BP 12: Poster 2

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

BP 12.1 Tue 17:30 P4

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

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

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

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

BP 12.2 Tue 17:30 P4

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

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

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

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

BP 12.3 Tue 17:30 P4

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

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

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

BP 12.4 Tue 17:30 P4

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

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

BP 12.5 Tue 17:30 P4

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

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

BP 12.6 Tue 17:30 P4

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

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

duction during durotaxis from different points of view. Our preliminary results regarding the neutrophil durotaxis show a surprising and transient force peak on the soft substrate during cell shifting.

BP 12.7 Tue 17:30 P4

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

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

BP 12.8 Tue 17:30 P4

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

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

BP 12.9 Tue 17:30 P4

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

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

BP 12.10 Tue 17:30 P4

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

Many important cellular functions such as organelle positioning and internal cargo transport are dependent on the viscoelastic intracellular mechanical properties of cells. A range of different mechanical models has been proposed to describe these properties. Whilst simple models such as Maxwell or Kelvin-Voigt models don't seem sufficient to capture the full complexity of cells, more elaborate models like generalized Kelvin-Voigt models require a huge number of parameters. This hinders the comparison and interpretation of experimental findings. Further, from a physics perspective, cells are systems out of thermodynamic equilibrium, permanently consuming metabolic energy to carry out mechanical work. The level of "non-equilibrium" can be proposed as an indicator for cell type, cell state or even diseases. To determine both, the viscoelastic properties and the cellular activity, we use optical tweezers based active and passive microrheology in a diverse group of 9 different cell-types. Surprisingly, despite differences in origin and function, the complex moduli of all cell types can be described using a 4 parameter based fractional Kelvin-Voigt model. Additionally, the frequency dependent activity can be described with a simple power law. This approach allows to reduce those complex and frequency dependent properties down to a fingerprint of 6 parameter. Further principal component analysis shows that only 2 of them may be sufficient to characterize the mechanical intracellular state.

BP 12.11 Tue 17:30 P4

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

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

BP 12.12 Tue 17:30 P4

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

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

BP 12.13 Tue 17:30 P4

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

Göttingen, Germany — [2]ZMBE - Institute of Cell Biology, University of Münster, Germany

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

BP 12.14 Tue 17:30 P4

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

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

BP 12.15 Tue 17:30 P4

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

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

BP 12.16 Tue 17:30 P4

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

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

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

In preliminary experiments, we measure the membrane tension and simultaneously image the cells to perform RT-DC leading to the cell mechanical properties. Having access to the ensemble mechanical properties of a cell as well as its membrane tension, the method allows for studying the interaction between the latter and the derived cortex tension. In future studies, we also want to investigate the tension distribution on the cell membrane.

BP 12.17 Tue 17:30 P4

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

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

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

BP 12.18 Tue 17:30 P4

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

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

BP 12.19 Tue 17:30 P4

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

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

BP 12.20 Tue 17:30 P4

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

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

BP 12.21 Tue 17:30 P4

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

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

BP 12.22 Tue 17:30 P4

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

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

BP 12.23 Tue 17:30 P4

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

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

BP 12.24 Tue 17:30 P4

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

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

BP 12.25 Tue 17:30 P4

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

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

BP 12.26 Tue 17:30 P4

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

Vascular endothelial cells (VECs) need to be able to constantly sense, withstand and adapt to varying mechanical stresses. One way cells adapt their mechanics to these varying requirements is through differential expression of cytoskeletal proteins. Here, we focus on the

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

BP 12.27 Tue 17:30 P4

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

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

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

BP 12.28 Tue 17:30 P4

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

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

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

BP 12.29 Tue 17:30 P4

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

2D polarization fluorescence imaging (2DPOLIM) provides complete in-plane evaluation of the polarization state of the sample[1,2], giving access to macromolecular arrangement in the range of 2-10 nm via Förster resonance energy transfer between similar fluorophores (homo-FRET, emFRET). Phalloidin-dye complexes map the structure of F-Actin, by binding specifically. We applied 2DPOLIM to phalloidin-DY490 stained liver tissue of mice from different treatment groups in the context of polymicrobial sepsis[1,3]. Qualitative analysis showed significant differences in the molecular arrangement of F-actin in agreement with the survival of the animals. Further information will be obtained from comparing the experimental data to a series of simulations[2]. – Funding by DAAD-GSSP, DFG-Ta1049/2, Interdisziplinäre Zentrum für Klinische Forschung Jena (AMSP-05). – [1] D. Täuber et al. ELMI 2021, https://doi.org/10.22443/RMS.ELMI2021.6. [2] R. Camacho et al. Commun. Biol. 2018, 1, 157. [3] A.T. Press et al. EMBO Mol. Med. 2021, 13 (10), e14436.

BP 12.30 Tue 17:30 P4

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

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

BP 12.31 Tue 17:30 P4

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

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

BP 12.32 Tue 17:30 P4

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

For voluntary movements, all animal life relies myofibrils in striated muscle, which are highly organised crystal-like cytoskeletal structures comprising chains of micrometer-sized sarcomeres. The size of sarcomeres is supposedly set by giant proteins such as titin. Titin elastically links myosin molecular motors in the middle of a sarcomere to a structure called Z-disc rich in actin crosslinkers at the sarcomere boundary. To investigate putative mechanisms for the self-assembly of myofibrils, we develop minimal mathematical models. We show that minimal models accounting for non-local interactions between three key proteins is sufficient to account for the spontaneous emergence of periodic sarcomeric patterns. We employ mean-field models, as well

as agent-based simulations, which reveal the influence of small-number fluctuations on emergent patterns. Additionally, analysing images of the *Drosophila* flight muscle during early development provided by the Schnorrer lab (IBDM, Marseilles), we were able to identify titin as the first protein forming periodic patterns, with myosin and later actin following subsequently, which constrains possible models.

BP 12.33 Tue 17:30 P4

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

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

BP 12.34 Tue 17:30 P4

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

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

BP 12.35 Tue 17:30 P4

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

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

BP 12.36 Tue 17:30 P4

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

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

BP 12.37 Tue 17:30 P4

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

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

BP 12.38 Tue 17:30 P4

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

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

BP 12.39 Tue 17:30 P4

3D Force Model of early zebrafish development via NeuralODEs — •Leon Lettermann, Sebastian Herzog, Alejandro Jurado, Florentin Wörgötter, and Timo Betz — 3rd Institute

of Physics - Biophysics, University of Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen

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

BP 12.40 Tue 17:30 P4

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

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

BP 12.41 Tue 17:30 P4

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

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

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

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

BP 12.42 Tue 17:30 P4

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

The coupling of two or more cellular membranes is an important part of cell interactions and therefore affects many biological mechanisms. Cells may restrict the movement of proteins in certain areas of their membrane creating functionally specialized regions, or membrane domains. Here we analyse whether the arrangement of proteins in different patterns changes the binding kinetics of the proteins. In our investigation we combine kinetic Monte Carlo simulations and explicit calculations of the binding rates of the patterns. Results show that there is indeed a difference in binding of the different patterns. An important factor seems to be the amount of proteins within a pattern due to the correlations between the proteins. The exact difference of the binding rates depends on the mechanical properties of the membrane and the proteins. We furthermore analyse the dynamics of bond formation and compare the results to experimental data on the activation of natural-killer cells binding to analogous patterns (experiment by the group of Mark Schvartzman at the Ben-Gurion Univeristy of the Negev).

BP 12.43 Tue 17:30 P4

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

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

BP 12.44 Tue 17:30 P4

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

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

BP 12.45 Tue 17:30 P4

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

Cooperative cell dynamics resulting from a complex interplay of single cell migration and cell-to-cell interactions plays a fundamental role in maintaining a confluent cell layer despite continuous changes in cell numbers and environmental conditions. It is the aim of this work to extract the essential components of this dynamics. Therefore, we seeded human umbilical vein endothelial cells and stained their nuclei with a fluorescent dye. Cells were observed within 48 hours (dt = 10 minutes). We obtained up to 50.000 cell trajectories within an area of 6 x 7 millimeters for 10 different experiments. All analyses were performed under nearly confluent conditions. Cells continued to

show lively proliferations and a non-stationary behavior indicated by a two-phase decay of the mean squared velocity. This behavior is accompanied by a decay of the velocity correlation. In addition, we found an exponential repulsion between cells that could transiently rise cell velocities due to cell proliferations. We put these observations into a mathematical model coupling cell proliferation and mean squared velocities over time. Bayesian analysis was applied to determine the best model and its parameters. In summary, we are able to perform a characterization of the complex cell dynamics. This approach can be used for simulations and application to different experimental conditions.

BP 12.46 Tue 17:30 P4

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

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

BP 12.47 Tue 17:30 P4

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

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

BP 12.48 Tue 17:30 P4

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

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

BP 12.49 Tue 17:30 P4

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

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

BP 12.50 Tue 17:30 P4

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

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

BP 12.51 Tue 17:30 P4

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

P. Univ. Católica de Chile — [4]Departamento de Física, UTFSM, Valparaíso, Chile — [5]Departamento de Física, Technische Universität Clausthal, Clausthal, Germany.

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

BP 12.52 Tue 17:30 P4

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

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

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

BP 12.53 Tue 17:30 P4

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

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

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

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

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

BP 12.54 Tue 17:30 P4

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

The European XFEL provides state-of-the-art instrumentation for absolving single-pulse, single-particle coherent diffractive imaging, which we have used to investigate synaptic vesicles, harvested from rat brain, with high spatial resolution. The method involves serial bio-sample delivery by aerosol jet such that droplets incorporating single particles are probed by femto-second pulses. In this way two prevalent challenges of SAXS (polydispersity and radiation damage for high brilliance beams) can be met. Stochastic distribution of sample and a nano-focused beam means only a fraction of the recorded data was of interest (1.2 PB in total, roughly $3 \cdot 10^8$ images). We present technical details behind the data acquisition used for this proof-of-concept experiment at the SPB instrument of the European FEL as well as our strategy in "hit-finding". Further, first steps towards electron density reconstruction will be presented as well as comparison to preceding SAXS work.

BP 12.55 Tue 17:30 P4

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

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

BP 12.56 Tue 17:30 P4

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

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

BP 12.57 Tue 17:30 P4

Spatial-Stochastic Model of Cell Fate Decisions in Early Mouse Development — •Michael Alexander Ramirez Sierra[1], Tim Liebisch[1,2], Sabine C. Fischer[3], Franziska Matthäus[1,2],

and Thomas R. Sokolowski[1] — [1]Frankfurt Institute for Advanced Studies (FIAS), Frankfurt am Main, Germany — [2]Goethe Universität Frankfurt am Main, Germany — [3]Julius-Maximilians-Universität Würzburg, Germany

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

BP 12.58 Tue 17:30 P4

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

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

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

BP 12.59 Tue 17:30 P4

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

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

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

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

BP 12.60 Tue 17:30 P4

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

In the absence of light, photosynthetic microbes can still sustain essential metabolic functionalities and motility by switching their energy production from photosynthesis to oxygen respiration. For suspensions of motile *C. reinhardtii* cells above a critical density, we demonstrate that this switch reversibly controls collective microbial aggregation [1]. Aerobic respiration dominates over photosynthesis in conditions of low light, which causes the microbial motility to sensitively depend on the local availability of oxygen. For dense microbial populations in self-generated oxygen gradients, microfluidic experiments and continuum theory based on a reaction-diffusion mechanism show that oxygen-regulated motility enables the collective emergence of highly localized regions of high and low cell densities.

[1] Fragkopoulos et al., J.R. Soc. Interface 18, 20210553 (2021).

BP 12.61 Tue 17:30 P4

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

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

BP 12.62 Tue 17:30 P4

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

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

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

BP 12.63 Tue 17:30 P4

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

Animals need to detect and discriminate odors for survival. In contrast to other senses, olfaction is shaped by physical processes, including odorant transport by the airflow and adsorption in the nasal mucus layer. These processes crucially affect what the brain can learn about the chemical composition of the environment. We study how the olfactory system relays information by using a simplified theoretical description of the airflow and the adsorption in the mucus. We predict the length scales over which odorants absorb along the olfactory epithelium. This length scale depends significantly on the odorant's solubility but is only weakly affected by odorant diffusivity and adsorption strength of mucus wall. We use these predictions to obtain the optimal arrangement of odorant receptor neurons that maximizes the information relay to the brain. We notice that the receptors sensitive

to odorants with shorter adsorption length scale always reside closer to the cavity inlet side and cover the cavity in an increasing fraction of total cavity length with adsorption length scale. Taken together, we study design principles of optimal odor information encoding using a simple fluid dynamical model and information theory. Our approach could help to understand the natural olfaction process and develop artificial noses.

BP 12.64 Tue 17:30 P4

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

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

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

BP 12.65 Tue 17:30 P4

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

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

BP 12.66 Tue 17:30 P4

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

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