ali Calim[1], and Ernest Barreto[3] — [1]Department of Biomedical Engineer-

ing, Bulent Ecevit University, Turkey — [2]Department of Electromagnetism and Physics of the Matter, University of Granada, Spain — [3]Department of Physics and Astronomy, George Mason University, USA

In neural systems, synchronization is widely considered to be responsible for the origin of oscillatory brain rhythms. Findings from experimental and theoretical studies suggest that it results from interplay between intrinsic properties of individual neurons, synaptic interaction dynamics and topological features. An interesting synchronization-induced emergent behavior is termination of ongoing population activity. We observe and study this phenomenon whereby neural activity spontaneously ceases. Here, we investigate the behavior of three types of networks composed of bistable HH neurons with a scale-free topology, involving either electrical or chemical synapses that are either excitatory or inhibitory. We find that periodic synchronous population activity emerges in all three networks, and strongly synchronized population spiking events lead to complete cessation of activity in excitatory networks, but not in gap junction or inhibitory networks. We identify the underlying mechanism responsible for this phenomenon by examining the particular shape of excitatory postsynaptic currents. We also examine the effects of the synaptic time constant, coupling strength, and channel noise on the occurrence of the phenomenon.

BP 12.50 Tue 14:00 Poster B2

Taming the bias when estimating correlations from spike recordings — Jens Wilting[1], Johannes Zierenberg[1], •Leonhard Leppin[1,2], and Viola Priesemann[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Georg-August-Universität Göttingen, Germany

What can we infer about a dynamical system if we can only observe a very small part of it? The problem of subsampling is common to the study of many systems. It is particularly severe in neuroscience, because electrophysiological recordings of spiking activity can only assess a small fraction of all neurons simultaneously. This subsampling has hindered characterizing even most basic properties of collective spiking in cortical networks. We proved that whenever a population is subsampled, the observed spike count cross-correlation between the populations can be strongly underestimated. The same holds for the autocorrelation strength of subsampled activity of a single population. These limitations hinder the correct inference of the underlying network dynamics. To overcome the systematic bias, we derived a novel estimator, which can infer properties of activity propagation even under strong subsampling. In this framework, the dynamical state is characterized by the average number of spikes triggered causally by a single spike in a neuron. Our generalization of the estimator to many populations now enables us to infer afferent contributions, recurrent propagation within a population, and reciprocal propagation between populations, and thereby enables us to contribute to identifying functional connections between brain areas.

BP 12.51 Tue 14:00 Poster B2

Tailored dynamic range using an ensemble of networks — •Johannes Zierenberg[1], Jens Wilting[1], Viola Priesemann[1], and Anna Levina[2] — [1]Max Planck Institute for Dynamics and Self-Organization — [2]Tübingen University

The dynamic range quantifies the range of inputs that a neural network can discriminate. It is maximized at a non-equilibrium phase transition. However, besides the actual size of the dynamic range, it is crucial that the interval of discriminable inputs covers the relevant inputs. We show analytically for a generic spiking model that – while the dynamic range indeed is maximal at criticality – the discriminable intervals are virtually indistinguishable from each other in the vicinity of the phase transition. We identify the constrained discriminable interval to be a result of *coalescence* (the simultaneous activation of the same unit from multiple sources). In our model, we can compensate coalescence by implementing adaptive synaptic weights and thereby obtain specific discriminable intervals that can be tuned by changing the distance to criticality. This enables us to optimally address particular tasks by constructing tailored ensembles of coalescence-compensated networks, e.g., discriminating very broad or bimodal input distributions, with implications for machine learning approaches such as reservoir computing networks.

BP 12.52 Tue 14:00 Poster B2

Signatures of criticality in efficient coding networks — •Shervin Safavi[1,2], Matthew Chalk[3], Nikos Logothetis[1], and Anna Levina[1,2] — [1]MPI for Biological Cybernetics — [2]University of Tübingen — [3]Institut de la Vision, Sorbonne Universite

Theoretical and experimental evidence brought forward a hypothesis that the brain operates close to a critical state. Numerous studies investigated neural models that can attain various distances to criticality depending on a control parameter and quantified information processing capabilities as a function of closeness to criticality. However, quantifying these capabilities in a general sense is not sufficient to assure usefulness of criticality for the brain. Therefore, we introduce a complementary approach. We study a network that is optimized for a task relevant for the brain. Then, we investigate whether we observe the scale-free neuronal avalanches exclusively in the optimized network. More specifically, we used a network of leaky integrate-and-fire neurons with parameters optimized for efficient coding. Previously, it was shown that performance of such networks varies non-monotonically with the noise amplitude. We discovered, that only in the network with optimal noise level the avalanche size distribution follows a power-law and with too low or too high noise, the network appears either super-critical or sub-critical, respectively. We demonstrate that scale-free distribution of neuronal avalanches might be a consequence of optimal efficient coding in spiking neural networks. This result has important implications, as it shows how two influential, and previously disparate fields - efficient coding, and criticality - might be intimately related.

BP 12.53 Tue 14:00 Poster B2

Evidence of quantum consciousness in evoked zero-spin echoes — •Christian Kerskens[1] and David Lopez[1,2] — [1]Trinity College Institute Neuroscience, Trinity College Dublin — [2]Faculty of Psychology, University of Warsaw, Warsaw, Poland

That consciousness could have its' basis in quantum computing has been speculated for many years. Unfortunately, unitary quantum gates, the main ingredient of quantum computing, are not compatible with irreversible biological systems which are effectively non-unitary. This is in line with experiments which so far haven't connected consciousness to quantum computing. Here, we used magnetic resonance imaging (MRI) to study long-range quantum coherence in the human brain. We were surprised to find that the cardiac pressure pulse evoked zero-spin echoes (ZSEs) in brain parenchyma. The ZSE signals, which are thought to be generated by long-range intermolecular zero-quantum coherence (iZQC), were much higher than expected. In contrast, single quantum coherence (SQC) imaging, which is also indirectly related to iZQC, was not affected. These findings suggest that we observed a non-classical effect originated from a small subdomain of the parenchyma. This evoked quantum effect was directly connected to consciousness as only sporadic ZSE signals were detected during sleep while a loss of the evoked quantum effect would probably always result in unconsciousness because the cardiac pressure pulse is necessary for consciousness. Our findings are unexpected but in line with recent biological research.

BP 12.54 Tue 14:00 Poster B2

Topological reinforcement as a principle of modularity emergence in brain networks — •Fabrizio Damicelli[1], Claus-Christian Hilgetag[1,3], Marc-Thorsten Hütt[2], and Arnaud Messé[1] — [1]Institute of Computational Neuroscience, University Medical Center Hamburg-Eppendorf, Hamburg University, Germany — [2]Department of Life Science and Chemistry, Jacobs University Bremen, Germany — [3]Department of Health Sciences, Boston University, USA

The self-organization of modular structure in brain networks is mechanistically poorly understood. We propose a simple plasticity model based on a fundamental principle, the Topological Reinforcement (TR), which promotes connections between nodes with high neighborhood similarity. This mechanism systematically evolves synthetic random networks toward a modular architecture by enhancing initial weak "proto-modules". Moreover, we show that this topological selection principle can also be implemented in biological neural networks evolving in a Hebbian fashion, where what "fires together, wires together" and, under proper conditions, the results were consistent between both scenarios, i.e., TR and Hebbian rule. We propose the selective reinforcement of topological overlap as a fundamental principle guiding the emergence of modular structure in brain networks. This bridges the gap between previous pure generative and activity based models of modularity emergence in brain networks, offering a common underlying principle at the topological level.

BP 12.55 Tue 14:00 Poster B2

Taming Stochastic, Nonlinear Rate Neurons With Field The-

ory — •Jonas Stapmanns[1,2], Tobias Kühn[1], David Dahmen[1], Carsten Honerkamp[2], and Moritz Helias[1,3] — [1]Institute of Neuroscience and Medicine (INM-6), Forschungszentrum Juelich, Germany — [2]Institute for Theoretical Solid State Physics, RWTH Aachen, Germany — [3]Department of Physics, Faculty 1, RWTH Aachen, Germany

Many phenomena observed in biological neural networks can only be explained by assuming nonlinear interactions. Due to effects like synaptic failure and channel noise, neuronal dynamics is also inherently stochastic. The investigation of the interaction of both of these properties is challenging because due to the nonlinearity, correlations of higher order influence those of lower order.

To cope with this problem, the dynamics of a self-interacting stochastic rate neuron is reformulated in the language of field theory by means of the Martin, Siggia, Rose, de Dominicis and Janssen formalism. The loop-wise fluctuation expansion of the corresponding effective action then incorporates corrections to the mean dynamics and time-dependent statistics due to fluctuations in the presence of nonlinear neuronal gain. From this, we derive a deterministic non-Markovian equation of motion of the mean value which illustrates that the interaction of nonlinearity and stochasticity introduces memory into the system.

BP 12.56 Tue 14:00 Poster B2

Estimating autocorrelation times of subsampled autoregressive processes under non-stationary parameters — •Jorge de Heuvel, Jens Wilting, Viola Priesemann, Johannes Zierenberg, and Paul Spitzner — Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen, Deutschland

Collective cortical dynamics are often approximated by linear autoregressive models. Only recent methodological advances enable us to infer network autocorrelation times even under subsampling, assuming stationarity. However, cortical dynamics are likely subject to non-stationary input, which can lead to a severe overestimation of the network autocorrelation time. Here, we present a novel approach for the subsampling-invariant estimation of network autocorrelation even under non-stationary input. A trial based experimental setup is applied, where the external input is time-dependent but similar over each trial. Our estimator is verified on both numerical data and experimental recordings.

BP 12.57 Tue 14:00 Poster B2

Synchronization of cilia — •Benjamin M. Friedrich — cfaed, TU Dresden, Dresden, Germany

I will present a historical overview on synchronization of cilia and flagella, featuring key experiments in the field. Two mechanisms, (i) synchronization by direct hydrodynamic interactions and by (ii) mechanical self-stabilization in self-propelled swimmers will be addressed. I will review the minimal model of rotating spheres of Vilfan and Jülicher, which has been influential in the field. This model highlights how synchronization depends on broken parity-time symmetry. Recently, this theoretical model has been realized experimentally using colloidal particles driven by optical tweezers.

BP 12.58 Tue 14:00 Poster B2

Reconstitution of cilia-like beating — •Veikko F. Geyer — Technische Universität Dresden, B CUBE - Center for Molecular Bioengineering, Dresden, Germany

I will present a historical overview on the study and reconstitution of bending oscillations in filament bundles and cilia-like beating, featuring key experiments and major challenges in the field.

To study ciliary beating, two approaches have been used: (i) the top-down (study of the dynamics of ciliary fragments) and (ii) the bottom-up (combining ciliary components - filaments, motors,cross-linkers) approach.

I will review the known requirements for bending oscillations in a minimal motor-filament system and discuss how those requirements have been tested experimentally by different approaches and by different groups.

BP 12.59 Tue 14:00 Poster B2

Interaction of superparamagnetic iron oxide nanoparticles and transferrin — •Ulrike Martens[1], Ali Abou-Hassan[2], and Mihaela Delcea[1] — [1]Institute for Biochemistry/ZIK HIKE, Greifswald University, Germany — [2]Laboratoire PHENIX, Sorbonne Université, Paris, France

Recent research demonstrated that nanoparticles (NPs) can enhance or suppress the immune response by binding to proteins of the blood stream. One important blood protein is transferrin which is composed of two distinct domains each containing an iron binding site. Its main role is to deliver iron to all biological tissues. By applying various biophysical techniques we investigated the interactions of superparamagnetic iron oxide nanoparticles (SPIONs) including maghemite γ-Fe_2O_3 and magnetite Fe_3O_4 with different coatings (e.g. citrate, chitosan) with transferrin. SPIONs present many advantages related to their magnetic properties, including magnetic manipulation and separation. The tools used allowed the characterization of the functionalized NP surface and the identification of structural changes of the proteins (e.g. circular dichroism spectroscopy) upon interaction with nanoparticles. In particular, dynamic light scattering measurements as well as SDS-PAGE revealed the corona formation of our model protein transferrin on the NPs, while transferrin also acted as a stabilizing agent of the colloidal suspension as verified by zeta potential measurements. In addition, the influence of the NPs on the iron binding site of transferrin in comparison to the binding to iron-free transferrin (apotransferrin) was studied via UV-Vis spectroscopy and urea PAGE.

BP 12.60 Tue 14:00 Poster B2

Principal component analysis of constrained molecular dynamics simulations — •Matthias Post, Steffen Wolf, and Gerhard Stock — Biomolecular Dynamics, Institute of Physics, Albert Ludwigs University, Freiburg, Germany

Describing the structure and dynamics of biomolecular systems via conventional unbiased molecular dynamics simulations becomes impractical, if their states are separated by high energy barriers such that conformational changes of interest to not occur in reasonable computer time. One way to overcome this problem is to pull these systems with a constant force ensuring this conformational change. While data from constrained molecular dynamics simulations do not allow for a direct estimate of the free energy from their biased probability distribution, they can be readily reweighed via Jarzynski's identity to do so. Using this approach, we apply principal component analysis on these non-equilibrium data to construct a multi-dimensional free energy landscape able to distinguish between different reaction pathways. We compare unbiased and constrained data on deca-alanine, a well-established model problem of testing biased simulations and understanding fundamental mechanisms of protein folding.

BP 12.61 Tue 14:00 Poster B2

Identification of metastable conformational states of protein dynamics — •Daniel Nagel — Biomolecular Dynamics, Institute of Physics, Albert Ludwigs University, 79104 Freiburg, Germany

Well-defined microstates, describing metastable conformational states, are the key to generate a Markov state model of protein dynamics. Taking a dimensional-reduced trajectory, these can be found by a recently proposed density-based geometrical clustering algorithm by Sittel et al., which is self-consistent in its data-based input parameters and computationally efficient. While for simple geometrical clustering methods such as k-means it was necessary to rely on a large number of microstates to properly discretize barriers and subsequently use dynamic clustering techniques to reduce the large set of microstates to a manageable number of macrostates, density-based clustering by design cuts at the energy barriers producing directly a reasonable number of microstates. Even though the latter algorithm performs much better, projection artifacts in the transition regions artificially shorten the estimated lifetimes. A simple corrective is to use dynamical boundary corrections, namely dynamical coring which requires staying for a minimum time after a state transition in the new state for the transition to be counted. This method increases metastability and Markovianity significantly by identifying misclassified interstate fluctuations as intrastate fluctuations. To illustrate the simplicity and performance of the workflow, two well-established biomolecular systems (alanine dipeptide and villin headpiece) are examined.

BP 12.62 Tue 14:00 Poster B2

Optimizing PDMS Stamp Transfer Preparation of MoS_2-Nanopores for DNA Translocation Experiments with Optical Tweezers — •Julian Cremer[1], Inga Ennen[2], Sebastian Knust[1], Martina Viefhues[1], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanoscience, Bielefeld University, Germany — [2]Thin Films & Physics of Nanostructures, Bielefeld University, Germany

To better understand the translocation of biological molecules through nanopores we measure the forces acting on λ-DNA during a translo-

cation through solid-state nanopores with Optical Tweezers. For high sensitivity, we milled pores smaller than 10 nm with a transmission electron microscope (TEM) in freestanding MoS_2-monolayers with a thickness of 0.67 nm.

The defect-free MoS_2-monolayers are produced by a simple but efficient viscoelastic PDMS stamp transfer technique. Since the contact with PDMS causes minute but nevertheless relevant residues on the MoS_2 we investigated the removal of these residues particularly with regard to enable nanopore experiments. Thus, we performed high resolution TEM as well as atomic force microscopy (AFM) measurements to optimize the preparation. These include pretreatments of the PDMS e. g. UV-ozone cleaning as well as variations of the PDMS stamp thicknesses and steps after the transfer like annealing or plasma treatment.

In this work we present first results towards the preparation of freestanding residue-free MoS_2-nanopores and controlled translocation experiments.

BP 12.63 Tue 14:00 Poster B2

Protein interactions studied by single molecule force spectroscopy — •Annelie Klein[1,2], Ina Buchholz[1,2], Felix Nagel[1,2], and Mihaela Delcea[1,2] — [1]Biochemistry Institute, University of Greifswald, Felix-Hausdorff-Str. 4, 17487 Greifswald, Germany — [2]ZIK HIKE, University of Greifswald, Fleischmannstr. 42, 17489 Greifswald, Germany

Endogenous proteins (i.e. self-proteins) which undergo mutations or post-translational modifications under stress conditions (e.g. pH, salt, drugs) may suffer alterations of their function often leading to autoimmune diseases. For example, the soluble non-blood protein serine protease inhibitor Kazal type 1 (SPINK1) is associated with chronic pancreatitis. The mechanism of this disease is not well understood. Here, we investigate the interaction of wild type and mutant SPINK1 with trypsin by single molecule force spectroscopy (SMFS). SPINK1 is a trypsin inhibitor in the pancreas and its mutation N34S is associated with hereditary chronic pancreatitis. In a biological trypsin inhibition assay we showed that wild type and mutant have the same inhibitory activity. However, the sensitive SMFS technique revealed a clear difference in the binding of trypsin to wild type SPINK1 (˜94 pN) and to mutated N34S (˜45 pN), respectively. Our results indicate that N34S mutation affects SPINK1 inhibitory efficiency, which could lead to chronic pancreatitis.

BP 12.64 Tue 14:00 Poster B2

Characterization of Magnetic Field Generating Tips for Spatio-Temporally Controlled Manipulation of Magnetic Nanoparticles — •Mohammad R. Safari and Cornelia Monzel — Experimental Medical Physics, Heinrich-Heine University Düsseldorf, 40225 Düsseldorf, Germany

The manipulation of magnetic nanoparticles is a powerful approach to probe and actuate biological functions in living systems and bears high potential for future medical applications. In comparison to complementary approaches involving chemical and electrical field manipulation, magnetic fields bear the advantage of applying a remote and spatio-temporally defined stimulus, which is nondestructive in the context of a biological sample. In view of realizing the manipulation of single cell functions, we here utilize micrometer magnetic tips to take advantage of their high spatial flexibility, variability in shape, and hence the possibility to dynamically tune magnetic fields and forces. We combine experimental magnetic nanoparticle tracking with in vitro attraction assays and finite element modeling, in order to obtain a comprehensive understanding of the magnetic forces applied (˜ 10fN). Via systematic characterization of a library of different magnetic tips, we assess their suitability for nanoparticle manipulation approaches on submicrometer scales.

BP 12.65 Tue 14:00 Poster B2

AFM-based Single-Molecule Force Spectroscopy on the Streptavidin:Biotin Interaction — •Steffen M. Sedlak[1], Leonard C. Schendel[1], Katherine R. Erlich[1], Achim Löf[1], Rafael C. Bernardi[2], Magnus S. Bauer[1], Carleen Kluger[1], and Hermann E. Gaub[1] — [1]Department of Physics and Center for NanoScience, LMU Munich, Germany — [2]University of Illinois at Urbana-Champaign, Urbana, IL , USA

The high-affinity interaction of the small molecule biotin with the tetrameric protein streptavidin (SA) is a widely applied tool for detection, labeling and immobilization of molecules. We study single biotin:SA interactions under force using AFM-based single-molecule force-spectroscopy (SMFS) and steered Molecular Dynamics (sMD) simulations. Probing monovalent SA in various specific tethering geometries, we investigated how the mechanical stability of the biotin:SA interaction depends on the force loading geometry and revealed the underlying molecular mechanism. We made use of the different unbinding forces to realize a protein-based bottom-up nanoscale assembly of single fluorescent molecules by single-molecule cut-and-paste; a unique approach that enables spatially controlled arrangements of diverse molecules into a single ensemble. We also studied SA of different valencies and distinguished unbinding forces of biotin from different SA subunits in AFM-based SMFS. sMD allowed to understand the force-propagation pathways through the SA tetramer. Identifying a long-lived tethering geometry, we can reliably measure single molecules at comparably high constant forces for many hours in magnetic tweezers.

BP 12.66 Tue 14:00 Poster B2

Narrow escape: How long does it take for a camel to go through the eye of a needle? — •Elisabeth Meiser[1], Susanne Fenz[1], Reza Mohammadi[2], and Nicolas Vogel[2] — [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 (NEP) 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. The mean first passage time of the particle can be calculated analytically for diffusion in two and three dimensions in several geometries. We aim to systematically test the solution of the NEP in two dimensions with micro-patterned planar model membranes. Micro-patterned membranes were produced by a lithography-based method to achieve patterned glass followed by vesicle fusion. Two lithography methods were tested: UV- and colloid-lithography. UV-lithography relies on a UV-cross-linkable resist to produce a pattern of hydrophilic and hydrophobic regions on the substrate by selective illumination. Colloid-lithography is alternative approach to prepare particular small membrane patches (d=1um). It exploits the shadowing effect of polymeric microspheres whilst coating the substrate with a thin layer of gold to achieve a structured gold film. After appropriate functionalization of the gold, membranes will only form on the bare glass. We will present our first results on membrane patterning and diffusion in solid supported lipid bilayers on the single-molecule level.

BP 12.67 Tue 14:00 Poster B2

Microfluidic rock-like reactors to study the synthesis of the first nucleotides — •Thomas Matreux[1], Maximilian Weingart[1], Victor Sojo[1], David Lappe[1], Saidul Islam[2], Matt Powner[2], Christof B. Mast[1], and Dieter Braun[1] — [1]Systems Biophysics, Ludwig-Maximilian University of Munich (LMU) — [2]Department of Chemistry, University College London (UCL)

The emergence of the first biomolecules is one of the most intriguing questions in the origins of life field. While synthesis pathways of nucleotides, amino acids and lipids were widely addressed in the last decade [1], their feasibility under geologically plausible boundary conditions is still unclear. How do laboratory experiments transfer to a realistic, prebiotic scenario with catalytic rock surfaces and thermal non-equilibrium boundary conditions and without clearly separated pipetting steps?

To address these questions, we have developed a microfluidic setup that allows for controlled, but prebiotically plausible sequential mixing by the presence of porous geo-material and provides an uninterrupted flow to produce activated nucleotides [1]. Microfluidic structures are made from FEP, which lets us focus on the interactions with the added synthetic rock. The reaction chambers are sandwiched between highly heat conducting sapphire plates ensuring complete thermal control including possible thermal gradients. This new experimental approach offers a variety of new reaction schemes by connecting prebiotic chemistry with geoscience and non-equilibrium physics.

[1] Sutherland Nature doi.org/10.1038/nature08013 (2009)

BP 12.68 Tue 14:00 Poster B2

Correlated Single Molecule Twist and Fluorescence Measurements on CRISPR-Cas Systems — •Pierre Aldag[1], Julene Madariaga[2], Inga Songailiene[3], Virginijus Siksnys[3], and Ralf Seidel[1] — [1]Peter Debye Institute for Soft Matter Physics, University of Leipzig — [2]Centro Nacional de Biotecnología (CSIC), Madrid — [3]Institute of Biotechnology, Vilnius University

CRISPR-Cas systems are RNA-guided ribonucleoprotein (RNP) com-

plexes with nuclease activity that provide prokaryotes with an adaptive defense mechanism against foreign nucleic acids. The RNP complex recognizes complementary target sites by base-pairing its RNA component with one of the strands of the target DNA while displacing the other one forming a so-called R-loop structure. Considering the vast potential of CRISPR-Cas systems in gene editing technology, it is crucial to fully understand the mechanism behind the targeting process by these enzymes. Here, we employed a combined magnetic tweezers and total internal reflection fluorescence microscopy setup to carry out correlated single-molecule force and fluorescence spectroscopy measurements. The magnetic tweezers allow us to probe the R-loop formation of the CRISPR system. Using fluorescently-labelled Cascade complexes we are able to additionally follow association and dissociation events prior to the actual R-loop formation. These measurements reveal information about the timescales of the target search as well as about the efficiencies of the search under varying torque conditions. This leads to a better understanding of the target recognition mechanisms by CRISR-Cas enzymes.

BP 12.69 Tue 14:00 Poster B2

Understanding the Sequence-Structure-Mechanics Relationship of Coiled Coil Dimers under Shear — Melis Goktas, Chuanfu Luo, Patricia Lopez-Garcia, Isabell Tunn, Ruby M. A. Sullan, Ana E. Bergues-Pupo, Ana Vila Verde, Reinhard Lipowsky, and •Kerstin G. Blank — Max Planck Institute of Colloids and Interfaces, Potsdam Golm Science Park, 14424 Potsdam, Germany

Coiled coils (CCs) are superhelical motifs found in many cytoskeleton and extracellular matrix proteins, suggesting that they possess mechanical function in Nature. Despite their wide abundance, surprisingly little is known about their molecular, mechanistic response to forces. With the goal of shedding light on their sequence-structure-mechanics relationship, we have characterized a series of CC heterodimers with AFM-based single molecule force spectroscopy (SMFS) and Molecular Dynamics simulations. The SMFS experiments show that CCs with a length of 3-5 heptads rupture at forces between 20-55 pN, when mechanically loaded in 'shear' geometry. Simulations show an initial rise in the force, followed by a force plateau and ultimately chain separation. During the plateau phase, the individual helixes uncoil and recoil, with recoiling being more frequent at lower pulling speeds. Modifications that stabilize the individual helices are thus expected to increase the mechanical stability of CCs. These results aid the design of CC-based molecular force sensors and material building blocks.

BP 12.70 Tue 14:00 Poster B2

Simultaneous Force and Fluorescence Spectroscopy inside Zero-Mode Waveguides — •Leonard C. Schendel, Steffen M. Sedlak, Magnus S. Bauer, and Hermann E. Gaub — Department of Physics and Center for NanoScience, LMU Munich, Germany

In the past years, Zero-Mode Waveguides (ZMWs) have emerged to a powerful application in modern life science. They provide subdiffraction detection volumes in single-molecule fluorescence measurements and hence experimental performance at physiological concentrations of fluorescently labeled biomolecules.

Here, single-molecule force spectroscopy using an atomic force microscope and ZMWs are combined in order to investigate force-activation pathways of enzymes. For this purpose, high concentrations are dictated by experimental conditions and requirements, this being high Michaelis-Menten constants of enzymes and the limited time span of keeping the protein's binding pocket open/accessible.

The implementation of a covalent site-specific chemistry together with an optical non-invasive cantilever localization routine shows the ability to probe monovalent streptavidin in an automated fashion. We mechanically remove a bound biotin and are able to simultaneously observe reoccupation of the vacant site by fluorescently labeled biotin. In the future, this improved methodology will be applied to investigate enzymes upon possible force-activation mechanisms.

BP 12.71 Tue 14:00 Poster B2

Influence of Ligand Binding on the Mechanical Stability of a Single Protein Revealed by AFM-based Force Spectroscopy — •Philipp R. Müller, Steffen M. Sedlak, Leonard C. Schendel, Jonas C. Fischer, Magnus S. Bauer, Carleen Kluger, and Hermann E. Gaub — Department of Physics and Center for NanoScience, LMU Munich, Germany

AFM-based force spectroscopy enables a large number of measurements of individual proteins. Covalent and site-specific immobilization strategies are key for consistent and reproducible force spectroscopy data. Fingerprint domains that exhibit a characteristic unfolding pattern serve as internal force reference and to reliably identify single-molecule interactions.

Streptavidin (SA) is a tetrameric protein that is frequently used in force spectroscopy experiments and binds biotin, as well as desthiobiotin and Strep-tag II with high affinity.

Here, we investigate the effect of ligand binding on the mechanical stability of a single SA subunit. In a tetrameric SA, we tether one of the four SA subunits by its C- and N-terminus and unfold it in the presence and absence of different ligands. Furthermore, combining functional and non-functional SA subunits, which cannot bind any ligands, we are able to create SA of different valencies in a controlled way. Using these SA variants, we analyze the influence of different ligands, binding to the tethered or the neighboring subunit, on the mechanical stability of the molecule. Unfolding patterns and rupture forces depend on the type of ligand employed.

BP 12.72 Tue 14:00 Poster B2

Comparing the Mechanical Strengths of the Interaction of Biotin with Avidin-like proteins by AFM-based Single Molecule Force Spectroscopy — •Jonas C. Fischer, Steffen M. Sedlak, Leonard C. Schendel, Philipp R. Müller, Magnus S. Bauer, Carleen Kluger, and Hermann E. Gaub — Department of Physics and Center for NanoScience, LMU Munich, Germany

Avidin-like proteins are a wildly applied tool in nano- and biotechnology for immobilization, labeling and detection of molecules.

Here, we investigate the interaction of the tetrameric proteins streptavidin, traptavidin and streptactin with the small molecule biotin by AFM-based Single-Molecule Force Spectroscopy. Site-specific and covalent immobilization of different receptor molecules on the same surface enables stable and parallel long-term measurements of unbinding events. By the use of fingerprint domains providing characteristic unfolding patterns true single-molecule interactions are identified.

Both traptavidin and streptactin differ from wild-type streptavidin from *Streptomyces avidinii* only by three amino acids. The unbinding force of biotin from streptavidin is strongly dependent on tethering geometry. The rupture forces for the C-terminal anchoring is about two times higher as for N-terminal attachment. While traptavidin behaves in a similar manner, the rupture forces for streptactin differ: We observe a loading rate dependent transition from a low force binding to a high force binding state.

BP 12.73 Tue 14:00 Poster B2

A classification scheme for clustering and identification of DNA events through a nanopore — •Ángel Díaz Carral[1], Chandra Shekar Sarap[1], Ke Liu[2], Aleksandra Radenovic[2], and Maria Fyta[1] — [1]Institute for Computational Physics, Universität Stuttgart, Allmandring 3, 70569 Stuttgart, Germany — [2]Institute of Biotechnology, Ecole Polytechnique Federale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland

DNA molecules can electrophoretically be driven through a nanoscale opening in a material giving rise to measurable electronic current blockades important for DNA sensing. In this work, we propose a methodological approach to interpret nanopore events based on experimental ionic current data of DNA homopolymers through molybdenum-disulphide nanopores. Experimental ionic traces are used to train an unsupervised Machine Learning model for identifying molecular events related to different conformations of DNA molecules threading the nanopore. We have tested different features for the classification of the translocation events, and conclude on the efficiency of using the current blockade height for classification. This allows us to indeed distinguish folded over unfolded DNA events through the pore. We discuss the impact of such a scheme in sensing the identity of DNA with a nanopore.

BP 12.74 Tue 14:00 Poster B2

Topological insulator and semiconductor beads as micro-oscillators induced by laser beam — •Warlley H. Campos[1,2], Tiago A. Moura[1], Jakson M. Fonseca[1], Joaquim B. S. Mendes[1], Márcio S. Rocha[1], and Winder A. Moura-Melo[1] — [1]Departamento de Física, Universidade Federal de Viçosa, Viçosa 36570-900, Brazil — [2]Institut für Physik, Johannes Gutenberg-Universität Mainz, Mainz 55128, Germany

The optical tweezers (OT) is a powerful technique used to trap microscopic objects with light. It became an essential tool for high accuracy

measurements in areas such as biological and soft matter physics. We perform the first experimental studies upon the optical trapping of topological insulator (TI) [Bi_2Te_3 and Bi_2Se_3] and Germanium (Ge) microparticles under a Gaussian laser beam OT. For such materials gradient and radiometric forces compete, generating oscillatory dynamics perpendicular to the optical axis. We describe the oscillations with an effective model that captures the forces acting on the particle, amplitude of oscillation, periodicity and their dependence on particle size. Ge beads oscillate in a preferential direction determined by the polarization of the laser beam, this was not observed for neither of the TI materials. Our results open an avenue for dynamical measurements with unprecedented simplicity and purely optical control. Among the possible applications for the near future, stand out the optical rheology of soft matter interfaces and biological membranes, as well as dynamical force measurements in macromolecules and biopolymers.

BP 12.75 Tue 14:00 Poster B2

Planar Antennas for Biosensing and Diagnostics — •Navid Soltani[1,2], Nemanja Markesevic[1,2], Avijit Kumar Das[2,3], Sergey Druzhinin[2,4], Heiko Ihmels[2,3], Holger Schönherr[2,4], and Mario Agio[1,2] — [1]Laboratory of Nano-Optics — [2]Research Center of Micro and Nanochemistry and Engineering (Cμ) — [3]Organic Chemistry II — [4]Laboratory of Physical Chemistry I, University of Siegen, Siegen, Germany

Molecular fluorescence plays an important role in biosensing and diagnostics. However, dye molecules in conventional biochips exhibit radiation patterns such that even with high numerical aperture (NA) objectives a large fraction of the emitted photons is lost. Here, we investigate the implementation of a biosensor based on planar antennas [1], which change the radiation pattern of a dipole emitter and increase the photon collection efficiency by orders of magnitude without requiring high NA objectives. We focus on specific biological relevant molecules [2], interfaces [3] and bioassays to investigate the physical limit of detection down to the single-molecule level and to study the interaction of organic dyes and DNA molecules in nanostructured environments.

[1] S. Checcucci, P. Lombardi, S. Rizvi, F. Sgrignuoli, N. Gruhler, F. B. C. Dieleman, F. S Cataliotti, W.H. P. Pernice, M. Agio and C. Toninelli, Light: Science & Applications 6, 16245 (2017) [2] P. M. Pithan, D. Decker, S. I. Druzhinin, H. Ihmels, H. Schönherr, Y. Voß, RSC Advances, 7, 10660 (2017). [3] N. Hain, D. Wesner, S. I. Druzhinin, H. Schönherr, Langmuir, 32, 11155 (2016).

BP 12.76 Tue 14:00 Poster B2

Competition between mutant and wild-type E. coli cells during carbon starvation — •Zara Gough[1], Felix Fleschhut[1], Elena Biselli[1], Hamid Seyed-Allaei[1], Severin Schink[1,2], and Ulrich Gerland[1] — [1]Technical University of Munich, Physics Department, James-Franck-Str 1, 85748 Garching, Germany — [2]Harvard Medical School, Department of Systems Biology, 200 Longwood Ave, Boston 02115 MA, USA

Surviving nutrient limitation is an important part of the microbial life cycle. Recently, it was shown that survival of carbon starved E. coli is quantitatively characterized by two parameters that set the exponential death rate of the population: maintenance rate and recycling yield. Following this exponential death, E. coli enter a long-term phase exhibiting cycles of death and regrowth. Mutant subpopulations have been observed to thrive during regrowth cycles, eventually overtaking wild type cells. We investigate how maintenance rate and recycling yield change in mutants harvested during this phase and how these cells compete with wild type cells in order to dominate the entire population, despite exhibiting traits of poorer fitness, such as slower growth rate and faster death rate, compared to wild type cells grown in identical conditions. Our work will extend our quantitative understanding of bacterial physiology in environments where, due to lack of nutrients, population competition is crucial for survival.

BP 12.77 Tue 14:00 Poster B2

A mathematical model for an inducible CRISPR-dCas9 based switch in yeast — Anja Hofmann[2] and •Johannes Falk[1] — [1]Technische Universität Darmstadt, Institut für Festkörperphysik, Germany — [2]Technische Universität Darmstadt, Clemens-Schöpf-Institut, Germany

The robust and precise on and off switching of one or more genes of interest, followed by expression or repression is essential for many biological circuits as well as for industrial applications. However, many regulated systems published to date influence the viability of the host cell, show high basal expression or enable only the overexpression of the target gene without the possibility of fine regulation. By combining the advantages of well-established systems, namely the scaffold RNA CRISPR/dCas9 platform, and LexA-ER-AD as heterologous transcription factor it is possible to overcome these limitations. On our poster, we compare experimental data with a minimal model that only captures the most basic processes but is still capable of covering all important results of the experiment. Our research hence helps to gain a better understanding of the underlying principles and the functioning of the inducible CRISPR/dCas9 system.

BP 12.78 Tue 14:00 Poster B2

How to generate a long-range signalling gradient based on short-range molecular interactions? — •Johanna Dickmann[1,2], Steffen Werner[1], 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

Animal bodies show a fascinating degree of organisation as testified by their complex body plans. In the context of embryonic development, signalling gradients (spatially graded profiles of signalling intensity) emerged as key concepts of body plan patterning. They have been explained by a substance diffusing away from a local source and being degraded. In case of regeneration, new tissue has to be patterned on adult length scales. It is debatable if a diffusion-based mechanism is fast enough to explain gradient formation on adult length scales. Flatworms are masters of regeneration, re-growing a perfectly patterned body from arbitrary amputation fragments at an adult length of up to 2 cm. Their main body axis - as for most animals - is patterned by a Wnt signalling gradient. In addition to a local Wnt source, they show spatially graded Wnt expression. Based on these observations, we hypothesise that additional Wnt sources are generated in response to signalling, organised by a local, signalling-independent source. We formalise the suggested mechanism in a physical model using differential equations, analyse the model both analytically and numerically, and test it experimentally by interfering with the gradient. This way, we hope to unravel a novel mechanism for long-range gradient formation.

BP 12.79 Tue 14:00 Poster B2

Understanding the lifespan of worm dauer by modeling its metabolic pathway — •Xingyu Zhang[1], Damla Kaptan[2], Sider Penkov[2], Vamshidar Gade[2], Bharath Raghuraman[2], Woberta Galli[3], Edmund Koch[3], Andrej Shevchenko[2], Teymuras Kurzchalia[2], and Vasily Zaburdaev[1] — [1]FAU Erlangen-Nürnberg,Germany — [2]MPI-CBG,Germany — [3]TU Dresden, Germany

Understanding a lifespan of an organism, which is governed by multiple mechanisms, is an intrinsically complex problem. Here, we focus on *C. elegans* dauer larvae, the stage of an organism development where the mechanisms of survival are dominant. Recently, we discovered that dauer of *C. elegans* can intake and metabolize external ethanol as a carbon source, somewhat contradicting the conventional picture of dauer worms as almost an isolated system. Interestingly, the lifespan of dauer increases when small amounts of ethanol are supplied, but starts to decrease when ethanol concentration becomes higher. To understand the mechanism of how the lifespan of dauer is related to the supplied ethanol, we developed a theoretical model based on the known metabolic pathway of *C. elegans* dauer accounting for the ethanol utilization. The model considers the lack of energy resources and the accumulation of toxic compounds from the metabolic activity as two factors that can potentially limit the lifespan of dauer. Results of the model show a qualitative agreement of the lifespan when compared to experimental data including dauers with various mutations in the metabolic pathway.

BP 12.80 Tue 14:00 Poster B2

Load distribution among the main structures of a passively flexed lumbar spine — Falk Mörl[1], Syn Schmitt[2], •Julia Maria Riede[2], and Michael Günther[2] — [1]Biomechanics & Ergonomics, FSA mbH Erfurt, Germany — [2]Biomechanics and Biorobotics, SimTech, Universität Stuttgart, 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 their connecting joints, ligaments and intervertebral discs. Currently there exists no measurement method to capture the function of all spinal structures at the same time. Therefore, computer simulations are the method

of choice to overcome the need of in vivo measurements. Still, the model with its initial conditions has to reproduce the biophysics of the human spine.

To get a good prediction for the load distribution of spinal structures we therefore combined experimental with simulation methods. On the simulation side we have a valid forward dynamics multibody model of the human spine. Hence we obtain valid simulation results that can subsequently be compared to the experimental results. On the experimental side stands a precise and objective measurement of human lumbar spine flexion torque. Both the experiment and the simulation were laid-out for a passive spine, i.e. no muscle activation, in the lumbar region. This allows for a detailed investigation of load distribution ensuring reasonable basic conditions for a passive human spine.

BP 13: Active matter I (joint session BP/CPP/DY)

Time: Wednesday 9:30–13:00 Location: H4

BP 13.1 Wed 9:30 H4

Self-assembled active systems - from individuals to a collective behaviour — •Aitor Martin-Gomez, Gerhard Gompper, and Roland G. Winkler — Forschungszentrum Juelich (ICS-2), Juelich, Germany

Active matter is comprised of agents which either convert internal energy or exploit energy from the environment to generate directed motion. Its associated out-of-equilibrium character is the origin of a number of fascinating phenomena. In particular, active systems with many internal degrees of freedom like filamentous, polymer-like structures are involved in various biological processes and exhibit novel conformational and dynamical properties. Moreover, the study of collective behavior emerging from the non-linear contributions of many individuals is an ongoing, open question. In conclusion, to shed light onto the effect of such active systems, or their passive counterparts embedded in an active environment, we perform analytical calculations combined to advanced computer simulations.

BP 13.2 Wed 9:45 H4

Light-dependent microbial motility induces pattern formation in confinement — •Alexandros Fragkopoulos[1], Johannes Frey[1], Flora-Maud Le Menn[1], Jeremy Vachier[1], Michael Wilczek[1], Marco Mazza[1,2], and Oliver Bäumchen[1] — [1]Max Planck Institute for Dynamics and Self-Organization, D-37077 Göttingen, Germany — [2]Loughborough University, Loughborough LE11 3TU, United Kingdom

A collection of active swimmers can undergo complex dynamics due to hydrodynamic and steric interactions. For sufficiently concentrated suspensions, it is possible to form large-scale concentration patterns, where the active suspension separates into regions of high and low particle concentrations. Here we present that a collection of *Chlamydomonas reinhardtii* cells, a unicellular soil-dwelling microalgae and a model organism of puller-type microswimmers, form patterns of high and low cell density regions in confinement and under specific light conditions. We find that the motility of the cells differs significantly for different light intensities and cell densities, which regulate the pattern formation in such active suspensions. In addition, we observe that the emerged pattern follows the shape of the confinement that encloses the motile cells, which indicates that the boundaries enclosing the motile cells play a crucial role for pattern formation. Finally, by performing active Brownian dynamics simulations of active particles with the observed motility characteristics, we show that we can reproduce the experimentally observed patterns.

BP 13.3 Wed 10:00 H4

Active Matter Invasion into Capillaries — •Felix Kempf[1], Romain Mueller[2], Erwin Frey[1], Juila Yeomans[2], and Amin Doostmohammadi[2] — [1]Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Department of Physics, Ludwig-Maximilians-Universität München - Theresienstr. 37, D-80333 München, Germany — [2]The Rudolf Peierls Centre for Theoretical Physics - Clarendon Laboratory, Parks Road, Oxford, OX1 3PU, UK

Biological active materials such as bacterial biofilms and eukaryotic cells thrive in confined microspaces. Here, we numerically show that combining growth dynamics with their intrinsic activity active material can use confinement as a mechanical guidance to achieve distinct modes of collective invasion. We assess the dynamics of the growing interface and classify these collective modes of invasion based on the activity of the active substance. While at small and moderate activities the active material grows as a coherent unit, we find blobs of active materials collectively detaching from the cohort above an activity threshold in a process reminiscent of the intravasation in cancer cells. We further characterise the mechanical mechanisms of transition between different modes of invasion.

BP 13.4 Wed 10:15 H4

Collective Responses of Magnetic Swimmers in a Poiseuille Flow — •Fanlong Meng[1,2], Daiki Matsunaga[2], 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

Magnetotactic bacteria can be focused at the radial centre of a microfluidic channel under an external magnetic field, and found to form clusters if the external magnetic field is strong or the flow speed is large [1]. However, the underlying mechanism was missing. We show that the magnetic microswimmers (not only for magnetotactic bacteria, but also applicable to synthetic magnetic microswimmers) can form interesting large-scale clusters when the magnetic attractive interaction dominates thermal fluctuations. By applying analytic techniques and conducting Brownian dynamics simulation, we provide the critical conditions for clustering of magnetic microswimmers, which matches well with the experiment. Hydrodynamic interactions between the microswimmers are also incorporated as a generalisation. Understanding the physics of magnetic active matter will help advance the cause of studying matter out of equilibrium, and provides new insight for technological applications of synthetic magnetic microrobots (for drug delivery, solution stirring, etc.) with desired collective properties. References: [1] N. Waisbord, C. T. Lefèvre, L. Bocquet, C. Ybert, C. Cottin-Bizonne, Phys. Rev. Fluids, (2016) 1, 053203 [2] F. Meng, D. Matsunaga, R. Golestanian, Phys. Rev. Lett., (2018) 120, 188101

BP 13.5 Wed 10:30 H4

Hydrodynamic simulations of flagellated bacteria in polymer solutions and polymer networks — •Andreas Zöttl and Julia M Yeomans — University of Oxford, UK

Many cells in the human body have to move through dense complex fluids such as various cells in the extracellular matrix or bacteria in mucus. While the motion of swimming bacteria in simple Newtonian fluids can be well quantified using continuum low Reynolds number hydrodynamics, the presence of supramolecular elements such as biopolymers leads to a much more complex behavior. Although the presence of polymers generally lowers particle mobility, surprisingly, several experiments have shown that bacterial speeds increase in polymeric fluids, but there is no clear understanding why.

We perform extensive coarse-grained MPCD simulations of a bacterium swimming in explicitly modeled solutions of supramolecular model polymers of different lengths, stiffness and densities. We observe an increase of up to 60% in swimming speed with polymer density and show that this is a consequence of a non-uniform distribution of polymers in the vicinity of the bacterium leading to an effective slip. However, this alone cannot explain the large speed-up, but coupling to the chirality of the bacterial flagellum is essential. Finally we present results for swimming in crosslinked polymer networks where hydrodynamics is screened and speed enhancement is also observed.

BP 13.6 Wed 10:45 H4

Memory-induced persistent motion — •Bernhard Georg Mitterwallner, Laura Lavacchi, and Roland Netz — Institut für theoretisch Physik, Frei Universität Berlin, Berlin, Germany

We investigate the mean-square displacement (MSD) for random motion governed by the generalized Langevin equation for different two-

scale memory-kernel models: In the first model, the memory kernel consists of a delta peak and a single exponential and in the second model of the sum of two exponentials. In particular, we investigate the scenario where the long-time exponential kernel contribution is negative. The competition between positive and negative friction contributions produces an enhanced transient ballistic regime in the MSD, which is relevant for biological motility and active matter systems.

15 minutes break.

Invited Talk BP 13.7 Wed 11:15 H4

Non-equilibrium dynamics in biological matter — •Christoph F Schmidt — Georg-August-Universität, Fakultät für Physik, Drittes Physikalisches Institut - Biophysik, Friedrich-Hund-Platz 1, 37077 Göttingen — Duke University, Department of Physics, 2316 French Family Science Center, 124 Science Drive, Durham, NC 27708, USA

Thermodynamic non-equilibrium is a defining feature of living systems on all levels of organization. Cells and tissues are built of active matter, dynamic materials with built-in force generators. Such materials self-organize in biological systems into well-ordered dynamic steady states, sustained by the dissipation of metabolic energy. The materials show striking collective phenomena on a mesoscopic scale. We used light microscopy to characterize the complex mechanical properties of and the motion and stress patterns in biological active matter, in particular the actin cortex, both in reconstituted model systems and in cells. I will introduce a method to detect and quantitate thermodynamic non-equilibrium in the dynamics of primary cilia of kidney epithelial cells using the principle of detailed balance.

BP 13.8 Wed 11:45 H4

Enhanced rotational diffusion of squirmers in viscoelastic fluids — •Kai Qi[1], Elmar Westphal[2], Gerhard Gompper[1], and Roland Winkler[1] — [1]Theoretical Soft Matter and Biophysics, Institute for Advanced Simulation and Institute of Complex Systems, Forschungszentrum Jülich, D-52425 Jülich, Germany — [2]Peter Grünberg Institute and Jülich Centre for Neutron Science, Forschungszentrum Jülich, D-52425 Jülich, Germany

Squirmers are generic models for biological microswimmers and synthetic self-propelled particles. Fluid-mediated interactions are essential for their swimming behavior, which can be strongly affected by the fluid viscoelasticity. Here, we perform mesoscale hydrodynamic simulations via the multiparticle collision dynamics (MPC) method for a spherical squirmer in a viscoelastic fluid, which is composed of MPC fluid particles and polymers. Polymers are either of phantom nature or self-avoiding. The concentration of monomers on the squirmer surface is enhanced by introducing a short-range attraction between the squirmer and polymers. This leads to a decrease of the rotational diffusion for a passive colloid in the presence of polymers. Self-propulsion reduces the monomer concentration on the surface and the squirmer's rotational diffusion is enhanced considerably, up to a factor 20 for phantom polymers. The actual change of the rotational diffusion D_r depends on the polymer length. An increasing polymer length reduces D_r^0 of the passive colloid, but D_r of the squirmer is enhanced. Both effects contribute to the obtained substantial increase of the ratio D_r/D_r^0.

BP 13.9 Wed 12:00 H4

Modelling coordinated motion in simplest multicellular animals — •Stephan Meschede[1] and Pawel Romanczuk[2] — [1]Department of Physics, Humboldt Universität zu Berlin — [2]Institute for Theoretical Biology, Department of Biology, Humboldt Universität zu Berlin

Placozoa, Trichoplax adhaerens, are structurally simplest known multicellular animals. Their bodies are flat and irregular, up to few milimeters in diameter and $10-15\mu m$ thick [1]. They consists of three layers, an upper and a lower epithelium enclosing a fiber cell layer. The Trichoplax body plan is completely decentralized without any hierarchical structure or a central nervous system. However, they are capable of amoeba-like, coordinated active motion on substrates through ciliary locomotion. We show that individual Trichoplax motion behavior can be modeled as a two-dimensional 'sheet' of active particles coupled through elastic forces, building upon previous models of cellular migration model proposed by Szabo et al [2]. We discuss the emergence of coordinated motion and the role of animal size and elastic coupling strength for the stochastic motility. Our aim is to understand how the self-organized active sheet dynamics shapes and constrains the motion behavior of these simple animals and their ability to navigate the environment.

[1]: Miller, D. J., & Ball, E. E. (2005). Animal Evolution: The Enigmatic Phylum Placozoa Revisited. Current Biology, 15(1), 26-28.

[2]: Szabó, B. et al.(2006). Phase transition in the collective migration of tissue cells: Experiment and model. Phys. Rev. E, 74(6), 1-5.

BP 13.10 Wed 12:15 H4

Phase space geometry of reaction–diffusion systems — •Fridtjof Brauns, Jacob Halatek, and Erwin Frey — Arnold Sommerfeld Center for Theoret- ical Physics, Ludwig-Maximilians-Universität München, Germany

Self-organized pattern formation — typically studied in terms of spatially extended dynamical systems — is as ubiquitous in nature as it is difficult to deal with conceptually and mathematically. We build on the phase space geometric methods of Nonlinear Dynamics, using geometric structures like nullclines and fixed points, to develop a comprehensive theory for two-component mass-conserving reaction–diffusion systems — a paradigmatic model class for pattern formation, e.g. intracellular polarization. A dissection of space into (notional) compartments enables us to characterize the spatio-temporal dynamics based on the ODE phase space of local reactions. Diffusive coupling leads to mass redistribution between the compartments which, in turn, changes the local phase space properties.

We show that all aspects of pattern formation, from linear instability and excitability to the bifurcations of stationary patterns, can be extracted from the geometric features of the line of chemical equilibria in phase space. Furthermore, our analysis points towards a deep connection between the far from equilibrium reaction–diffusion dynamics to phase separation of binary mixtures near equilibrium, and thus offers a new perspective on phase separation far from equilibrium.

BP 13.11 Wed 12:30 H4

Diffusive dynamics of complex particles in active colloidal suspensions of motile algae — •Florian von Rüling and Alexey Eremin — Institute of Physics, Otto von Guericke Universität Magdeburg, Germany

We report experimental studies on the dynamics of complex passive particles in the presence of motile algae Chlamydomonas reinhardtii in thin capillaries. Employing video microscopy and particle tracking algorithm, the enhancement of the diffusion of elongated particles due to interactions with the microswimmers was explored. Depending on the number of motile algae, the translational and rotational diffusion constants of doublets of silica beads close to a solid boundary can be increased by several orders of magnitude in comparison to purely Brownian motion. At a high concentration of Chlamydomonas reinhardtii, the algae formed dense dynamic clusters at the lower capillary wall. In this state of the system, swimming and clustering algae interact with passive particles. Clustering algae can restrict both translational and rotational dynamics of the silica doublets. We explore the effect of the motion of algae in such active clusters on the dynamic of the passive silica doublets.

BP 13.12 Wed 12:45 H4

Self-propelled Dipolar Nanocubes — •Martin Kaiser[1], Sofia Kantorovich[1,2], Yeimy Martinez[3], and Annette Schmidt[3] — [1]University of Vienna, Austria — [2]Ural federal University, Russia — [3]Universität zu Köln, Germany

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" describes the ability of certain particles or units, to convert energy from their environment into motion, hence, kinetic energy.

In this study, we use active matter to create a new type of nanomotor, which is oriented by an applied magnetic field and propelled by an active particle. One of those units consists of a dipolar cube that can be directed due to its interaction with a magnetic field. A non-dipolar active particle attached to the cube, with a propulsion force directed into the cubes centre of mass, creates a field controlled swimming unit.

This scenario is investigated using molecular-dynamic simulations, setting the above described unit in an obstacle free environment while applying a constant magnetic field.

In collaboration with Dr. Schmidt from the University of Cologne, those nanomotors are also investigated experimentally.

BP 14: Cell mechanics I

Time: Wednesday 9:30–13:00 Location: H10

BP 14.1 Wed 9:30 H10

A large scan area AFM for measurements on large biological samples and on many cells — •Todor Krastev, David Grunwald, 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 biological samples. However, the scan range of typical AFMs (100 μm in xy- and 10 μm in z-direction) is limiting its use on large samples. We present a Macro-AFM with a scan range of 25 mm in xy- and 0.25 mm in z-direction. The Macro-AFM allowed us to map the elastic modulus of a cross section of a whole mouse aorta in a single scan. Furthermore, we applied image detection techniques to fluorescently stained cells to facilitate automated, autonomous measurements of many cells. We demonstrate the robustness of the method by comparing the elastic modulus of cells in a control group to a group treated with cytochalasin D. By performing measurements on over 1000 single cells per group, we achieved a remarkably low statistical p-value.

BP 14.2 Wed 9:45 H10

Repetitive failures and success in particle retraction of macrophage filopodia — •Rebecca Michiels and Alexander Rohrbach — Lab for Bio- and Nano-Photonics, University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

Macrophages take up pathogens like viruses and bacteria in a process called phagocytosis. On their surface, macrophages express abundant filopodia, thin, needle-like protrusions, which they use to catch and retract pathogens, which are later engulfed. We investigate the adaptive mechanics of filopodia and analyze the biophysical principles governing the attachment and retraction of particles. To this end, we use a Photonic Force Microscope in which we combine DIC microscopy, fluorescence microscopy, optical tweezers and interferometric particle tracking. Filopodia retractions are induced by presenting optically trapped polystyrene beads to macrophage cells. The information gained from interferometric particle tracking is used to analyze the stiffness of the bond between cell and bead, the viscosity of the surroundings, the velocity of the retraction and the force-dependence of all these parameters. It can be shown that the strength of the attachment between cell and bead evolves dynamically during pulling. The experiments are complemented by fluorescence microscopy with live cells with labeled actin cytoskeleton. The characteristics of the movement of the bead are compared with the dynamics of the underlying actin retrograde flow. The results indicate that the bead retraction is mediated by a force-dependent coupling to the actin cytoskeleton.

BP 14.3 Wed 10:00 H10

Measuring cellular reactions upon particle approach on a broad bandwidth by photonic force microscopy — •Felix Jünger and Alexander Rohrbach — Department of Microsystems Engineering, Laboratory for Bio- and Nano-Photonics, University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

A particle diffusing in the vicinity of a living cell exerts broadband mechanical stimuli onto the cell membrane and influences the molecular processes of the cellular response. In this study, we demonstrate that molecular stimuli and the following cellular reorganization occur on different time scales.

We use photonic force microscopy (PFM) to approach optically trapped microbeads to the membrane of different biological cells and to track the bead's temporal fluctuations with nanometer precision and on a broad spectral bandwidth up to 2 MHz. The autocorrelation of the bead motion reveals the friction coefficient $\gamma(d)$, which changes significantly with the bead-membrane distance d. In addition, the frequency-resolved viscoelastic modulus $G(\omega,d)$ is obtained by analyzing the fluctuation data via the Kramers-Kronig relations.

Our results show that fluctuations of the incoming particle are slowed down and momentum transfer onto the cell is increased. Furthermore, we found evidence of a viscoelastic interaction of the bead with the cell coat, which is unique to HT29 cells and additionally regulates the momentum transfer to the cell surface and its mechanosensitive receptors.

BP 14.4 Wed 10:15 H10

Tuning Mechanics and Biochemical Recognition using Hyaluronic Acid Hydrogels — •Martin Schilling and Florian Rehfeldt — Third Institute of Physics - Biophysics, Georg-August-University, Göttingen, Germany

Many aspects of cell behavior are influenced by the mechanical properties of their microenvironment. To mimic the various elastic Young's moduli E of different in vivo environments of cells, it is necessary to design and mechanically characterize hydrogels for cell culture that are biocompatible and allow for a tunable elasticity.

Hyaluronic acid (HA), a polysaccharide consisting of disaccharide units, was chosen as base for the hydrogel system as it is biocompatible and not toxic for cells, thus allowing for 3D encapsulation.

Native HA hydrogels exhibit a visco-elasticity at the lower end of the physiologically relevant stiffness range. Here, we show that by chemical modification and subsequent covalent cross-linking, we can cover the required range from 0.1 kPa to 100 kPa. Additionally, altering the degree of modification of HA allows distinct and independent tuning of Young's modulus and biochemical recognition of HA by cells. Mixtures of both high and low modified HA are examined to combine both properties. The gelation kinetics of the resulting hydrogels are investigated by rheology using oscillatory shear tests both in the low and high strain (LAOS) regime. The resulting influence of mechanics and biochemistry of those HA substrates are investigated with hMSCs and RPM-MCs.

Invited Talk BP 14.5 Wed 10:30 H10

Physical determinants of phagocytic uptake and transport — •Holger Kress — Biological Physics Group, Department of Physics, University of Bayreuth, Germany

Phagocytosis is an essential part of the human immune system and an evolutionary highly conserved fundamental cellular process. Although a large number of molecules that are involved in phagocytosis are known already, a quantitative physical understanding of this intrinsically mechanical process is still lacking. Therefore we investigate physical determinants of phagocytic uptake and transport. We examine the cellular resolution limit for particle uptake by using holographic optical tweezers in combination with correlative light and electron microscopy to measure the ability of cells to discriminate between two spatially separated objects. These studies provide insights into the spreading of cell signaling during particle uptake. In addition, we investigate the influence of basic spatial factors for the transport of intracellular organelles and we show that not all phagosomes are transported directly from the cell periphery to the perinuclear region, but that they exhibit more complex transport characteristics which depend strongly on the size of the phagosomes. This transport behavior might be the foundation for a size-dependent cellular sorting mechanism for organelles. In addition, we quantify how the intracellular transport forces scale with the organelle size by using magnetic tweezers, which can provide cues for the number of motors involved in the transport of different-sized organelles.

15 minutes break.

BP 14.6 Wed 11:15 H10

Blood platelet formation - a biological Rayleigh-Plateau instability — •Christian Bächer and Stephan Gekle — Biofluid Simulation and Modeling, Bayreuth, Germany

Active stresses in the cell cortex, which can trigger changes in cell shape, are highly important for cell mechanics. Based on active gel theory and thin shell theory we incorporate active stresses in 3D simulations of elastic cell membranes in flows [1]. We combine the active force calculation with immersed boundary/lattice Boltzmann method to couple an active membrane to an external fluid.

Blood platelets are formed out of fragmenting protrusions of stem cells called megakaryocytes under presence of active stresses. Our simulations provide an explanation for this fragmentation: active stresses trigger a pearling instability of an elastic, biological cell membrane. This instability can be understood as a biological Rayleigh-Plateau instability with the active stress playing the same role as the surface tension of a liquid jet.

[1] C. Bächer, S.Gekle, J. Comput. Phys. (submitted), 2018

BP 14.7 Wed 11:30 H10

Numerical-experimental observation of shape bistability of red blood cells flowing in a microchannel — Achim Guckenberger[1], Alexander Kihm[2], Thomas John[2], Christian Wagner[2], and •Stephan Gekle[1] — [1]Biofluid Simulation and Modeling, Theoretische Physik VI, Universität Bayreuth — [2]Experimental Physics, Universität des Saarlandes

Red blood cells flowing through capillaries assume a wide variety of different shapes owing to their high deformability. In this work we construct the shape phase diagram of a single red blood cell with a physiological viscosity ratio flowing in a microchannel. We use both experimental in-vitro measurements as well as 3D numerical simulations to complement the respective other one. Two different major shapes are found, namely croissants and slippers. Notably, both shapes show coexistence at low (<1 mm/s) and high velocities (> 3mm/s) while in-between only croissants are stable. This pronounced bistability indicates that RBC shapes are not only determined by system parameters such as flow velocity or channel size, but also strongly depend on the initial conditions.

[1] Guckenberger et al. Soft Matter 14, 2032-2043 (2018)

BP 14.8 Wed 11:45 H10

Dynamic RT-DC: time-resolved mechanical single cell analysis at 100 cells / second — •Bob Fregin[1], Fabian Czerwinski[1], Konstanze Aurich[2], Doreen Biedenweg[2], Salvatore Girardo[3], Stefan Gross[4], and Oliver Otto[1] — [1]ZIK HIKE, Universität Greifswald, Greifswald, Germany — [2]Universitätsklinikum Greifswald, Greifswald, Germany — [3]Biotechnology Center, Technische Universität Dresden, Dresden, Germany — [4]DZHK, Universität Greifswald, Greifswald, Germany

Real-Time Deformability Cytometry (RT-DC) is a label-free technique for single cell mechanical analysis with high-throughput of up to 1,000 cells / second. Capturing the steady-state deformation at the end of a microfluidic channel RT-DC is currently limited to time-independent parameters like the elastic Young's modulus.

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

BP 14.9 Wed 12:00 H10

The role of cell culture topology in cell mechanics: comparing 2D with 3D microenvironments — •Venkata AS Dabbiru[1], Muzaffar H Panhwar[1], Doreen Biedenweg[2], Fabian Czerwinski[1], Ricardo H Pires[1], and Oliver Otto[1] — [1]ZIK HIKE, University of Greifswald, Greifswald, Germany — [2]University Medicine Greifswald, Greifswald, Germany

Despite the widespread use of cell monolayers to culture cells in vitro, this 2D format does not recapitulate many of the physical cues present in the 3D environment that characterizes a tissue. In turn, these topological differences influence gene expression patterns and modulate the physiological behaviour of cells. However, the effect of topology on the mechanics of single cells has so far never been investigated systematically. Here, we apply real-time deformability cytometry (RT-DC) for the high-throughput mechanical phenotyping of single cells and cell spheroids. We compare HEK 293 cells obtained from planar monolayers (2D) and spheroidal (3D) formats and show that cells cultured in a 3D microenvironment have a larger Young's modulus when compared to those cultured in a 2D cell culture format. Furthermore, we show that cell confluency determines the average cell size but does not impact their mechanical properties.

BP 14.10 Wed 12:15 H10

High-throughput cell and tissue mechanics in virtual fluidic channels — •Muzaffar Hussain Panhwar[1], Venkata A.S. Dabbiru[1], Doreen Biedenweg[2], Ricardo H. Pires[1], Fabian Czerwinski[1], and Oliver Otto[1] — [1]ZIK HIKE, University of Greifswald, Greifswald, Germany — [2]University Medicine Greifswald, Greifswald, Germany

The biomechanical properties of cells and tissues are of utmost importance for a number of regulatory processes and complex functions, e.g., cell activation and migration. We use a novel development of real-time deformability cytometry (RT-DC) to access cell and spheroid mechanics of large samples. To accommodate the size range between cells and spheroids, we show that microfluidic geometries can be modified on-the-fly by polymer solutions creating virtual fluidic channels between two immiscible interfaces. After establishing virtual fluidic channels in the mesoscopic environment of a glass cuvette commonly used in flow cytometers, we explore their capability for high-throughput mechanical characterization. Performing RT-DC on an embryonic cell line cultured in 2D and comparing the results to several hundreds of spheroids as a 3D model system, a greater elastic modulus was found for single cells. These results might lead to a better understanding of tissue growth and could reveal insights into the mechanical dynamics of cell-cell interactions.

BP 14.11 Wed 12:30 H10

Stretching Adherent Cells with Light — •Tobias Neckernuss, Daniel Geiger, Jonas Pfeil, and Othmar Marti — Institute of Experimental Physics, Ulm University

In natural science and medicine mechanical properties of cells are important parameters. Over the years, countless techniques to assess all kinds of parameters have been developed for all kinds of cells. The most important ones are: stiffness, creep and relaxation constants. However, the investigation often relies on the interaction of a probe with the cells. Hence, the measured properties are always those of the joint system cell and probe. In 2001 Guck et al. demonstrated that it is possible to investigate the mechanical properties of suspended cells in a microfluidic channel with laser light. We present a setup to determine the mechanical properties of adherent cells in their physiological environment without having to alter their biochemistry or influence the measurement results by interaction of a probe with the cells. A setup for stretching and a method to detect the deformation of the cell have been developed together with the necessary data analysis algorithms. The deformation data are fitted to different kinds of viscoelastic models to describe the behavior of the cells with networks of springs and dashpods. The best models are selected by methods of information theory and the properties of 3T3 fibroblasts measured as cultured are compared to latrunculin treated ones.

BP 14.12 Wed 12:45 H10

A microfluidic method to sort capsules and cells according to their size and deformability — •Doriane Vesperini[1,2] and Anne Le Goff[1] — [1]Sorbonne universités, Université de technologie de Compiègne, CNRS, UMR 7 338 Biomécanique et Bioingénierie — [2]INM, Leibniz Institute for New Materials, Cytoskeletal fibers, (F. Lautenschläger Group)

Cell mechanical properties depend on their functions or pathologies such as cancer or infections. Sorting cells according to their stiffness is thus particularly interesting to help diagnosis. We propose a microfluidic device that consists of a half-cylinder obstacle located at the end of a rectangular straight channel. Upstream of the obstacle, a flow-focusing module centers cells on the obstacle. Downstream of the obstacle, a diffuser ends on 5 symmetrical outlets. Trajectories in the diffuser depend on several parameters, such as cell size, deformability and the capillary number Ca. The capillary number expresses the competition between elastic and viscous forces when the micro-object is squeezed onto the obstacle. Large and stiff micro-objects are more deflected than small and soft ones. We first demonstrate the efficiency of our device to sort micro-capsules according to their size at low flow strength and to their deformability at high flow strength. It is a passive, non-destructive, and sensitive system. We then downscale the microfluidic device in order to sort non-adherent cells.

BP 15: Focus session: Collective Dynamics in Neural Networks

Time: Wednesday 9:30–13:00 Location: H11

Invited Talk BP 15.1 Wed 9:30 H11

Statistical physics of correlated neuronal variability — •Moritz Helias — INM-6, Forschungszentrum Juelich, Germany — Condensed matter theory, RWTH Aachen University, Germany

Neuronal networks can be considered as many particle systems with interesting physical properties: They operate far from thermodynamic equilibrium and show correlated states of collective activity [1].

We here discuss recent progress in understanding the structure of these correlated states by methods from statistical physics and disordered systems [2,3,4].

Our analysis shows that the heterogeneity of the network connectivity enables critical dynamics that unfolds in a low-dimensional subspace. The structure of correlations predicted by this theory is found in line with massively parallel recordings from motor cortex [2]. We then demonstrate that networks in such regimes possess optimal capacity to memorize past input sequences [3]. We find that they operate in a hitherto unreported regime that combines instability on short time scales with asymptotically non-chaotic dynamics. As an outlook, we demonstrate how methods from field theory [4] help us understand the interplay of non-linearities and fluctuations that is vital to neuronal network dynamics.

1. Dahmen, Bos, Helias (2016) Phys. Rev. X 6, 031024; 2. Dahmen, Grün, Diesmann, Helias (2018) arXiv:1711.10930; 3. Goedeke, Helias (2018) Phys. Rev. X 8, 041029; 4. Kühn, Helias (2018) J Phys A 51, 37

BP 15.2 Wed 10:00 H11

Precise Synaptic Balance in a Homolog of Olfactory Cortex — Peter Rupprecht[1,2] and •Rainer Friedrich[1,2] — [1]Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland — [2]University of Basel, Basel, Switzerland

In the classical balanced state, uncorrelated excitatory and inhibitory inputs result in irregular spiking that is inefficient for specific computations. More recently, theoretical studies have shown that correlating excitatory and inhibitory inputs on a short timescale (tight balance) and in a multi-dimensional coding space (detailed balance) can neutralize these drawbacks of balanced networks.

We used whole-cell voltage-clamp recordings in the intact zebrafish brain to directly analyze synaptic inputs to neurons in a distributed olfactory memory network. We found that large excitatory and inhibitory recurrent inputs establish a transient balanced state during odor stimulation. Using 20 Hz upstream oscillations as a reference clock to align excitatory and inhibitory inputs in time, we found a tight balance, with inhibition tracking excitation by a 3 ms delay. Finally, by studying the odor-specificity of excitatory and inhibitory inputs, we found inhibition and excitation to be co-tuned, as a signature of a detailed, high-dimensional balance in stimulus space. This precise synaptic balance implies specific and non-random connectivity among neurons, despite the absence of an obvious topography in olfactory cortex. We propose that this network is the substrate for a pattern classification process that is fast, as in classical balanced networks, but also stable in many coding directions.

BP 15.3 Wed 10:15 H11

Long-Range Collective Dynamics in the Balanced State — •Moritz Layer, Lukas Deutz, David Dahmen, and Moritz Helias — Forschungszentrum Juelich, INM-6, Wilhelm-Johnen-Strasse, 52428 Juelich, Germany

Experimental findings suggest, that cortical networks operate in a balanced state, in which strong recurrent inhibition suppresses single cell input correlations. The balanced state, however, only restricts the average correlations in the network, the distribution of correlations between individual inputs is not constrained. We here investigate this distribution and establish a functional relation between the distance to criticality and the spatial dependence of the statistics of correlations. Therefore, we develop a mean-field theory that goes beyond self-averaging quantities by taking advantage of the symmetry of the disorder-averaged effective connectivity matrix. We demonstrate that spatially organized, balanced networks can show rich pairwise correlation structures, extending far beyond the range of direct connections. Strikingly, the range of these correlations depends on the distance of the network dynamics to a critical point. This relation between the operational regime of the network and the range of correlations is a potential dynamical mechanism that controls the spatial range on which neurons cooperatively perform computations. In the future we will compare our results with data from multi channel recordings to infer new constraints on realistic network models.

BP 15.4 Wed 10:30 H11

Effects of cellular excitatory-inhibitory composition on neuronal dynamics — •Oleg Vinogradov[1,2], Nirit Sukenik[3], Elisha Moses[3], and Anna Levina[1,2] — [1]University of Tübingen — [2]MPI for Biological Cybernetics — [3]Weizmann Institute of Science

Excitation/Inhibition balance is essential for stable neuronal dynamics. It is considered to be strongly related to the relative counts of excitatory and inhibitory neurons. However, it is not clear if the relative counts indeed change the excitation/inhibition balance on a synaptic level and affect the neuronal dynamics. To investigate these effects, we recorded Ca-activity of hippocampal cultures with various numbers of inhibitory neurons. In experiments, all cultures developed network bursting. The cultures with various fractions of inhibitory neurons showed stable average inter-burst intervals. The variance of inter-burst intervals, however, grew with the number of inhibitory neurons. We reproduced the results of experiments in a model network of leaky integrate-and-fire neurons with different numbers of inhibitory neurons, but balanced strength of excitation and inhibition, and adaptation. The model showed that the stable mean and increasing variance of inter-burst intervals can be achieved by the synaptic balance between excitation and inhibition that regulates effects of adaptation. We also show that an equivalent mean-field model of excitatory and inhibitory rate-neurons with adaptation can account for these effects in terms of simple attractor dynamics. Overall, our results suggest that hippocampal cultures with various cellular compositions tend to maintain the balance.

BP 15.5 Wed 10:45 H11

Functional Renormalization Group for Stochastic Rate Neurons — •Tobias Kühn[1], Jonas Stapmanns[1,2], David Dahmen[1], Carsten Honerkamp[2], and Moritz Helias[1,3] — [1]Institute of Neuroscience and Medicine (INM-6), Forschungszentrum Juelich, Germany — [2]Institute for Theoretical Solid State Physics, RWTH Aachen, Germany — [3]Department of Physics, Faculty 1, RWTH Aachen, Germany

It is often suggested that the cortex operates close to a critical point at which linear response theory fails since the neural dynamics is dominated by large fluctuations on all length scales. The functional Renormalization Group (fRG) is not stained with this flaw because in principle it treats statistics of arbitrary order in an unbiased and self-consistent way. We apply fRG to a self-interacting, stochastic, quadratic rate neuron and show how this method incorporates corrections to the mean dynamics and time-dependent statistics due to fluctuations in the presence of nonlinear neuronal gain. To obtain a simplified treatment of the frequency-dependence of all observables, we adapt the Blaizot Méndez-Galain Wschebor (BMW) scheme to the vertex expansion, which yields good predictions.

We expect that the insights into fRG-techniques gained within our study will help to tackle challenges occurring in the description of phenomena in spatially extended networks, notably the calculation of critical exponents and the coarse-graining of microscopic models.

15 minutes break.

BP 15.6 Wed 11:15 H11

Resonant chaos in random networks of adapting neurons — Samuel Muscinelli[1], Wulfram Gerstner[1], and •Tilo Schwalger[2,3] — [1]Brain Mind Institute, École polytechnique fédérale de Lausanne (EPFL), 1015 Lausanne, Switzerland — [2]Institut für Mathematik, Technische Universität Berlin, 10623 Berlin — [3]Bernstein Center for Computational Neuroscience, 10115 Berlin

The dynamical response of cortical neurons to inputs is governed by several history-dependent mechanisms. One prominent example are slow negative feedback mechanisms that lead to spike frequency adaptation – a widely observed feature of neurons. Despite the importance of adaptation, it is theoretically poorly understood how such neuronal properties shape the collective activity of recurrent networks.

Here, we study the dynamics of a random recurrent network of multi-dimensional rate neurons admitting adaptation. Using dynamical mean-field theory and an iteratative map for the self-consistent second-order statistics of neural activity, we show how local adaptation and recurrent feedback from the network give rise to two distinct types of chaotic behavior, resonant and non-resonant chaos. The type of chaos as well as the resonance frequency can be predicted by the single neuron susceptibility. Interestingly, the emerging correlation time of the network activity cannot be increased by slow adaptation. We also find that suppression of chaos is maximized by input frequencies close to the resonant one. More generally, our work sheds light on the complex interplay between local neuron properties and recurrent network connectivity beyond adaptation.

BP 15.7 Wed 11:30 H11

Growing Critical: Self-Organized Criticality in a Developing Neural System — •Sven Goedeke[1], Felipe Yaroslav Kalle Kossio[1], Benjamin van den Akker[2], Borja Ibarz[3], and Raoul-Martin Memmesheimer[1,2] — [1]Neural Network Dynamics and Computation, University of Bonn, Germany — [2]Department of Neuroinformatics, Radboud University Nijmegen, Netherlands — [3]Nonlinear Dynamics and Chaos Group, Universidad Rey Juan Carlos, Madrid, Spain

Experiments in various neural systems found avalanches: bursts of activity with characteristics typical for critical dynamics. A possible explanation for their occurrence is an underlying network that self-organizes into a critical state. We propose a simple spiking model for developing neural networks, showing how these may "grow into" criticality [1]. Avalanches generated by our model correspond to clusters of widely applied Hawkes processes. We analytically derive the cluster size and duration distributions and find that they agree with those of experimentally observed neuronal avalanches.

[1] Kalle Kossio, F. Y., Goedeke, S., van den Akker, B., Ibarz, B., and Memmesheimer, R. M. (2018). Growing Critical: Self-Organized Criticality in a Developing Neural System. Phys. Rev. Lett. 121(5), 058301.

BP 15.8 Wed 11:45 H11

Homeostatic plasticity and external input shape neural network dynamics — •Johannes Zierenberg[1,2], Jens Wilting[1], and Viola Priesemann[1,2] — [1]Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen — [2]Bernstein Center for Computational Neuroscience, Göttingen

In vitro and in vivo spiking activity clearly differ. Whereas networks *in vitro* develop strong bursts separated by periods of silence, *in vivo* cortical networks show continuous activity. This is puzzling as both networks presumably share similar single-neuron dynamics and plasticity rules. We propose that the defining difference between *in vitro* and *in vivo* dynamics is the strength of external input. *In vitro*, networks are virtually isolated, whereas *in vivo* every brain area receives continuous input. We analyze a model of spiking neurons in which the input strength, mediated by spike rate homeostasis, determines the characteristics of the dynamical state. Our analytical and numerical results on various network topologies show that under increasing input, homeostatic plasticity generates distinct dynamic states, from bursting, to close-to-critical, reverberating and irregular states. This implies that the dynamic state of neural networks can readily adapt to the input strengths. Our results match experimental spike recordings: *in vitro* bursts are consistent with a state generated by very low network input ($< 0.1\%$), whereas *in vivo* activity suggests that on the order of 1% recorded spikes are input-driven, resulting in reverberating dynamics. This implies that one could impose *in vivo*-like activity in *in vitro* preparations by exposition to weak long-term stimulation.

BP 15.9 Wed 12:00 H11

Critical dynamics in models and experimental data — •Anna Levina — Tübingen University — BCCN Tübingen

Understanding the complex dynamics of the human brain is one of the most exciting challenges in modern science. Novel experimental methods allow acquiring unprecedented amounts of high-quality data. However, making sense of all these data requires an integrative theoretical approach to foster a deeper understanding of brain activity. Here I will discuss the critical dynamics approach that provides an explanation for a plethora of empirical results regarding scale-free spatiotemporal dynamics observed through a multitude of experimental methodologies across different spatial and temporal scales. The hypothesis that the brain operates close to the critical state is supported by the theoretical evidence suggesting multiple aspects of information processing to be optimized at the second order phase transition. I will give an overview of the experimental evidence and theoretical modeling of criticality in neuronal systems. Using an example of an efficient coding network, I will demonstrate how optimization of the network for particular function might result in a critical-like dynamics. Considering the problem from the other side, I present evidence that approaching critical state can improve the general computational capabilities in the developing cortical and hippocampal cultures.

BP 15.10 Wed 12:30 H11

Critical avalanches in a spatially structured model of cortical On-Off dynamics — •Roxana Zeraati[1,2], Tatiana Engel[3], and Anna Levina[1,2] — [1]University of Tübingen — [2]MPI for Biological Cybernetics — [3]Cold Spring Harbor Laboratory

Spontaneous cortical activity unfolds across different spatial scales. On a local scale of individual columns, activity spontaneously transitions between episodes of vigorous (On) and faint (Off) spiking, synchronously across cortical layers. On a wider spatial scale of interacting columns, activity propagates as neural avalanches, with sizes distributed as an approximate power-law with exponential cutoff, suggesting that brain operates close to a critical point. We investigate how local On-Off dynamics can coexist with critical avalanches. To this end, we developed a branching network model capable of capturing both of these dynamics. Each unit in the model represents a cortical column, that spontaneously transitions between On and Off episodes and has spatially structured connections to other columns. We found that models with local connectivity do not exhibit critical dynamics in the limit of a large system size. While for a critical network, it is expected that the cut-off of the avalanche-size distribution scales with the system size, in models with nearest-neighbor connectivity, it stays constant above a characteristic size. We demonstrate that the scaling can be recovered by increasing the radius of connections or by rewiring a small fraction of local connections to long-range random connections. Our results highlight the possible role of long-range connections in defining the operating regime of the brain dynamics.

BP 15.11 Wed 12:45 H11

Inferring network wiring from recorded activity — •Nataliya Kraynyukova and Tatjana Tchumatchenko — Max-Planck-Institute for Brain Research, Frankfurt am Main, Germany

The cortical circuits are able to perform a variety of nonlinear computations. One of the most ubiquitous representations of neural activity observed throughout sensory modalities is a tuning curve. In the visual cortex the tuning curves have been often shown to be contrast invariant. Contrast invariance means that after normalizing by the peak value tuning curves recorded at different contrast values will have a universal shape. We show that if the activity of a neural rate network is contrast invariant, then network connectivity and input profiles have a specific, mathematical relation to activity tuning curves. This simple theoretical observation provides constraints on the possible network connectivities and we show how it serves to infer connectomes.

BP 16: Dynamics of multilayer networks I (joint session SOE/DY/BP)

Recently, multilayer networks have been suggested to offer a better representation of the topology and dynamics of real-world systems in comparison with isolated one-layer structures. The prime objective of multiplex networks is to explore multiple levels of interactions where functions of one layer get affected by the properties of other layers. One of the most promising applications of the multilayer approach is the study of the brain, or technological interdependent systems, i.e., those systems in which the correct functioning of one of them strongly depends on the status of the others. The purpose of this focus session is to bring together researchers working on multilayer networks and to share recent ideas and results in the field. (The sessions Dynamics of Multilayer Networks I + II have been organized by Anna Zakharova and Sarika Jalan.)

Time: Wednesday 9:30–12:00 Location: H17

Topical Talk BP 16.1 Wed 9:30 H17

Inhibition induced explosive synchronization in multiplex network — •Sarika Jalan — Complex Systems Lab, IIT Indore, Indore 453552

To date, explosive synchronization (ES) is shown to be originated from either degree-frequency correlation or inertia of phase oscillators. Of late, it has been shown that ES can be induced in a network by adaptively controlled phase oscillators. We show that ES can occur in any network by appropriately multiplexing it with another layer. We devise an approach which leads to the occurrence of ES with hysteresis loop in a network upon its multiplexing with a negatively coupled (or inhibitory) layer. We discuss the impact of various structural properties of positively coupled (or excitatory) and inhibitory layer along with the strength of multiplexing in gaining control over the induced ES transition. This investigation is a step forward in highlighting the importance of multiplex framework not only in bringing novel phenomena which are not possible in an isolated network but also in providing more structural control over the induced phenomena.

Topical Talk BP 16.2 Wed 10:00 H17

Percolation on multi-layer networks — •Filippo Radicchi — Indiana University, Bloomington, Indiana, United States

In this talk, I will review some of my recent papers about percolation on multi-layer networks. I will first illustrate a theoretical approach consisting in a system of heuristic equations able to approximate the phase diagram of the ordinary percolation model for arbitrary multi-layer networks. Second, I will introduce and characterize the redundant percolation model, a genuine model for multi-layer networks where the addition of new layers boosts system robustness by creating redundant interdependencies among layers. Third, I will generalize the problem of optimal percolation from single-layer to multi-layer networks, and present several algorithms for finding approximate solutions to the problem. Finally, I will present a large-deviation approach to ordinary percolation able to shed light on the importance of fluctuations in the study of percolation on real-world multi-layer networks.

15 min. break

Topical Talk BP 16.3 Wed 10:45 H17

Mean field phase synchronization across multilayer networks in chimera states — •Ralph Gregor Andrzejak[1], Giulia Ruzzene[1], Kaspar Schindler[2], Eckehard Schöll[3], and Anna Zakharova[3] — [1]Dept. of Information and Communication Technologies, Univ. Pompeu Fabra, Barcelona, Spain — [2]Dept. of Neurology, Sleep-Wake-Epilepsy-Center, Inselspital, Univ. Bern, Switzerland — [3]Inst. für Theoretische Physik, Technische Univ. Berlin, Germany

Chimera states are an intriguing interplay of synchronous and asynchronous motion in networks of coupled oscillators. While chimera states were traditionally studied in one-layer networks, recent work studies interactions of chimera states across coupled layers in multilayer networks. We here review our recent work in which we applied different types of couplings between pairs of networks that individually show chimera states when there is no coupling between them. We show that these couplings across network layers can lead to generalized synchronization [1] and phase synchronization [2] between networks, while both layers continue to exhibit distinct chimera states. We show that these synchronization phenomena are in close analogy to those found for low-dimensional chaotic dynamics.

References: [1] Andrzejak, R. G., Ruzzene, G., & Malvestio, I. (2017). Generalized synchronization between chimera states. Chaos, 27(5), 053114.

[2] Andrzejak, R. G., Ruzzene, G., Malvestio, I., Schindler, K., Schöll, E., & Zakharova, A. (2018). Mean field phase synchronization between chimera states. Chaos, 28(9), 091101.

BP 16.4 Wed 11:15 H17

Weak multiplexing induces coherence resonance — •Nadezhda Semenova[1,2] and Anna Zakharova[3] — [1]Department of Physics, Saratov State University, Saratov, Russia — [2]FEMTO-ST / Optics Dept., Univ. Bourgogne Franche-Comté, Besançon Cedex, France — [3]Institut für Theoretische Physik, Technische Universität Berlin, Berlin, Germany

Using the model of a FitzHugh-Nagumo system in the excitable regime, we study the impact of multiplexing on coherence resonance in a two-layer network [1]. We show that multiplexing allows for the control of the noise-induced dynamics. In particular, we find that multiplexing induces coherence resonance in networks that do not demonstrate this phenomenon in isolation. Examples are provided by deterministic networks and networks where the strength of interaction between the elements is not optimal for coherence resonance. In both cases, we show that the control strategy based on multiplexing can be successfully applied even for weak coupling between the layers. Moreover, for the case of deterministic networks, we obtain a counter-intuitive result: the multiplex-induced coherence resonance in the layer which is deterministic in isolation manifests itself even more strongly than that in the noisy layer.

[1] N. Semenova, A. Zakharova, Weak multiplexing induces coherence resonance, Chaos 28, 051104 (2018)

Topical Talk BP 16.5 Wed 11:30 H17

Relay synchronization in multiplex networks — •Inmaculada Leyva[1,2], Irene Sendina-Nadal[1,2], Ricardo Sevilla-Escoboza[3], and Victor Vera-Avila[3] — [1]Complex Systems Group & GISC, Universidad Rey Juan Carlos, Madrid, Spain — [2]Center for Biomedical Technology, Universidad Politécnica de Madrid, Madrid, Spain — [3]Centro Univ. de los Lagos, Universidad de Guadalajara, Jalisco, Mexico

The relay synchronization is observed when two dynamical units synchronize despite not being directly linked, due to the intermediation of a relay mismatched unit. In our work we have extended the concept of relay synchronization to the case of a multiplex network, showing that the intermediation of a relay layer can lead to inter-layer synchronization of a set of paired layers, both topologically and dynamically different from the transmitter. The phenomenon can be extended to indefinitely higher order relay configurations, provided a mirror symmetry is preserved in the multiplex. The coherent state is very robust to changes in the dynamics, topology, and even to strong multiplex disconnection.Our results provide a new path for starting the study of the role of symmetries in setting long distance coherence in real systems, specially in brain networks, where remote synchronization is of outstanding relevance for coordination between remote cortical areas.

BP 17: Statistical physics of biological systems I (joint session BP/DY)

Time: Wednesday 15:00–17:30 Location: H4

BP 17.1 Wed 15:00 H4

Active noise fuels the heterogeneous anomalous diffusion of inert nanoparticles in the cytoplasm — •Adal Sabri[1], Xinran Xu[2], Diego Krapf[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth, Germany — [2]School of Biomedical Engineering, Colorado State University, CO, USA

Diffusive motion of inert particles in the cytoplasm of living cells is generally assumed to be driven by thermal noise. This assumption appears particularly justified for the frequently observed sublinear growth of the particles' mean square displacement ('subdiffusion').

In order to probe quantitatively to which extent also active noise contributes to (sub)diffusional motion in living matter, we have introduced inert quantum dots into the cytoplasm of living cells and performed extensive single-particle tracking experiments in untreated cells and after disrupting the cytoskeleton. In all cases a pronounced subdiffusive motion of the particles with a distinct anti-correlation of successive steps was observed. Yet, the degree of the diffusion anomaly and the generalized diffusion coefficients showed marked changes when the integrity of the cytoskeleton was compromised, i.e. particles moved less vivid when cytoskeleton-associated active transport was erased. This observation highlights that cytoplasmic subdiffusion is partially fueled by active noise. In line with this notion, several measures of the trajectories, e.g. the gaussianity, highlight a strongly heterogeneous random walk with a temporally and/or spatially varying noisy driving.

BP 17.2 Wed 15:15 H4

Self-organised segregation of bacterial chromosomal origins — •Sean Murray — Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

In spite of much effort, many aspects of chromosome segregation in bacteria remain unclear. Like many other bacteria, the chromosomal origin of replication in Escherichia coli is dynamically positioned throughout the cell cycle. Initially maintained at mid-cell, where replication occurs, origins are subsequently partitioned to opposite quarter positions. However the mechanism underlying this is unknown. Here, we provide an explanation based on the self-organisation of the Structural Maintenance of Chromosomes complex, MukBEF. We propose that a non-trivial feedback between the self-organising MukBEF gradient and the origins leads to accurate positioning and partitioning as an emergent property. We find excellent agreement with quantitative experimental measurements and confirm key predictions. In particular, we show that origins exhibit biased motion towards MukBEF, rather than mid-cell, consistent with the model. Overall, our findings suggest that MukBEF and origins act together as a self-organising system for chromosome segregation and introduces protein self-organisation as an important consideration for future studies of chromosome dynamics.

BP 17.3 Wed 15:30 H4

Perfect anomalous transport of subdiffusive cargos by molecular motors in viscoelastic cytosol — •Igor Goychuk — Institute for Physics and Astronomy, University of Potsdam, Karl-Liebknecht-Str. 24/25, 14476 Potsdam-Golm, Germany

Multiple experiments show that various submicron particles such as magnetosomes, RNA messengers, viruses, and even much smaller nanoparticles such as globular proteins diffuse anomalously slow in the viscoelastic cytosol of living cells. Hence, their sufficiently fast directional transport by molecular motors such as kinesins is crucial for the cell operation. It has been shown recently that the traditional flashing Brownian ratchet models of molecular motors are capable to describe both normal and anomalous transport of such subdiffusing cargos by molecular motors with a very high efficiency. This work elucidates further an important role of mechanochemical coupling in such an anomalous transport. It shows a natural emergence of a perfect subdiffusive ratchet regime due to allosteric effects, where the random rotations of a "catalytic wheel" at the heart of the motor operation become perfectly synchronized with the random stepping of a heavily loaded motor, so that only one ATP molecule is consumed on average at each motor step along microtubule. However, the number of rotations made by the catalytic engine and the traveling distance both scale sublinearly in time. Nevertheless, this anomalous transport can be very fast in absolute terms.

[1] I. Goychuk, Biosystems, in press, arXiv:1809.08032 [physics.bio-ph]

Invited Talk BP 17.4 Wed 15:45 H4

Chaos in self-propelled droplets — •Annette Zippelius and Reiner Kree — Georg-August-Universität Göttingen, Institut für Theoretische Physik, Friedrich-Hund Platz 1, 37077 Göttingen

Intracellular flow can be generated by a variety of active mechanisms, such as motors transporting cargo. The actively generated flow has at least two effects: it can drive cell locomotion and simultaneously play a central role for intracellular transport. We develop increasingly more complex, but analytically solvable models, starting from a simple fluid droplet or a biphasic droplet, consisting of a fluid and a rigid gel. Active forces or stresses, which are co-localised on the gel, generate internal flow. The trajectories of tracer particles which are advected by the internal flow, are shown to display the full richness of dynamical systems, ranging from closed orbits to quasiperiodic motion and chaotic trajectories in general. We discuss the mixing properties of the internal flow as well as its significance in comparison to diffusive transport. Despite chaos inside the droplet, locomotion of the droplet as a whole remains simple and regular, e.g. motion on a straight line or a spiral.

BP 17.5 Wed 16:15 H4

Three-dimensional membrane confinement and geometry dictate excitable signaling dynamics in Dictyostelium cells. — •Marcel Hörning[1,2,3] and Tatsuo Shibata[2] — [1]Institute of Biomaterials and Biomolecular Systems, University of Stuttgart, 70569 Stuttgart, Germany — [2]Laboratory for Physical Biology, RIKEN Center for Biosystems Dynamics Research, Kobe 650-0047, Japan — [3]Institute for Integrated Cell-Material Sciences, Kyoto University, 606-8501, Kyoto, Japan

Propagating waves on the plasma membrane mediate the membrane protrusive activities in Dictyostelium and mammalian cells. Most studies focus on the dynamics extracted from single focal planes only. Thus, the relation between the dynamics and three-dimensional cell shape remains elusive, due to the lack of signaling information about the unobserved part of the membrane.

We show that PtdInsP3 wave dynamics are directly regulated by the three-dimensional geometry - size and shape - of the plasma membrane. By introducing an analysis method that extracts the three-dimensional spatiotemporal activities on the entire cell membrane, we show that PtdInsP3 oscillatory waves self-regulate their dynamics within the confined membrane area. This leads to changes in speed, orientation and pattern evolution, following the underlying excitability of the signal transduction system. This findings emphasize the role of the plasma membrane topology in reaction-diffusion driven biological systems and indicate its importance in other mammalian systems.

BP 17.6 Wed 16:30 H4

Non-equilibrium spatial scaling reveals intrinsic features of the active driving — •Federica Mura, Grzegorz Gradziuk, and Chase Broedersz — Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universität München

Recent experiments indicate non-equilibrium activity in a host of biological systems, including chromosomes, cell membranes, and the cytoplasm. Measuring and quantifying non-equilibrium dynamics in such systems is a major challenge in biophysics, due to their many-body nature and the limited number of variables accessible in an experiment. We investigate what information concerning the system's non-equilibrium state can be extracted by non-invasively tracking a subset of degrees of freedom. To this end, we develop a general, yet simple stochastic model of soft elastic networks with spatially-varying internal driving, representing internal enzymatic force generation. With this model, we determine the scaling behavior of non-equilibrium dynamics from the phase space currents of tracer particles with varying spatial separations in the system. Finally, we will discuss how the non-equilibrium dynamics measured on different length scales can reflect the intrinsic microscopic features of the internal active driving.

BP 17.7 Wed 16:45 H4

Dynamical states of a living network — •Philipp Fleig, Mirna

Kramar, Michael Wilczek, and Karen Alim — Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen, Germany

Understanding the emergence of behaviour in living systems from underlying physical mechanisms is a major goal of biophysics. Even very simple, non-neural organisms like the slime mould *Physarum polycephalum* show remarkably complex behaviour including growth, adaptation of the network morphology and foraging for food - despite only being a single, giant, network-shaped cell.

Behavioural dynamics, here, emerge directly from living matter, namely the coordinated contractions of the cell's tubular shaped actomyosin cortex undergoing rhythmic contraction every 100 seconds. We decompose this spatiotemporal dynamics into principal components and identify a reduced set of characteristic large-scale contraction patterns spanning the network. Based on this dictionary of patterns we are able to determine the typical sequence of the network's response patterns to a controlled stimulus, mimicking a natural response scenario. We also find spontaneously occurring breaking of coherent contraction dynamics into decoherent patterns over short time-scales. Finally, we note a power law distribution of the relative amplitudes of the principal components. This may be key in explaining the observed dynamical features from the underlying biomechanics. Our findings connect behaviour with characteristic states of living matter.

BP 17.8 Wed 17:00 H4

Active droplets can center internal particles — •David Zwicker[1,2], Anthony Hyman[3], and Frank Jülicher[2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen — [2]Max Planck Institute for the Physics of Complex Systems, Dresden — [3]Max Planck Institute of Cell Biological and Genetics, Dresden

Active droplets are non-equilibrium systems where chemical reactions drive fluxes of the droplet material. These fluxes can control the droplet nucleation as well as the droplet size and thereby stabilize many droplets against the typical coarsening observed in passive systems. Here, we study how the non-equilibrium fluxes affect solid particles inside such active droplets. We find that particles get centered when the droplet is maintained externally, while particles are expelled in the opposite case of autocatalytic droplets. In this case, only catalytically active particles can be centered. An example of such a situation are centrosomes in biological cells. Our theory thus accounts for the observed central positioning of centrioles and it generally provides a mechanism for controlling the morphology of active droplets.

BP 17.9 Wed 17:15 H4

Mesoscopic roughness analysis of propagating cell fronts: physical statistics as an in-vitro phenotype probe — •Guillaume Rapin[1], Audrey Rawleigh[2], Aziza Merzouki[3], Ermano Moriggi[2], Bastien Chopard[3], Thierry Giamarchi[1], Steven A. Brown[2], and Patrycja Paruch[1] — [1]DQMP, University of Geneva, Switzerland — [2]IST, Universtiy of Zurich, Switzerland — [3]CSD, University of Geneva, Switzerland

The competition between elasticity and disorder governs the geometry and dynamics of interfaces in many systems, from ferroic domain walls to bacterial colonies. In the latter case, it has been used as a framework to explore cell front evolution, with local mapping of displacements and forces, and the origin of the cell front roughness.

Here, we report on the geometry and dynamics of propagating rat epithelial cell fronts in artificial wound healing assays over 72 hours, studied over 5 orders of magnitude in length scale ranging from $1\mu m$ to $2cm$. Under standard conditions, they present 3 distinct regimes: power law growth of the roughness with characteristic roughness exponent values of $\zeta = 0.55$ at sub-cell length scales, and of $\zeta \approx 0.3$ at few-cell length scales, reaching a scale-independent maximum beyond $400\mu m$. Exposure to a selection of chemical inhibitors targeting cell division rates, mobility, or intercellular communications changes this roughening behaviour, as well as the initial and steady-state dynamics of the cell front. Our results suggest that collective motion on the order of 4-10 cells plays a key role in the roughness evolution of the front. These experimental results will be compared to numerical simulations.

BP 18: Cell mechanics II

Time: Wednesday 15:00–17:15 Location: H10

BP 18.1 Wed 15:00 H10

Combined Traction Force and Scanning Probe Microscopy for Investigation of Active and Passive Cell Mechanics — •Johannes Rheinlaender, Nicolas Schierbaum, and Tilman E. Schäffer — Institute of Applied Physics, Eberhard Karls University Tübingen, Germany

Living cells are highly complex systems and their mechanics are governed by the cytoskeleton, which exhibits two outstanding characteristics: "passive" viscoelastic material properties and "active" contractile forces. Understanding their interplay is subject of current research, but there is no technique for the direct measurement of both viscoelastic material properties and contractile forces in parallel. We therefore for the first time directly combined traction force microscopy (TFM) and scanning probe microscopy (SPM), specifically, scanning ion conductance and atomic force microscopy (AFM). Using combined TFM and AFM, we directly measured the relation between viscoelastic material properties in terms of stiffness and fluidity and contractile forces in terms of the net contractile moment on the single-cell level. We found a strong correlation between each stiffness, fluidity, and net contractile moment, suggesting a common mechanism controlling all three parameters. Myosin II inhibition results in concurrent change of all three parameters to this correlation, confirming that the actomyosin machinery concurrently controls both viscoelastic material properties and contractile forces. Further experimental and theoretical work is required for a complete understanding of cell mechanics, but combined TFM and SPM is powerful tool for this purpose.

BP 18.2 Wed 15:15 H10

Investigating cancer cell behaviour during migration through a confining microenvironment — •Carlotta Ficorella — University of Leipzig, Linnéstraße 5, 04103 Leipzig, Germany

The extra-cellular microenvironment plays a fundamental role in tumour growth and progression, strongly affecting the migration strategies adopted by single cancer cells during metastatic invasion. Here we use a novel microfluidic device to investigate the ability of mesenchymal and epithelial breast tumour cells to migrate through quasi-three-dimensional narrowing microstructures upon chemoattractant stimulation.

Our results show that both epithelial and invasive cells are able to easily disassemble and rearrange their cytoskeleton, in order to achieve migration through the constriction openings. Metastatic mesenchymal cells, on the other hand, exhibit no invasive behaviour. We also demonstrate that migration of epithelial cells through a highly compressive environment can occur in absence of a chemoattractive stimulus, thus suggesting that they are just as prone to react to mechanical cues as invasive cells.

BP 18.3 Wed 15:30 H10

Spatial heterogenity of the mechanics of solid tumors — •Thomas Fuhs, Erik W. Morawetz, Frank Sauer, Steffen Grosser, and Josef A. Käs — Peter Debye Institut für Physik weicher Materie, Universität Leipzig, Deutschland

In solid tumors tissue that is stiffer than healthy tissue is formed by cells that are softer than healthy cells. We try to address this contradiction by spatially resolved investigation of the mechanics of solid tumors tissues. We are able to measure the elasticity of slices of solid tumors on the millimeter scale with micrometer spatial resolution by AFM. This avoids measuring only heavily selected regions or only single cells extracted from dissected tissue. At the same time we are able to precisely align our AFM data with immunohistological stains. We can correlate the spatial heterogeneity of the elasticity maps with the distribution of cytokeratin. We complete these measurements with elasticity data on the whole tissue scale obtained by magnetic resonance elastography and single cell data from optical stretcher measurements. Each set of measurements is performed with tissue and from the same tumor, minimizing the error through biological variance within a dataset. Through the combination of the measurements we are able to bridge the scales from single cells to tissue level, to see how the individual cells contribute to the whole.

BP 18.4 Wed 15:45 H10

Modeling of T-Cell polarization — •Ivan Hornak and Heiko Rieger — Saarland University, Center for Biophysics, Theoretical Physics Saarbrücken, Germany

Cytotoxic T lymphocytes (T) and natural killer (NK) cells are the main cytotoxic killer cells of the human body to eliminate pathogen-infected or tumorigenic cells (i.e. target cells). They form a tight contact, the immunological synapse (IS), with targets and release their lytic granules containing perforin/granzyme and cytokine containing vesicles. Once a NK or T cell has identified a target cell and established a contact zone one observes a re-polarization of the cell involving the rotation of the microtubule (MT) half-spindle and a movement of the centrosome or microtubule organizing center (MTOC) to a position that is just underneath the plasma membrane at the center of the IS. Concomitantly a massive relocation of organelles attached to MTs is observed, including the Golgi apparatus, lytic granules and mitochondria. Since the mechanism of this relocation is poorly understood we devised a theoretical model for the molecular motor driven motion of the MT half-spindle confined between plasma membrane and nucleus during T cell polarization. We analyze different scenarios currently discussed in the literature, including cortical sliding and capture shrinkage mechanism, and compare quantitative predictions about the spatio-temporal evolution of MTOC position and spindle morphology with experimental observations. We propose that our model opens a way to infer details of the molecular motor distribution from the experimentally observed features of the MT half-spindle dynamics.

BP 18.5 Wed 16:00 H10

Toward theoretical model for cell blebbing — Sebastian Hillringhaus, Gerhard Gompper, and •Dmitry A. Fedosov — Institute of Complex Systems, Forschungszentrum Jülich, Jülich, Germany

Cell blebbing corresponds to the dissociation of cell membrane from the inner cellular network as result of internal stresses. Therefore, it represents the instability of the connection between the membrane and actin cortex. We employ a coarse-grained cell model to study cell blebbing for a number of involved parameters, including membrane rigidity, cytoskeletal stress, and binding strength between the membrane and bulk cytoskeleton. Furthermore, theoretical model for the detachment of bound solid surfaces is extended in order to include the effect of deformable cellular structures on the blebbing process.

BP 18.6 Wed 16:15 H10

How the cytoskeleton and cell shape directs pollen tube outgrowth in Arabidopsis thaliana — Lucie Riglet[1], •Karin John[2], Frédérique Rozier[1], Thierry Gaude[1], Catherine Quilliet[2], and Isabelle Fobis-Loisy[1] — [1]RDP, ENS Lyon, France — [2]LIPhy, CNRS, U. Grenoble-Alpes, France

In the flowering plant Arabidopsis thaliana, the pollen tube that transports male gametes grows within the cell wall of the epidermal cells of the female reproductive organ, also named stigmatic papilla. In the katanin mutant (ktn), the shape of the papilla is slightly altered and cortical microtubules (CMT) are completely disorganized compared to the wild type. At the same time the directionality of pollen tube growth is disturbed. We show by Atomic Force Microscopy and measurements of pollen tube growth speed, that alterations in the CMT organization affect the mechanical properties of the stigmatic cell wall, which could be responsible for the disoriented pollen tube growth. We propose a simple model mechanism, where pollen outgrowth is directed by two basic principles: (i) minimizing locally the curvature of the pollen tube path on the papilla surface and (ii) mechanical anisotropy of the papilla wall stiffness.

Invited Talk BP 18.7 Wed 16:30 H10

Physics of epithelial folding — •Guillaume Salbreux — The Francis Crick Institute

The shape of a biological tissue is determined by mechanical stresses acting within the tissue cells. During embryonic morphogenesis, forces generated in the actomyosin cytoskeleton in the cells of epithelia result in cell deformation, cell rearrangements, and 3D bending of the epithelium. To understand tissue morphogenesis, force generation at the cellular scale must be related to flows and deformation occurring at the tissue scale. Here I will discuss how this relation can be captured by a 3D vertex model or by a continuum theory of active surfaces subjected to internal torques. Using this framework, I will discuss epithelial fold formation in the Drosophila wing disc and the formation of pancreatic cancerous tumours.

BP 18.8 Wed 17:00 H10

Mechanical Properties of Head and Neck Squamous Carcinoma Cells — •Hsiao-Ching Tsai[1], Julia Kristin[2], Jörg Schipper[2], and Mathias Getzlaff[1] — [1]Institute of Applied Physics, Heinrich-Heine-Universität Düsseldorf — [2]Hals-Nasen-Ohren-Klinikum Düsseldorf

Several studies have shown that many human diseases can be associated to the mechanical properties of living cells. Additionally, elastic properties of cancer cells may play a major role in malignant processes. Since cell stiffness is related to invasiveness, we suggest that the elasticity parameter is a useful parameter to distinguish between cancer and non-malignant cells. Atomic Force Microscopy (AFM) is a powerful technique to determine mechanical properties. However, the characterization of mechanical properties of cells or tissue with AFM is relatively costly, difficult and time-consuming. Moreover, the experimental result is hard to reproduce due to the aquatic environment. Therefore, the discrimination of elastic properties of Head and Neck Squamous Carcinoma Cells (HNSCC), one of the most severe tumor cells, is not determined yet. In this study, we culture both normal cells and cancerous human oral cells from different location of head-neck area and applied them with an indentation study of AFM. With this measurement, we can get not only the cell morphology, but also the elastic modulus using Hertz Contact Model.

BP 19: Focus session: Physics of cilia: Dynamics of synchronized oscillators

Time: Wednesday 15:00–17:00 Location: H11

Invited Talk BP 19.1 Wed 15:00 H11

Self-organized wave-like beating of actin bundles — Marie Pochitaloff[1], Mathieu Richard[1], Takagi Yasuharu[2], Wenxiang Cao[3], Enrique De La cruz[3], Jim Sellers[2], Jean-François Joanny[1], Frank Jülicher[4], Laurent Blanchoin[5], and •Pascal Martin[1] — [1]Institut Curie, Paris, France — [2]NHLBI-NIH, Bethesda, USA — [3]Yale University, New Haven, USA — [4]MPIPKS, Dresden, Germany — [5]CEA, Grenoble

The emergent active behaviors of systems comprising large numbers of molecular motors and cytoskeletal filaments remain poorly understood, even though individual molecules have been extensively characterized. Here, we show in vitro with a minimal acto-myosin system that flagellar-like beating emerges naturally and robustly in polar bundles of filaments. Using surface micro-patterns of a nucleation-promoting factor, we controlled the geometry of actin polymerization to produce thin networks of parallel actin filaments. With either myosin Va or heavy-mero myosin II motors added in bulk, growing actin filaments self-organized into bundles that displayed periodic wave-like beating resembling those observed in eukaryotic cilia and flagella. We studied how varying the motor type or changing the size of the actin bundles influenced the properties of the actin-bending waves. In addition, using myosin-Va-GFP to visualize the motors within the actin bundle, we identified a novel feedback mechanism between motor activity and filament bending. Overall, structural control over the self-assembly process provides key information to clarify the physical principles underlying flagellar-like beating.

BP 19.2 Wed 15:30 H11

Toward synthetic cilia: bending oscillations of a microtubule-dynein system — •Isabella Guido[1], Ramin Golestanian[1], Andrej Vilfan[1], Eberhard Bodenschatz[1], and Kazuhiro Oiwa[2] — [1]Max-Planck Institute for Dynamics and Self-organization, Göttingen, Germany — [2]National Institute of Information and Communications Technology , Kobe, Japan

Cilia and flagella produce rapid and regular bending waves responsible for the propulsion of organisms in fluids or for the promotion of fluid transport. It is known that the main contribution to their beating is due to motor proteins, dynein, which drives sliding of the micro-

tubule doublets. However, the fundamental mechanism of the dynein-microtubule interaction is still a puzzle. Here we investigate their mechanical interaction and emergent behavior by analyzing a minimal synthetic system that we experimentally assemble with two microtubules and few dynein motors. We observe that the microtubule pair undergoes cyclical association/dissociation interaction through rhythmic bending, followed by a complete detachment of the microtubules and subsequent re-attachment. By considering the shearing force produced by the motors when they move along the adjacent microtubule and the finite elasticity of the system, we describe this beating cycle in terms of the curvature and dynein-microtubule binding force.

This work is supported by the BMBF and MPG through the MaxSynBio initiative.

BP 19.3 Wed 15:45 H11

Reconstitution of bio-mechanical oscillations in a minimal system — •Monique Honsa, Veikko F. Geyer, and Stefan Diez — B CUBE, TU Dresden, Germany

Bio-mechanical oscillations drive important biological processes through the dynamic interplay of molecular motors and filaments. To better understand the fundamental mechanism of the generation of oscillations in a minimal system, we realized a bottom-up approach of a bio-mechanical oscillator by using only three components – molecular motors, filaments and cross-linkers. In an *in vitro* kinesin-1 gliding motility assay, we cross-linked the leading tips of microtubules to the glass surface and observed the rhythmical buckling of the trailing parts of the microtubules with frequencies of 40 mHz and amplitudes of 2.5 μm. Remarkably, during buckling, parts of the microtubules moved up to three times faster than the gliding velocity of the microtubules. Our observations provide insight into the fundamental mechanisms involved in the generation of oscillations in motor-filament systems and are expected to lead to a better understanding of dynamic biological processes such as the flagellar beat.

BP 19.4 Wed 16:00 H11

SpermQ - a simple analysis software to comprehensively study flagellar beating and sperm steering — •Jan N Hansen[1], Sebastian Rassmann[1], Jan F Jikeli[1], and Dagmar Wachten[1,2] — [1]Institute of Innate Immunity, Biophysical Imaging, University Hospital Bonn, University of Bonn, 53127 Bonn, Germany — [2]Center of Advanced European Studies and Research (caesar), Molecular Physiology, 53175 Bonn, Germany

Motile cilia, also called flagella, are found in many species; some cilia propel cells like sperm, while cilia on epithelia create complex fluid patterns e.g. in the brain or lung. For sperm, the picture has emerged that the flagellum is not only a motor, but also a sensor, computing the beat pattern based on environmental cues and thereby, navigating the sperm through the female genital tract. It has been proposed that distinct flagellar signaling domains control the flagellar beat. However, a detailed analysis has been mainly hampered by the fact that current comprehensive analysis approaches rely on complex microscopy and analysis systems. Thus, knowledge on signaling regulating the flagellar beat is based on custom quantification approaches that are limited to only a few parameters, do not resolve the entire flagellum, rely on qualitative descriptions, and are little comparable among each other. Here, we present SpermQ, a ready-to-use and comprehensive analysis software to quantify sperm motility in common time-lapse images acquired by dark-field microscopy. We envision SpermQ becoming a standard tool in motile cilia and flagella research that allows to readily link individual signaling components and distinct flagellar beat patterns.

BP 19.5 Wed 16:15 H11

Meet the beat: an inter-species study of the 3-dimensional flagellar beat — •An Gong[1], Sebastian Rode[2], Rene Pascal[1], Benjamin Friedrich[3], Jens Elgeti[2], Stephan Irsen[1], Luz Perez[4], Gerhard Gompper[2], Benjamin Kaupp[1], and Luis Alvarez[1] — [1]Center of Advanced European Studies and Research (caesar), Bonn, Germany — [2]Institute of Complex Systems, Jülich, Germany — [3]Center for Advancing Electronics, Dresden, Germany — [4]Instituto de Ciencia y Tecnología Animal, València, Spain

Sperm capture sensory cues that are processed and translated into a time pattern of three-dimensional (3D) flagellar beat for propulsion and steering to find the egg. However, sperm of different species are confronted with quite different fertilization habitats and, accordingly, differ greatly in behaviors. The 3D flagellar beat pattern underlying behaviors and the molecular mechanism involved are not yet understood.

We used holographic microscopy to study the 3D movement of sperm flagella and the resulting swimming behaviors across different species including two external (sea urchin and eel) and two internal (human and mouse) fertilizers. The difference and commonalities among sperm from diverse species are described with a focus on sea urchin and human sperm. Furthermore, we describe novel features of the beat that underlie the sperm behaviors and we propose a link between these 3D beat features and internal flagellar structures.

BP 19.6 Wed 16:30 H11

Actuation of artificial cilia with surface acoustic waves — •Gerhard Lindner — Institut für Sensor- und Aktortechnik, Hochschule Coburg, 96450 Coburg, Germany

Surface acoustic waves such as Rayleigh or Lamb waves generate displacements at the surface with larger amplitudes than in the bulk volume. By them a periodic movement of cilia, whose tracing point is fastened at the surface, can be actuated. In case of an asymmetric bending stiffness of such cilia it is possible to excite a directional streaming in a fluid, which enables a pumping of this fluid. In particular, this allows an advantageous modification of the streaming profile in the boundary layer neighboring a solid wall. Corresponding estimations will be presented in this contribution. The concept is matter of the European patent EP 2545369 "Apparatus producing and/or detecting a flow in a medium" granted on May 30, 2018.

BP 19.7 Wed 16:45 H11

Light-Switchable Adhesive Functionalities of Eukaryotic Flagella — Christian Titus Kreis, Christine Linne, Marine Le Blay, Anni Röse, and •Oliver Bäumchen — Max Planck Institute for Dynamics and Self-Organization, D-37077 Göttingen, Germany

In contrast to marine phytoplankton, many photoactive microbes live in complex environments, such as liquid-infused soil and moist rocks, where they encounter and colonize a plethora of surfaces. We discovered that the flagella-mediated adhesion of the unicellular, eukaryotic microalga *Chlamydomonas* to surfaces can be reversibly switched on and off by light [1]. Our *in vivo* micropipette force spectroscopy (MFS) experiments [2] suggest that light-switchable adhesiveness is a natural functionality of flagella to actively regulate the transition between freely swimming (planktonic) and surface-associated state, which yields an adhesive adaptation of microbes to optimize their photosynthetic efficiency in variable and inhomogeneous light conditions. The kinetics of this transition can be readily probed by MFS experiments, where the cell actively pulls itself towards the substrate (auto-adhesion) until the cell achieves its gliding configuration on the surface. We show that the associated forces are exerted by molecular motors, which are connected to individual flagella-surface contacts. In conclusion, eukaryotic flagella are multifunctional cellular appendages that are not only essential for microbial propulsion but also for cellular adhesion to surfaces.

[1] C.T. Kreis et al., *Nature Physics* 14, 45-49 (2018).
[2] M. Backholm & O. Bäumchen, *Nature Protocols* (in press).

BP 20: Dynamics of multilayer networks II (joint session SOE/DY/BP)

Time: Wednesday 15:00–16:45 Location: H17

Topical Talk BP 20.1 Wed 15:00 H17

Delay controls chimera relay synchronization in multiplex networks — •Eckehard Schöll, Jakub Sawicki, Iryna Omelchenko, and Anna Zakharova — Institut für Theoretische Physik, Technische Universität Berlin, Germany

We study remote (or relay) synchronization in multilayer networks between parts of one layer and their counterparts in a second layer, where these two layers are not directly connected. A simple realization of such a system is a triplex network where a relay layer in the middle, which is generally not synchronized, acts as a transmitter between two outer layers; an example is provided by the hippocampus connecting distant parts of the brain. We find various partial synchronization patterns, in particular chimera states, i.e., complex patterns of coexisting coherent and incoherent domains, and establish time delay in the interlayer coupling as a powerful tool of control [1]. We demonstrate that the three-layer structure of the network allows for synchronization of the coherent domains of chimera states in the first layer with their counterparts in the third layer, whereas the incoherent domains either remain desynchronized or synchronized. As model dynamics we use the paradigmatic FitzHugh-Nagumo system.

[1] J. Sawicki, I. Omelchenko, A. Zakharova, and E. Schöll, arXiv:1807.11223v2 (2018).

BP 20.2 Wed 15:30 H17

Spiral wave patterns and their synchronization in lattices of nonlocally coupled discrete-time systems — Andrei Bukh, Galina Strelkova, and •Vadim Anishchenko — Saratov State University, Saratov, Russia

We investigate numerically the spatio-temporal dynamics of a 2D lattice of coupled discrete-time systems with nonlocal interaction. The individual map is given by a universal discrete system (the Nekorkin map) proposed for modeling the neural activity. The network behavior is studied for periodic and open boundary conditions. It is shown that for certain values of the nonlinear coupling parameters, rotating spiral waves and spiral wave chimeras can be observed in the considered lattice. We analyze and compare statistical and dynamical characteristics of the local oscillators from coherence and incoherence clusters of a spiral wave chimera. We also explore the effects of partial and complete synchronization of spiral wave chimeras in two coupled lattices of discrete maps with varying the intercoupling between the networks.

BP 20.3 Wed 15:45 H17

Synchronization of spiral wave patterns in coupled 2D lattices of discrete maps — •Andrei Bukh[1], Eckehard Schöll[2], and Vadim Anishchenko[1] — [1]Saratov State University, Saratov, Russia — [2]Technical University, Berlin, Germany

We study numerically the dynamics of two symmetrically and unidirectionally coupled lattices of nonlocally coupled two-dimensional Nekorkin maps. The phenomena of external and mutual synchronization of spiral wave patterns including chimera states are explored. The partial and complete synchronization is analyzed by calculating the number of synchronous elements in the coupled lattices depending on the coupling strength between them. Synchronous regimes are quanitified by using mutual correlation coefficients between the relevant elements in the lattices.

BP 20.4 Wed 16:00 H17

Transmission and synchronization of chimeras in a multilayer network of nonlocally coupled chaotic maps — •Galina Strelkova and Tatiana Vadivasova — Saratov State University, Saratov, Russia

We explore numerically transmission and external synchronization of chimera states in a multilayer network of unidirectionally coupled rings of nonlocally coupled logistic maps. We consider two cases: when all M coupled layers are identical (homogeneous) and when (M-1) identical layers differ from the first driving layer in their nonlocal coupling parameters. It is shown that the master chimera state in the first layer can be retranslating along the network with small distortions which are defined by a parameter mismatch. The synchronization effect is evaluated by calculating the mean-square deviation of the structure in the layers when varying the nonlocal coupling parameters.

BP 20.5 Wed 16:15 H17

Synchronization of chimera states in multilayer heterogeneous network of nonlocally coupled maps — •Elena Rybalova[1], Galina Strelkova[1], Tatiana Vadivasova[1], and Anna Zakharova[2] — [1]Saratov State University, Saratov, Russia — [2]Technical University, Berlin, Germany

We present numerical results on the study of a complex network composed of many asymmetrically coupled heterogeneous layers of nonlocally coupled logistic maps. Transmission and synchronization of chimera states realized in the first (master) layer is considered for mutual and unidirectional inter-coupling between the layers. It is shown that there is a threshold of the forced synchronization, which is different for various chimeras (phase and amplitude) in the master layer. It is established that the presence of feedback (backward) inter-coupling is a significant obstacle for global synchronization across the network. We also analyze and compare the role of heterogeneity in control and coupling parameters on the degree of forced synchronization.

15 min. break

BP 21: Biopolymers, biomaterials and bioinspired functional materials (joint session CPP/BP)

Time: Wednesday 15:45–18:30 Location: H13

Invited Talk BP 21.1 Wed 15:45 H13

Many Weak Interactions Make a Difference - from Fuzzy Biomolecular Self Assembly to Superselectivity — •Ralf Richter — School of Biomedical Sciences, Faculty of Biological Sciences, School of Physics and Astronomy, Faculty of Mathematics and Physical Sciences, and Astbury Centre for Structural Molecular Biology, University of Leeds, Leeds, LS2 9JT, United Kingdom

Multivalent interactions are key to molecular and cellular communication in biological systems, yet remain poorly understood. I shall present results of our efforts to better understand the role of multivalent interactions in two biological systems that involve biological polymers: (i) the nuclear pore permeability barrier, a meshwork of intrinsically disordered proteins that fills the nuclear pores and makes nucleo-cytoplasmic transport selective, and (ii) the interface between polysaccharide-rich extracellular matrix and the cell surface which is key to the communication of cells with their environment.

To study these systems on the supramolecular level, we take a multidisciplinary approach that combines surface science tools (to reconstitute well-defined model systems from the constituent molecules), biophysical characterization techniques (for quantitative analysis) and soft matter physics theory (to establish structure/property/function relationships).

The insights gained help us to uncover physical mechanisms underpinning functions, such as 'superselectivity' in the targeting of cell surfaces or the permeability of membranes, and help develop materials with new functions for applications in the life sciences.

BP 21.2 Wed 16:15 H13

DNA crookedness regulates DNA mechanical properties at short length scales — •J.G. Vilhena[1], Alberto Marin-Gonzalez[2], Fernando Moreno-Herrero[2], and Ruben Perez[3] — [1]Department of Physics, University of Basel — [2]Centro Nacional de Biotecnologia, CSIC, Spain — [3]Universidad Autonoma de Madrid, Spain

Sequence-dependent DNA conformation and flexibility play a fundamental role in specificity of DNA-protein interactions. Here we quantify the DNA crookedness: a sequence-dependent deformation of DNA that consists on periodic bends of the base pair centers chain. Us-

ing extensive 100 μs-long all-atom molecular dynamics simulations, we found that DNA crookedness and its associated flexibility are bijective: unveiling a one-to-one relation between DNA structure and dynamics. This allowed us to build a predictive model to compute the stretch moduli of different DNA sequences from solely their structure. Sequences with very little crookedness show extremely high stretching stiffness and have been previously shown to form unstable nucleosomes and promote gene expression. Interestingly, the crookedness can be tailored by epigenetic modifications, known to affect gene expression. Our results rationalize the idea that the DNA sequence is not only a chemical code, but also a physical one that allows to finely regulate its mechanical properties and, possibly, its 3D arrangement inside the cell.

BP 21.3 Wed 16:30 H13

Fast and on demand mussle-inspired adhesives by enzymatic polymerization of decapetides — •Maximilian Seuss[1], Justus Horsch[2], Patrick Wilke[2], Matthias Pretzler[3], Inga Melnyk[1], Dario Remmler[2], Annette Rompel[3], Hans G. Börner[2], and Andreas Fery[1] — [1]Leibniz-Institut für Polymerforschung Dresden e.V. — [2]Humboldt-Universität Berlin — [3]Universität Wien

A novel strategy to generate adhesive protein analogues by enzyme-induced polymerization of peptides is presented. Inspired by the repetitive nature of certain peptide sequences in mussel-foot protein mfp-1 we designed a polymerization reaction using these sequences as macromonomers. Peptide polymerization relies on tyrosinase oxidation of tyrosine residues to Dopaquinone, which rapidly forms cysteinyldopa with free thiols from cysteine residues. This forms a covalent bond between macromonomers and generates adhesive polymers. The resulting artificial protein analogues show strong adsorption to different surfaces, even resisting hypersaline conditions. Adhesion energies up to 10.9 mJ/m^2 are found in single adhesion events and average values are superior to those reported for mussel foot proteins that constitute the gluing interfaces.

BP 21.4 Wed 16:45 H13

Inequivalence of fixed-force and fixed-extension statistical ensembles for a flexible polymer tethered to a planar substrate — •Panayotis Benetatos[1] and Sandipan Dutta[2] — [1]Department of Physics, Kyungpook National University, Daegu, S. Korea — [2]Center for Soft and Living Matter, Institute for Basic Science, Ulsan, S. Korea

Recent advances in single macromolecule experiments have sparked interest in the ensemble dependence of force-extension relations (Gibbs versus Helmholtz). The thermodynamic limit may not be attainable for such small systems, that leads to inequivalence of the fixed-force and the fixed-extension ensemble. We consider an ideal Gaussian chain described by the Edwards Hamiltonian with one end tethered to a rigid planar substrate. We analytically calculate the force-extension relation in the two ensembles and we show their inequivalence which is caused by the confinement of the polymer to half space. The inequivalence is quite remarkable for strong compressional forces. We also perform Monte-Carlo simulations of a tethered wormlike chain with contour length 20 times its persistence length which corresponds to experiments measuring the conformations of DNA tethered to a wall. The simulations confirm the ensemble inequivalence and qualitatively agree with our analytical predictions for the Gaussian model. Our analysis shows that spatial confinement due to tethering causes ensemble inequivalence, irrespective of the polymer model.

15 min. break

BP 21.5 Wed 17:15 H13

Transverse viscoelastic properties of cellulose fibers investigated by atomic force microscopy — •Caterina Czibula[1,3], Christian Ganser[1,3], Ulrich Hirn[2,3], and Christian Teichert[1,3] — [1]Institute of Physics, Montanuniversitaet Leoben, Austria — [2]Institute of Paper, Pulp and Fibre Technology, Graz University of Technology, Austria — [3]CD Laboratory for Fiber Swelling and Paper Performance, Graz University of Technology, Austria

Cellulosic fibers are used in the paper and textile industry. To gain more insight on how mechanical properties of cellulose fibers are related to properties of end-products like paper, our work focusses on the transverse viscoelastic behavior of single cellulose fibers. To reach this ambitious goal we implemented an atomic force microscopy (AFM) based method. Probing nanoscale mechanical properties of soft materials with AFM yields information on the performance of the material. With the Johnson-Kendall-Roberts model, the contact between AFM tip and sample surface can be well described. The evaluation of the experimental data combines contact mechanics and viscoelastic models which consist of springs and dashpots in series or parallel describing elastic and viscous behavior, respectively. Here, it will be demonstrated that the so-called Generalized Maxwell model yields reasonable results for single pulp as well as viscose fibers at five different relative humidity (RH) values and in water. The RH increase leads to a steady decrease of the viscoelastic properties. Especially in water, the viscoelastic behavior shows a pronounced decrease, proving that the interaction of the fibers in water is different than at varying RH levels.

BP 21.6 Wed 17:30 H13

Elastic-Plastic Transition of Filament Networks — •Fanlong Meng[1] and Eugene Terentjev[2] — [1]Max Planck Institute for Dynamics and Self-Organization, Am Faßberg 17, 37077 Göttingen, Germany — [2]Cavendish Laboratory, University of Cambridge, JJ Thomson Avenue, Cambridge CB3 0HE, U.K.

Filament networks are ubiquitous in biological systems, such as cytoskeleton, extracellular matrix and connective tissue. The elasticity of a permanently crosslinked filament network is relatively well understood [1, 2]. However, the filament networks are usually transient because the filaments can dynamically break from and re-bonded to crosslinks including various proteins and biological motors. Because of the complexity in the spatial and the temporal evolution of the network structure induced by crosslink dynamics, the rheological properties of a transiently crosslinked is poorly investigated. Recently, we proposed a model where the total energy of a transient filament network is a function of time due to the breakage and the re-formation of crosslinks [3]. With the model, we successfully explain experimental observations including stress relaxation, shape recovery, and necking formation. Moreover, we provide a phase diagram detailing the conditions for a transient filament network to behave elastically, plastically or in a mixed way. References: [1] F. Meng, E. Terentjev, Soft Matter 12, 6749 (2016) [2] F. Meng, E. Terentjev Polymers, 9, 52 (2017) [3] F. Meng, E. Terentjev, Macromolecules 51, 4660 (2018)

BP 21.7 Wed 17:45 H13

Permanent Damage in Reversible Cross-linked Fiber Bundles — •Huzaifa Shabbir[1] and Markus Hartmann[2] — [1]Faculty of Physics, University of Vienna, Austria — [2]Ludwig Boltzmann Institute of Osteology at the Hanusch Hospital of WGKK and AUVA Trauma Centre Meidling, Vienna, Austria

Cross-linking is a common strategy to tailor the mechanical properties of polymeric systems. In natural systems, these cross-links are usually weaker than covalent bonds, which helps to maintain the structural integrity of the system preventing permanent damage [1].

Addition of cross-links to a polymeric system shows positive effects on many mechanical parameters, recent computational studies on cross-linked fiber bundles showed the surprising result that weak cross-links may deteriorate the strength of these systems [2]. This effect is strongly dependent on the coordination of cross-links [3], being most pronounced for the classical case of two-fold coordinated cross-links, i.e. one additional bond connecting two monomers. This presentation will discuss in detail the influence of cross-link coordination on this effect. In particular, Monte Carlo simulations have been used to detect the onset of permanent damage, the corresponding work and strength as a function of cross-link density and coordination. The results clearly indicate that systems with cross-links of higher coordination are more damage tolerant than classical two-fold coordinated cross-links.

[1] Fantner et al., Biophys. J. 90, 1411 (2006) [2] Nabavi & Hartmann, Soft Matter 12, 2047 (2016) [3] Shabbir & Hartmann, New Journal of Physics 19, (2017)

BP 21.8 Wed 18:00 H13

Capabilities of photoresists based on polysaccharides for Direct LaserWriting — •Marie-Christin Heep[1], Agnes Koerfer[1], Maximilian Rothammer[2], Cordt Zollfrank[2], and Georg von Freymann[1,3] — [1]Physics Department and Research Center OPTIMAS, TU Kaiserslautern, Germany — [2]Chair of Biogenic Polymers, TU Munich, Campus Straubing of Biotechnology and Sustainability, Germany — [3]Institute for Industrial Mathematics ITWM, Germany

Direct laser writing is a common method for fabrication of three dimensional micro- and nanostructures. The available materials have recently been expanded to polysaccharides [1]. These resists consist of

a photo-curable polysaccharide, a photo initiator and a solvent. The exact mixture defines the properties of the final material. A detailed discussion on the crosslinking density and hence the stability of the written structures as well as on the resolution and the feature size of the resist will be provided. These properties are most crucial for applications. Furthermore, we examine the surface roughness of the resist as well as the ability to self-assemble. The self-assembling of the resist is investigated with respect to the concentration of initiator. Different solvents are taken into account, to observe their influence on the handling of the resist. The knowledge about the influence of the exact mixture on the properties of the material allows the development of new resist for specific requierenments. This also allows the use of self-assembling processes for micro- and nanostructures with a tailored disorder.

[1] M. Rothammer et al., Cellulose **25**, 6031 (2018).

BP 21.9 Wed 18:15 H13

Towards an artificial human nail plate — •Kim Thomann[1], Andreas Späth[1], and Rainer H. Fink[1,2] — [1]Lehrstuhl für Physikalische Chemie II, Friedrich-Alexander Universität Erlangen-Nürnberg, Germany — [2]CENEM, Friedrich-Alexander Universität Erlangen-Nürnberg

Human fingernails cannot be studied ex vivo with the same ease as for example hair since only clippings can be obtained which do not necessarily reflect the behavior of the whole nail. Thus, we aim to create an artificial nail plate model that resembles the adhesive characteristics of the human finger nail suited for ex vivo studies. In order to mimic the surface free energy (SFE) as well as the morphology of the nail, we first investigated the surface properties of the natural fingernail using a number of methods. In vivo contact angle (CA) measurements were performed to determine the SFE. Water CAs along resin replicas of fingernails were measured and scanning electron micrographs were taken to correlate SFE with topography. Our first approach for an artificial nail plate model is based on mixed alkane thiol self-assembled monolayers, terminated with either -OH or -COOH and -CH3. CA measurements revealed that either the total SFE or the relation between the polar and dispersive component could be replicated, but both requirements could not be met simultaneously. Thus, microcontact printing (micro-CP) is considered to produce patterned SAMs at various periods to match the nail's microstructure.

BP 22: Annual general meeting of the BP division (BP Mitgliederversammlung)

Time: Wednesday 18:00–19:00 Location: H4

Report, discussion and election

BP 23: Biomaterials and biopolymers I (joint session BP/CPP)

Time: Thursday 9:30–12:45 Location: H10

BP 23.1 Thu 9:30 H10

A unifying perspective on rigidity in under-constrained materials — •Matthias Merkel[1,3], Karsten Baumgarten[2], Brian Tighe[2], and Lisa Manning[1] — [1]Department of Physics, Syracuse University, Syracuse, NY, USA — [2]Delft University of Technology, Delft, The Netherlands — [3]Centre de Physique Théorique, Université Aix-Marseille, France

We present a novel approach to understand rigidity in under-constrained materials, including sub-isostatic spring networks as well as 2D and 3D vertex models for dense biological tissues. We show that the onset of rigidity is determined by a purely geometric criterion. This allows us to analytically predict the elastic material properties close to the transition, which depend only on few geometric coefficients. We obtain exact expressions for the magnitudes of bulk modulus and shear modulus discontinuities at the rigidity transition, several scaling relations of the shear modulus, and the magnitude of the anomalous Poynting effect. Moreover, we show that the ratio of the excess shear modulus to the shear stress is inversely proportional to the critical shear strain with a prefactor of three, which we expect to be a general hallmark of rigidity in under-constrained materials induced by geometric incompatibility. This could be used in experiments to distinguish whether strain-stiffening as observed for instance in biopolymer networks arises from nonlinear characteristics of the microscopic material components or from effects of geometric incompatibility.

BP 23.2 Thu 9:45 H10

Heat and light - non-equilibrium tools to break early symmetry — Matthias Morasch[1], Corinna Kufner[2], Stefan Krebs[3], Hannes Mutschler[4], Wolfgang Zinth[5], Dieter Braun[1] und •Christof Mast[1] — [1]Systems Biophysics, LMU Munich, Amalienstr. 54, 80799 Munich, Germany — [2]Harvard-Smithsonian Center for Astrophysics, Harvard University, 60 Garden Street, Cambridge, MA 02138 — [3]Gene Center, LMU Munich, Feodor-Lynen-Straße 25, 81377 Munich, Germany — [4]MPI Biochemistry, Am Klopferspitz 18, 82152 Martinsried, Germany — [5]BMO, LMU Munich, Öttigenstrasse 67, 80538 Munich, Germany

Modern lifeforms perpetuate their highly evolved molecular structures by using them to convert external energy-fluxes for self-replication and evolution. It is an open question how this closed cycle could start around four billion years ago. At that time, no sophisticated enzymes were available to initiate that process from the initially random and racemic pool of early prebio-polymers. We investigate how physical non-equilibria could help this issue by breaking early symmetry and locally enrich oligomer pools with a reduced sequence space and with a homochiral backbone. We are especially interested in the effect of thermal gradients across small water-filled pores and of incident UV-light. Thermal convection chambers could have selected for interacting, hence homochiral, sequences by their thermophoretic and lengthdependent concentration while UV-light is known to damage oligomers in a sequence dependent manner.

BP 23.3 Thu 10:00 H10

Kinetic Control of Peptide Self Assembly Pathways — •Joshua T. Berryman and Ali Asghar Hakami Zanjani — University of Luxembourg, Luxembourg

Naturally occurring peptides may aggregate to form 3D amyloid-like crystals, or may take on quasi one-dimensional amyloid fibril structures. Mltiple distinct polymorphic structures often exist as subbranches within both the crystallising and fibril-forming pathways, differing either in overall symmetry or in only local conformational degrees of freedom.

We examine and discuss a system of aggregating peptides in which the available polymorphs are observed to differ in the macroscopic chirality of their assembly, with right-twisted fibrils, left-twisted fibrils, and non-twisted crystals forming sometimes even in the same sample. Using atomistic and also coarse-grained calculations we develop a structural and kinetic model for assembly of the amyloid-forming peptides and validate against light scattering and microscopy results [1,2]. We are able to provide a simple analytical expression to predict if a given set of experimental conditions (parameterised by temperature, concentration and pH) will lead to left-handed fibrils, right-handed fibrils or mesoscopic twist-free microcrystals [1].

[1] Reynolds et al., Nat. Comms. 8:1338 (2017)
[2] Lara et al., J. Am. Chem. Soc. 136(12):4732 (2014)

BP 23.4 Thu 10:15 H10

Early Stage Self Assembly of Flexible Peptides — •Ali Asghar Hakami Zanjani and Joshua T. Berryman — University of Luxembourg, Luxembourg

We use accelerated simulation methods to investigate the early stage nucleation processes of a homologous series of hexapeptides: ILQINS (from hen's egg-white lysozyme), IFQINS (from human lysozyme) and TFQINS (a disease-related mutation in humans). We observe that the majority of initially formed one-dimensional single beta sheets in

these systems have antiparallel alignment of peptide strands, in contrast to experimentally observed mature multi-sheet aggregates which have parallel strand alignment in all structures found to date [1-3].

We confirm the stability of the antiparallel aggregates by molecular dynamics simulations showing greater configurational stability for the antiparallel rather than parallel single beta sheets [4]. As mature antiparallel aggregates have not been observed for these systems we assume that such structures represent a kinetic trap, with limited potential to mature into amyloid fibrils or the related microcrystals. The existence of this kinetic trap offers the possibility to control amyloid formation by chemically directing small structures either towards or away from the antiparallel structures, depending if formation of macroscopic aggregates is considered beneficial or harmful.

[1] Reynolds et al., Nat. Comms. 8:1338 (2017)
[2] Lara et al., J. Am. Chem. Soc. 136(12):4732 (2014)
[3] Sievers, PhD Dissertations, (ProQuest, UMI: 3322087, 2008)
[4] Cooper, Beta-Sheet Geometry, (Birkbeck College, 1995)

BP 23.5 Thu 10:30 H10

The force spectroscopy of a biomimetic polymer in molecular simulations via perturbation theory — •Aviel Chaimovich[1], Christian Leitold[2], Kurt Kremer[3], and Christoph Dellago[4] — [1]Max Planck Institute of Colloids and Interfaces, 14476 Potsdam — [2]University of California, Santa Barbara 93106 — [3]Max Planck Institute for Polymer Research, Mainz 55128 — [4]University of Vienna, 1090 Vienna

It has become a common practice of probing various aspects of biological polymers via force spectroscopy. Considering that many proteins exhibit similar phenomena, we are interested in their corresponding universal signatures. For this purpose, we invoke molecular simulations of a biomimetic polymer: Although this homopolymer is solely based on a bead-spring model with a square-well potential, it is capable of universally capturing the protein-like unfolding of any heteropolymer [1]. Foremost, via the Wang-Landau procedure, we calculate at zero force the free energy as a function of the potential energy of the polymer [2]. We continue via perturbation theory, determining the free energy at nonzero force, applying it on different sets of monomeric sites. We in turn find scaling relations for the activation and transition of the biomimetic unfolding, relating these to various polymeric characteristics (e.g. the radius of gyration). Our findings consequently have important ramifications for protein unfolding.

[1] M. P. Taylor, W. Paul, and K. Binder (PRE, 2009). [2] C. Leitold and C. Dellago (JCP, 2014).

BP 23.6 Thu 10:45 H10

Heated microbubbles condense and encapsulate prebiotic molecules and enhance ribozymatic activity — •Matthias Morasch[1], Alan Ianeselli[1], Alexandra Kühnlein[1], Saidul Islam[2], Kristian Le Vay[3], Hannes Mutschler[3], Matthew W. Powner[2], Christof B. Mast[1], and Dieter Braun[1] — [1]Systems Biophysics, LMU Munich, Amalienstrasse 54, 80799 München — [2]Department of Chemistry, University College London, 20 Gordon Street, London, WC1H 0AJ, UK — [3]Max-Planck Institute for Biochemistry, Am Klopferspitz 18, 82152, Martinsried, Germany

Interfaces in an otherwise homogeneous system can drastically change local reaction dynamics. Here, we studied microscale water cycles by the application of a temperature gradients to microbubbles in water and found that it triggered a wide range of processes crucial for the origin of life. We could show that biomolecules increase in concentration more than 1000-fold by the capillary flow at the air-water interface. RNA precursors are found to crystallize around the bubble, allowing for a possible enantiomeric selection, while monomers undergo an enhanced phosphorylation. In the presence of vesicles, nucleic acids are concentrated and encapsulated in vesicle clusters, which are frequently ejected into the bulk solution. In addition, self-complementary RNA is demonstrated to form sequence-pure hydrogels, while the catalysis of the hammerhead ribozyme drastically increased at the interface compared to the bulk. The studied setting is hypothesized to be ubiquitous on early Earth.

15 minutes break.

BP 23.7 Thu 11:15 H10

Mechanical properties of UV-irradiated collagen fibrils studied with atomic force microscopy — •Marcus Schulze, Melanie Rogge, and Robert Stark — Physics of Surfaces, Materialwissenschaften, TU Darmstadt, Alarich-Weiss-Straße 16, 64287 Darmstadt

Collagen is a widely used component for the synthesis of substrates in the field of Tissue Engineering (TE). Cell adhesion and proliferation on theses substrates is strongly dependent on their mechanical properties which makes a controlled adjustment of these properties a key requirement for a more elaborated substrate design. Among several approaches, the irradiation of the collagen-based substrates with UV light proved itself a valuable technique to modify the mechanics without introducing cytotoxicity. For the evaluation of the influence of UV light on the mechanical properties of collagen fibrils in a liquid environment the atomic force microscope was used. Varying combinations of UV light sources (UV-A, UV-B, and UV-C) and fluids (deionized water and phosphate buffered saline (PBS)) were applied to two kinds of samples. The indentation modulus was measured on surface supported fibrils and a tensile modulus was derived from bending experiments on freely suspended collagen fibrils. Results suggested an increase in modulus within 30 minutes of treatment with UV-B or UV-C light in PBS.

BP 23.8 Thu 11:30 H10

The effect of surface functionalization and pH on protein-gold nanoparticle interactions — •Brahmaiah Meesaragandla[1,2], Isabel Garcia[3], Luis.M Liz-Marzán[3,4], and Mihaela Delcea[1,2] — [1]Institute of Biochemistry, University of Greifswald, Greifswald, Germany — [2]ZIK HIKE, University of Greifswald, Greifswald, Germany — [3]CIC biomaGUNE and CIBER de Bioingeniería, Biomateriales y Nanomedicina (CIBER-BBN), San Sebastián, Spain — [4]Ikerbasque, Basque Foundation for Science, Bilbao, Spain

In this work, we have investigated the interactions between differently functionalized gold nanoparticles (citrate, PEG-OMe, PEG-COOH, PEG-NH2, and glycan coated AuNPs) and human serum albumin (HSA) with pH using UV-Vis absorption, dynamic light scattering (DLS), and circular dichroism (CD) spectroscopy techniques. HSA exhibit different isomeric forms and undergoes conformational changes at different pH conditions (e.g. pH 3.8, 7.4, and 9.3). Both UV-Vis and DLS measurements have indicated the formation of protein corona. CD spectroscopy studies suggested that HSA conjugated to AuNPs undergoes a change in the secondary structure (decrease in alpha-helix) at various pH for all functionalized AuNPs. This change in protein secondary structure might be due to the type of dominant interaction between NPs and HSA (i.e electrostatic, hydrogen bonding). Our results indicated that both, surface charge and pH of the medium, influences the changes in HSA structure.

BP 23.9 Thu 11:45 H10

Temperature dependence of the elastic modulus of vapor deposited phospholipid bilayers on solid substrates — Maria J. Retamal[1], •Rodrigo Catalan[2], Marcelo Cisternas[2], Nicolas Moraga[2], Diego Diaz[2], Tomas P. Corrales[3], Mark Busch[4], Patrick Huber[4], Marco Soto-Arriaza[1], and Ulrich G. Volkmann[2] — [1]Faculty of Chemistry and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [2]Institute of Physics and CIEN-UC, P. Univ. Catolica de Chile, Santiago, Chile — [3]Department of Physics, UTFSM, Valparaiso, Chile — [4]TUHH, Hamburg, Germany

Phospholipid membranes (PMs) play a key role in most physiological processes. Besides the function of membrane proteins, changes in the fluidity of the phospholipid membrane are crucial in the permeability of certain molecules, such as oxygen or glucose. We analyze with Atomic Force Microscopy (AFM) and Surface Force Spectroscopy (SFS) the temperature dependence of Young's modulus (YM) of non-functional PMs (DPPC, DMPC and DSPC). Phospholipids were vapor-deposited in high vacuum onto silicon substrates. AFM measurements in liquid confirm the self-assembly of the phospholipid bilayer and YM measurements with SFS indicate the main transitions of the phospholipid bilayers. We show that PMs made by PVD in high vacuum preserve their structure and mechanical properties after proper hydration. This study opens new pathways to assemble phospholipid mixtures by means of solvent-free membrane formation. Acknowledgements: FONDECYT Nos. 3160803 (MJR), 1180939 (UGV), 1171047 (MSA) and 11160664 (TPC), CONICYT Fellowship (MC) and CONICYT-PIA ACT 1409.

BP 23.10 Thu 12:00 H10

Sequence effects on size, shape, and structural heterogeneity in Intrinsically Disordered Proteins — •Upayan Baul[1], Debayan Chakraborty[2], Mauro L. Mugnai[2], John E. Straub[3], Devarajan Thirumalai[2], and Joachim Dzubiella[1] — [1]Institute of Physics, Albert-Ludwigs-University of Freiburg, Hermann-Herder-Strasse 3, 79104 Freiburg, Germany — [2]Department of Chemistry, The

University of Texas at Austin, Austin, Texas 78712 — [3]Department of Chemistry, Boston University, Boston, Massachusetts 02215

Intrinsically disordered proteins (IDPs) lack well-defined three-dimensional structures, thus challenging the archetypal notion of structure-function relationships in proteins. We present the development of a coarse grained simulation model that quantitatively characterizes the structural features of IDPs as a function of sequence and length (N_T). For diverse IDP sequences, with N_T ranging from 24 to 441, our simulations not only reproduce the radii of gyration (R_g) obtained from experiments, but also predict the scattering intensity profiles in near quantitative agreement with Small Angle X-ray Scattering experiments. While R_g values are well-described by the standard Flory scaling law, $R_g = R_0 N_T^{\nu}$, with $\nu = 0.588$, analyses reveal that the extent of conformational heterogeneity for IDPs is highly sequence-dependent, even though ensemble-averaged properties suggest synthetic polymer-like behavior in a good solvent. In conclusion, we comment on the effects of external stimuli such as salt concentration and temperature on the conformational properties of polypeptide sequences.

BP 23.11 Thu 12:15 H10

Co-survival and competition relationship between bacteria analyzed in millifluidic droplet sequence — •Xinne Zhao[1], Larysa Baraban[1,2], and Gianaurelio Cuniberti[1,2] — [1]Institute of Materials Science and Max Bergmann Center of Biomaterials Dresden, TU Dresden, Dresden, Germany — [2]Center for advancing electronics Dresden, cfaed, Dresden

Analysis of living systems, e.g. bacterial or cells populations plays significant role in fundamental research of population diversity, and evolution.1 Here, we present an optical detection system, combining the encapsulation of bacteria into numerous emulsion droplets to monitor their long term behavior and their relationship in co-culture environment. The bacteria we choose here are BFP E.coli and YFP E.coli which can express blue fluorescence and yellow fluorescence separately under different light illuminations. By detecting the emission wavelength from different E.coli, we can obtain the information of growth state of each bacteria strain. Compared to the classical cell culture methods, the strategy we use here can avoid the influence of getting sample during bacteria growing, as well achieve real-time and automatic monitoring. In order to find out the co-survival and mutual competition relationship between the two bacteria strains, we plan to get the reference growth curve of individually culturing both strains, co-culture them with different initial cell concentration ratios, add antibiotics, as well as compare their maximum cell concentration and generation time.

[1] R. Illing et al, Biomicrofluidics, 2016, 10, 024115.

BP 23.12 Thu 12:30 H10

Collagen gels determine the viscoelastic properties of tissue without hindering the diffusion of the aqueous solvent — Frank Sauer[1], Linda Oswald[1], Angela Ariza de Schellenberger[3], Heiko Tzschätzsch[3], •Felix Schrank[3], Tony Fischer[2], Jürgen Braun[4], Claudia T. Mierke[2], Rustem Valiullin[5], Ingolf Sack[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 Radiology, Charité-Universitätsmedizin, Berlin, Germany — [4]Institute of Medical Informatics,Charité-Universitätsmedizin, Berlin, Germany — [5]Applied Magnetic Resonance, Felix Bloch Institute for Solid State Physics, Leipzig, Germany

Collagen accounts for the major extracellular matrix component in many tissues providing mechanical support for cells. Little is known whether water diffusion interacts with viscoelastic properties of tissues. We are combining highfield MR based diffusion measurements, novel compact tabletop MRE and confocal microscopy in collagen networks of different cross-linking states (untreated versus additional treatment with glutaraldehyde). The MRE-measured shear modulus is sensitive to interactions on the intrafiber level (e.g. fiber stiffness) and is able to depict the pronounced transition from viscous-soft to elastic-rigid gel properties. 3D pore size analysis indicate an unaltered overall network structure and MR based diffusion measurements further allude that there is free extracellular diffusive water transport in connective tissue.

BP 24: Cell adhesion and migration, multicellular systems I

Time: Thursday 9:30–13:00 Location: H11

Invited Talk BP 24.1 Thu 9:30 H11

Active motion in living systems: from molecules to assemblies of organisms — •Ben Fabry — Department of Physics, University of Erlangen-Nuremberg, Erlangen, Germany

The dynamics of active motion in living system is governed by intermittency and approach to kinetic arrest in striking analogy with inert non-equilibrium systems, including soft glasses and jammed colloidal assemblies. The emerging collective behavior of active agents, from molecules, cells, groups of cells up to the level of individual organisms, appears to depend on the shape and magnitude of the interaction potential between the agents and on the distance of the system's effective temperature from a critical point. These well-established concepts in condensed matter physics link dynamic interactions between the underlying elements to integrative biological functions at the macroscale, such as cytoskeletal arrangements at the leading edge of migrating cells, heterogeneity of immune cell migration, collective matrix invasion in metastasizing cancer cell assemblies, and the organization of penguin colonies.

BP 24.2 Thu 10:00 H11

Mechanics of tissue competition: Interfaces stabilize coexistence — Nirmalendu Ganai[1,2], •Tobias Büscher[1], Gerhard Gompper[1], and Jens Elgeti[1] — [1]Theoretical Soft Matter and Biophysics, Institute of Complex Systems, Forschungszentrum Jülich, 52425 Jülich, Germany — [2]Department of Physics, Nabadwip Vidyasagar College, Nabadwip, Nadia 741302, India

Cells grow and divide, which implies a change in volume. In physical terms, the conjugate force to a change in volume is pressure. Thus, in order to grow, cells must exert mechanical pressure on the neighbouring tissue. In turn, mechanical stress influences growth. This effect leads to a mechanical contribution when tissues compete for space. The tissue with higher homeostatic pressure, i.e. the pressure at which cell division and death balance, overwhelms the weaker one [2,3,4]. We expand these works to include different adhesion properties. Surprisingly, a weaker tissue can persist in stable coexistence with a stronger tissue, if adhesion between them is small enough. An analytic continuum description can quantitatively describe the underlying mechanism and reproduce the resulting pressures and cell-number fractions. Computer simulations furthermore display a variety of coexisting structures, ranging from spherical inclusions to a bicontinuous state.

[1] Ganai *et al*, 2018, arXiv:1809.10990
[2] Basan *et al*, 2011, *Phys. Biol.* **8**, 026014
[3] Podewitz *et al*, 2016, *EPL* **109**, 58005
[4] Podewitz *et al*, 2016, *New J. Physics* **18**, 083020

BP 24.3 Thu 10:15 H11

Interkinetic nuclear migration - a stochastic process constrained by tissue architecture — •Anne Herrmann[1], Afnan Azizi[2], Salvador J. R. P. Buse[2], Yinan Wan[3], Philipp J. Keller[3], William A. Harris[2], and Raymond E. Goldstein[1] — [1]Department of Applied Mathematics and Theoretical Physics, University of Cambridge, Cambridge, United Kingdom — [2]Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, United Kingdom — [3]Howard Hughes Medical Institute, Janelia Research Campus, Ashburn, VA, USA

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 develop a quantitative model for the phenomenological properties of IKNM in the retinal system. Both the data and our model support the hypoth-

esis of IKNM being a stochastic process during the majority of the cell cycle. Furthermore, our model reveals the remarkable and previously overlooked importance of simple physical constraints imposed by the overall tissue architecture. Because IKNM has been suggested to fulfil a regulatory role for retinal cell differentiation, our results have important implications for understanding proper eye development. Moreover, our findings will inform future work on IKNM in other organs and on the developmental regulation in these systems.

BP 24.4 Thu 10:30 H11

Continuum theory of bacterial aggregates — •Hui-Shun Kuan[1,2], Frank Jülicher[2], and Vasily Zaburdaev[1,2] — [1]Department of Biology, Friedrich-Alexander Universität Erlangen-Nürnberg, Erlangen, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Cellular aggregates are common in many biological settings, ranging from bacterial biofilms to organoids and tumors. The dynamics of these systems is intrinsically non-equilibrium and driven by active processes in individual cells. In this work, motivated by *Neisseria gonorrhoeae* bacteria we develop a continuum theory to study bacterial aggregates driven by attractive pili-mediated forces and with excluded volume interactions. We describe the process of aggregate formation as an active phase separation phenomenon and identify the physics of the coalescence between two aggregates. In addition, within the same framework we can describe the demixing process of two bacterial types differing in the properties of their pili–pili interactions and thus can recover the patterns observed in experiments. Furthermore, this general hydrodynamic approach offers a way to incorporate the viscoelastic nature of the bacterial colonies and provide a link to the experiments focusing on material properties of cellular aggregates.

BP 24.5 Thu 10:45 H11

External forces generated by the attachment between blastoderm and vitelline envelope impact gastrulation in insects — •Stefan Münster[1,2,3], Alexander Mietke[2,3], Akanksha Jain[1], Pavel Tomancak[1], and Stephan Grill[1,2] — [1]MPI-CBG, Dresden — [2]TU Dresden, Biotec — [3]MPI-PKS, Dresden

Gastrulation is a critical step during the development of multicellular organisms in which a single-layered tissue folds into a multi-layered germband. This shape change is characterized by tissue folding and large-scale tissue flow. The myosin-dependent forces that underlie this process have been increasingly investigated; however, thus far, the possible interaction between the moving tissue and the rigid shell surrounding the embryo has been neglected. Here, we present our quantitative findings on the physical mechanisms governing gastrulation in the red flour beetle, Tribolium castaneum. We investigated the forces expected within the tissue given the myosin distribution observed by multi-view light-sheet microscopy and discovered that an additional external force must be counteracting this tissue-intrinsic contractility. We then identified that a specific part of the tissue tightly adheres to the outer rigid shell. This attachment is mediated by a specific integrin whose knock-down leads to a complete loss of the counter-force. Moreover, in the fruit fly Drosophila melanogaster, knock-down of another integrin leads to a severe twist of the germband, suggesting that the integrin-mediated interaction between tissue and vitelline envelope may be conserved in insects.

15 minutes break.

BP 24.6 Thu 11:15 H11

Complex fluid flow and cell polarity in the brain ventricular system — •Christian Westendorf[1], Shoba Kapoor[2], Yong Wang[1], Gregor Eichele[2], and Eberhard Bodenschatz[1] — [1]Max Planck Institute for Dynamics and Self-Organisation, Goettingen, Germany. — [2]Max Planck Institute for Biophyscial Chemistry, Goettingen, Germany.

Brain ventricles, that are filled with cerebrospinal fluid (CSF), are coated by specialized epithelial cells each of which carries a bundle of beating cilia. The cilia beats create complex and directional flow patterns that transport CSF and its constituents within the ventricles. The proximal cause of such an organized transport network rests on intricate domains of beating cilia [1]. We used antibody staining and DIC microscopy to explore ciliary polarity and dynamics in the domains and now show that the foundation of the organized flow within and across domains is grounded on the translational and rotational polarities of the cilia bundles. In areas of straight CSF flow, cilia are oriented in a uniform and unidirectional manner. In domains of circular flow, cilia in adjacent cells are oriented in their beating directions so as to generate a circular architecture. In cases where two flow domains are in opposite direction, the beating direction is opposite and changes abruptly over just a few cells. In conclusion, the complex transport network in the ventricle is determined by the polarity properties of the ciliated cells and their cilia.

[1] R. Faubel, C. Westendorf, E. Bodenschatz and G. Eichele, Science 2016, 353(6295) p176-178.

BP 24.7 Thu 11:30 H11

Mechano-response and multicellular organization — •Sara Kaliman[1], Carina Wollnik[2], Damir Vurnek[1], Diana Dudziak[3], Florian Rehfeldt[2], and Ana-Suncana Smith[1] — [1]PULS group, Theoretical Physics I, Friedrich-Alexander-University, Erlangen — [2]3rd Institute of Physics - Biophysics, Georg-August-University, Göttingen — [3]Department of Dermatology, University Hospital, Friedrich-Alexander-University, Erlangen

Today, we know that mechano-response is one of the key regulators of a number of biological processes, including morphogenesis, cell differentiation and cancer progression. However, while there is good understanding of these effects in isolated cells, mechano-sensitivity in tissues remains heavily debated, and it remains unclear if tissue formation and individuals cells in a tissue are affected by surrounding rigidity. Here we show that mechano-response of multi-cellular colonies affects cell density in a steady state (homeostasis) as well as the cell density distribution within the colony. On the cellular level, decreasing substrate rigidity modulates cell proliferation and focal adhesions and induces switch from cuboidal to tubular epithelial structure. Surprisingly, despite strikingly different cell densities, different steady states are characterized by the same morphological features. On the other hand, tissues which are not in the steady state have different morphological properties. These results unequivocally relate cellular and macroscopic lengths scales in a tissue mechano-response.

BP 24.8 Thu 11:45 H11

Dynamics of vortices formed by active malaria parasites — •Pintu Patra[1], Anna Battista[1], Johanna Kratzer[2], Konrad Beyer[2], Astha Jaiswal[3], Karl Rohr[3], Friedrich Frischknecht[2], and Ulrich S. Schwarz[1] — [1]Institute for Theoretical Physics & BioQuant, Heidelberg University, Heidelberg, Germany — [2]Center for Infectious Diseases, Heidelberg University Medical School, Heidelberg, Germany — [3]Bioquant, University of Heidelberg & DKFZ, Heidelberg, Germany

Self-organised vortices can be observed in many biological systems, including schools of fish, groups of bacteria and active biopolymers. Here we study dynamic vortices formed by crescent-shaped Plasmodium sporozoites, the highly motile forms of the malaria parasite. Image processing of our experimental movies shows that the angular speed of sporozoites within a vortex is inversely proportional to their distance from the vortex centre, while their speed remains uncorrelated. Further, the distance of sporozoites from vortex centre is found to oscillate over time. To explain the characteristic features of sporozoite vortices, we develop an agent-based simulation, where each agent mimics the biophysical behaviour of an individual sporozoite. Our simulation shows that at high-density sporozoites can self-organize into vortices that recapitulate the experimentally observed features. Our quantification of motility statistics of sporozoites in the vortex state shows that vortex sporozoites are more dynamic than isolated sporozoites. Our study presents a new model system for the emergence of stable patterns by active particles with curved shapes.

BP 24.9 Thu 12:00 H11

Crawling to rolling: adhesion of malaria-infected red blood cells in shear flow — •Anil Kumar Dasanna[1] and Ulrich Sebastian Schwarz[2] — [1]Institute of Complex Systems (ICS-2), Forschungszentrum Jülich, Jülich, Germany — [2]BioQuant & Institute for Theoretical Physics, Heidelberg University, Heidelberg, Germany

During malaria infections, the adhesion of infected red blood cells (iRBC) in hydrodynamic flow is an essential step for parasite survival. The gradual change in morphology, stiffness and adhesiveness that takes place over the 48 hour cycle in the blood leads to complex adhesion dynamics in flow such as crawling, flipping and rolling. Earlier we have employed multiparticle collision dynamics for hydrodynamics combined with a deformable red blood cell model for simulating iRBC-adhesion in shear flow [1]. We now show that constant stiffening and change in the morphology drives the cells to unstable adhesion states

whereas growth in the number of knobs works in the reverse direction, resulting in middle-stage infected cells to achieve stable adhesion in flow with maximum contact area with the substrate, which is essential for increasing the residency time in the vasculature. We summarize our findings in a phase diagram.

[1] Christine Lansche, Anil K. Dasanna et al., The sickle cell trait affects contact dynamics and endothelial cell activation in Plasmodium falciparum-infected erythrocytes, Nature communications biology 2018 (in press).

BP 24.10 Thu 12:15 H11

Parallelized Manipulation of Single Cell Behaviour with Magnetic Nanoparticles and Micromagnetic Arrays — Koceila Aïzel[1], •Cornelia Monzel[1,2], Elie Balloul[1], Chiara Vicario[1], Loïc Toraille[3], João Sampaio[4], Stanislas Rohart[4], Nicolas Vernier[5], Mathieu Coppey[1], Loïc Rondin[3], Jean-François Roch[3], and Maxime Dahan[1] — [1]Laboratoire Physico-Chimie, Institut Curie, Paris, France — [2]Experimental Medical Physics, Heinrich-Heine Univ., Düsseldorf, Germany — [3]Laboratoire Aimé Cotton, CNRS, Univ. Paris-Sud, ENS Cachan, Orsay, France — [4]Laboratoire de Physique des Solides, CNRS, Univ. Paris-Sud, Univ. Paris-Saclay, Orsay, France — [5]Centre de Nanosciences et de Nanotech., CNRS, Univ. Paris-Sud, Univ. Paris-Saclay, Orsay, France

The spatial manipulation of functionalized magnetic nanoparticles (MNPs) on subcellular scales is a powerful approach to probe and actuate biological processes in cells. In order to realize the manipulation of MNPs in a remote and well-defined manner, micromagnets are placed in the vicinity of the cell. The magnetic fields generated by these micromagnetic cuboids are quantified using optical magnetometry. Here, the spin properties of NV color centers in diamond enable determination of mT magnetic field distributions with micrometer sensitivity. We then arrange the micromagnets in arrays surrounded by cells, to realize a parallelized high-throughput manipulation. Using these arrays, we show that MNPs are efficiently redistributed in multiple cells and that functionalized MNPs can activate smallGTPases of cell signalling pathways.

BP 24.11 Thu 12:30 H11

Probing the interface structure of adhering cells by contrast variation neutron reflectometry — •Bert Nickel[1], Philip Böhm[1], Joachim Rädler[1], and Erich Sackmann[2] — [1]Fakultät für Physik & CeNS, Ludwig-Maximilians-Universität, 80539 München — [2]Physikdepartment E22, Technische Universität München, 85748 Garching

The cell substrate distance and the amount of water in the membrane substrate gap is difficult to determine. Here, we present a neutron reflectometry study of confluent epithelial cell monolayers on silicon substrates. The neutron experiments have been performed at MLZ in Garching, using MARIA and REFSANS, in collaboration with A. Koutsioubas and J.F. Moulin, respectively. The cell chamber enabled perfusion with cell medium and allowed for contrast variation in-situ by sterile exchange of buffer with different H2O-to-D2O ratio. Contrast variation reduces the ambiguity of data modelling for determining the thickness and degree of hydration of the interfacial cleft between the adherent cells and the substrate. Our data suggest a three-layer interfacial organization. The first layer bound to the silicon surface interface is in agreement with a very dense protein film with a thickness of 10 nm, followed by a highly hydrated 25 nm thick layer, and a several ten nm thick layer attributed to the composite membrane. Hence, the results provide clear evidence of a highly hydrated region between the composite cell membrane and the substrate.

BP 24.12 Thu 12:45 H11

The heat is on: Understanding germ granule segregation in *C. elegans* — •Anatol W. Fritsch[1], Matthäus Mittasch[1], Carsten Hoege[1], Frank Jülicher[2], Moritz Kreysing[1], and Anthony Hyman[1] — [1]MPI-CBG, Dresden, Germany — [2]MPI-PKS, Dresden, Germany

During embryonic development sexually reproducing species rely on the segregation of germ granules as one characteristic to specify their germ line. In *C. elegans*, P granules, a type of germ granule, have been found to behave as liquid-like protein condensates. The underlying biochemical control of the segregation has been described as an mRNA competition mechanism. Furthermore, it has been suggested that this drives segregation via spatially defined changes in the phase separation behavior of the condensates.

Using physical principles underlying phase separation, we are able to rescue the asymmetric localization of P granules in mutants with defective segregation *in vivo*. We replace wild type biochemical control with a localized temperature gradient that mimics its physical mechanism. Furthermore, with this approach, we are able to invert the endogenous spatial distribution of P granules in zygotes. This enables us to study the dynamics of *in vivo* phase separation via controlled physical perturbations. In this study we conclude, that P granule segregation is a spatially tuned, diffusive-flux dependent, dissolution-condensation phenomenon.

BP 25: Physics of self-organization in DNA nanostructures (joint session CPP/BP)

Time: Thursday 12:15–13:00 Location: H13

BP 25.1 Thu 12:15 H13

Synthetic cells: Bottom-up assembly with DNA nanotechnology — •Kerstin Göpfrich[1,2], Kevin Jahnke[1,2], Ilia Platzman[1,2], and Joachim P. Spatz[1,2] — [1]Max Planck Institute for Medical Research, Department of Cellular Biophysics, Jahnstraße 29, D 69120, Heidelberg — [2]Department of Biophysical Chemistry, University of Heidelberg, Im Neuenheimer Feld 253, D 69120 Heidelberg

Bottom-up synthetic biology has been successful at isolating components from cells and reconstituting subcellular functions inside compartments. Progress towards a fully functional synthetic cell, however, requires strategies to recombine and arrange a multitude of components in space and time. We therefore propose to merge two precision technologies, namely microfluidics and DNA nanotechnology, to position and manipulate components in synthetic cells. In particular, we demonstrate that DNA can be used as a near-universal tool for responsive and programmable compartment functionalization. Our method relies on the self-assembly of single-stranded cholesterol-tagged DNA handles, which provide an addressable anchoring point for complementary DNA carrying an arbitrary functional group. Using this DNA handle approach, we demonstrate the stimuli-responsive attachment of reactive groups, DNA nanostructures, microspheres, an actin cortex and even living cells to the periphery of surfactant-stabilized droplets. We further employ DNA to construct functional components, including a pH-responsive DNA-based cytoskeleton mimic, which serves as a stabilizing cortex inside synthetic cells.

BP 25.2 Thu 12:30 H13

DNA-Assembled Plasmonic Waveguides for Nanoscale Light Propagation — •Thorsten-Lars Schmidt — Department of Physics, Kent State University, Kent, OH, USA — cfaed, TU Dresden, Germany

Plasmonic waveguides consisting of metal nanoparticle chains can localize and guide light well below the diffraction limit, but high propagation losses due to lithography-limited large interparticle spacing have impeded practical applications. We previously demonstrated a robust DNA-origami-based self-assembly pipeline of monocrystalline gold nanoparticles. More recently, we demonstrated that this method allows the interparticle spacing to be decreased below 2 nm, thus reducing propagation losses to 0.8 dB per 50 nm at a deep subwavelength confinement of 62 nm ($\sim\lambda/10$). We characterize the individual waveguides with nanometer-scale resolution by electron energy-loss spectroscopy. Light propagation towards a fluorescent nanodiamond is directly visualized by cathodoluminescence imaging spectroscopy on a single-device level, therefore realizing nanoscale light manipulation and energy conversion. Simulations suggest that longitudinal plasmon modes arising from the narrow gaps are responsible for the efficient waveguiding. With this scalable DNA origami approach, micrometer-long propagation lengths could be achieved, enabling applications in information technology, sensing and quantum optics.

BP 25.3 Thu 12:45 H13

Functionalized DNA Origami Nanostructures for Molecu-

lar Electronics — •Turkan Bayrak[1], Jingjing Ye[2], Richard Weichelt[3], Amanda Reyes[4], Alexander Eychmüller[3], Enrique Samano[4], Ralf Seidel[2], and Artur Erbe[1] — [1]Helmholtz-Zentrum Dresden-Rossendorf, Dresden, Germany. — [2]Peter Debye Institute for Soft Matter Physics, Universität Leipzig, Germany. — [3]Physikalische Chemie, Technische Universität Dresden, Germany. — [4]Centro de Nanociencias y Nanotecnología, Ensenada, México.

The DNA origami method provides a programmable bottom-up approach for creating nanostructures of any desired shape, which can be used as scaffolds for nanoelectronics and nanophotonics device fabrications. Based on this technique, the precise positioning of metallic and semiconducting nanoparticles along DNA nanostructures can be achieved. In this study, various DNA origami nanostructures (nanomolds, nanotubes and nanosheets) are used for the fabrication of nanoelectronic devices. To this end, gold nanoparticles, semiconductor quantum dots/rods are used in/on the DNA origami structures to create nanowires and transistor-like devices. The DNA origami nanowires and transistors were electrically characterized from room temperature (RT) down to 4.2K. Temperature-dependent characterizations of wires were performed in order to understand the dominant conduction mechanisms. Some nanowires showed pure metallic behavior. Transistor like devices showed Coulomb blockade behavior at RT. The study shows that self-assembled DNA structures can be used for nanoelectronic patterning and single electron devices.

BP 26: Single molecules biophysics

Time: Thursday 15:00–16:00 Location: H4

Invited Talk BP 26.1 Thu 15:00 H4

Understanding molecular machines by single-molecule FRET — •Thorsten Hugel — Institute of Physical Chemistry, livMatS and CIBSS, University of Freiburg, Germany

Many molecular machines associate and dissociate dynamically and/or alternate dynamically between multiple conformations. Common techniques are not ideal for studying such dynamics on relevant time scales from sub-micro-seconds to several hours. This dynamic information, ideally in and out of equilibrium, is crucial for a thorough understanding of the machines' function.

We have used networks of distance distributions obtained with single molecule FRET to simultaneously quantify large global conformational changes (seconds) and local dynamics (microseconds to milliseconds) in the molecular chaperone and heat shock protein Hsp90. The data reveal a state-specific suppression of the sub-millisecond fluctuations by dynamic Hsp90-substrate interactions, enabling an additional (orthogonal) regulation mechanism. The fundamental precision and accuracy of single-molecule FRET measurements as well as multi-color single molecule FRET will also be discussed.

In addition, we have developed a plasmon-ruler based single-molecule approach to study the conformational dynamics of Hsp90 over 24 hours at video rate. This unprecedented dynamic bandwidth reveals states with surprisingly long dwell times of many minutes. To be discussed are the impact of these findings on our understanding of conformational heterogeneity among proteins, protein denaturation, ergodic behavior, and non-Markovian dynamics (memory effects).

BP 26.2 Thu 15:30 H4

AFM-based Single-Molecule Force Spectroscopy on the Streptavidin:Biotin Interaction — •Steffen M. Sedlak[1], Leonard C. Schendel[1], Katherine R. Erlich[1], Achim Löf[1], Rafael C. Bernardi[2], Magnus S. Bauer[1], Carleen Kluger[1], and Hermann E. Gaub[1] — [1]Department of Physics and Center for NanoScience, LMU Munich, Germany — [2]University of Illinois at Urbana-Champaign, Urbana, IL, USA

The high-affinity interaction of the small molecule biotin with the tetrameric protein streptavidin (SA) is a widely applied tool for detection, labeling and immobilization of molecules. We study single biotin:SA interactions under force using AFM-based single-molecule force-spectroscopy (SMFS) and steered Molecular Dynamics (sMD) simulations. Probing monovalent SA in various specific tethering geometries, we investigated how the mechanical stability of the biotin:SA interaction depends on the force loading geometry and revealed the underlying molecular mechanism. We made use of the different unbinding forces to realize a protein-based bottom-up nanoscale assembly of single fluorescent molecules by single-molecule cut-and-paste; a unique approach that enables spatially controlled arrangements of diverse molecules into a single ensemble. We also studied SA of different valencies and distinguished unbinding forces of biotin from different SA subunits in AFM-based SMFS. sMD allowed to understand the force-propagation pathways through the SA tetramer. Identifying a long-lived tethering geometry, we can reliably measure single molecules at comparably high constant forces for many hours in magnetic tweezers.

BP 26.3 Thu 15:45 H4

Angstrom precision distance measurements in dynamic protein structures with single-molecule FRET — •Christian Gebhardt, Rebecca Mächtel, Niels Zijlstra, and Thorben Cordes — LMU München, Faculty of Biology, Großhaderner Str. 2-4, 82152 Planegg, Germany

Single-molecule Förster resonance energy transfer (smFRET) has evolved towards a mature toolkit for the study of distances, structures and dynamics of biomolecules in a physiologically relevant context in vitro and in vivo. There is, however, no generally accepted way to derive and use quantitative distance information from the FRET-ruler to derive structural models or constraints in the protein data base. Hellenkamp et al. (Nat. Methods, 2018) recently presented a quantitative smFRET study of oligonucleotide ruler structures that revealed high precision, accuracy and reproducibility of FRET-derived distances in a worldwide comparative study of 20 labs with a distance uncertainty below 6 angstrom. While this establishes smFRET as a suitable technique for accurate distance measurements of static biological reference structures, we raise the question if smFRET is applicable for proteins with dynamic conformational motions or allosteric modulations of protein structure by an effector. Proteins are more challenging targets for site-specific fluorophore labelling. We identified a model system to benchmark FRET-derived distance uncertainties in proteins for situations of (i) stochastic labelling and (ii) allosteric and dynamic modulation of the structure and show similar angstrom precision comparable to DNA.

BP 27: Biomaterials and biopolymers II (joint session BP/CPP)

Time: Thursday 15:00–17:00 Location: H10

BP 27.1 Thu 15:00 H10

Cell Adhesion as a Function of Hydrogel Layer Thickness: From Thin Layers to Bulk Samples — •Sandra Sindt, Galen Ream, and Christine Selhuber-Unkel — Institute of Materials Science, CAU Kiel, Germany

Cells are in vivo in contact with a large range of different mechanical environments. However, many tissues have complicated structures without distinct elasticity values, which can result in stiffness gradients close to their interfaces and cells are known to be capable of sensing a more rigid substrate underneath a soft structure. For example, Buxboim et al. have recently shown that mesenchymal stem cells show increased adhesive spreading on thin soft hydrogels due to a stiff underlying substrate. A threshold of rigidity sensing of fibroblasts was reported to be 60-70 micrometer thickness at approximately 1 kPa of elastic modulus. We here report results on the dependency of cell adhesion on hydrogel thickness and elasticity. This is of great importance for the design and development of coatings for various biomedical applications. We use polyacrylamide layers on glass slides with thicknesses below 100 micrometer to semi-infinite bulk samples (ca. 500 micrometer). Furthermore, we use two different elasticities to determine, if the effective cellular substrate sensing depth is affected by the elasticity of the samples. Our results demonstrate that the spreading area and circularity is strongly influenced by the thickness of the polyacrylamide samples. However, there was no conclusive difference in this effect for both stiffnesses.

BP 27.2 Thu 15:15 H10

Liquid-like protein condensates are glassy — •Louise Jawerth[1,2], Elisabeth Fischer-Friedrich[3], Suropriya Saha[1], Anthony Hyman[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 — [3]Biotechnology Center, Technische Universitat Dresden

Liquid-like protein condensates (LLPCs) 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 viscosity, surface tension and other material properties determine how segregated species diffuse into and within condensates; they, thus, critically impact the biological function of the condensates. It has become increasingly clear that some LLPCs 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 two proteins, PGL-3 and FUS, 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. This and other features we observe bear a striking resemblance to the behaviors observed in materials with glass-like aging suggesting that LLPCs are in fact not simple liquids but, rather, a type of soft glass.

BP 27.3 Thu 15:30 H10

The Poisson ratio of the cellular actin cortex is frequency-dependent — Marcel Mokbel[1], Kamran Hosseini[2], Sebastian Aland[1], and •Elisabeth Fischer-Friedrich[2] — [1]Hochschule für Technik und Wirtschaft, Dresden, Germany — [2]Biotechnology Center, Technische Universität Dresden, Dresden, Germany

Cell shape changes are vital for many physiological processes such as cell proliferation, cell migration and morphogenesis. They emerge from an orchestrated interplay of cellular force generation and cellular force response both crucially influenced by the actin cytoskeleton. To model cellular force response and deformation, cell mechanical models commonly describe the actin cytoskeleton as a contractile isotropic incompressible material. However, in particular at slow frequencies, there is no compelling reason to assume incompressibility as the water content of the cytoskeleton may change. Here we challenge the assumption of incompressibility by comparing computer simulations of an isotropic actin cortex with tunable Poisson ratio to measured cellular force response. Comparing simulation results and experimental data, we determine the Poisson ratio of the cortex in a frequency-dependent manner. Our results show that the Poisson ratio of the cortex depends on the frequency and may deviate from the incompressible case. In addition, our results suggest that the assumption of cortex isotropy is violated at large time scales likely due to anisotropic actin cortex repolymerization from the membrane.

Invited Talk BP 27.4 Thu 15:45 H10

3D scaffolds as cell-instructive biomaterials — •Christine Selhuber-Unkel — Institute for Materials Science, University of Kiel, Kiel, Germany

In vivo, many cell types are embedded in densely structured 3D environments. Such environments typically contain nano- and micropores or consist of nano- and microfibrous interwoven biopolymer structures. Mimicking such natural environments by synthetic materials can provide novel functionalities in many applications, particularly in tissue engineering. We therefore investigate 3D scaffold materials for their impact on cellular properties. As a first example, microchannels are embedded in a hydrogel matrix of well-defined stiffness, chemistry and conductivity. The scaffold provides a large and spatially controlled cell-surface contact area through the specific architecture of its pores, such that the specific properties of the environment have large impact on the cells and induce, e.g., cell capture. As a second example, carbon-based fibrous scaffolds will be introduced. These are highly attractive for applications that require conductive materials. In addition, they resemble the structural features of the natural extracellular environment and can be equipped with bioactive particles. Hence, 3D microstructured environments are promising candidates for instructing cells to execute specific and coordinated functions.

BP 27.5 Thu 16:15 H10

Effect of drug treatment on the formation of malaria pigment crystals — •Szilvia Mucza[1], Ana Strinic[2], Agnes Orban[1], Petra Molnar[3], Peter Furjes[4], Beata Vertessy G.[3], and Istvan Kezsmarki[1,2] — [1]Department of Physics, Budapest University of Technology and Economics — [2]Experimental Physics V, University of Augsburg — [3]Hungarian Academy of Sciences Research Centre for Natural Sciences — [4]Institute of Technical Physics and Materials Science, Centre for Energy Research, Hungarian Academy of Sciences

The malaria pigment crystals are a by-product of the metabolic process of malaria parasites. These few-hundred-nanometer sized needle-like crystals are unique indicators of the presence of infection. Our group developed a magneto-optical device for malaria diagnosis, which can precisely measure the concentration of the crystals produced by the parasites. The increasing crystal concentration in time indicates the growth of the parasites in a culture, thus, the device is also sufficient for drug screening using parasite cultures. In the present study, we found that the magneto-optical method is able to determine the size distribution of the crystals in addition to their concentration. By following the size distribution of the crystals throughout the life cycle of the parasites for drug-treated and untreated cultures we could specify the stage when the drug action takes place. The same method can also be used to reveal if the drug action is related to the blocking of crystal formation or has a different pathway.

BP 27.6 Thu 16:30 H10

Efficient hemozoin extraction from Plasmodium falciparum parasites — •Ana Strinic[1], Agnes Orban[2], Szilvia Mucza[2], Petra Molnar[3], Beáta Vértessy[3], Stephan Krohns[1], and Istvan Kezsmarki[1,2] — [1]Experimental Physics V, University of Augsburg — [2]Department of Physics, Budapest University of Technology and Economics — [3]Hungarian Academy of Sciences Research Centre for Natural Sciences

Hemozoin crystals are a natural biomarker of malaria infection. A prototypical magneto-optical setup uses magnetic and optical properties of hemozoin for a rapid and cheap, yet sensitive detection of malaria parasites within blood samples. As the parasites mature the volume of the crystallites produced within their food vacuole continuously increases. However, the age distribution of parasites within human blood and cell cultures is not homogenous. Thus, unveiling the relation between their age distribution and the size distribution of the hemozoin crystals may facilitate the monitoring of stage-specific drug actions and target oriented drug testing. Taking advantage of the high

sensitivity of the magneto-optical method not only to the crystal concentration but also to their size distribution, we aim to determine the relation of size versus age distribution. This however strongly depends on a successful hemozoin extraction from in vitro cultures. Here, I show, how the crystal extraction process and sample preparation affect the quality of the extracted crystals and the magnitude of the magneto-optical signal. This allows determining the optimal procedure and investigating reactions along the preparation, which reduce the hemozoin concentration.

BP 27.7 Thu 16:45 H10

Results of field trials of the rotating-crystal magneto-optical method for malaria detection — •Agnes Orban[1], Leandra Arndt[2], Tamarah Koleala[2], Jetsumon Sattabongkot[3], Stephan Karl[2], and Istvan Kezsmarki[1,4] — [1]Dept. of Phys., Budapest Uni of Tech. and Econ., Hungary — [2]Papua New Guinea Inst. of Med. Res., Madang, PNG — [3]Mahidol Vivax Res. Unit, Fac. of Tropical Medicine, Mahidol Uni, Bangkok, Thailand — [4]Exp. Phys. V, Center for Electronic Correlations and Magnetism, Uni. of Augsburg

Although malaria is still a global health burden, the current standard for its detection still remains the microscopic observation of stained blood smears. A novel cost-effective, automated, yet sensitive diagnostic method is needed for malaria detection both as an in-field instrument and as a laboratory tool.

Our group aims to design such a compact and inexpensive diagnostic device based on the detection of the magnetically induced linear dichroism exhibited by malaria pigment (aka. hemozoin). These micrometer-size crystals are promising malaria-diagnostic targets as they are unique indicators of the infection.

The rotating magnetic field employed in our system enables a very high sensitivity detection of hemozoin as tested on suspensions of synthetic crystals; on *Plasmodium falciparum* cultures, on mouse models and on human samples from field trials performed in Thailand and Papua New Guinea, the latter being the main focus of the talk.

BP 28: Statistical physics of biological systems II (joint session BP/DY)

Time: Thursday 15:00–17:30 Location: H11

BP 28.1 Thu 15:00 H11

Experimental evidence of symmetry breaking of transition-path times — •Jannes Gladrow[1], Marco Ribezzi-Crivellari[2,3], Felix Ritort[3,4], and Ulrich F. Keyser[1] — [1]Cavendish Laboratory, University of Cambridge, Cambridge CB3 0HE, UK — [2]Laboratoire de Biochimie (LBC), ESPCI Paris, PSL Research University, CNRS UMR8231 Chimie Biologie Innovation, Paris, France — [3]Condensed Matter Physics Department, University of Barcelona, 08028 Barcelona, Spain — [4]CIBER-BBN de Bioingenieria, Biomateriales y Nanomedicina, 28029 Madrid, Spain

While thermal rates of state transitions in classical systems have been studied for almost a century, associated transition-path times have only recently received attention. Uphill and downhill transition paths between states at different free energies should be statistically indistinguishable. Here, we systematically investigate transition-path-time symmetry and report evidence of its breakdown on the molecular- and meso-scale out of equilibrium. In automated Brownian dynamics experiments, we establish first-passage-time symmetries of colloids driven by femtoNewton forces in holographically-created optical landscapes confined within microchannels. Conversely, we show that transitions which couple in a path-dependent manner to fluctuating forces exhibit asymmetry. We reproduce this asymmetry in folding transitions of DNA-hairpins driven out of equilibrium and suggest a topological mechanism of symmetry breakdown. Our results are relevant to electrophysiology and single-molecule fluorescence experiments.

BP 28.2 Thu 15:15 H11

Unveiling lineage decisions in zebrafish neurogenesis — Emmanuel Than-Trong[1,2], •Bahareh Kiani[3], Alessandro Alunni[1,2], Benjamin D. Simons[4,5,6], Laure Bally-Cuif[1,2], and Steffen Rulands[3] — [1]Institut Pasteur, Unit Zebrafish Neurogenetics, Department of Developmental & Stem Cell Biology, 25 rue du Dr Roux, 75015 Paris, France — [2]CNRS, UMR3738, 25 rue du Dr Roux, 75015 Paris, France — [3]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Deutschland — [4]Cavendish Laboratory, Department of Physics, University of Cambridge, Cambridge CB3 0HE, UK — [5]The Wellcome Trust/Cancer Research UK Gurdon Institute, University of Cambridge, Cambridge CB2 1QN, UK — [6]The Wellcome Trust/Medical Research Council Stem Cell Institute, University of Cambridge, Cambridge CB2 1QN, UK

Zebrafish neural tissue hosts specialised precursor cells which fuel the ongoing production of neurons into discrete brain regions. To understand how neural maintenance is achieved in this system, we performed a quantitative clonal analysis of the fate of precursor cells. Lineage tracing in growing tissues is complicated by the fact that labelled clones fragment into disconnected clusters, rendering the retrospective analysis of cell fate highly ambiguous. Combining statistical inference with biophysical modelling we reconstructed the clonal origin of labelled cells, revealing that progenitor containing clones persist over the lifetime of the animal. Using stochastic modelling, we unveiled lineage relationships and proliferation kinetics in the adult zebrafish pallium.

BP 28.3 Thu 15:30 H11

Revealing chromosome organization from Hi-C data using a maximum entropy approach — •Joris Messelink[1], Jacqueline Janssen[2], and Chase Broedersz[1] — [1]Arnold Sommerfeld Centre for Theoretical Physics, LMU Munich — [2]Max Planck Institute for the Physics of Complex Systems, Dresden

The bacterial DNA outsizes the cell by roughly a factor of a thousand. The DNA must not only be highly condensed to fit inside the cell, but this condensed DNA must be organized inside the cell to facilitate functional processes of the chromosome. Thus, understanding the three-dimensional spatial organization of the bacterial chromosome is important to understand how the core biological processes are regulated inside of the cell. Recent chromosome conformation capture experiments provide genome-wide data on chromosome folding. In particular, the Hi-C method provides contact frequency maps of the chromosome, revealing its highly organized structure. We develop a maximum entropy approach to extract the three-dimensional structure of the bacterial chromosome from such data. The aim of our method is to develop a coarse-grained model for the statistical mechanics of the folding of the whole bacterial chromosome. From this model, we obtain the full distribution of chromosome configurations in the cell.

BP 28.4 Thu 15:45 H11

Control of droplet coarsening in active emulsions — •Christoph Weber[1], Marta Tena-Solsona[2], Jacqueline Janssen[1], Caren Wanzke[2], Fabian Schnitter[2], and Job Boekhoven[2] — [1]MPIPKS, Dresden — [2]TUM, Munich

Spatial-temporal regulation of liquid phase separation is crucial inside living cells. While spatial control can be achieved through concentration gradients, temporal control is often limited by the slow coarsening processes of droplet fusion and Ostwald ripening. Here we present a new class of active emulsions where the rate of coarsening can be dramatically accelerated in a controlled manner. This class of active emulsions involves a fuel that drives a chemical reaction from thermodynamically stable precursor molecules to metastable building blocks. At large enough concentrations of building blocks liquid droplets can form. We show by experimental studies of various active emulsions and a theory which quantitively coincides with the experimental measurements, how the metastable building blocks actually accelerate the coarsening kinetics in this novel class of phase separated systems. This class of active emulsions indicates novel possibilities to control sizes of assemblies in chemical engineering and may also rely on a mechanism used for the size regulation of membrane-less organelles in living cells.

BP 28.5 Thu 16:00 H11

Immune Repertoire Dynamics out of Steady State — •Mario Udo Gaimann[1], Jonathan Desponds[2], and Andreas Mayer[3] — [1]Ludwig-Maximilians-Universität München, Faculty of Physics, Munich, Germany — [2]University of California San Diego, Department of Physics, La Jolla, CA, USA — [3]Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, NJ, USA

Over the last ten years high-throughput sequencing of lymphocyte receptor repertoires has provided an increasingly precise view of how immune defenses are organized. A highly reproducible finding of these sequencing efforts has been that the clone sizes of lymphocytes which share the same receptor are heavy-tail distributed. Here, we present a simple neutral birth-death model kept out of steady-state by the arrival of new clones in which competition between cells for a global resource couples the birth rate to the total size of the immune repertoire. We show that this model produces transient, but long-lived power-law scaling of clone sizes through a rich-get-richer mechanism resembling preferential attachment. Our model predicts an onset of power-law scaling early in life, which should persist throughout the human lifespan in the biologically relevant parameter regime. We verify both predictions by reanalyzing previously published T cell receptor sequencing data from a human aging study. Furthermore, we demonstrate that our mechanism is robust to relaxations of the model assumptions including when competition is based on the lymphocyte receptor specificity. Overall, our work suggests that early life has a strong influence on the long-term structure of the immune repertoire.

BP 28.6 Thu 16:15 H11

Topological dynamics of small degree networks: percolation, rate equation, and stochastic network growth — •Adrian Fessel and Hans-Günther Döbereiner — Universität Bremen, Bremen, Deutschland

In self-organizing networks, topology and dynamic processes interact in a unique way: the network adapts its structure based on local activity, enabling the emergence of global dynamic properties on an optimized topology.
Working with *Physarum polycephalum* as an experimentally accessible model for an adaptive transportation system, we seek to formalize topological development into a sequence of discrete events intended to serve as basis for studying the interaction of flow and topology. We focus on reorganization of *P. polycephalum* networks after fragmentation, a process occurring in a prominent percolation transition in a system where system size is not fixed.
The theoretical description follows a master equation with parameters obtained from statistical analysis of experimental data. Computational investigation of the model recreates the dynamics of the topological phase transition and enables characterization of finite size effects and critical exponents. Comparing the influences of system growth and fusion within the system reveals a significant shift of the transition when system growth dominates.

Invited Talk BP 28.7 Thu 16:30 H11

Spontaneous buckling of active matter — •Karsten Kruse — NCCR Chemical Biology, Departments of Biochemistry and Theoretical Physics, University of Geneva, 1211 Geneva, Switzerland

Active matter in living systems is often organized in the form of quasi two-dimensional sheets. Examples are the actin cortex of animal cells or epithelial cell monolayers in organisms. In many processes, these sheets fold, for instance, during cell division or gastrulation, which is the developmental process of inward folding of a single-cell layered sphere in early embryogenesis. The molecular players and signaling cascades involved in these processes have been studied in detail. In contrast, the underlying mechanics remains poorly characterized. This is in large part due to technical difficulties in measuring the material properties of these systems as well as the forces acting on them. Theoretical analysis can shed light on the mechanics governing the spontaneous buckling of active matter as I will illustrate by two model systems: One system consists of an initially homogenous actomyosin sheet reconstituted *in vitro* that can buckle spontaneously into states of positive and negative Gaussian curvature upon contraction. The other example is provided by a cell monolayer growing on the inside of an elastic sphere. It buckles spontaneously as cells continue to proliferate beyond the state when the whole inner surface of the sphere is covered with cells. In both cases, theoretical analysis allows to extract mechanical properties of the active materials that are difficult to assess otherwise.

BP 28.8 Thu 17:00 H11

Phase separation in the ensemble of fixed pH — •Omar Adame-Arana[1], Christoph A. Weber[1], Vasily Zavurdaev[1,2], Jacques Prost[3], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]Friedrich-Alexander Universität Erlangen-Nürnberg, Cauerstr. 11, 91058 Erlangen, Germany — [3]Institut Curie, 26 rue d'Ulm, 75248 Paris Cedex 05, France

Recent developments at the interface of biology and physics brought to light the importance of phase separation in explaining biological processes in the cell. It has been shown that some proteins are able to phase separate in solution and form liquid-like droplets in the cytoplasm that carry out a distinct biological function. Particularly, a drop in the cytosolic pH leads to a widespread protein assembly in the cytoplasm, this phenomenon triggered our interest to the mechanism of protein phase separation as a function of pH. In order to study this mechanism, we define a model of a solution composed of macromolecules which can exist in three different charge states and have a tendency to phase separate. The pH dependence is introduced in terms of chemical reactions which control the charge state of the macromolecules. Using conservation laws and chemical equilibrium, we identify the conjugate variables of the system. We then perform a Legendre transform which defines the free energy corresponding to a fixed pH ensemble. We conclude by showing phase diagrams as a function of pH, where we find that under most conditions, phase separation is most pronounced near the isolectric point.

BP 28.9 Thu 17:15 H11

Kleiber's law scaling of the metabolic rate in planarians — Albert Thommen[1,2], Steffen Werner[2,3], Olga Frank[1], Jenny Philipp[4], Oskar Knittelfelder[1], Yihui Quek[2,5], Karim Fahmy[4], Andrej Shevchenko[1], •Benjamin M. Friedrich[2,6], Frank Jülicher[2], and Jochen C. Rink[1] — [1]MPI CBG, Dresden. Germany — [2]MPI PKS, Dresden, Germany — [3]AMOLF, Amsterdam, Netherlands — [4]HZDR, Dresden, Germany — [5]MIT, Cambridge, USA — [6]cfaed, TU Dresden, Germany

Kleiber's law states that the metabolic rate of animals scales with the 3/4 power of their body mass. It is considered one of the few quantitative laws in biology, yet its mechanistic basis remains unknown. Here, we take advantage of the reversible changes in body size by 2 orders of magnitude as function of food abundance in the planarian *Schmidtea mediterranea*. Using microcalometry, we show that Kleiber's law applies to adult organisms of this flatworm species. Intriguingly, the metabolic rate per cell is independent of organism size. Instead, Kleiber's law in planarians results from a size-dependent increase in mass per cell, reflecting a higher proportion of energy stores in large animals. Using a minimal energy balance model, we relate energy currents to growth and degrowth rates, in quantitative agreement with experiment. Our study is a first step to link energy fluxes, metabolism, and pattern formation in living matter.

[1] Thommen et al. BioRxiv; doi: https://doi.org/10.1101/332916 (accepted in eLife)

BP 29: PhD Focus session: Theory of stochastic processes with applications in biology (joint session SOE/BP/DY/AKjDPG)

Session initiated and organized by Rosalba Garcia Millan, Johannes Pausch and Ignacio Bordeu Weldt (Imperial College, UK), in cooperation with divisions DY, BP, SOE and the jDPG.

Time: Thursday 15:00–18:45 Location: H17

Invited Talk BP 29.1 Thu 15:00 H17

Ecosystem stability and altruistic advantage — •Nick Jones — Imperial College Mathematics, London, UK

In this talk I consider why many, empirically observed, directed networks might contain a lack of feedback loops. An answer might be network growth mechanisms that favour clear trophic levels and which generate assymetries between the in degrees and out degrees of nodes. This is a partial answer to May's (Complexity-Stability) Paradox. Finally I will outline an, ageing relevant, concrete biological example of spatial demographic stochasticity where altruists can dominate a system even when actively selected against.

BP 29.2 Thu 15:45 H17

Thermodynamics of steady-state switching — •Jacob Cook[1,2] and Robert G. Endres[1,2] — [1]Department of Life Sciences, Imperial College, London, UK — [2]Centre for Integrative Systems Biology and Bioinformatics, Imperial College, London, UK

Entropy production is a hallmark of nonequilibrium processes in stochastic thermodynamics. Multistable nonequilibrium systems are abundant outcomes of nonlinear dynamics with feedback yet relatively little is known about what determines the stability of the steady states and their switching rates in terms of entropy and entropy production. Here, we will link the fluctuation theorem for the entropy production along trajectories and the large-deviation approach of minimum-action-path theory to elucidate the thermodynamics of steady-state switching. Interestingly, we find that the entropy production at steady state plays no explicit role, but the entropy production along switching trajectories is key. Alternative stabilising and destabilising mechanisms such as steady-state entropy and diffusive noise are also investigated.

BP 29.3 Thu 16:00 H17

Dynamical phase transition in assemblies of chemotactic cells — •Charlie Duclut — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

We consider a large number of chemotactic cells that diffuse, die, divide and interact at long range via the release of chemicals. We investigate the dynamics at long time and focus on the phase transition that occurs between a dilute and a dense phase using a renormalization group analysis. If we consider only interactions that conserve the particles number, exact scaling exponents can even be obtained; this analysis predicts in particular a superdiffusive behaviour of the cells close to the phase transition.

Invited Talk BP 29.4 Thu 16:15 H17

Topological Hindrance and Jamming Transitions in Multi-Species Transport — •Erwin Frey — Arnold-Sommerfeld-Center for Theoretical Physics, Ludwig-Maximilians-Universität München, München, Germany

Motivated by recent experimental studies that have addressed the stepping behavior of kinesins, we investigate a lattice gas model for simultaneous transport of two species of active particles on a microtubule. The species are distinguished by their different gaits: While the first species moves straight ahead, the second follows a helical path. We show that the collective properties of such systems critically differ from those of one-species transport as described by generalised totally asymmetric exclusion processes. This is most evident in a jamming transition far below full occupation, as well as in nonequilibrium pattern formation. The altered behavior arises because - unlike the case in single-species transport - any given position may be targeted by two particles from different directions at the same time. However, a particle can leave a given position only in one direction. This simple change in connectivity significantly amplifies the impact of steric interactions and thus becomes a key determinant of mixed species transport. We computationally characterize this type of hindrance and develop a comprehensive stochastic theory for collective two-species transport along a cylinder. Our observations show high robustness against model extensions that account for additional biomolecular features which suggests relevance also in a biological context.

15 min. break

Invited Talk BP 29.5 Thu 17:00 H17

Seeing and believing at super-resolution — •Susan Cox — Randall Centre for Cell and Molecular Biophysics, King's College London

Super-resolution microscopy is a powerful tool for imaging structures at a lengthscale of tens of nm, but its utility for live cell imaging is limited by the time it takes to acquire the data needed for an image. For localisation microscopy the acquisition time can be cut by more than two orders of magnitude by using advanced algorithms which can analyse dense data, trading off acquisition and processing time. Information can be traded for resolution: for example, the whole dataset can by modelled as arising from blinking and bleaching fluorophores (Bayesian analysis of Blinking and Bleaching), although at a high computational cost. However, all these approaches will come with a risk of artefacts, which can mean that the image does not resemble the underlying sample. We have recently developed Harr Wavelet Kernel Analysis, a multi-timescale prefiltering technique which enables high density imaging without artefacts. The results of benchmarking with other techniques reveal that at high activation densities many analysis approaches may achieve high apparent precision (very sharp images), but poor accuracy (the images don't look like the sample). I will discuss the relationship between precision, accuracy and information content in super-resolution microscopy images.

BP 29.6 Thu 17:45 H17

Filament flexibility enhances power transduction of F-actin bundles — •Alessia Perilli[1], Carlo Pierleoni[2], Giovanni Ciccotti[1], and Jena-Paul Ryckaert[3] — [1]Dept. of Physics, Sapienza University of Rome, Italy — [2]Dept. of Physical and Chemical Sciences, University of L'Aquila, Italy — [3]Dept. of Physics, Free University of Brussels, Belgium

In different biophysical cellular processes, semiflexible biofilaments like Factin and F-tubulin are known to exploit chemical free energy, associated to their growth by polymerization, to perform mechanical work against an external load. In vitro experiments have recently been set up to measure the force-velocity relationship of an actin bundle or to equilibrate the bundle polymerizing force by an optical trap restoring force. Theoretical interpretation is usually based on multi filament brownian ratchet models assuming perfectly rigid filaments (Mogilner-Oster). In this talk, we will exploit statistical mechanics tools and a coarse grained stochastic dynamic approach based on the discrete Wormlike Chain (WLC) model, to study the influence of filament flexibility on the non-equilibrium velocity-load relationship for a bundle of parallel un-crosslinked actin filaments pressing against a mobile wall. Using a realistic value of the actin persistence length, we show that flexibility enhances the power developed by the polymerizing force against the load in a way which increases with the length of the bundle, as long as the pushing filaments remain in the nonescaping regime.

Topical Talk BP 29.7 Thu 18:00 H17

Reconstructing the topographic landscape of epithelial-mesenchymal plasticity — •Francesc Font-Clos, Stefano Zapperi, and Caterina A. M. La Porta — Center for Complexity and Biosystems, University of Milan, Italy

We construct a topographic map underlying epithelial-mesenchymal plasticity by combining numerical simulations, statistical physics methods and analysis of bulk and single-cell gene expression data. The map reveals a multitude of metastable hybrid phenotypic states, separating stable epithelial and mesenchymal states, and is reminiscent of the free energy measured in glassy materials and disordered solids.

Topography of epithelial-mesenchymal plasticity, Francesc Font-Clos, Stefano Zapperi, Caterina A. M. La Porta, Proceedings of the National Academy of Sciences Jun 2018, 115 (23) 5902-5907; DOI:

10.1073/pnas.1722609115

BP 29.8 Thu 18:30 H17

Beating cancer 'escape room': let's use mathematical modelling to unlock cells! — •Núria Folguera-Blasco — The Francis Crick Institute, London, UK

The inherent capacity of differentiated cells to switch their phenotype in vivo in response to damage stimuli might have a pivotal role in ageing and cancer. However, how the mechanisms of phenotype reprogramming are established remains poorly understood. In order to elucidate such mechanisms, we present a stochastic model of combined epigenetic regulation (ER)-gene regulatory network (GRN) to study the plastic phenotypic behaviours driven by ER heterogeneity. Our analysis of the coupled system reveals the existence of pluripotent stem-like and differentiated steady-states. Crucially, ER heterogeneity is responsible for conferring abnormal robustness to pluripotent stem-like states, which cause the locking of the cells in a stem cell-like state prone to cancer development. By analysing the ER heterogeneity, we formulate epigenetic heterogeneity-based strategies capable of unlocking and facilitating the transit from differentiation-refractory (pluripotent stem-like) to differentiation-primed epistates. Our results suggest that epigenetic heterogeneity regulates the mechanisms and kinetics of phenotypic robustness of cell fate reprogramming. The occurrence of tunable switches capable of modifying the nature of cell fate reprogramming from pathological to physiological might pave the way for new therapeutic strategies to regulate reparative reprogramming in ageing and cancer.

BP 30: Cell mechanics III

Time: Thursday 16:15–17:00 Location: H4

BP 30.1 Thu 16:15 H4

Passive and active response of bacteria under mechanical compression — •Renata Garces[1], Samantha Miller[2], and C.F. Schmidt[1,3] — [1]DPI, University of Goettingen — [2]The Institute of Medical Sciences, University of Aberdeen — [3]Department of Physics, Duke University

The ability to maintain a positive turgor pressure, by means of higher osmolarity of the cell interior than the exterior, is a requirement for proper metabolism in walled microbial cells. Turgor pressure is sensitive to changes in external osmotic conditions, and is drastically increased upon osmotic downshock, together with cell volume. Bacteria prevent lysis caused by excessive osmotic pressure through mechanosensitive (MS) channels: membrane proteins that release solutes (ions) in response to mechanical stress. The exact mechanism of channel gating in the natural setting, however, has been elusive due to the lack of experimental methods appropriate for the small dimensions of prokaryotes. We here present experimental data on the gating of MS channels of E. coli subjected to compressive force under iso-osmotic conditions. We indent living cells with micron-sized beads attached to the cantilever of an atomic force microscope (AFM) and characterize the mechanical response. We show that turgor pressure can be monitored through the measured response and quantify its value and fluctuations for individual single cells before and after MS channel gating.

BP 30.2 Thu 16:30 H4

Moving chromosomes in intact cell nuclei — Matthäus Mittasch[1], Anatol Fritsch[1], Michael Nestler[2], Juan Iglesias[1], Archit Bhatnagar[1], Kaushikaram Subramanian[1], Axel Voigt[2], and •Moritz Kreysing[1] — [1]MPI of Cell Biology, Dresden — [2]Department of Mathematics, TU Dresden

Recently we have described that we can move the cytoplasm of cells and developing embryos in a non-invasive manner (1). Here we demonstrate that we can optically generate hydrodynamic flows also in the nucleoplasm of developing C. elegance embryos during mitosis. Induced flows cause the instantaneous motion of chromosomes, indicating the absence of inertia and elastic creep relaxation in the nucleoplasm. Furthermore, chromosomes may be moved in time-reversal manner, which characterizes the mitotic nucleus as Stokes fluid type suspension of colloidal particles. We explicitly show that prophase chromosomes are free to exchange neighbors. Using the Stokes Einstein relation we estimate flow induced forces to be on the order of 10-100fN only, emphasizing the non-invasive character of induced flows. Biologically interesting, we find that altering chromsome position does not impact developmental success. This largely rules out a functional relevance of trans-mitotic inheritance of chromosome positioning.

Reference: Mittasch et al., " Non-invasive perturbations of intracellular flow reveal physical principles of cell organization", Nature Cell Biology 1 (2018)

BP 30.3 Thu 16:45 H4

Microtissues as an In-vitro platform for Investigating Muscle Mechanics — •Delf Kah, Ingo Thievessen, Marina Spörrer, Wolfgang Goldmann, and Ben Fabry — Department of Physics, Biophysics Group, Friedrich-Alexander-University Erlangen-Nuremberg, D-91052, Erlangen, Germany

In-vitro engineered muscle tissue grafts are of growing interest for different applications including regenerative therapy, replacement of infarcted cardiac sites, or as a drug testing platform. Critical for the successful development of suitable models for engineered muscle grafts is the maturation into an in-vivo-like, highly aligned, and contractile tissue. To achieve this, we established a stretchable and electrically paceable system consisting of an array of 4x2x2 mm microwells with two elastic pillars that serve as force sensors. Our system provides a universal platform for a variety of cell-mechanical investigations of different types of muscle tissue. Cardiomyocytes mixed with collagen, for example, form aligned tissues that show distinct mechanical response depending on the stiffness of the PDMS pillars. This indicates a force feedback in response to the mechanical regime similar to the classic Frank-Starling mechanism. Tissues from skeletal muscle cells, on the other hand, show increased static contractility when exposed to mechanical stress during early tissue development.

BP 31: Cell adhesion and migration, multicellular systems II

Time: Friday 9:30–12:00 Location: H10

Invited Talk BP 31.1 Fri 9:30 H10

Mechano-chemical self-organization determines search pattern in migratory cells — •Milos Galic — Institute of Medical Physics and Biophysics, University of Muenster, Germany

Efficient signal detection is fundamental for motile cells. To optimize their search strategy, cells seeking signal inputs employ non-Brownian motion pattern. Combining experimental and theoretical analysis, we identify a self-organizing system for super-diffusive two-state motion. We demonstrate that nanoscale plasma membrane deformations at the leading edge nucleate a mechano-chemical feedback loop that mediates polarization longevity and in consequence migration persistence. The resulting two-state motion, defined by continuous transitions between random and persistent phases, reduces oversampling to expand the search area. Collectively, the findings establish a mechanism for optimized search efficiency of vertebrate cells in the absence of polarized signal inputs.

BP 31.2 Fri 10:00 H10

Entropic DNA swelling drives complex cellular behavior — •Sebastian Kruss — Universität Göttingen, Göttingen, Germany

Neutrophilic granulocytes are able to release their own DNA as neutrophil extracellular traps (NETs) to capture and eliminate pathogens. DNA expulsion (NETosis) has also been documented for other cells and organisms, thus highlighting the evolutionary conservation of this process. Moreover, dysregulated NETosis has been implicated in many diseases, including cancer and inflammatory disorders. During NETosis, neutrophils undergo dynamic and dramatic alterations of their cellular as well as sub-cellular morphology whose biophysical basis is poorly understood. Here we investigate NETosis in real-time on the single-cell level using fluorescence and atomic force microscopy. Our results show that NETosis is highly organized into three distinct phases with a clear point of no return defined by chromatin status. Entropic chromatin swelling is the major physical driving force that causes cell morphology changes and the rupture of both nuclear envelope and plasma membrane. Through its material properties, chromatin thus directly orchestrates this complex biological process.

BP 31.3 Fri 10:15 H10

Stochastic Nonlinear Dynamics of Confined Cell Migration — •David Brückner[1], Alexandra Fink[2], Christoph Schreiber[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

In many biological phenomena, cells migrate through confining structured environments. We study how migrating cells overcome physical obstacles in the form of a thin constriction. Specifically, we ask whether such confined migration exhibits emergent stochastic dynamical laws. To this end, we develop two-state micropatterns, consisting of two adhesive sites connected by a thin constriction, allowing the cells to perform repeated stochastic transitions between the sites. For this minimal system, we obtain a large data set of single cell trajectories, enabling us to infer an equation of cell motion, which decomposes the dynamics into deterministic and stochastic contributions. Our data-driven approach reveals that these cells exhibit intricate non-linear migratory dynamics, with qualitatively similar features for cancerous (MDA-MB-231) and non-cancerous (MCF10A) cells. In both cases, the cells drive themselves deterministically into the thin constriction, a process that is sped up by noise. Interestingly, the deterministic dynamics of the cancerous cells exhibits a limit cycle, while the non-cancerous cells show excitable bistable dynamics. Our approach yields a conceptual framework that may be extended to describe active motility on different scales, and in more complex confining environments.

BP 31.4 Fri 10:30 H10

Rotating lamellipodium waves prior to cell polarization — Cody Reeves[1,2], Benjamin Winkler[3], Igor S. Aranson[2,4], and •Falko Ziebert[5] — [1]Engineering Sciences and Applied Mathematics, Northwestern University, Evanston, USA — [2]Materials Science Division, Argonne National Laboratory, USA — [3]Physikalisches Institut, Albert-Ludwigs-Universität Freiburg, Germany — [4]Department of Biomedical Engineering, Pennsylvania State University, University Park, USA — [5]Institute for Theoretical Physics, Heidelberg University, Germany

Cellular protrusion and lamellipodium waves are widespread and observed for many cell types. They are involved in the cells' exploration of the substrate, their internal organization, as well as for the establishment of self-polarization prior to the onset of motion. Here we apply a recently developed phase field approach to model shape waves and their competition on the level of a whole cell. We derive analytic descriptions for the emergence of a single wave deformation. Further we develop an amplitude equation approach to study competition of multiple waves, describing how cells can transition from a non-moving state towards a polarized, steady moving state. Reference: C. Reeves et al., Comms. Phys. 1,73 (2018).

BP 31.5 Fri 10:45 H10

Placing the power plants: functional crosstalk between mitochondrial homeostasis and active cellular dynamics — •Sufi O. Raja and Christoph F. Schmidt — Third Institute of Physics-Biophysics, Georg-August University of Gottingen, Friedrich-Hund-Platz 1, Gottingen-37077, Germany

Dynamic actomyosin organization is an energy dependent active process and the key to several cellular processes related to shape change and movement. But our knowledge regarding how living cells spatiotemporally control such dynamic organization is still limited. In this context studying the functional role of mitochondrial homeostasis can be a potential target as mitochondria are the cellular energy (Adenosine Tri-Phosphate, ATP) hub and directly regulate the homeostasis of Ca+2 and reactive oxygen species which in turn can potentially regulate actomyosin dynamics locally. On the other hand the mobility of mitochondria is solely determined by the cytoskeleton elements. So, the question is if and how a functional feedback circuit does exists or not. In this context, we are trying to revisit cellular processes like cell adhesion spreading kinetics in the context of mitochondrial homeostasis. How dynamics of the mitochondria (activity/mobility) gets coupled with actomyosin dynamics locally through modulation of local supply of energy and level of small signaling molecules. Lastly, we are also trying to study the response of mitochondrial dynamics during mechanical perturbation of cell to establish a direct connection between cellular energetics and dynamics.

BP 31.6 Fri 11:00 H10

Cortical Actin Contractility of Single Suspended Cells Might Determine Tissue Surface Tension — •Enrico Warmt, Steffen Grosser, Erik Morawetz, and Josef Käs — University of Leipzig, Faculty of Physics and Earth Sciences, Peter Debye Institute, Soft Matter Physics Division, Linnéstr. 5, 04103 Leipzig, Germany

Here, we investigate suspended cells regarding active contractility, lacking stress fibers and adhesion points. Epithelial cells assemble a strong actomyosin cortex providing pretension forming round cells and exhibiting more contractile behavior. Contrastly, mesenchymal cells behave much less contractile. In tissue development experiments, epithelial suspended cells rapidly form stable cell-cell contacts, which is accompanied with rearrangement of their actomyosin cortices building up a collective actomyosin rim. This collective actomyosin rim envelops whole cell clusters visible in round shaped cell spheroids suggesting high tissue surface tension. In contrast, suspended mesenchymal cells do not form stable cell-cell contacts. No collective actomyosin rim forms and envelops cell clusters, resulting in rough cell spheroid surfaces, suggesting low tissue surface tension. Demixing experiments, where we observe segregation behavior of epithelial and mesenchymal cells, show that epithelial cells form always a compact inner core, supporting the theory of expressing higher tissue surface tension. Altogether we hypothesize, that the contractile potential, in particular of epithelial cells, is highly correlated with the ability to rearrange actomyosin assembly. Furthermore, cells contractile potential is thus a driving force in tissue development and essential in tissue integrity.

BP 31.7 Fri 11:15 H10

Efficient outgrowth of primordia is mechanically driven — •Jason Khadka, Jean-Daniel Julien, and Karen Alim — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Morphogenesis of plants and animal often emerges from mechanical

moulding and deformations. Yet, how precisely cells as individual mechanical entities can act to shape a tissue reliably and efficiently in three dimensions is still puzzling. In plants, the mechanics of cells within a tissue is particularly well defined as individual cell growth is essentially mechanical yielding of cell-wall in response to internal turgor pressure. Most intriguingly, cell-wall stiffness is controlled by biological signalling and is observed to respond to mechanical stresses building up within a tissue. What is the role of such a mechanical feedback during morphing in three dimensions? Here, we propose a three dimensional vertex model to investigate tissue mechanics at the onset of organ outgrowth at the tip of a plant shoot. We find that organ height is primarily governed by the ratio of growth rates of faster growing cells initiating the organ to slower growing tissue cells surrounding them. Remarkably, the outgrowth rate is more efficient when cells can remodel their cell-wall stiffness in response to the tissue-wide mechanical stresses. Our quantitative analysis of simulation data shows that the feedback acts by not only modulating cell growth by reorganising walls but also by changing the stress pattern within the tissue promoting organ outgrowth.

BP 31.8 Fri 11:30 H10

Visualization of intracellular calcium levels in Dictyostelium discoideum with a genetically encoded reporter — •Manuel Frey, Sven Flemming, Serena Cucinotta, and Carsten Beta — University of Potsdam, Potsdam, Germany

Calcium is an important second messenger in eukaryotic cells and is crucial for several signaling pathways related to cellular functions such as chemotaxis and cell motility. To visualize calcium in the social amoeba Dictyostelium discoideum, we expressed a genetically encoded GFP based calcium reporter at the plasma membrane. This enabled us to monitor spatiotemporal changes in the intracellular Ca2+ levels.

We could detect global increases in Ca2+ levels after chemotactic stimulation with cAMP. Mechanical stimulation of cells led to a local Ca2+ response. Furthermore, we could detect short, focal increases of Ca2+ at the basal plasma membrane, which coincided with the appearance of F-actin foci at the same location. In cells exposed to continuous shear flow, we observed periodic oscillations of the intracellular Ca2+ levels. Interestingly, once excited these oscillations continued for several minutes even after the shear flow was stopped. In contrast, application of a short pulse of shear flow induced only single responses.

Inhibitor experiments suggested that the observed Ca2+ response at the plasma membrane is caused by an influx of Ca2+ needed to replenish the internal stores for Ca2+. Our results show that localized increases in calcium can be visualized with our new reporter in live cell imaging experiments and revealed interesting oscillatory behavior under shear flow.

BP 31.9 Fri 11:45 H10

Coiled coils as molecular force sensors for the extracellular matrix — •Melis Goktas, Chuanfu Luo, Ruby May Arana Sullan, Ana Elisa Bergues-Pupo, Reinhard Lipowsky, Ana Vila Verde, and Kerstin Blank — Max Planck Institute of Colloids and Interfaces, Science Park Potsdam-Golm, 14424 Potsdam, Germany.

Cells sense the mechanical properties of the extracellular matrix (ECM) and use this information for regulating a wide range of cellular functions. Even though it is well understood that mechanical signals play a crucial role in directing cell fate, surprisingly little is known about the range of forces that define cell-ECM interactions at the molecular level. To determine the single molecular forces required to maintain initial cell adhesion, we developed a library of coiled coil (CC)-based molecular force sensors (MFSs). Using AFM-based SMFS, we have calibrated the rupture forces of a series of short heterodimeric CCs (3-5 heptad repeats) under shear geometry. We show that the rupture forces lie in the range of 20-50 pN and depend on CC length (i.e. number of heptads). Using these mechanically calibrated CCs as molecular building blocks, we developed a two-component MFS approach. Proof-of-concept experiments performed with fibroblasts and endothelial cells revealed that single integrin-ligand bonds transmit forces lower than 40 pN during initial cell adhesion and that cells with endothelial lineage exert lower cell-ECM forces compared to fibroblasts. These results aid the future design of 2D and 3D CC-based MFS platforms for investigating cellular mechanosensing processes at the single molecule level.

BP 32: Active matter II (joint session BP/CPP/DY)

Time: Friday 9:30–12:00 Location: H11

BP 32.1 Fri 9:30 H11

Dynamics of an active model microswimmer in an anisotropic fluid — •Abdallah Daddi-Moussa-Ider and Andreas M Menzel — Institut für Theoretische Physik II: Weiche Materie, Heinrich-Heine-Universität Düsseldorf, Düsseldorf

Several recent experiments investigate the orientational behavior of self-propelled bacteria and colloidal particles in anisotropic fluids such as nematic liquid crystals. Correspondingly, we study theoretically the dynamics of a simple model microswimmer in a uniaxially anisotropic fluid. The behavior of both puller- and pusher-type swimmers in the anisotropic fluid is analyzed. Depending on the propulsion mechanism as well as the relative magnitude of different involved viscosities, we find alignment of the microswimmer parallel or perpendicular to the anisotropy axis. The observed swimmer reorientation results from the hydrodynamic coupling between the self-induced fluid flow and the anisotropy of the host fluid. Our theoretical predictions are found to be in qualitative agreement with recent experiments on swimming bacteria in nematic liquid crystals. They support the objective of utilizing the anisotropy of a surrounding fluid to guide individual swimmers and self-propelled active particles along a requested path, enabling controlled active transport.

Reference: A. Daddi-Moussa-Ider and A. M. Menzel. Dynamics of a simple model microswimmer in an anisotropic fluid: Implications for alignment behavior and active transport in a nematic liquid crystal, Phys. Rev. Fluids 3, 094102 (2018).

BP 32.2 Fri 9:45 H11

Dynamics of bottom-heavy squirmers — •Felix Ruehle and Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, Germany

The self-propulsion of biological or synthetic microswimmers is often influenced by a gravitational field [1,2], where a density mismatch leads to sedimentation and an offset center of mass triggers reorientation along the direction of gravity so that they swim upwards [2]. Combining these passive effects with the non-equilibrium properties of active motion creates novel and interesting dynamics, both in dense and dilute suspensions [3]. In particular, a large variety of dynamical behaviours has been observed for the squirmer microswimmer model [4,5].

In this contribution we focus on bottom-heavy squirmers and determine their state diagram, depending on the gravitational force and acting torque. For strong gravitational forces we observe conventional sedimentation, whereas the density profile is inverted for weaker forces. Additionally, we find stable convective plumes for neutral squirmers that become metastable as the torque increases. We also observe spawning clusters at the bottom if the sedimentation velocity almost equalizes the swimming speed. Spawning clusters and continuous plumes do not occur for pusher and puller type swimmers.

[1] J. Palacci, et al., *Phys. Rev. Lett.* **105**, 088304 (2010).
[2] K. Drescher et al., *Phys. Rev. Lett.* **102**, 168101 (2009).
[3] K. Wolff, A. M. Hahn and H. Stark, *EPJE* **36**, 1 (2013).
[4] J.-T. Kuhr et al., *Soft Matter* **13**, 7548 (2017).
[5] F. Rühle et al., *New J. Phys.* **20**, 025003 (2018).

BP 32.3 Fri 10:00 H11

Bead-spring modelling of triangular microswimmers — •Sebastian Ziegler[1], Alexander Sukhov[2], Jens Harting[2,3], and Ana-Sunčana Smith[1,4] — [1]PULS Group, Institute for Theoretical Physics, Department of Physics, Friedrich-Alexander Universität Erlangen-Nürnberg, Erlangen, Germany — [2]Helmholtz Institute Erlangen-Nürnberg for Renewable Energy, Germany — [3]Dep. of Applied Physics, Eindhoven University of Technology, The Netherlands — [4]Division of Physical Chemistry, Ruder Bošković Institute Zagreb, Croatia

A customary approach to model mechanical micropropulsion is to prescribe the swimming stroke. However, with this approach, the hydro-

dynamic features of the motion are in essence smoothed over and the problem becomes a purely geometrical one. The alternative approach, yet significantly more demanding, is to impose not the stroke itself but the forces driving the device. The swimming stroke then emerges as a result of the various forces acting in the system. We use a perturbative approach to examine a triangular swimmer's behaviour in the Stokes regime that is also eligible for general geometries of bead-spring swimmers. The device shows a multifaceted comportment dependent on a number of therefore identified effective parameters. The triangular swimmer is further used as a prototype to study the influence of variations in the viscosity of the surrounding fluid on its motion.

BP 32.4 Fri 10:15 H11

Simple Swimmers Reverse Direction near a Surface — •Michael Kuron[1], Philipp Stärk[1], Joost de Graaf[2], and Christian Holm[1] — [1]Institut für Computerphysik, Universität Stuttgart, Deutschland — [2]Institute for Theoretical Physics, Universiteit Utrecht, Nederland

The motion of a microswimmer can change substantially in the presence of a surface. Sperm are known to move in circular trajectories near a wall, paramecia move in sinusoidal trajectories through a tube, and chemical swimmers can orbit around spherical obstacles. Spherical squirmers are one of the simplest model microswimmers, commonly defined by the first two Legendre modes of their surface slip velocity. In this talk, we use the squirmer to numerically investigate the effect of the environmental geometry. We discuss how the transition between scattering and orbiting/hovering depends on the strength of the squirmer's hydrodynamic dipole moment. Interestingly, we observe cases where the squirmer orbits/hovers along a surface in a direction opposite to that observed in bulk. This effect is present both in a far-field theoretical model and our lattice Boltzmann calculations, which accurately account for the near-field flow. These results extend the understanding of the effect of geometry on microswimmer motion and show the importance of finite swimmer size and associated near-field effects.

BP 32.5 Fri 10:30 H11

Bacterial Swarming Dynamics — •Hannah Jeckel[1,2,3], Eric Jelli[1,2], Raimo Hartmann[1], Praveen Singh[1], Rachel Mok[3,4], Jan Frederik Totz[5], Lucia Vidakovic[1], Bruno Eckhardt[2], Jörn Dunkel[3], and Knut Drescher[1,2] — [1]Max Planck Institute for Terrestrial Microbiology, Marburg, Germany — [2]Department of Physics, Philipps-University Marburg, Germany — [3]Department of Mathematics, Massachusetts Institute of Technology, Cambridge, MA — [4]Department of Mechanical Engineering, Massachusetts Institute of Technology, Cambridge, MA — [5]Institute for Theoretical Physics, Technical University Berlin, Germany

Coordinated dynamics of individual components in active matter are an essential aspect of life on all scales. Establishing a comprehensive, causal connection between intracellular, intercellular, and macroscopic behaviors has remained a major challenge due to limitations in data acquisition and analysis techniques suitable for multiscale dynamics. Here, we combine a high-throughput adaptive microscopy approach with machine learning, to identify key biological and physical mechanisms that determine distinct microscopic and macroscopic collective behavior phases which develop as *Bacillus subtilis* swarms expand over five orders of magnitude in space. Our experiments, continuum modeling, and particle-based simulations reveal that macroscopic swarm expansion is primarily driven by cellular growth kinetics, whereas the microscopic swarming motility phases are dominated by physical cell-cell interactions. These results provide a unified understanding of bacterial multi-scale behavioral complexity in swarms.

BP 32.6 Fri 10:45 H11

Effects of collective bacterial motility on their chemotactic navigation — •Remy Colin and Victor Sourjik — Max Planck Institute for Terrestrial Microbiology, Marburg, Germany

At high cell density, swimming bacteria exhibit collective motility patterns, self-organized through physical interactions of a however still debated nature. Although high-density behaviors are frequent in natural situations, it remains unknown how collective motion affects chemotaxis, the main physiological function of motility that enables bacteria to follow chemical and other gradients in their environment. Here, we systematically investigated this question in the model organism *Escherichia coli*, varying cell density, cell length and suspension confinement. The characteristics of the collective motion indicated that its emergence is dominated by hydrodynamic interactions between swimmers. We observed that moderate increase in cell density enhanced the chemotactic drift of bacteria, whereas it was suppressed at higher densities, because the collective motion disturbed the choreography necessary for chemotactic sensing. We suggest that this physical hindrance imposes a fundamental constraint on high-density behaviors of motile bacteria, including swarming as well as the formation of multicellular aggregates and biofilms.

BP 32.7 Fri 11:00 H11

Feedback Control of Active Microswimmers — •Alexander Fischer[1], Haw Yang[2], and Frank Cichos[1] — [1]Uni Leipzig — [2]Princeton University

Collective motion created by the interaction of autonomous individuals plays a major role in flocks of birds, bacterial growth or the motion of robotic swarms. Sensing and reacting to signals is a fundamental issue of life. Microswimmers, which are artificial objects that mimic the active motion of biological systems, do not have such sensing and response features built in yet, but may gain them through an external control of their propulsion. Here we explore an information exchange between artificial microswimmers by computer-controlled feedback processes. We have created a setup where multiple active microswimmers can react to their position in space or their distance to other microswimmers. We investigate the influence of different interaction potentials or a delay in the information exchange. Our results demonstrate so far that particles can be coupled to each other by the used feedback by designed virtual potentials. The collective motion of such coupled particles reveals oscillating modes with emergent features like spontaneous rotation. The experiments shall help to understand the emergence of complex behavior in biological systems.

BP 32.8 Fri 11:15 H11

Out-of-plane beating components of active axonemes isolated from Chlamydomonas reinhardtii — Azam Gholami[1], •Soheil Mojiri[2], Eberhard Bodenschatz[1], and Jörg Enderlein[2] — [1]Max-Planck Instiute for Dynamics and Self-Organization, Göttingen, Germany — [2]Georg-August Universität, Göttingen, Germany

Cilia and flagella are ubiquitous in the living world. They are essential for micro-scale driven transport of fluids or cells by cilia/flagellar beating. Their slender bodies are composed of a microtubule/molecular motor structure that when taken independently are called an axoneme. Axonemes move by bending waves that emerge from the interplay between internal stresses generated by dynein motor proteins . Here we use the novel multi-plane phase contrast imaging technique to record the three dimensional beating pattern of isolated axonemes from Chlamydomonas reinhardtii that beat in the vicinity of a substrate. We measure the torsion of the axoneme along the contour length with high spatiotemporal resolution. High precision information on out-of-plane beating component of axonemes allows us to check the validity of the resistive-force theory.

BP 32.9 Fri 11:30 H11

Nanoscale chemotaxis of enzymes and small molecules — •Jaime Agudo-Canalejo[1,2], Tunrayo Adeleke-Larodo[1], Pierre Illien[3], and Ramin Golestanian[4,1] — [1]University of Oxford, Oxford, UK — [2]Penn State University, State College, USA — [3]ESPCI Paris, Paris, France — [4]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

We present a microscopic theory for the observed chemotaxis of enzymes and other small molecules. [1,2] We find that two distinct mechanisms contribute to enzyme chemotaxis: a diffusiophoretic mechanism due to non-specific interactions, and a new type of mechanism due to binding-induced changes in the diffusion coefficient of the enzyme. For a typical enzyme, the two mechanisms compete against each other, one dominating at high substrate concentration, the other at low concentration. The competition between the two mechanisms may be used to engineer nanovehicles that move towards or away from regions with a specific substrate concentration. Finally, we include the effects of anisotropy and flexibility of the enzyme, [3] and show that enzymes can be aligned by gradients, and shape fluctuations lead to corrections in the diffusion and chemotactic mobility of enzymes. [1] Agudo-Canalejo, J., Adeleke-Larodo, T., Illien, P., & Golestanian, R. (2018) Acc. Chem. Res. 51, 2365 [2] Agudo-Canalejo, J., Illien, P., & Golestanian, R. (2018) Nano Lett. 18, 2711 [3] Adeleke-Larodo, Agudo-Canalejo, J., & Golestanian, R. (2018) arXiv:1811.09631

BP 32.10 Fri 11:45 H11

High-motility visible light-driven Ag/AgCl Janus mi-

croswimmers interacting with passive beads — •Xu Wang[1], Larysa Baraban[2], Vyacheslav R Misko[3,4], Franco Nori[4,5], Petre Formanek[6], Tao Huang[2], Gianaurelio Cuniberti[2], Jürgen Fassbender[1], and Denys Makarov[1] — [1]Helmholtz-Zentrum Dresden-Rossendorfe.V., Institute of Ion Beam Physics and Materials Research, 01328 Dresden, Germany — [2]Technische Universität Dresden, 01062 Dresden, Germany — [3]Universiteit Antwerpen, B-2610 Antwerpen, Belgium — [4]RIKEN Cluster for Pioneering Research, 351-0198 Saitama, Japan — [5]University of Michigan, 48109-1040 Michigan, USA — [6]Leibniz-Institut für Polymerforschung Dresden e.V., 01069 Dresden, Germany

Visible light driven nano/micro swimmers typically show mean squared displacement (MSD) values in the range of up to 200 μm^2 (over 10 s) under favorable UV light illumination.[1] Here, we demonstrate Ag/AgCl-based spherical Janus micromotors that reveal an efficient propulsion with a MSD to 3000 μm^2 (over 10 s) in pure H_2O under visible blue light illumination (λ = 450-490 nm).[2] Furthermore, we show the micromotors reveal efficient exclusion effect to their surrounding passive polystyrene beads in pure H_2O experimentally and using numerical simulations of the Langevin equations.[3]

1. Simmchen, J., et al., ChemNanoMat 2017, 3, 65.
2. Wang, X., et al., Small DOI: 10.1002/smll.201803613.
3. Wang, X., et al., Small 2018, 14, 1802537 (Frontispiece paper)

BP 33: Closing talk (joint session BP/CPP/DY)

Time: Friday 12:30–13:15 Location: H1

Invited Talk BP 33.1 Fri 12:30 H1

Pattern formation in active cytoskeletal systems — •Andreas R. Bausch — Lehrstuhl für Biophysik, Technische Universität München, 85747 Garching

Living cells rely on the self-organization mechanisms of cytoskeleton to adapt to their requirements. In processes such as cell division, or cellular motility rely on the controlled self-assembly and disassembly of well defined active cytoskeletal structures interacting with lipid membranes. One important and promising strategy to identify the underlying governing principles is to quantify the underlying physical processes in model systems mimicking functional units of living cell. Here I*ll present in vitro minimal model systems consisting of active microtubule and actin filament systems which show pattern formation resulting from active transport processes. I will discuss how small variations in local interactions results in nematic or polar patterns in high density motility essays. With the example of reconstituted active vesicles I will discuss how to relate local force exertion and tension generation to shape transformations, blebbing, invagination or tethering of lipid membranes