BP 11: Poster A: Single Molecule, Multicellular, Bioimaging, Focus Sessions, etc.

Time: Monday 16:30–19:00 Location: BPp

BP 11.1 Mon 16:30 BPp

How fast do PMCA pumps transport Ca^{2+}? — •Barbara Schmidt[1], Cristina E. Constantin[2], Bernd Fakler[2], and Heiko Rieger[1] — [1]Center for Biophysics and Dep. Theoretical Physics, Saarland University, 66123 Saarbrücken, Germany — [2]Institute of Physiology, University of Freiburg, 79104 Freiburg, Germany

Plasma membrane protein complexes of two PMCA subunits and two Neuroplastin or Basigin proteins are responsible for Ca^{2+} ion transport out of cells. Here we make use of BK-type Ca^{2+}-activated K^+ channels to determine the Ca^{2+} transport activity of PMCA. Due to their large conductance and their particular gating kinetics the BK channels may be used as fast and reliable sensors for intracellular Ca^{2+}-concentration ($[Ca^{2+}]_i$) beneath the plasma membrane. Experimentally we monitor the PMCA-mediated Ca^{2+} clearance (or transport) by the decay of BK-currents following their activation by a short (0.8 ms) period of Ca^{2+}-influx through Cav2.2 channels. To relate the experimentally observed temporal evolution of the K^+ current to the underlying temporal evolution of the Ca^{2+} concentration we implement a theoretical model for the Ca^{2+}-dependence of the BK-current and of the PMCA pump strength. The maximum PMCA pump strength is used to fit the predicted time course of the K^+ current to the experimental data, which turns out to be at least 2 orders of magnitude larger than what has been assumed so far. Implication of this finding for Ca^{2+} signaling in general are discussed.

BP 11.2 Mon 16:30 BPp

Molecular Friction and Adhesion on Porous Membranes — •Kordula Schellnhuber[1,2], Hanna Hübner[2], Johanna Blass[1], Markus Gallei[2], and Roland Bennewitz[1] — [1]INM-Institut für Neue Materialien, Campus D.2.2 Universität des Saarlandes, 66123 Saarbrücken, Germany — [2]Lehrstuhl für Polymerchemie, Naturwissenschaftlich-Technische Fakultät, Universität des Saarlandes, 66123 Saarbrücken, Germany

Understanding and controlling the dynamics of polymer-surface interactions are key to a functional design of nanoscale objects and to reveal mechanisms underlying biological processes. We study friction and adhesion of single polymers at the solid-liquid interface by means of atomic force microscopy (AFM) with focus on entanglement dynamics. As a model system, a single M13mp18 DNA-molecule with a length of 2.5 μm is attached to an AFM probe. Friction measurements are performed by moving the cantilever in parallel to the surface at a height of a few hundred nanometers. Deflection of the cantilever reveals adhesive interactions between the DNA polymer and the membrane. Entanglement of the DNA in the membrane pores is probed by adhesion measurements after varying waiting time at a constant height of few hundred nanometers above the surface.

BP 11.3 Mon 16:30 BPp

The mechanics of single cross-links which mediate cell attachment at a hydrogel surface — Arzu Colak, Bin Li, Johanna Blass, Aranzazu del Campo, and •Roland Bennewitz — INM - Leibniz Institute for New Materials, Saarbrücken, Germany

Cells attach to the surface of a poly(ethylene glycol diacrylate) (PEGDA) hydrogel if linkers are functionalized with the RGD cell adhesive motif. Attachment and spreading of cells on the hydrogel depend on its mechanical properties, for examples when Young*s modulus E of the hydrogel is varied. We were interested in the effective stiffness of those linkers which mediate cell attachment and measured it by means of single-molecule force spectroscopy [1]. For these experiments, the linkers were functionalized with biotin and the tip of an atomic force microscope with streptavidin. A factor of ten in the elastic modulus E of the hydrogel corresponded to a factor of five in the effective spring constant k of single crosslinks, indicating a transition in scaling with the mesh size ζ from the macroscopic $E \propto \zeta^{-3}$ to the molecular $k \propto \zeta^{-2}$. The effective stiffness of single linkers was also measured for a second polymer network based on four-arm star-PEG molecules which interpenetrated the PEGDA hydrogel. The quantification of stiffness and deformation at the molecular length scale contributes to the discussion of mechanisms in force-regulated phenomena in cell biology. [1] A. Colak, B. Li, J. Blass, K. Koynov, A. del Campo, R. Bennewitz, The mechanics of single cross-links which mediate cell attachment at a hydrogel surface, Nanoscale, 11 (2019) 11596-11604.

BP 11.4 Mon 16:30 BPp

Deep reinforcement learning of molecular mechanisms — •Roberto Covino[1], Hendrik Jung[2], Arjun Wadhawan[3], Peter G. Bolhuis[3], and Gerhard Hummer[2,4] — [1]Frankfurt Insitute for Advanced Studies, Frankfurt am Main, Germany — [2]Max Planck Institute of Biophysics, Frankfurt am Main, Germany — [3]Van 't Hoff Institute for Molecular Sciences, University of Amsterdam, Amsterdam, The Netherlands — [4]Institute of Biophysics, Goethe-University Frankfurt, Frankfurt, Germany

We present a deep reinforcement learning artificial intelligence (AI) that learns the molecular mechanism from computer simulations. The AI simulates molecular reorganizations and progressively learns how to predict their outcome. We integrate path theory, transition path sampling (TPS), and deep learning. TPS is a Markov Chain Monte Carlo method to sample the rare trajectories connecting metastable states. Using reinforcement learning, we iteratively train a deep neural network on the outcomes of TPS simulation attempts. In this way, we increase the rare-event sampling efficiency while gradually revealing the underlying mechanism. At convergence, the AI learns the rare events' committor function, encoded in the trained neural network. By using symbolic regression, we distill simplified quantitative models that reveal mechanistic insight in a human-understandable form. Our innovative AI enables the sampling of rare events by autonomously driving many parallel simulations with minimal human intervention and aids their mechanistic interpretation.

BP 11.5 Mon 16:30 BPp

Acidic amino acids do not affect the robustness of protein hydration layers to changes in KCl concentration — •Hosein Geraili[1] and Ana Vila Verde[2] — [1]MPI of Colloids and Interfaces, Dept Theory and Bio-Systems, Potsdam, Germany — [2]U. Duisburg-Essen, Physics, Duisburg, Germany

The proteins of halophilic microorganisms have a higher content in negatively charged amino acids compared to microorganisms living in normal environments. One proposed hypothesis explaining this large content in acidic residues is that they are necessary to maintain the proteins at normal hydration levels in an environment with high salt concentration, i.e., in low water activity. To investigate protein hydration in high salt concentration using Molecular Dynamics, we optimized the interaction potential between potassium ions and the carboxylate side-chain of acidic amino acids; the optimized potential is compatible with the widely-used suite of AMBER force fields and the TIP3P water model. We compared hydration levels of 5 halophilic proteins and 5 non-halophilic ones. Our simulations show that all proteins have almost identical levels of hydration in high and low KCl concentrations: the large fraction of acidic amino acids in halophilic proteins is not necessary to ensure that they remain hydrated. We quantified the translational dynamics of the solvation shell of the halophilic and non-halophilic proteins, and observe almost no difference between them. The claim that acidic residues cooperatively interacting with the solvated network of ions would markedly decrease the dynamics of the protein solvation shell is not supported by our calculations.

BP 11.6 Mon 16:30 BPp

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

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

BP 11.7 Mon 16:30 BPp

Molecular mechanisms of single alpha helix deformation under tension — Ana Bergues-Pupo[1], Reinhard Lipowsky[2], and •Ana Vila Verde[3] — [1]Max Delbrück Center for Molecular Medicine, Berlin, Germany — [2]MPI of Colloids and Interfaces, Dept Theory and Bio-Systems, Potsdam, Germany — [3]U. Duisburg-Essen, Physics, Duisburg, Germany

Alpha helices (SAHs) that are stable in isolated form have been found in motor proteins, where they connect spatially separated domains. We investigate the force-estension curve and molecular deformation mechanisms of SAHs pulled from the termini, at pull speeds approaching the quasi-static limit, using molecular dynamics simulations with atomistic resolution of the protein and an implicit model for the solvent. SAHs unravel starting from the termini, in a residue-by-residue manner. Contrary to prior simulations of metastable helices, hydrogen bond breaking is not the main event determining the barrier to unfolding of SAHs at all pull speeds we tested. We fit the force-extension curves to the cooperative Sticky Chain model, and extract the distance, $x_E = 0.13$ nm, to the transition state, the natural frequency of bond vibration, $\nu_0 = 0.82\ \mathrm{ns}^{-1}$, and the height, V_0=2.9 kcal/mol, of the free energy barrier associated with the deformation of single residues. The results confirm that the Sticky Chain model could be used to analyze experimental force-extension curves of SAHs and other biopolymers.

BP 11.8 Mon 16:30 BPp

Structural Dynamics Correlation of Peptides derived from Nucleoporins: Time-resolved X-ray Scattering and Computational Modelling — •Naireeta Biswas[1,2], Markus Osterhoff[2], Jakob Soltau[2], Sheung Chun Ng[3], Dirk Görlich[3], and Simone Techert[1,2] — [1]FS-SCS, Deutsches Elektronen-Synchrotron (DESY), Notkestraβe 85, 22607 Hamburg, Germany — [2]University of Göttingen, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [3]Department of Cellular Logistics, Max Planck Institute for Biophysical Chemistry, Göttingen, Germany

FG nucleoporins are intrinsically disordered proteins located in the nuclear pore complexes (NPCs) consist of FG repeating motifs. It has been proposed that repeating motifs play an important role in the formation of hydrogel due to their cohesive interactions and hydrophobic nature. These protein hydrogels show unique features of non-covalent interactions such as hydrogen bonding, Vander Waals interaction or π-π stacking, driving the protein self-assembly, leading to an anisotropic structural growth, thus forming hydrogels with unusual materials properties. Our computational simulations, suggest different conformations and interactions between these FG repeating motifs and that these conformational variety may be the driving forces for the co-existing domains. To understand this molecular rationale of the protein kinetics during their gelation process, we have studied the first steps of self-assembling and structural organization of the protein hydrogels during the formation .

BP 11.9 Mon 16:30 BPp

Heat flows adjust local ion concentrations in favor of prebiotic chemistry — •T. Matreux[1], K. LeVay[2], A. Schmid[1], P. Aikkila[1], L. Belohlavek[3], Z. Caliskanoglu[3], E. Salibi[2], A. Kühnlein[1], C. Springsklee[3], B. Scheu[3], D.B. Dingwell[3], D. Braun[1], H. Mutschler[2], and C.B. Mast[1] — [1]Systems Biophysics, LMU, Amalienstr. 54, 80799 Munich, Germany — [2]MPI für Biochemie, Am Klopferspitz 18, 82152 Martinsried, Germany — [3]Earth and Environmental Sciences, LMU, Theresienstr. 41, 80333 Munich, Germany

Prebiotic reactions often require certain initial concentrations of ions. For example, the activity of RNA enzymes requires a lot of divalent magnesium salt, whereas too much monovalent sodium salt leads to a reduction in enzyme function. However, it is known from leaching experiments that prebiotically relevant geomaterial such as basalt releases mainly a lot of sodium and only little magnesium. A natural solution to this problem is heat fluxes through thin rock fractures, through which magnesium is actively enriched and sodium is depleted by thermogravitational convection and thermophoresis. This process establishes suitable conditions for ribozyme function from a basaltic leach. It can take place in a spatially distributed system of rock cracks and is therefore particularly stable to natural fluctuations and disturbances.

BP 11.10 Mon 16:30 BPp

Structured keratin films as artificial nail plate model — •Kim Thomann, Andreas Späth, and Rainer H. Fink — Lehrstuhl für Physikalische Chemie II, Friedrich-Alexander Universität Erlangen-Nürnberg, Egerlandstr. 3, D-91058, Erlangen, Germany

Human fingernails can be studied ex vivo only in form of clippings which offer limited insight as they do not necessarily reflect the behavior of the whole nail. Keratin films (KFs) can potentially serve as human fingernail substitute which is especially relevant for the medical and beauty sector. In order to model the nail's adhesive characteristics, structured and unstructured films from keratin extracted from human hair and nails were produced.

The fingernail being the reference, the KFs were characterized with a number of methods, including SEM, AFM, contact angle (CA) measurements, XPS, ATR-FTIR and Raman spectroscopy. In terms of composition, KFs show a good resemblance, regardless of keratin origin. The nail's microstructured topography is well matched by the structured KFs. CA measurements revealed that the surface free energy is in the same range for both KF types. However, the unstructured KFs exhibit a much stronger polar component compared to the nail while the structured KFs fit the nail's component composition well. Thus, the structured KFs represent a good approach to achieve a satisfying model in terms of wetting while combining both composition and topography aspects. The research is funded by the BMBF within project 05K19WE2.

BP 11.11 Mon 16:30 BPp

Activity of hydrogel-encapsulated cells monitored by atomic force microscopy — •Mengxiao Li[1,2], Kordula Schellnhuber[1,2], Shardul Bhusari[1,2], Johanna Blass[1], Shrikrishnan Sankaran[1], and Roland Bennewitz[1,2] — [1]INM - Leibniz for New Materials, Campus D22, 66123 Saarbrücken — [2]Saarland University, Naturwissenschaftlich Technische Fakultät, 66123 Saarbrücken

Living materials are an emerging concept in biomaterial research. Living organisms become part of the material and equip it with tailored functions. For example, genetically engineered bacteria are encapsulated in hydrogels to release drugs when triggered by an external stimulus [1]. The aim of this study is to develop a new technique for highly sensitive measurements of mechanical perturbances arising from growth and motion of bacteria trapped in a thin hydrogel film by means of Atomic Force Microscopy (AFM). To probe the activity of E. coli bacteria enclosed in a pluronic diacrylate hydrogel, we contact its surface with a colloidal probe cantilever. Normal and lateral displacements of the contact caused by motion or division of bacteria are recorded for a contact time of 300s at various positions of the hydrogel surface. Over 24 hours, we observe an increase of the mechanical signals with time that we attribute to bacterial colony growth inside the hydrogel film. Characteristic time scales of the processes are determined by means of continuous wavelet transform.

[1] S. Sankaran et al., Small 15 (2019) 1804717.

BP 11.12 Mon 16:30 BPp

Cohesin and condensin extrude DNA loops in a cell cycle-dependent manner — •Stefan Golfier[1,2], Thomas Quail[1,2], and Jan Brugues[1,2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]MPI-PKS, Nöthnitzer Straße 38, Dresden, Germany

How cells spatially organise long DNA polymers inside the confinements of the cell nucleus without creating knots and tangles has been a central question in cell biology. Recent observations have unveiled the physical architecture of the genome as a hierarchy of higher-order structures that deeply impact biological function. Despite their role for gene regulation, DNA repair and genome propagation, the underlying mechanisms shaping the 3D genome remained elusive. The active formation of vast DNA loops by the molecular motors cohesin and condensins has been proposed as a general mechanism to spatially organize the genome across the cell cycle. However, the requirements for genome organisation change dramatically during the cell cycle. To date it remained unclear, if DNA loops shape the drastically different chromatin architectures in inter- and metaphase. Using Xenopus laevis egg extracts, we reconstitute and directly observe DNA loop formation for the first time in a native environment and dependence of the cell cycle. We show that DNA loops are actively formed in both meta- and interphase, but with distinct biophysical properties and responsible factors. Our findings provide fundamental evidence that DNA loops are the physical building blocks of genome architecture, that are molecularly regulated during the cell cycle.

BP 11.13 Mon 16:30 BPp

UV-Induced Selectivity of Short DNA Oligonucleotides in

Early Evolution — •Corinna L. Kufner[1], Dominik B. Bucher[2], Wolfgang Zinth[3], Christof B. Mast[3], Gabriella G. Lozano[1], Sukrit Ranjan[4], Zoe R. Todd[5], and Dimitar D. Sasselov[1] — [1]Harvard University, USA — [2]TU München — [3]LMU München — [4]Northwestern University, USA — [5]University of Washington, USA

At early stages of the evolution of life, between 3.5 and 4.2 billion years ago, the ultraviolet (UV) irradiation on the surface of the Earth was much higher than today. In the prebiotic era, particularly in the absence of complex enzymes, UV light both served as an important energy source for photochemical reactions and imposed a strong selection pressure on the building blocks of life. Here, we study the photophysics of short DNA oligonucleotides by irradiation experiments and ultrafast UV pump (266 nm) IR probe (5-7 um) spectroscopy. We find a strong sequence selectivity in the photostability of short oligonucleotides. Charge transfer states can promote sequence selective self-repair of adjacent photolesions via an entirely intrinsic mechanism which resembles the enzymatic repair by photolyases. Particularly charge transfer states which involve Guanine, the strongest electron donor among the canonical nucleobases, play a key role in the photostability of short oligonucleotides. It may be assumed that photophysical mechanisms have strongly influenced the selection of base sequences at early stages of evolution.

BP 11.14 Mon 16:30 BPp

Nanomechanics of DNA self-assemblies and light driven molecular motors — Michael Penth[1,2], Yijun Yijun[1], Arzu Çolak[1], Kordula Schellnhuber[1,2], Mitchell K.L. Han[1], Aránzazu del Campo[1,3], Roland Bennewitz[1,2], and •Johanna Blass[1] — [1]INM - Leibniz for New Materials, Campus D22, 66123 Saarbrücken — [2]Saarland University, Physics Department, 66123 Saarbrücken — [3]Saarland University, Chemistry Department, 66123 Saarbrücken

Single-molecule force spectroscopy has become an essential tool to unravel the structural and nanomechanical properties of biomolecules. In this study, we present Flow Force Microscopy (FlowFM) as a massively parallel approach to study the nanomechanics of hundreds of molecules in parallel. The high-throughput experiments performed in a simple microfluidic channel enable statistically meaningful studies with nanometer scale precision in a time frame of several minutes. A surprisingly high flexibility was observed for a self-assembled DNA construct typically used in DNA origami. The persistence length was determined to be 12.6 nm, a factor of four smaller than for native DNA. The enhanced flexibility is attributed to the discontinuous backbone of DNA self-assemblies. We also quantified the forces actuated by a unique molecular machine that can apply forces at cell-matrix and cell-cell junctions using light as an energy source. Micrometer-sized beads tethered to the surface via entangled rotary motors were retracted against drag forces from 1 pN to 5 pN within the first minute of UV-irradiation.

BP 11.15 Mon 16:30 BPp

In-situ GiSAXS investigations of sprayed drugs on Peptide Hydrogel based matrix — •Naireeta Biswas[1,2], Elisabeth Erbes[1,2], Krishnayan Basuroy[1], Jose Velaquez Garcia[1], Sreevidya Thekku Veedu[1], Matthias Schwartzkopf[1], Calvin Brett[1,4], Stephan Roth[1,3], and Simone Techert[1,2] — [1]Deutsches Elektronen-Synchrotron (DESY), Notkestraβe 85, 22607 Hamburg, Germany — [2]University of Göttingen, Institute for X-ray Physics, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [3]Department of Fibre and Polymer Technology, KTH Royal Institute of Technology, 100 44 Stockholm, Sweden. — [4]Department of Mechanics, KT Royal Institute of Technology, 100 44 Stockholm, Sweden

A controlled and personalized treatment is key to successful medication. We have designed a novel hybrid material- a matrix made of a mixture of hydrophilic carboxymethylated nanocellulose (CMC) hydrogel and disordered hydrophobic peptide hydrogel (P). Our investigations into this material are the first steps towards a novel drug delivery/carrier strategy that allows a controlled dosage of anti-COVID drugs embedded in the system. This gives us the opportunity to vary the local uptake in a hydrophobic or hydrophilic compartment in the matrix. The structural intercalation and the time-resolved process were investigated with in-situ grazing-incidence small-angle X-ray scattering (GISAXS) experiments while spraying the drug on the matrix. In this work, we have focused on the structural analysis of the peptide hydrogel system with the drugs. The structural analysis of the CMC fibers will be presented in the poster of Elisabeth Erbes.

BP 11.16 Mon 16:30 BPp

Cytoplasmic streaming enables inter-nuclear signaling in the giant syncytium *Physarum polycephalum* — •Nico Schramma[1], Siyu Chen[1,2], and Karen Alim[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Technical University of Munich, Physics Department, Munich, Germany

The slime mold *Physarum polycephalum* is known for its optimized active transport network, which is utilized to spread signals and nutrients over its up to meter-sized cell-body. Intriguingly, this syncytium contains up to billions of nuclei, which are said to divide in a mitotic wave. However, direct experimental evidence of this finding is still missing and the possibility of inter-nuclear signaling remains elusive. Here, by observing fluorescent labeled nuclei with high-speed microscopy, we uncover that individual nuclei not only can be transported in the tubes of the network, but can also get immobilized in the porous, gel-like endoplasm wrapping the tubes. Then, using particle image velocimetry, we resolve the slow flow within the endoplasmic tube-walls. Furthermore, we use a simplified advection-diffusion-reaction model to show that inter-nuclear exchange of large molecules such as mRNA can only happen within physiological time scales between stuck nuclei in the endoplasm, rather than between transported nuclei. Our study provides evidence that immobilised nuclei may play a crucial role in the coordination of mitotic waves or gene-expression patterns in *Physarum* and may pave the way to use *Physarum* as a model syncytium to understand the interplay of fluid-driven transport and signaling of nuclei.

BP 11.17 Mon 16:30 BPp

Resolving Energy Storage in Extra-Embryonic Membranes — •Zoë Lange[1,2], Franziska Krämer[1,3,4], Frederic Strobl[3,4], Ernst Stelzer[3,4], and Franziska Matthäus[1,4] — [1]Frankfurt Institute for Advanced Studies (FIAS) — [2]IfB, FB Physik, Uni Frankfurt/Main — [3]Buchmann Institute for Molecular Life Sciences (BMLS) — [4]IZN, FB Biowissenschaften, Uni Frankfurt/Main

Efficient energy use and storage is crucial in living organisms. In the context of evolution, energy management is continuously optimized to ensure an individual's ability to successfully compete. This is especially true for oviparous species, as all required energy has to be provided at the moment of oviposition in order to give rise to a fully functional organism. Based on our preliminary imaging data in the emerging insect model *Tribolium castaneum*, we formulate the hypothesis that extra-embryonic serosa cells utilize shape change during gastrulation to allocate and store energy that is later on required for their extensive movement during dorsal closure. To investigate this possible functional connection, we want to gain further insights into the multi-scale effects of force propagation from cellular to tissue level. Spatial and temporal dynamics of forces are calculated using non-invasive Force Inference (FI). FI utilizes a biomechanical model, a mathematical inverse method and a Bayesian framework to estimate cell and tissue stress from segmented image data and for the whole system simultaneously. Here we highlight our workflow from obtaining 3D time-lapse light sheet-based fluorescent microscopy images of live *Tribolium* embryos to multi-scale estimation of tensions and pressures acting in the serosa membrane.

BP 11.18 Mon 16:30 BPp

Cell Fate Clusters in Inner Cell Mass Organoids Arise from Cell Fate Heredity — •Tim Liebisch[1,2], Armin Drusko[1,2], Biena Mathew[1,3], Ernst Stelzer[1,3], Sabine Fischer[4], and Franziska Matthäus[1,2] — [1]GU Frankfurt — [2]FIAS — [3]BLMS — [4]JMU Würzburg

Recently, inner cell mass (ICM) organoids have been published as an in vitro model system towards preimplantational development. ICM organoids mimic the second cell fate decision taking place in in vivo mouse embryos. It was shown that cells of the same fate tend to cluster stronger than expected for the currently hypothesised random cell fate distribution. Three major processes contribute to the cell fate arrangements at the 24 h old and 48 h old ICM organoids or mid and late blastocyst, respectively: chemical signalling; cell sorting process; cell proliferation.

An agent-based model was developed, accounting for cellular interactions, cell growth and division. The model was applied to compare current assumptions of how the ICM neighbourhood is formed. The model supports the hypothesis that initial cell fate acquisition is a stochastically driven process. Subsequently, the observed neighbourhood structures can emerge due to cell fate heredity.

Simulations show that the initial cell differentiation process takes place only during a small time window, during ICM organoid composition. Our results leave little room for cellular signalling believed to be

important in cell fate decision. Hence, we are discussing an alternative role of chemical signalling in this process.

BP 11.19 Mon 16:30 BPp

Migration of Cytotoxic T Lymphocytes in Collagen Matrices — •Zeinab Sadjadi[1], Heiko Rieger[1], Markus Hoth[2], Bin Qu[2], and Renping Zhao[2] — [1]Department of Theoretical Physics and Center for Biophysics, Saarland University — [2]Department of Biophysics, Center for Integrative Physiology and Molecular Medicine, School of Medicine, Saarland University

Cytotoxic T lymphocytes (CTLs) need to migrate to search for their target cells in complex biological microenvironments, a key component of which is extracellular matrix (ECM). The mechanisms underlying CTL*s navigation are not well understood so far. Here we use a collagen assay as a model for the ECM and analyze the migration trajectories of primary human CTLs in collagen matrices with different concentrations. We observe different migration patterns for individual T cells. Three different motility types can be distinguished: slow, fast and mixed motilities. Slow CTLs remain nearly stationary within the collagen matrix and show slightly anti-persistent motility, while the fast ones move quickly and persistent. We hypothesize that the slow mode describes CTLs creating channels through the collagen matrix by deforming and tearing apart collagen fibers, and that the fast motility mode describes CTLs moving within these channels. The dynamics of the mixed type consists of periods of slow and fast motions. The dynamics can be well described by a two-state persistent random walk model. We extract the parameters of the model by analyzing experimental data.

BP 11.20 Mon 16:30 BPp

Is Cell segregation just like oil and water: A phase field approach — •Florian Franke, Steffen Lange, Hans-Joachim Böhme, Sebastian Aland, and Anja Voss-Böhme — Hochschule für Technik und Wirtschaft Dresden (HTW), Dresden, Germany

Understanding the segregation of cells is crucial to answer questions about tissue formation in embryos or tumor progression. According to Steinberg's differential adhesion hypothesis the separation of cells can be compared to the separation of two liquids, e.g. water and oil. Specifically, it was proposed, that similarly to the demixing of fluids, differences in the strengths of the adhesive forces in homo- and heterotypic cell contact lead to all sorting. This hypothesis has been tested on the basis of cell-based models which simulate motile cells with differential adhesive interaction on the basis of probability cellular automaton models. On the other hand, the segregation of fluids like water and Oil can be well described by phase-field models as the Cahn-Hilliard-Navier-Stokes-equation.

Here we investigate the relation between the two approaches and to what extent parameters can be transformed between the two models. Further, by comparing simulations of either model to in-vitro experiments from the literature, we conclude that cells segregation is best described by the cellular automaton. Only a specific time regime of the segregation resembles the demixing of two liquids. However, experimentally observed cell segregation displays both regimes of logarithmic and power-law segregation with varying exponent. This rich behavior is reproduced by the cellular automaton model.

BP 11.21 Mon 16:30 BPp

Theoretical approaches to mechanics of biofilms — •Hui-Shun Kuan[1], Wolfram Pönisch[2], Leander Self[3], Frank Jülicher[4], Michael Schmiedeberg[3], and Vasily Zaburdaev[1] — [1]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]MRC Laboratory for Molecular Cell Biology, University College London, United Kingdom — [3]Institut für Theoretische Physik 1, Friedrich-Alexander-Universität Erlangen-Nürnberg — [4]Max Planck Institute for the Physics of Complex Systems

Mechanics of biofilms is intrinsically affected by biological processes at different scales: from the activity of molecular motors to motility, and to cell death and division. As a result, the rheological properties of these bacterial colonies are markedly different from those exhibited by systems at thermal equilibrium. In this work, motivated by biofilms of *Neisseria gonorrhoeae* bacteria, we use a continuum theory and agent-based numerical simulations to study dense bacterial colonies shaped by attractive intercellular interactions. We can describe the formation of a colony as a phase separation process while the colony itself behaves as a viscoelastic material. By studying the behaviour of the colonies under oscillatory shear, we can link their mechanical properties to the dynamics of the intercellular forces. Due to the turnover of these active forces, the colonies show a liquid-like behaviour at large times and strong shear-thinning effect under the large amplitude of the oscillatory shear. Our study provides an important insight on how the active intercellular forces define the material properties of living aggregates which can now also be tested experimentally.

BP 11.22 Mon 16:30 BPp

Nanoprobing of osteoblasts adhered to molecular landscapes of dendrimer and protein — Christian Völkner[1], Issam Assi[1], Willi Karberg[1], •Regina Lange[1], Martina Grüning[2], Barbara Nebe[2], Ingo Barke[1], and Sylvia Speller[1] — [1]University of Rostock, Institute of Physics, Physics of Surfaces & Interfaces, 18059 Rostock — [2]Rostock University Medical Center, Dept. of Cell Biology, 18057 Rostock

Molecular surface gradients can constitute electric field landscapes and serve to control local cell adhesion and migration. This may allow the discovery of routes to improve osseointegration of implants. Flat molecule aggregate landscapes of amine-terminated dendrimers (PAMAM, generation 1) or proteins (BSA) were prepared on glass by micro contact printing [1] to provide lateral electric field gradients through their less negative zeta potentials compared to the glass substrate.
The local as well as the mesoscopic responses of adhered osteoblasts (MG-63) were studied by means of Scanning Ion Conductance Microscopy (SICM) [2] and Fluorescence Microscopy, in situ.
A distinct spindle shape oriented parallel to the stripe pattern as well as a preferential adhesion of the cells on the glass site have been observed when the width of the stripes and the spacing is 6 or 20 μm. To explain this effect, we suggest a retraction mechanism according to cathodic taxis, a subtype of galvanotaxis [3].
[1] Whitesides et al., Chem. Rev. 105, 1171 (2005)
[2] Korchev et al., Biophys. J. 73, 653 (1997)
[3] Djamgoz et al., J.of Cell Science 117, 1631 (2004)

BP 11.23 Mon 16:30 BPp

Kinetics of light-switchable surface association of *C. reinhardtii* populations — •Rodrigo Catalan[1], Alexandros Fragkopoulos[1], Nicolas von Trott[1], Simon Kelterborn[2], Peter Hegemann[2], and Oliver Bäumchen[1,3] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), Am Fassberg 17, 37077 Göttingen, Germany — [2]Humboldt University of Berlin, Institute of Biology, 10115 Berlin, Germany. — [3]University of Bayreuth, Experimental Physics V, 95440 Bayreuth, Germany

Bacterial and microalgal colonization on surfaces produce favorable and adverse effects in technological and medical settings. Therefore, the fundamental aspects of biofilm formation on solid substrates are actively studied. While bacteria have been the main focus of research to understand microbial surface colonization, analogous studies using archetypes in microalgae are thus far elusive. We exploit light-switchable flagellar adhesion of *C. reinhardtii* [Kreis et al., Nature Physics, 2018] to study the kinetics of adsorption and desorption of cell suspensions on glass using bright field microscopy and image analysis. We observe that both processes exhibit a lag response relative to the time at which blue- or red-light conditions are set and we model this feature using time-delayed Langmuir kinetics. We find that adsorption occurs significantly faster than desorption, with the delay to be an order of magnitude larger. Adsorption experiments of phototactically blind *C. reinhardtii* mutants show that phototaxis does not affect the kinetics of either process. Hence, our method can be used as an assay for characterizing surface colonization.

BP 11.24 Mon 16:30 BPp

Unravelling the biomolecular origin of light-switchable adhesion of *Chlamydomonas* to surfaces — •Antoine Girot[1], Rodrigo Catalán[1], Alexandros Fragkopoulos[1], Marzieh Karimi[1], Simon Kelterborn[2], Peter Hegemann[2], Michael Hippler[3], and Oliver Bäumchen[1,4] — [1]Max Planck Institute for Dynamics and Self-Organization (MPIDS), 37077 Göttingen, Germany — [2]Institute of Biology, Humboldt University of Berlin, 10099 Berlin, Germany — [3]Institute of Plant Biotechnology and Biology, University of Münster, 48143 Münster, Germany — [4]Experimental Physics V, University of Bayreuth, 95440 Bayreuth, Germany

In this work, we focus on the adhesion of the biflagellated microalga *Chlamydomonas reinhardtii*. We discovered that this alga exhibits light-switchable adhesion, i.e. the flagella of the cells stick to surfaces under blue but not under red light. In order to unravel the biomolecular origin of this specific light-regulated behaviour, two different experimental approaches are carried out. First, we record the kinetics

of the adsorption and desorption of a cell suspension to a surface in response to a light switch. Second, we employ *in vivo* micropipette force spectroscopy to measure the adhesion force of single cells. By applying these methods for different wild-type strains, we aim at identifying characteristic gene sequences associated to cells adhesion. To unravel the blue-light sensitive photoreceptor responsible for adhesion, these experiments are performed with specific photoreceptor-deleted mutants. Finally, we investigate how the glycosylation of the flagellar membrane proteins affects the adhesion of *Chlamydomonas*.

BP 11.25 Mon 16:30 BPp

Determination of the effective adhesion parameter for the sorting behavior of a cell system with several cell types using statistical learning methods — •Philipp Rossbach, Steffen Lange, Hans-Joachim Böhme, and Anja Voss-Böhme — Hochschule für Technik und Wirtschaft Dresden

The process of cell sorting plays an essential role in development and maintenance of tissues. To understand this process, mathematical modeling can assist cell biological research by providing means to analyze the consequences of different hypotheses on the underlying mechanisms. In the Differential Adhesion Hypothesis (DAH) by Steinberg (1962) it is assumed that cell sorting is determined by quantitative differences in cell type specific intercellular adhesion strengths. An implementation of the DAH is the Differential Migration Model (DMM) by Voss-Böhme and Deutsch (2010). From this DMM an effective adhesion parameter (EAP) for systems with two cell types can be derived analytically which predicts the asymptotic sorting pattern. However, the existence and form of such an parameter for more than two cell types is unclear.

Here, we investigate numerically the existence of an EAP for systems with more than two cell types. We rely on in-silico time-series data that is produced by a cellular automaton which emulates the DMM and classify the segregation behavior using statistical learning methods such as SVM and Logit Model. We use these tools to demonstrate the existence of an EAP for three cell types which matches our analytical prediction for systems with arbitrary many cell types.

BP 11.26 Mon 16:30 BPp

Optogenetic control of intracellular flows and cell migration: a minimal active gel model — •Oliver M. Drozdowski[1,2], Falko Ziebert[1,2], and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, Heidelberg University, Philosophenweg 19, 69120 Heidelberg, Germany — [2]BioQuant, Heidelberg University, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany

The actin cytoskeleton of cells is in continuous motion due to both polymerization of new filaments and their contraction by myosin II molecular motors. Through adhesion to the substrate, such intracellular flow can be converted into cell migration. Recently, optogenetics has emerged as a new powerful experimental method to control both actin polymerization and myosin II contraction. While optogenetic control of polymerization can initiate cell migration by effecting protrusions, it is less clear if and how optogenetic control of contraction can effect cell migration. Here we analyze the latter situation using a minimal variant of active gel theory into which we include optogenetic activation as a spatiotemporally constrained perturbation. The model can describe the symmetrical flow of the actomyosin system observed in optogenetic experiments but not the long-lasting polarization required for cell migration. Motile solutions become possible if cytoskeletal polymerization is added to the boundary conditions. Optogenetic activation of contraction can then initiate locomotion in a symmetrically spreading cell and strengthen motility in an asymmetrically polymerizing one. If designed appropriately, it can also arrest motility even for protrusive boundaries.

BP 11.27 Mon 16:30 BPp

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

Force generation and motion of individual cells and cell collectives are fundamental constituents for many biological processes, including development, wound healing and cancer metastasis. Wound healing assays are quantitative experiments in which a 2D cell monolayer moves into empty space, often forming finger-like protrusions. Such experiments have revealed that migrating cell monolayers are both dynamic and elastic at the same time. However, such a combination of properties is very challenging to model with conventional approaches. Here we present a new phase field approach enabling us to predict the dynamics of thin elastic sheets under the action of active stresses and localized forces while ensuring reversibility as required by elasticity[1]. The continuum equations of our model can be solved by a combination of spectral and matrix methods and the numerical solutions can be compared to analytical ones. We demonstrate the potential of our modelling approach by studying several biologically relevant situations and geometries for single cells and cell monolayers, including elastic bars, contractile discs and the formation of elastic protrusions in an expanding monolayer scenario.

[1] R. Chojowski, U.S. Schwarz, F. Ziebert, Reversible elastic phase field approach and application to cell monolayers, Eur. Phys. J. E 43, 63 (2020)

BP 11.28 Mon 16:30 BPp

Morphodynamics in the Foraging of *Physarum polycephalum* — •Lisa Schick and Karen Alim — Technische Universit"at M"unchen

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

BP 11.29 Mon 16:30 BPp

A general theoretical framework to describe the influence of electric field on Mesechymal stem cell differentiation — •Jonathan Dawson[1], Ursula van Rienen[1,2,4], Poh Soo Lee[3], and Revathi Appali[1,4] — [1]Institute of General Electrical Engineering, University of Rostock, Germany — [2]Life, Light and Matter, Interdisciplinary Faculty, University of Rostock, Germany — [3]Max Bergmann Center for Biomaterials, Institute for Materials Science, Technical University of Dresden, Dresden, Germany — [4]Ageing of Individuals and Society, Interdisciplinary Faculty, University of Rostock, Germany

Bone regeneration is a highly complex and tightly regulated process which involves concerted and controlled action of human mesenchymal stem cell (hMSC) proliferation and differentiation into osteoblasts. Multiple physiological and environment factors influence the osteogenic differentiation and proliferation of hMSCs. Here we present a quantitative study investigating the influence of external electric field on stem cell dynamics, specifically proliferation and differentiation. In experiments, hMSCs were exposed to a low-frequency electrical field applied via a transformer-like-coupling (TLC). Osteogenic differentiation was quantified by measuring expression levels of cell alkaline phosphate (ALP) activity over time. Our mean-field theory describes the dynamics of a population of ALP stained hMSCs and takes into account cell division, cell differentiation, and intracellular ALP activity. Our results show that the stem cell differentiation rate is electric field dependent, and the proliferation rate is cell-density dependent.

BP 11.30 Mon 16:30 BPp

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

To enable differentiation of cells and to facilitate cell organization the establishment of gradients is crucial in early embryogenesis. We have used the model organism C. elegans and a custom built light-sheet microscope to study the formation of protein and organelle gradients in three dimensions over time. Due to the low phototoxicity and reduced bleaching induced by this selective illumination long term observations without developmental perturbations are made possible. The focus of the current study is on evolution until the first cell division, which, next to the different sized daugther cells, is characterized by a lot of accompanying asymmetries. We study the protein concentration of two vital proteins in early development with respect to their axial as well

as radial distribution. Also, two organelles with opposing gradients are investigated. Since diffusion plays a vital role in the establishment of gradients a new multiplexed diffusion measurement technique (SPIM-FCS) is used to quantify changes in diffusive behavior of proteins in space and time.

BP 11.31 Mon 16:30 BPp

Characterisation of local membrane height fluctuations on live cells — •Max Ulbrich[1], Christian Völkner[1], Regina Lange[1], Sophie Kussauer[2], Robert David[2], Martina Grüning[3], Barbara Nebe[3], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, Physics of Surfaces & Interfaces, University of Rostock, 18059 Rostock — [2]University Medical Center, Cardial Regeneration, University of Rostock, 18057 Rostock — [3]Rostock University Medical Center, 18057 Rostock

Assessment of cellular membrane fluctuations may aid monitoring of physiologic and pharmacologic effects [1]. Scanning Ion Conductance Microscopy (SICM) is a nanoprobing method to acquire morphology and dynamics on live cells. We operate the nanopipette-probe on fixed lateral locations and record SICM time traces in order to assess membrane fluctuations and cell activities [2]. Membrane fluctuations of live osteoblasts and cardiomyocytes are analysed in the time and frequency domain. Living osteoblasts and paused pacemaker cells, in average, exhibit scaling exponents of -2.8 and -2.5, respectively, however with large variations from cell to cell and site to site. We discuss this behavior in view of reference measurements on fixed cells and in the context of optically obtained results [3].

[1] B Rappaz, et al, Blood Cells Mol. Dis. 42 (2009) 228
[2] S-O Kim, et al, Nano Convergence (2017) 4:5
[3] B Sinha, et al, Biophys. J. (2017) 113

BP 11.32 Mon 16:30 BPp

A single-molecule view of the cytosolic membrane of Trypanosoma brucei — •Paula Büttner, Marie Schwebs, and Susanne Fenz — Julius-Maximilians-Universität Würzburg, Würzburg, Germany

African trypanosomes are the causative agents of sleeping sickness. In the bloodstream of their host, they express a dense coat of GPI-anchored variant surface glycoproteins (VSGs). Fluidity of this coat is fundamental for the evasion of the hosts immune system and thus for the survival of the parasite. However, VSG dynamics is also limited by the lipid matrix. We have recently introduced super-resolution imaging of intrinsically fast-moving flagellates based on cyto-compatible hydrogel embedding and found that the inner membrane leaflet appears to be structured [Glogger et al. JPD 17 & Exp. Parsitol. 17]. We hypothesize that the WCB (whole cell body) protein, that connects the cytoskeleton with the plasma membrane, causes this structure. We present two-color single-molecule measurements of a lipid probe and WCB to address this hypothesis.

BP 11.33 Mon 16:30 BPp

Multi-color fluorescence fluctuation spectroscopy in living cells via spectral detection — •Valentin Dunsing, Annett Petrich, and Salvatore Chiantia — Universität Potsdam, Potsdam, Deutschland

Signaling pathways in biological systems rely on specific interactions between multiple biomolecules. Fluorescence fluctuation spectroscopy is a powerful toolbox to quantify such interactions directly in living cells. Cross-correlation analysis of spectrally separated fluctuations provides information about inter-molecular interactions, but is conventionally limited to two fluorophore species. Here, we present scanning fluorescence spectral correlation spectroscopy (SFSCS), a versatile approach that can be implemented on standard confocal microscopes, allowing the investigation of interactions between multiple protein species at the plasma membrane of cells. We demonstrate that SFSCS enables cross-talk-free cross-correlation, diffusion and oligomerization analysis of up to four protein species labeled with strongly overlapping fluorophores. As an example, we investigate the interactions of influenza A virus (IAV) matrix protein 2 with two cellular host factors simultaneously. We furthermore extend raster spectral image correlation spectroscopy (RSICS) to four species analysis and apply it to determine the stoichiometry of ternary IAV polymerase complexes in the cell nucleus. Based on triple correlation analysis of RSICS data, i.e. detection of coincident fluctuations of fluorescence signals emitted by three fluorophore species, we provide direct evidence for the assembly of ternary protein complexes.

BP 11.34 Mon 16:30 BPp

Conditions for thermodynamic stability and critical points in multicomponent mixtures with structured interactions — •Isabella Graf and Benjamin Machta — Yale University, New Haven, CT, USA

Multicomponent mixtures are ubiquitous in biology, ranging from cellular membranes to liquid-like droplets. There is experimental evidence that their phase behavior plays a functional role for signaling and control of biochemical reactions and is under regulation itself. For instance, it has been demonstrated recently that membranes composed of a large variety of lipids are tuned close to a miscibility critical point. Theoretical work has shed light on the phase behavior of idealized systems with many components and random, mutually independent interactions, but there is little understanding of how these results generalize to systems with more structured interactions. To address this open question, we consider a family of multicomponent models with an interaction matrix of variable rank. The matrix is constructed so that each component is characterized by several scalar "features", each of which conveys an Ising-like interaction between neighboring components and could be interpreted as lipid tail length, headgroup or saturation in the case of membrane lipids. We derive analytical, mean-field conditions for the occurrence of thermodynamic stability and (higher-order) critical points and find that these conditions depend on the cumulants of the principal components of the feature distribution. These results might provide important insights into critical membrane behavior and phase behavior of multicomponent mixtures more generally.

BP 11.35 Mon 16:30 BPp

Modeling RNA Polymerase II clusters by lattice kinetic Monte Carlo simulations — •Tim Klingberg[1,2], Lennart Hilbert[3], and Vasily Zaburdaev[1,2] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg — [2]Max-Planck-Zentrum für Physik und Medizin — [3]Karlsruher Institut für Technologie

Eukaryotic genes are mainly transcribed by RNA polymerase II (Pol II). Before active transcription starts, Pol II is recruited to the promoter region of a specific gene and then released from a paused state into transcript elongation. Clusters of paused Pol II of various sizes and morphologies can be observed in zebrafish embryos (Pancholi et al.). Here, we aim to understand the physical mechanisms that are essential for the cluster formation and determine their emerging properties. To this end, we apply two-dimensional lattice kinetic Monte Carlo simulations with single Pol II particles interacting with DNA polymers, whose dynamics are determined by the Verdier-Stockmayer algorithm. The model suggests that formation of Pol II clusters can be rationalized as phase separating phenomenon where polymerases form a liquid phase that wets the chromatin at the promoter region. Cluster properties such as size and morphology can be linked to the size of the promoter region and the respective gene. Despite the simplicity of the model, it is sufficient to qualitatively describe the experimentally observed cluster properties in normal conditions and under drug treatments interfering with the transcription process.

BP 11.36 Mon 16:30 BPp

Euchromatin reorganisation during transcription resembles active microemulsion — •Rakesh Chatterjee[1,2], Hui-Shun Kuan[1,2], and Vasily Zaburdaev[1,2] — [1]Department of Biology, Friedrich-Alexander-Universität Erlangen-Nürnberg, 91058 Erlangen, Germany — [2]Max Planck Zentrum für Physik und Medizin, 91058 Erlangen, Germany

During transcription RNA polymerase II (Pol II) attaches and moves along the DNA strand to produce messenger-RNA (mRNA). The selective induction of transcription from DNA into RNA shapes and is being shaped by the chromatin organisation. To investigate this complex interplay, we aim to establish a phenomenological model, which qualitatively mimics the experimental results regarding transcription process in primary cell cultures obtained from zebrafish embryos. Our phenomenological lattice model is based on the framework of microphase separation or microemulsion. DNA, mRNA and Pol II serve as the three basic components similar to the oil-water-surfactant system, which exhibits two and three phase coexistence. Freely diffusing Pol II undergoes chemical transitions reflecting different stages of the transcription process. Similar behaviour can be realised by assuming transient dynamics of the surfactants which switches between active and inactive states. We use lattice model simulations and the correlation function approach to characterises different phases of this three component system. The resulting structures can be understood

via the continuum theory that we derive by coarse-graining the lattice model.

BP 11.37 Mon 16:30 BPp

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

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

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

BP 11.38 Mon 16:30 BPp

Mechanical phenotyping beyond geometrical constraints using virtual fluidic channels — •Muzaffar Panhwar[1], Fabian Czerwinski[1], Venkata A.S. Dabbirru[1], Yesaswini Komaragiri[1], Peter Nestler[1], Bob Fregin[1], Ricardo H. Pires[1], Doreen Biedenweg[2], and Oliver Otto[1] — [1]AG Biomechanic, ZIK-HIKE, Universität Greifswald, Greifswald, Deutschland — [2]Universitätsmedizin Greifswald, Greifswald, Deutschland

Microfluidic techniques have proven to be of key importance for achieving high-throughput cell mechanical measurements. However, their design modifications require sophisticated cleanroom equipment. Here, we introduce virtual fluidic channels as a flexible and robust alternative to Poly-dimethylsiloxane chips. Virtual channels are liquid-bound fluid flows that can be tailored in three dimensions within seconds for rheological studies on a wide size range of biological samples. While cell deformation inside standard hard-wall constrictions is mainly driven by shear stress, virtual channel possess an additional normal stress component originating from the liquid-liquid interface. We demonstrate that this interface acts as a high-frequency liquid cantilever for probing cell rheology on a millisecond timescale. In proof-of principle experiments, cells are treated with cytochalasin D to inhibit actin polymerization. A significant reduction in the Young's modulus is found compared to untreated cells. In addition, we utilize virtual channels to measure the mechanical properties of single cells and spheroids as a tissue model system. Our results indicate that the Young's modulus of single cells exceeds the one of tissue by one order of magnitude.

BP 11.39 Mon 16:30 BPp

Monitor, categorize and manipulate label-free water-in-oil droplets in microfluidic systems — •Tobias Neckernuss[1,3], Chrostoph Frey[2], Jonas Pfeil[1,3], Daniel Geiger[1,3], Ilia Platzman[2], Joachim Spatz[2], and Othmar Marti[1] — [1]Institute for Experimental Physics, Ulm University — [2]Max-Planck-Institute for Medical Research, Heidelberg — [3]Sensific GmbH, Germany

A key point of droplet based microfluidics is the availability of powerful but easy-to-implement methods for high throughput real-time analysis and automated manipulation of the droplets. We developed a novel optical device, consisting of a fast camera with integrated data processing for smart and fast algorithms enabling label-free real-time monitoring and active manipulation of passing droplets. The device continuously analyzes up to 3000 particles per second in real-time with respect to bright-field image parameters like size, brightness, granularity, circumference, speed and many more. According to these parameters and combinations thereof, the passing droplets can be sorted. We measure different droplet production parameters and demonstrate label-free detection of cells encapsulated in droplets. Furthermore, we performed label-free sorting of cell laden droplets from empty droplets. The peripheral sorting electronics are controlled by our device. Decision making is based on predefined parameter ranges that are compared to the measurement results of the droplets right before the sorting gate. Similarly, in another experiment we demonstrate efficient sorting of droplets depending on size.

BP 11.40 Mon 16:30 BPp

Transition of adherent to suspension state: relevance to cell mechanical properties — •Venkata Dabbiru[1], Emmanual Manu[1], Huy Tung Dau[1], Nora Bödecker[1], Doreen Biedenweg[2], Ricardo Pires[1], and Oliver Otto[1] — [1]University of Greifswald, Germany — [2]University Medicine Greifswald, Germany

Adherent cells often detach from their native surface as a result of important physiological changes such as those, for example, found in cancer. While many studies have examined the mechanical properties of cells in their native adherent or suspended state, few studies have addressed the consequences associated with the transition between them. We have approached this question by using atomic force microscopy for adherent and semi-adherent cells as well as real-time deformability cytometry to study the mechanical properties of cells in suspension. As a model system, HEK293T cells have been cultured in the presence and absence of surface-tethering molecules, respectively, to mimic the transition state. Our results show that cell detachment is associated with increased stiffening of cells. Interestingly, surface-tethered transiently suspended cells and fully suspended cells differ in their mechanical properties. Analysing the F-actin distribution by confocal microscopy indicates a passive cell-surface interaction, which is not driven by adhesion molecules.

BP 11.41 Mon 16:30 BPp

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

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