BP 7: Poster 1

Time: Monday 18:00–20:00 Location: P1

BP 7.1 Mon 18:00 P1

Assessing biomolecular interactions across scales using optical tweezers — •Roman Renger, Nicholas Luzzietti Luzzietti, and Philipp Rauch — LUMICKS, Amsterdam, Netherlands

Biological processes involving proteins interacting with nucleic acids, cell membranes or cytoskeletal filaments are key to cell metabolism and hence to life in general. Detailed insights into these processes provide essential information for understanding the molecular basis of physiology and the pathological conditions that develop when such processes go awry. The next scientific breakthrough consists in the direct, real-time observations and measurements of the most fundamental mechanisms involved in biology Single-molecule technologies offer a powerful opportunity to meet these challenges and to study dynamic protein function and activity in real-time and at the single-particle level. Here, we present our efforts for further enabling discoveries in the field of biology and biophysics using the combination of optical tweezers with correlative fluorescence microscopy (widefield, TIRF, confocal and STED) and label-free Interference Reflection Microscopy (IRM). We present several examples in which our technology has enhanced the understanding of basic biological phenomena, ranging from protein structure to intracellular organization. Furthermore, we show that advances in hybrid single-molecule methods can be turned into an easy-to-use and stable instrument that has the ability to open up new avenues in many research areas.

BP 7.2 Mon 18:00 P1

Transport in complex intracellular environments — •Mohammad Amin Eskandari, Bart Vos, Mattias Luber, and Timo Betz — Third Institute of Physics - Biophysics Georg August University Göttingen

Active transport is vital for targeted delivery of organelles, proteins and signaling molecules in eukaryotic cells and defects in active transport are linked to different diseases such as Alzheimer's disease. Kinesin and dynein are two motor proteins which are responsible to carry the cargoes along the microtubule filaments. Since the cytoplasm is a highly crowded environment, the motion of cargoes can be hindered by some sorts of obstacles and this brings us to the question how these motors can generate a processive motion in such an environment to bypass the roadblocks. In this project, we aim to investigate the possible mechanisms that kinesin and dynein can use to overcome the obstacles.

BP 7.3 Mon 18:00 P1

Single Particle Tracking of Molecular Motors under Different Physiological Conditions — •Adrian Lentz, Paulina Blair, Daniel Kuckla, Philipp Hagemann, and Cornelia Monzel — Experimental Medical Physics, Heinrich-Heine University, Düsseldorf, Germany

Single particle tracking (SPT) is a powerful tool to gain insights into the dynamics of molecular motors. These proteins convert the chemical energy of adenosine triphosphate (ATP) into a forward motion to transport vesicles along the microtubule network. In our study we investigate the linear motion of the kinesin variant Kif5C, which is normally found in neuronal cells. A genetically modified Kif5C with fused green fluorescent protein was monitored with millisecond resolution and analysed with an algorithm that links precisely detected particle positions to trajectories. We establish a point density based classification of trajectories into different molecular gaits and determine diffusion, velocity and processivity of the Kif5c motor. We show a systematic analysis of the influence of different acquisition times on the motor motion determination and compare Kif5C transport in the human cell lines HeLa, MCF-7, HEK, NIH/3T3 and COS-7. Of central interest was then to measure the effect of different physiological conditions, e.g. absence or high concentration of glucose and high amount of ATP, on the Kif5C dynamics.

BP 7.4 Mon 18:00 P1

Towards Advanced Single Particle Tracking of Molecular Motors by Quantum Dot Labeling and Monitoring of the Cytoskeletal Environment — •Paulina Blair, Adrian Lentz, Xiaoyue Shang, Daniel Kuckla, Philipp Hagemann, and Cornelia Monzel — Experimental Medical Physics, Heinrich-Heine Universität, Düsseldorf, Germany

The molecular motor Kif5C plays a central role in the intracellular transport and synaptic transmission of neuronal cells. To understand how Kif5C mediated transport depends on its environment, it is essential to track the motor in the cytoplasmic context. We aim to advance the single molecule tracking of Kif5C by Quantum Dot labeling as well as by characterising the cytoskeletal environment. Quantum Dots are nanoscale semiconductors, which in contrast to genetically encoded fluorophores, offer tracking at enhanced spatio-temporal resolution and over long time scales. In this project we express Kif5C genetically fused to a streptavidin molecule in live cells. Quantum Dots functionalised with biotin are added to the cell sample to bind via streptavidin-biotin interaction to Kif5C. Molecular motors are recorded with millisecond resolution and are analysed using a global Linear Assignment Approach. The microtubule is stained using a silicon rhodamine-based fluorophore. We then derive parameters such as network density or intersections to correlate it with the motor protein dynamics.

Our data will provide insights on the benefit of Quantum Dot labeling, on molecular motor gaits such directed, superdiffusive and subdiffusive motion as well as on effects of the cytoskeletal environment.

BP 7.5 Mon 18:00 P1

Quantification of molecule-spanning protein dynamics with fluorescence correlation spectroscopy — •Veronika Frank[1], Jean-Benoît Claude[2], Jérôme Wenger[2], and Thorsten Hugel[1,3] — [1]Institute of Physical Chemistry, University of Freiburg, Germany — [2]Fresnel Institute, CNRS, Aix Marseille University, France — [3]Signaling research centers BIOSS and CIBSS, University of Freiburg, Germany

Protein conformational kinetics and their regulation occur on many time and length scales. Fluorescence methods have mainly focused on the hundreds of microseconds to minutes time scale and NMR on the picosecond time scale. Here we explore the several nanoseconds to microseconds time scale for the multi-domain molecular chaperone heat shock protein Hsp90, a homodimer with a molecular weight of 90 kDa per monomer. Hsp90 is a therapeutic target for cancer therapy, but its dynamics and its dynamic interactions with other proteins are not yet fully understood.

Here we use fluorescence correlation spectroscopy and zero-mode waveguide nanoapertures to measure and understand fast molecule-spanning dynamics and how they are affected by interactors.

BP 7.6 Mon 18:00 P1

AniMol: A quick interactive web-based molecular trajectory visualiser — James Panayis, James Partington, and •Rudolf A. Römer — Department of Physics, University of Warwick, Coventry, CV4 7AL, UK

We present software developed to interactively visualise dynamic molecular trajectories in web browsers. This tool allows for quick and efficient interaction with large flexing/moving molecular structures and helps to more easily understand results of in-silico modeling processes, for example protein dynamics simulations. The browser-based software simplifies workflows as no installation is required, and there are very few limitations due to hardware or software compatibilities. We achieve this using a lightweight state-of-the-art graphics engine, and compiling our code to WebAssembly (WASM), a portable compilation target for programming languages supported by all major browsers since 2017. We also present a webserver (animol.warwick.ac.uk) utilising this software offering cloud storage and retrieval of molecular trajectories, to aid collaboration and communication of results.

BP 7.7 Mon 18:00 P1

Correlation-based feature selection to identify functional dynamics in proteins — •Georg Diez, Daniel Nagel, and Gerhard Stock — Physikalisches Institut, Albert-Ludwigs-Universität Freiburg

Molecular dynamic simulations provide an effective tool for a deeper understanding of proteins and their functioning. In order to shed light on the underlying mechanisms of processes, one typically models the dynamics using some key internal coordinates (or features) which capture the most important conformational changes of the protein. However, one often ends up in a high-dimensional feature space which hampers a straightforward interpretation of the typically very com-

plex dynamics. Adopting the Leiden community detection algorithm [1], we present an effective and scalable approach to divide the feature space into subsets which describe collective motion. By applying this approach to the functional dynamics of different protein systems with varying size, we show that it allows to identify and discard uncorrelated motion and noise. Moreover, it provides an effective dimensionality reduction scheme by extracting the key features, and leads to a detailed understanding of the underlying mechanisms.

[1] Traag et al., "From Louvain to Leiden: guaranteeing well-connected communities", Sci. Rep., 2019

BP 7.8 Mon 18:00 P1

Reversible protein immobilization and biosensing on liquid-gated GFETs — •Mykola Fomin[1], Lara Jorde[2], Changjiang You[2], Jacob Piehler[2], and Carola Meyer[1] — [1]Department of Physics, Osnabrück University, Germany — [2]Department of Biology/Chemistry and CellNanOs Center, Osnabrück University, Germany

Apart from the standard requirements such as selectivity, sensitivity, and biological compatibility, effective electronic biosensors are facing the demand for the fabrication of cost-efficient devices. Cost and resource efficiency would benefit from re-useage of the biosensor after detection, which can be achieved by reversible immobilization of the molecules in question. While multiple biosensors have already been demonstrated to generate a response to a specific analyte molecule and its various concentrations, reversible protein monitoring remains a challenging task. Besides, during such measurements on graphene exists a risk of unspecific attachment to the channel with following protein denaturation. This work aims to demonstrate reversible protein immobilization detected by current changes of a liquid-gated GFET. PEG-tris-NTA on a lipid monolayer is used for site-specific immobilization of histidine-tagged proteins. The lipid layer forms a 2,5 nm hydrophilic cover over the channel that prevents unspecific protein attachment and its denaturation, resulting in enhanced biocompatibility [1]. We track the current changes upon attachment of histidine-tagged GFP to the device and their removal upon imidazole wash.

[1] L. Jorde. et al.(2021), doi: 10.1063/5.0035871.

BP 7.9 Mon 18:00 P1

Hierarchical dynamics as result of log-periodic oscillations in proteins — •Emanuel Dorbath, Gerhard Stock, and Steffen Wolf — Albert-Ludwigs-Universität, Freiburg, Germany

Logarithmic oscillations were observed in earthquakes, financial crashes and several biomolecular systems such as proteins. In many protein systems it is generally assumed, that the time scales, ranging from femtoseconds up to microseconds and longer, are in fact not independent but structured hierarchical in the sense that the fast time scales are a prerequisite for the slower ones.

This hierarchy can be well described via the free energy landscape which then gives rise to the logarithmic oscillations and a power-law. From the logarithmic oscillations, multiple relaxation times can be derived extending over several orders of magnitude [Metzler 1999].

Here, an analysis is presented to derive the respective time scales using logarithmic oscillations in non-equilibrium simulations. For this three systems are studied: A 1-dimensional model with an inherent hierarchical energy landscape is used as proof of principle and demonstration of the method. The second one is the simple hierarchical peptide Aib9 with two helical states which has been researched already in the past [Buchenberg 2015]. Finally, the widely studied PDZ2 domain is studied which shows complex conformational folding and restructure mechanisms.

BP 7.10 Mon 18:00 P1

The effect of D_2O on the pressure dependent protein-protein interaction in aqueous lysozyme solutions — •Michelle Dargasz, Jaqueline Savelkouls, and Michael Paulus — Fakultät Physik/DELTA, TU Dortmund, 44221 Dortmund, Germany

In some experimental techniques such as neutron scattering, the substitution of H_2O with D_2O is used to obtain a useful signal. It was assumed that the exchange of the solvent does not have a major influence on the protein structure and interactions. However, measurements with lysozyme in D_2O revealed a larger attractive component of the protein-protein interaction potential [1]. In this study, the pressure-dependent behavior of high concentrated lysozyme solutions with H_2O and D_2O was considered using SAXS at the beamline BL2 of the synchrotron radiation source DELTA (Dortmund Germany). In previous measurements a non-linear relationship between the interaction potential and the exerted pressure was observed [2]. This was also visible in this study, as a shift in the correlation peak of the scattering curve occurs as a function of pressure. Up to approx. 2 kbar, a shift to larger q-values occurs, which is reversed with further increasing pressure up to 4 kbar. Since this effect occurs equally in H_2O as well as D_2O, it can be assumed that the water structure plays a rather minor role for the nonlinear correlation.

[1] C. Gripon, Journal of Crystal Growth 178, 575-584 (1997)
[2] Martin A. Schroer, Phys. Rev. Lett. 106, 178102 (2011)

BP 7.11 Mon 18:00 P1

Coarsening of biomolecular condensates regulate crossover placement in Meiosis I — •Marcel Ernst and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

During meiosis, genetic information from female and male chromosomes is exchanged in a process called crossover. The dynamics that determine the positioning of these crossovers is largely not understood. Experimental observations consistently reveal two key findings: First, the number of crossovers per chromosome is at least one and is usually small, between one and three. Second, there is crossover interference, which prevents nearby crossovers on a single chromosome. We hypothesize that crossovers are determined by biomolecular condensates, which coarsen by exchanging material along chromosomes. We present theoretical and numerical results suggesting scaling laws analogous to Lifshitz-Slyozov-Wagner theory that predict the final number of crossovers, and their spatial structure as a function of coarsening time, chromosome length, and the initial amount of material. These results are consistent with current experimental findings in *Arabidopsis thaliana* and suggest how cells use a fundamental coarsening process to regulate spatial patterns.

BP 7.12 Mon 18:00 P1

Controlling size, phase transitions, and reactions in microfluidic double-emulsion droplets — •Paula Girones Paya, Sebastian W. Krauss, and Matthias Weiss — Experimental Physics I, University of Bayreuth

Double-emulsion based assays have been widely used in a large number of experiments such as in bio-inspired microreactors or in direct evolution assays. Despite the advanced techniques that have been developed to produce picoliter-sized droplets, a better manipulation of the droplet interior remains a challenge. Here, we demonstrate how hundreds of double emulsion droplets, trapped in a microfluidic sieve, can be grown and shrunk by controlling the salt concentration in the carrier liquid. Alternating the osmotic pressure leads to a rapid and reversible volume change of the aqueous droplet interior, resulting in a reversible phase separation of an enclosed binary fluid. The phase separation is shown to be a versatile tool to control, for example, the dissociation and re-association of double-stranded DNA or to monitor an enzymatic reaction via a pH sensitive fluorescence reporter.

BP 7.13 Mon 18:00 P1

Nucleation of chemically active droplets — •Noah Ziethen and David Zwicker — Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Liquid-liquid phase separation emerged as a crucial organizing principle inside biological cells giving rise to a plethora of intracellular compartments. Unique to the cellular context, these condensates can consist of only a few hundred molecules and are affected by non-equilibrium processes. In particular, active chemical conversion between condensate material and proteins in the surrounding cytoplasm can control their size. Moreover, the significant concentration fluctuations due to the small molecule numbers imply that spontaneous nucleation and dissolution are likely. Yet, it is unclear how the driven reactions affect these stochastic processes. Here, we investigate the influence of chemical reactions on the nucleation behavior of active droplets using a stochastic field theory. We find a decrease in the nucleation rate with the increased strength of the chemical reactions. Using classical nucleation theory, we can reduce the full dynamics to an analytical expression for the free energy, which only depends on the droplet radius and the strength of the chemical reactions. The chemical reactions increase the energy barrier, which the system needs to overcome to form a droplet. Additionally, the binodal and the spinodal line are moved towards the center of the phase diagram. Cells might use these effects to control the nucleation behavior of intracellular droplets or even suppress their formation completely.

BP 7.14 Mon 18:00 P1

Liquid-liquid phase separation of promoter and gene-body condensates in multi-scale simulations — •Arya Changiarath Sivadasan[1,2] and Lukas stelzl[1,2] — [1]Institute of Physics, JGU Mainz — [2]Faculty of Biology JGU Mainz and institute of Molecular Biology (IMB), Mainz

Liquid-Liquid phase separation plays an important role in the formation of localized nuclear hubs of RNAPII during the transcription process. Our research is focused on understanding the molecular basis of phase separation of CTD, the largest subunit of RNAPII, using molecular dynamics (MD) simulation methods. We investigated how the CTD phase separation is affected by differences in CTD sequences using coarse-grained MD simulations and the results indicate that deviation from the ideal heptapeptide sequence has less tendency to phase separate, which suggests that these deviations from the ideal heptapeptide repeats are important for responsive regulation of transcription. Moreover, we are looking at how phosphorylation of CTD and the presence of other biomolecules that can influence CTD phase behavior. Hyperphosphorylation prevents phase separation as the negatively charged phosphate groups repel each other. We show how hyperphosphorylated CTD might co-phase separate in elongation with HRD of Cylin-T1 in accordance with the experiment. To explore more on this, we studied the phase behavior of CTD and phosphorylated CTD in the presence of HRD and the results show that they co phase separate into a large cluster, but do not mix, which may help to physically distinguish between the initiation and elongation stages of transcription.

BP 7.15 Mon 18:00 P1

Mechanical growth and auxin patterning in plant tissues — •Mathias Höfler[1] and Karen Alim[1,2] — [1]Physics Department and CPA, Technische Universität München — [2]Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen

Individual cell shape and growth underlies a high variance in living organisms. It is puzzling how on a larger scale, the morphogenesis of a tissue can be a reliably stable and efficient process. Theory and experiment show that there is a mechanical and biochemical feedback loop for tissue development and morphogenesis. Mechanical forces in plants have a pronounced effect on the microtubule orientation in cells, thereby changing the cell's mechanical properties, causing an impact on the magnitude and direction, hence anisotropy, of cell growth. Here we study the effect of cell mechanics on the bidirectional, radial growth of tissue in the plant stem. We investigate feedback mechanisms, stress patterns and how these affect tissue and early organ shape and development. For the latter, we furthermore study the role of the growth hormone auxin in the shoot apical meristem (SAM). Here, auxin induces cell wall loosening thus enhancing mechanical growth via biochemical feedback.

BP 7.16 Mon 18:00 P1

Characterizing flexibility and mobility in the natural mutations of the SARS-CoV-2 spikes — James Panayis[1], Dom Bellini[2], and •Rudolf A. Römer[1] — [1]Department of Physics, University of Warwick, Coventry, CV4 7AL, UK — [2]MRC Laboratory of Molecular Biology, Cambridge CB2 0QH, UK

We perform in-silico modelling of the SARS-CoV-2 spike protein and its mutations, using structures from the Protein Data Bank (PDB), to ascertain their dynamics, flexibility and rigidity. Identifying the precise nature of the dynamics for the spike proteins enables, in principle, the use of further in-silico design methods to quickly screen both existing and novel drugs that may hinder these natural dynamics. We use a recent protein flexibility modelling approach, combining methods for deconstructing a protein structure into a network of rigid and flexible units with a method that explores the elastic modes of motion of this network, and a geometric modelling of flexible motion. We also conduct this analysis on synthetic structures of some newer variants (α, β, γ, δ, λ, o) for some of which structure files are not yet available from the PDB. All proteins are thermalised for at least 1ns with NAMD to human body temperature before the flexibility analysis.

BP 7.17 Mon 18:00 P1

Effects of CTCF and Cohesin complexes and nucleosome positions on chromatin loops. — •Aymen Attou, TIlo Zülske, and Gero Wedemann — University of Applied Sciences Stralsund, Institute for Applied Computer Science, 18435 Stralsund, Germany

The spatial organization of the eukaryotic genome plays an important role in regulating transcriptional activity. In the nucleus, chromatin forms loops that assemble into fundamental units called topologically associating domains, which facilitate or inhibit long range contacts. These loops are formed and held together by a ring-shaped protein complex involving cohesin and CTCF. To analyse the effects of cohesin and CTCF, an established coarse-grained computer model of chromatin with a resolution of single nucleosomes was extended by integrating potentials describing CTCF and cohesin. We performed Monte Carlo simulations combined with replica exchange procedure with regular spaced nucleosomes and experimentally determined nucleosome positions in presence of cohesin-CTCF as well as depleted systems as control. The simulations generated a statistical representative ensemble of configurations in thermal equilibrium. We studied differences in the spatial structure and of contacts probabilities of different domains. That allowed us to understand the impact of cohesin and CTCF on the 3D structure of chromatin and how nucleosome positions can impact the conformations of the chromatin loops during the residence time of the loop anchor, with presumed consequences for transcriptional activity.

BP 7.18 Mon 18:00 P1

In Silico Tumor Invasion — •Eric Behle[1], Julian Herold[2], and Alexander Schug[1] — [1]JSC, Jülich Research Centre, Wilhelm-Johnen-Straße, 52428 Jülich, Germany — [2]Karlsruhe Institute of Technology, Kaiserstraße 12, 76131 Karlsruhe, Germany

To this day, cancer remains an insufficiently understood disease plaguing humanity. In particular, the mechanisms driving tumor invasion still require extensive study. Current investigations address collective cellular behavior within tumors, which leads to solid or fluid tissue dynamics. Furthermore, the extracellular matrix (ECM) has come into focus as a driving force facilitating invasion. To complement the experimental studies, computational models are employed, and advances in computational power within HPC systems have enabled the simulation of macroscopic tissue arrangements. In line with this, we hereby present our work using Cells in Silico (CiS), a high performance framework for large-scale tissue simulation developed by us. Combining a cellular potts model and an agent-based layer, CiS is capable of simulating tissues composed of millions of cells, while accurately representing many physical and biological properties. We aim to parameterize CiS via a bottom-up approach, starting with experimental data from small systems. We focused our studies on tumor spheroids, spherical aggregates composed of thousands of individual cells, which are one of the main workhorses of tumor analysis. We investigated the invasion dynamics and their dependence on the ECM density, and further aim to apply our model to the realistic simulation of larger systems.

BP 7.19 Mon 18:00 P1

Time resolved signal propagation in a photoswitched PDZ3 domain — •Ahmed Ali, Adnan Gulzar, Steffen Wolf, and Gerhard Stock — Institute of Physics, University of Freiburg, Germany

Allostery is one of the most important mechanisms for biomolecular regulation. Generally, it involves a perturbation such as a binding event at one side of a macromolecule to affect another distant functional site. However, how such a perturbation propagates through the protein in detail is still not well understood. To establish a minimal allosteric model system, the third PDZ domain (PDZ3) of the postsynaptic density-95 (PSD-95) protein has been considered. The PDZ3 domain binds to the C-terminus of target proteins and regulates the signal propagation in PSD-95. In addition to the common and conserved central β-sheets and two α-helices present in all PDZ variants, PDZ3 contains a third C-terminal α-helix (α_3–helix) that packs against the β-sheet at a considerable distance to the ligand binding pocket.

In this work, we aim for a detailed understanding of the microscopic dynamics of allosteric communication between α_3 and the ligand binding pocket. In addition, we explicitly aim at finding intraprotein changes appearing on the same time scales as found in recent time-resolved IR spectroscopic experiments. Consequently, we perform direct nonequilibrium molecular dynamics (MD) simulations of PDZ3. We characterize the α_3-switched response by a combination of principal component analysis, clustering methods, and machine learning and characterize the microscopic mechanism behind the allosteric communication between α_3 and the ligand binding site.

BP 7.20 Mon 18:00 P1

Enabling computer simulations of chromatin at physiological density with a resolution of individual nucleosomes — •Tilo Zülske, Aymen Attou, and Gero Wedemann — University of Applied Sciences Stralsund, System Engineering and Information

Management, 18435 Stralsund, Germany

The spatial structure of chromatin in the nucleus is important for processes such as the regulation of transcription by facilitating contacts over long distances or by hindering spatial accessibility. Despite extensive research, the spatial structure of chromatin remains enigmatic. Coarse-grained computer simulation models of chromatin help to understand the existing variation of experimental data. Nucleosomes were modelled as spherocylinders connected by elastic segments describing linker DNA. Interactions include stretching, bending, torsion, electrostatic and internucleosomal interactions. Nucleosomes were spaced equidistantly and randomly. Configurations were sampled utilizing Metropolis Monte Carlo and replica exchange algorithms. We studied synthetic fibers of 1.1 Mbp utilizing with periodic boundary conditions that mimic density behavior at different concentrations. The systems comprised 6000 nucleosomes which was more than an order of magnitude larger than the systems computed by us so far. Comparison with experimental results deliver crucial insights how nucleosome positions and density affect the spatial structure and contacts.

BP 7.21 Mon 18:00 P1

Numerical study of the driving forces behind the slipper formation for RBC cells in rectangular microchannels. — •Berin Becic — Biofluid Simulation and Modeling ,Theoretische Physik VI, Universität Bayreuth

Red blood cells in rectangular microchannel flows exhibit two types of motions. At low velocities they tend to migrate towards the center and take symmetric croissant like shapes whereas for high velocities they migrate along the axis with the larger dimension and take an asymmetric slipper shape. Based on these results the behavior of the asymmetric off-centered slipper-movement was studied further via the boundary integral method. There it was observed that surprisingly this motion is only weakly dependant on the cell's elastic properties. Additionally it was found that the flow profile perpendicular to the direction of the displacement of the centered position plays a crucial role in stabilizing the slipper state and surpressing the tumbling motion expected from considering the behavior in a pure shear flow.

BP 7.22 Mon 18:00 P1

Brownian dynamics simulations of deformable cells in ordered polymer networks — •Jan Timo Bachmann[1,2] and Andreas Zöttl[2] — [1]TU Darmstadt, Germany — [2]University of Vienna, Austria

Various Cells migrate in different environments and in response to different stimuli. Cell migration may include the navigation and locomotion through complex environments, as in the case of Leukocyte migration where cells have to translocate through small pores in the extracellular matrix (ECM) by squeezing their cell body considerably. To investigate the influence of pores in the ECM on cell velocity and deformation we study a simplified model of an externally driven deformable cell moving through ordered polymer networks by means of Brownian dynamics simulations.

The cell velocity shows oscillatory behaviour with minima before and maxima after each network pore. The speed maxima can exceed the terminal velocity of the respective cell in a network-free fluid, indicating that in the squeezing process elastic interaction energy with the network is utilized to locally enhance the cell speed. The mean velocity through the network as a function of the bending modulus of the cell surface bending potential shows a non-linear unimodal curve. We further show how the interplay of pore size and cell elasticity determines the cell velocity.

BP 7.23 Mon 18:00 P1

Modelling of cell proliferation in epithelial tissue — •Kevin Höllring[1], Sara Kaliman[1], Lovro Nuić[2], Luca Rogić[2], Simone Gehrer[1], Maxime Hubert[1], and Ana-Sunčana Smith[1,2] — [1]PULS Group, FAU Erlangen-Nürnberg, Germany — [2]Group for Computational Life Sciences, Ruđer Bošković Institute, Zagreb, Croatia

The extracellular microenvironment (ECM) of epithelial cells is known to mechanically govern the properties and behavior of cells and tissues like cell differentiation, size and motility. Yet its effect on the division rate of cells in tissues has not been analyzed in detail to our knowledge. In this work, we use MDCK-II cells grown on glass and 11 kPa PDMS substrates to provide evidence for a local cell density dependent division rate in an ECM stiffness dependent manner but independent of the age of the model- tissue, its internal structure or state.

We provide a theoretical model for microscopic tissue growth in a local microenvironment with well-defined average cell-density in agreement with experimental data and Dissipative Particle Dynamics (DPD) tissue simulations. We also propose an extension to the macroscopic tissue description via the Fisher-Kolmogorov equation (FK) accounting for our new findings that is able to reproduce characteristic edge behavior of tissues that has not been able to be reproduced by the FK formalism alone.

This work therefore sheds a new light on the influence of the ECM stiffness on the maturation of epithelial tissues and the important influences of different time scales for tissue growth and cell division.

BP 7.24 Mon 18:00 P1

Finding protein-ligand unbinding pathways in dcTMD simulations using distance-based clustering — •Victor Tänzel — Institute of Physics, Albert Ludwigs University, Freiburg, Germany

The exploration of protein-ligand dynamics by fully atomic simulations is of immense interest, for example in drug design, yet remains unfeasible in unbiased molecular dynamics (MD). To trigger rare events, we employ dissipation-corrected targeted MD (dcTMD) simulations, in which a moving distance constraint biases a prechosen reaction coordinate x, here the protein-ligand distance. The method combines a Markovian Langevin equation with a second-order cumulant expansion of the Jarzynski equality. From the required constraint forces, a free energy profile $\Delta G(x)$ as well as a friction coefficient $\Gamma(x)$ are extracted.

Transitions often occur along multiple pathways. In order to find these pathways, we study distance-based clustering approaches combining a pairwise ligand RMSD with the Leiden community detection algorithm. Here, we demonstrate the capabilities of this approach with the example of the A2A-ZMA complex and estimate (un-)binding rates.

BP 7.25 Mon 18:00 P1

Protein folding as described by different internal coordinates — •Sofia Sartore — Albert-Ludwigs-Universität Freiburg

Proteins reach their final structure (native state) through a process named folding. A powerful tool to investigate such process are molecular dynamics simulations, that can simulate the folding of a protein, giving as output a folding trajectory up to hundreds of microseconds long. This trajectory however needs to be further interpreted and analyzed in order to obtain an understandable model of the process, consisting of states that correspond to metastable conformation of the protein during the folding. To build such states, identifying the main features that are responsible for the folding of the protein is of utmost importance, as well as choosing appropriate coordinates to describe the dynamics under study. Using internal coordinates such as dihedral angles or interatomic distances proves to be convenient, since they disregard the overall motion of the system. In this poster we analyse what influence the choice of different input coordinates has on the resulting picture of the process: we compare an analysis of the fast folding protein HP35 based on dihedral angles as internal coordinates with one based on contacts, a particular set of interatomic distances that satisfy specific requirements. We find that using different input coordinates highlights different dynamics of the system, resulting in different descriptions of the same physical process.

BP 7.26 Mon 18:00 P1

Machine Learning based parametrization of tumor simulation — •Julian Herold[1], Eric Behle[2], and Alexander Schug[2] — [1]Karlsruhe Institute of Technology (KIT), Kaiserstraße 12, 76131 Karlsruhe, Germany — [2]JSC, Jülich Research Centre, Wilhelm- Johnen-Straße, 52428 Jülich, Germany

Despite decades of substantial research, cancer remains a ubiquitous scourge in the industrialized world. Effective treatments require a thorough understanding of macroscopic cancerous tumor growth out of individual cells in the tissue and microenvironment context.

Here, we aim to introduce the critical scale-bridging link between clinical imaging and quantitative experiments focusing on small clusters of cancerous cells by applying machine learning to drive model building between them. We deploy Cells in Silico (CiS), a high performance framework for large-scale tissue modeling developed by us. Based on both a cellular potts model and an agent-based layer, CiS is capable of accurately representing many physical and biological properties, such as individual cell shapes, cell division, cell motility etc.

The strong representational capacity of our model comes with the need to adjust a large number of parameters according to experimental findings. We present a generalized approach to optimize these param-

eters which allows the use of different sources of experimental data.

One major hurdle to achieve this goal is finding appropriate objective functions. To overcome this we implemented a variation of the Particle Swarm Optimization algorithm which learns the objective function during the optimization process.

BP 7.27 Mon 18:00 P1

Coarse-Grained Force Fields for Intrinsically Disordered Proteins — •Yannick Witzky, D. Janka Bauer, Arash Nikoubashman, and Friederike Schmid — Inst. für Physik, Universität Mainz, Germany

Simulations of systems containing many long proteins that perform liquid-liquid phase separation (LLPS) are usually computed with coarse-grained united residue force fields that allow for feasible runtime. One of these commonly used force fields was developed by Dignon et al.[1], where the proteins are modeled as bead-spring chains in an implicit solvent. As a reference we also used the bottom up coarse-grained UNRES force field [2] that resolves many more protein characteristics and is originally used for folding predictions. The results of simulations of four variants of an intrinsically disordered protein from both force fields are discussed in prospect of their polymer characteristics and the implications for simulations of LLPS-systems.

[1] Dignon et al.(2018) PLoS Comput Biol 14(1): e1005941

[2] Sieradzan et al.(2019) J. Phys. Chem. B, 123, 27, 5721-572

BP 7.28 Mon 18:00 P1

Nano-tribological investigation of the influence of specific synovial fluid components on lubrication of artificial joint materials — •Alex Kreis[1], Lukas Böttcher[1], Regina Lange[1], Paul Henke[2], Rainer Bader[2], Ingo Barke[1], and Sylvia Speller[1] — [1]Institute of Physics, University of Rostock — [2]Biomechanics and Implant Technology Research Laboratory, University Medical Center Rostock

The human synovial fluid in native and endoprosthetic joints enables outstanding lubrication and low wear. The question is how this fluid or its specific components, such as hyaluronic acid and albumin, participate in this performance on a nanoscopic scale. In this work we aim to determine the frictional forces between the force microscope (AFM) tip (Si3N4) and typical materials for articulating components of endoprosthetic implants, such as ceramics, ultra-high molecular weight polyethylene (UHWMPE) and cobalt-chromium (CoCr) based alloy by means of lateral force microscopy (LFM). As reference we use force loops acquired on borosilicate glass surfaces in water. Further we plan to investigate and discuss the influence of the chain length of hyaluronic acid on tribological properties of each of these materials.

BP 7.29 Mon 18:00 P1

Microscale resonators for microfluidic based Nuclear Magnetic Resonance spectroscopy — •Alaleh Mirhajivarzaneh[1], Piotr Lepucki[1], Adam P. Dioguardi[1], Aleksandr I. Egunov[1], Marco Rosenkranz[1], Renato Huber[1], Daniil Karnaushenko[1], Dmitry D. Karnaushenko[1], Oliver G. Schmidt[3,4], Bernd Büchner[1,2], and Hans-Joachim Grafe[1] — [1]Leibniz Institute for Solid State and Materials Research (IFW) Dresden — [2]Dresden University of Technology, Faculty of Physics — [3]Research Center for Materials, Architectures and Integration of Nanomembranes (MAIN), Chemnitz — [4]Chemnitz University of Technology, Material Systems for Nanoelectronics

Over the past few decades efforts to miniaturize Nuclear Magnetic Resonance (NMR) spectroscopy have resulted in the down-scaling of the core of an NMR system to microscale detectors. This achievement has unfolded a new era of NMR spectroscopy, with applications particularly in biological studies, where the sample size can scale down to micro- or nanoliters (nL), typical of microorganism and cell cultures. Our novel microcoil is a 3D microscale resonator with an integrated microfluidic system that offers high sensitivity and resolution (8ppb) for analyte volumes as small as 1.5nL, one of the smallest reported detection volumes in the field of NMR spectroscopy. Additionally, the integrated microfluidic system optimizes the filling factor of the device to reach almost 100%. The rolled-up microcoil can potentially be employed for high-resolution micro-NMR analysis of biological samples.

BP 7.30 Mon 18:00 P1

Altered local chromatin dynamics in stressed cells — •Rebecca Benelli and Matthias Weiss — Experimental Physics I, University of Bayreuth, Germany

The dynamic re-organization of chromatin is of crucial importance for cell viability and replication. During interphase, chromatin is mostly decondensed to allow for the transcription of genes, i.e. individual chromatin elements can be supposed to move like monomers of a polymer. Yet, recent reports have suggested chromatin to behave like a solid body on mesoscopic scales, questioning any free motion of chromatin elements. To explore the motion of integral chromatin markers, we have performed extensive single-particle tracking on telomeres under varying conditions. In agreement with previous findings, we observed a strongly subdiffusive and anti-persistent motion of telomeres in untreated culture cells, akin to the motion of monomers in a Rouse polymer. Reducing the ambient temperature or challenging cells by hyper- or hypo-osmotic stress resulted in a significant reduction of telomere mobility. In addition, significant jumps of telomeres between dynamically caged loci, observed in untreated cells, subsided or even vanished in response to these challenges. Altogether, our data indicate that local chromatin dynamics with long-range jumps between different loci are possible in untreated cells whereas a more compact/solid configuration of chromatin might explain the strongly reduced mobility of telomeres in stressed cells.

BP 7.31 Mon 18:00 P1

Image segmentation of irradiated tumour spheroids by Fully Convolutional Networks — •Matthias Streller[1], Sona Michlikova[2], Leoni A. Kunz-Schughart[2], Steffen Lange[1], and Anja Voss-Boehme[1] — [1]University of Applied Sciences Dresden — [2]OncoRay, National Center for Radiation Research in Oncology

Multicellular tumour spheroids are an established in-vitro model to quantify the effectiveness of cancer therapies. Spheroids are treated with radiotherapy and their therapeutic response over time is most frequently monitored via microscopic imaging. For analysis, it is necessary to segment the spheroids in these images, to extract their characteristics like the average diameter or circularity. While several image analysis algorithms have been developed for the automatic segmentation of spheroid images, they focus on more or less compact and circular spheroids with clearly distinguishable outer rim throughout growth. In contrast, treated spheroids are usually obscured by debris of dead cells and might be partly detached and destroyed. We train and optimize two Fully Convolutional Networks, in particular UNet and HRNet, to create an automatic segmentation which covers both cases, spheroids with and without therapy. While we successfully demonstrate the automatic segmentation for one spheroid type, we plan to extent the segmentation to other spheroid models.

BP 7.32 Mon 18:00 P1

Investigating Nanoparticle Dynamics in a High-Finesse Optical Microcavity — Larissa Kohler, •Shalom Palkhivala, and David Hunger — Karlsruhe Institute of Technology – Institute of Physics, Karlsruhe, Germany

We explore the dynamics of nanoparticles using a novel fibre-based high-finesse Fabry-Perot microcavity with integrated microfluidic channels. Silica nanospheres with radii down to 25 nm and gold nanorods with lengths of 20 nm have thus been investigated.

The three-dimensional Brownian motion of a single nanosphere in the cavity has been tracked by the simultaneous measurement of the fundamental and higher-order transverse modes. The particle's position was derived with spatial and temporal resolutions of down to 8 nm and 0.3 ms respectively.

To resolve the faster motion of even smaller nanoparticles, a cavity-locking system has been implemented. This achieved an rms stability of 4% of the resonance linewidth in a water-filled cavity having a finesse of 5×10^4. Hence, the dynamics of 20 nm gold nanorods could be detected with high measurement bandwidth. We shall report progress towards a quantitative evaluation of nanorod diffusion, and the measurement of nanoparticle rotation using a cavity-locked polarisation-splitting scheme.

Based on this, we aim to explore the dynamic and optical behaviour of single biomolecules, such as DNA.

BP 7.33 Mon 18:00 P1

Fixed 4-channel detection in 2D polarization fluorescence imaging (2DPOLIM) and compensation of depolarization caused by dichroic mirrors — •Yutong Wang[1,2], Asad Hafeez[1,2], Dijo Moonnukandathil Joseph[1,2], Mohammad Soltaninezhad[1,2], Rainer Heintzmann[1,2], and Daniela Täuber[1,2] — [1]Leibniz Institute of Photonic Technology — [2]Friedrich-Schiller-University Jena, Germany

Polarization resolved fluorescence imaging (POLIM) can reveal macromolecular structure in the range of 2-10 nm via Förster resonance energy transfer between similar fluorophores (homo-FRET, emFRET). 2D POLIM is superior to conventional fluorescence anisotropy methods for studies of anisotropic samples[1,2]. Implementing a variable electrooptic polarization control in the excitation together with a fixed 4-channel detection[3] speeds up the acquisition giving access to polarization resolved snapshots of dynamic samples. A major issue in POLIM setups is depolarization caused by the multilayer coating of dichroic mirrors, which introduces phase shifts between s- and p-polarized components. We implemented two pairs of dichroics with orientations crossed to each other. By this, incident s- and p-polarization is exchanged within each pair. The design proved to be an effective and reliable approach to significantly improve the quality of polarization by compensating the depolarization introduced by a single dichroic. – Funding: DFG-Ta1049/2 – [1] R. Camacho et al. Adv. Mater. 2019, 1805671. [2] R. Camacho et al. Commun. Biol. 2018, 1, 157. [3] F. Zimmermann et al. in Optically Induced Nanostructures, 2015.

BP 7.34 Mon 18:00 P1

Scanning small angle x-ray scattering of hydrated, keratin-rich cells — •Boram Yu[1], Chiara Cassini[1], Sophie-Charlotte August[1], Manfred Burghammer[2], and Sarah Köster[1] — [1]Institute for X-Ray Physics, Universität Göttingen, Germany — [2]ESRF, Grenoble, France

Intermediate filaments (IFs), one of the three main components of the cytoskeleton, form a network that contributes to cell mechanic. Thus, collecting structural information about IFs in their physiological setting, i.e., in whole cells, is crucial. We use scanning small angle x-ray scattering(SAXS) to obtain this information, as it offers both real space overview images with moderate resolution and reciprocal space information with high resolution. X-ray imaging of cells in aqueous state is challenging as their electron density contrast is low. Additionally, the aqueous environment contributes to extremely rapidly spreading radiation damage. For this reason, a fast-scanning mode is employed by moving the sample continuously through the beam rather than step by step, resulting in a significant reduction in exposure time, thus diminishing the radiation damage. As a benchmark for ordered intracellular structures, we investigate mammalian cells expressing the IF protein keratin. A purpose-built chamber maintains the cells hydrated while minimizing the volume of the liquid in the optical path. Despite weak contrast and short exposure times, we are able to retrieve the local main orientation of subcellular structures, thus demonstrating how scanning SAXS offers valuable information from hydrated cells.

BP 7.35 Mon 18:00 P1

Microfluidics-based analysis of the mobility and migration pattern of Trypanosoma brucei — •Hannes Wunderlich[1], Lucas Brehm[2], Jana Jentzsch[2], Sebastian Krauss[1], Klaus Ersfeld[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth, Germany — [2]Molecular Parasitology, University of Bayreuth, Germany

Trypanosoma brucei is a unicellular parasite that causes the African sleeping sickness after entering the human bloodstream. An active movement of trypanosomes, mediated by the beating of a microtubule-powered flagellum that spirals along the elastic cell body, is crucial for escaping the host's immune response. A highly ordered, subpellicular array of aligned microtubules beneath the cell membrane determines the effective elasticity of parasite and hence its propulsion during flagellar beating. Using soft lithography to create well-definded two-dimensional chambers, we have studied the mobility and migration pattern of trypanosomes without and with genetically induced changes of posttranslational microtubule modifications. Using a set of informative measures that have been developed for (persistent) random walks, we have analyzed trypanosome trajectories that exhibit clear run-and-tumble patterns. Our data reveal that posttranslational modifications of microtubules significantly alter trypanosome mobility and migration.

BP 7.36 Mon 18:00 P1

Topological artifacts in mid-IR photo-induced force microscopy (PiF-IR) — •Sajib Barua[1,2], Hardik Gadher[1,3], Uwe Hübner[1], 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]Leibniz University Hannover, Germany

The use of tapping mode atomic force microscopy (AFM) for detecting mid IR absorption can provide nanoscale chemical information. Several studies report on successful applications for qualitative characterization of biomaterials [1]. Implementing such methods for quantitative evaluation of chemical sample compositions requires further understanding of underlying physical processes [2]. In general, the surface of biological cells and tissue is rough on a sub-micron scale. This may cause artifacts in signal detection due to non-planar interactions with the AFM tip. We use structured polymer layers to investigate implications of sample topography on the signal intensity in mid-IR photo-induced force microscopy (PiF-IR). – [1] Wang et al. Super-Resolution Mid-Infrared Spectro-Microscopy of Biological Applications through Tapping Mode and Peak Force Tapping Mode Atomic Force Microscope. Adv. Drug Deliv. Rev. 2022, 180. [2] Täuber et al. Interference Effects in Nanoscale Infrared Spectroscopy Methods, submitted.

BP 7.37 Mon 18:00 P1

Investigation of biofilm formation on metal surfaces — •Bernhard Kaltschmidt[1], Annika Kiel[2], Ehsan Asghari[2], Julian Cremer[3], Dario Anselmetti[3], Barbara Kaltschmidt[2], Christian Kaltschmidt[2], and Andreas Hütten[1] — [1]Thin Films & Physics of Nanostructures, University of Bielefeld — [2]Department of Cell Biology, University of Bielefeld — [3]Biophysics & Nanosciences - "Physics of Life", University of Bielefeld

Biofilms can cause major problems in many different areas, such as corrosion and contamination of medical products. The aim of this work was to investigate biofilm formation on stainless steels and on sputtered transition metals. Steel disks of the chromium steels 1.4016, 1.4301 and 1.4510 were inoculated with bacteria in LB medium for 7 and 14 days. As bacteria we used Pseudomonas aeruginosa, which we use as our in vitro model for strong biofilm formation. After 14 days the first signs of bio-corrosion were detected by scanning electron microscopy (SEM) and atomic force microscopy. In another series of investigations, glass slides were coated with the transition metals Gold, Ruthenium and Tantal by magnetron sputtering and incubated with Pseudomonas aeruginosa for 24 hours. An uncoated glass surface served as a reference. Comparative studies of biofilm growth on the reference and on the different transition metals were carried out using SEM, confocal laser scanning microscopy and the colony forming unit assay. The analysis revealed that biofilm growth on transition metals is severely hindered compared to our non coated glass slide reference.

BP 7.38 Mon 18:00 P1

Observation of two-step aggregation kinetics of amyloid-β42 peptide from fractal analysis — •Soham Mukhopadhyay — Chair of Mathematics in Life Sciences, Friedrich-Alexander Universität Erlangen-Nürnberg, Cauerstr. 11, 91058 Erlangen, Germany — Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany

Proteins are responsible for controlling and catalyzing the reactions and processes that make life possible. Proper folding of protein molecules into their native states is critical for them to function correctly; conversely, misfolded proteins often cause damaging effects on the biological processes they are involved in. Misfolded proteins often undergo self-aggregation, a process that has been the subject of intense research due to its importance in biological contexts. Of particular interest is the formation of stable filamentous aggregates termed amyloids — implicated in the pathology of several diseases such as Alzheimer's, Parkinson's, type-II diabetes, etc. Several models propose a two-step aggregation mechanism, with linearly growing fibrils and branch formation through secondary growth.

In this work, we employ tools from fractal geometry to develop an analysis technique for images of protein aggregation obtained from TIRF microscopy. Fractal geometry provides an instinctive framework for analyzing 1- and 2-dimensional growth. We use this framework to study the aggregation of the amyloid-β42 peptide and find the initial aggregation to proceed in a one-dimensional fashion, with later branching events leading to two-dimensional growth. This provides direct evidence for the two-step aggregation model.

BP 7.39 Mon 18:00 P1

Influence of varying pH on individual and collective behavior of filamentous cyanobacteria — •Franziska Papenfuss, Maximilian Kurjahn, Antaran Deka, and Stefan Karpitschka — MPI for Dynamics and Self-Organization, Göttingen, Germany

Photoautotrophic cyanobacteria are responsible for about 10 % of global primary production of reduced carbon and represent a sustainable source of carbon dioxide neutral bio-fuel. Adaptation to envi-

ronmental changes is a key factor of their evolutionary success, but the emergent phenomena that couple the individual to their collective behavior remain elusive. Here, we investigate three species of filamentous cyanobacteria cultivated in pH-buffered and non-buffered medium over three weeks of cultivation. During cultivation, colony-scale properties like external pH and aggregate morphology were measured as well as properties of individual filaments like gliding velocity and absorption spectra. In the non-buffered cultures, pH varies in dependence on light-driven photosynthesis. Different species seem to adapt colony morphology from compact aggregates to reticulate layers at different pH values in the low alcalic range. Yet, the external pH has no influence on the gliding velocities, but influences the abundance of the dominant photo-pigments Chlorophyll-a, beta-carotene and phycocyanin in some species. Our investigations show that the pH is not only governed by the photosynthetic activity, but also influences the fate of the cyanobacterial colony in a regulating feedback mechanism.

BP 7.40 Mon 18:00 P1

Identifying malignant tissue using Laser Induced Breakdown Spectroscopy (LIBS) and Neural Networks — •Elena Ramela Ciobotea[1], Christoph Burghard Morscher[1], Cristian Sarpe[1], Bastian Zielinski[1], Hendrike Braun[1], Arne Senftleben[1], Josef Rüschoff[2], and Thomas Baumert[1] — [1]Kassel Universität, Kassel, Germany — [2]Institut für Pathologie Nortdhessen, Kassel, Germany

The problem of differentiating cancerous tissue from a healthy one is currently solved in the diagnostic process through microscopic imaging of stained biopsy sections by pathologists. During surgical removal of cancerous tissue, oncological safety margins must be established to ensure the complete removal of the tumor without affecting much of the neighboring healthy tissue. For this purpose, on-site pathological analysis is done on freshly frozen, stained cuts, which is time consuming. We investigate a new approach to minimize the time of discrimination between malign and benign tissue by an in situ, non-contact spectroscopic analysis. In a proof of principle experiment, a plasma is generated by focusing an 800 nm femtosecond laser on the pathologic postoperative sample. The spectrum of plasma radiation contains information on the element composition of the ablated tissue. Since the recorded spectra are complex and full of information, neural networks are employed to find differences between malign and benign tissue with a high speed and accuracy. This contribution presents the experimental parameters that allow for the best possible differentiation of some biological tissues through fs-LIBS by minimizing deviations between the measurements.

BP 7.41 Mon 18:00 P1

Deep learning for single particle tracking in noisy data — •Mattias Luber, Mohammad Amin Eskandari, and Timo Betz — University of Goettingen, Goettingen, Germany

The quantitative analysis of particle motion critically depends on the quality of particle trajectory detection. Especially the position detection of particles in fluorescence microscopy images is an important task faced in biophysics. Trajectories are used to study processes like intracellular transport protein diffusion within and through membranes and the reconstruction of force fields driving the particle motion. In such settings, high spatial and temporal resolution are be desired. However, in practice those factors have contradictory measurement requirements. High temporal resolution requires short exposure times, which limit the photon budget and thus lead to low signal to noise ratios. We developed an approach to reconstruct the particle position from noisy images, by applying U-NET based deep learning models to fluorescence microscopy images. Using this we can successfully track particles with shorter exposure times, compared to traditional denoising techniques.

BP 7.42 Mon 18:00 P1

Analyses of the outer membrane of vital mitochondria — •Eric Lieberwirth[1], Christian Völkner[1], Regina Lange[1], Anja Schaeper[2], Magdalena Otte[2], Armin Springer[3], Markus Frank[3], Ingo Barke[1], Simone Baltrusch[2], and Sylvia Speller[1] — [1]University of Rostock, Institute of Physics, 18059 Rostock, Germany — [2]Rostock University Medical Center, Institute for Medical Biochemistry and Molecular Biology, 18057 Rostock, Germany — [3]Rostock University Medical Center, Medical Biology and Electron Microscopy Center, 18057 Rostock, Germany

A network of mitochondria enables a cell to perform oxidative metabolism. These organelles have a double membrane that is subject to constant remodeling during the regular fusion and fission processes. This study aims to gain more knowledge about the outer membrane containing translocase, porin and ion channels. Via Scanning Ion Conductance Microscopy (SICM) is it possible to measure the outer membrane of vital mitochondria at lateral spatial resolution of approx. 50 nm and at height resolution of a few nanometer. We immobilize the organelle in phosphate buffered saline (PBS) on collagen-coated substrates and scan the outer membrane with nanopipettes. Though the nanoprobe was, on each pixel, approached from top, the observed shapes exhibit forward-backward hysteresis and flat plateaus. The corrugation amplitude amounts to a few 10 nm and soft steps are present. Labeling translocase of the outer membrane (TOM) with nanoscopic gold particles may help learning about their spatial distribution and help to identify signatures in SICM and SEM.

BP 7.43 Mon 18:00 P1

Multiple thermophoretic particle trapping at single molecule resolution — •Benjamin Fanselow, Tobias Thalheim, and Frank Cichos — Peter-Debye Institute for Soft Matter Physics, Leipzig University, Germany

Achieving single molecule resolution for microscopy enabled to gain valuable insight into processes, that otherwise would be hidden in the ensemble, such as amyloid fibril fragmentation, volume exclusion of DNA molecules, or localization of proteins within a cell. One technique is the combination of fluorescence microscopy with thermophoretic trapping. It utilizes thermophoresis for confining freely diffusing single molecules within a liquid into a region of interest and allows observing these molecules without surface immobilization, over a time period of several minutes. The required temperature fields are generated via optical heating using a focused laser beam steered on a thin chromium layer. So far, only one trap at a time could be used, entailing multiple time-consuming measurements to achieve a reasonable statistics. We present the realization and characterization of up to four thermophoretic traps, which can be controlled simultaneously while preserving the single molecule resolution. This mode is characterized by a model system of 200-nm polystyrene particles in water, trapped with a feedback assisted mode. Analyzing the molecule displacement framewise, the trap stiffness and temperature induced velocities can be calculated. While it could be shown, that the stiffness is scalable with the laser power and the number of used traps, it also revealed an upper limit caused by the feedback loop frequency.

BP 7.44 Mon 18:00 P1

adaptive interferometric light-sheets for resolution enhanced imaging — •meelad lalenejad and alexander rohrbach — Laboratory for Bio- and Nano-Photonics, Department of Microsystems Engineering (IMTEK), University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

The success of light-sheet microscopy bases on the idea that only the parts of the object being are illuminated with laser beams from the side, which are in focus of the objective lens. This concept leads to increased image contrast and reduces photo-bleaching / -toxicity. In addition, larger volumes are scanned plane-wise or line-wise, such that LSM is significantly faster than point-wise scanning methods. However, compromises in spatial resolution have had to be made because of objective lenses with limited numerical aperture and aberrations from light scattering. On the detection side, such phase aberrations could often be corrected with adaptive optics. However, spatial light modulation and phase adaptation of the illumination side still leave plenty of room for improvements. In our research we want to combine the principles of holographically shaped illumination beams with interferometric arrangements of the illumination beams. Since the modulation contrast can be deteriorated by refractive index inhomogeneities of the sample, future phase adaptation for each of the counter propagating beams shall be used as an effective aberration compensation. Using the principles of structured illumination microscopy, we show 3D images in scattering media such as cancer cell clusters obtained from two laterally scanned, counter-propagating Bessel beams.

BP 7.45 Mon 18:00 P1

Absorption-based specificity in ROCS microscopy — •Victor Chuman and Alexander Rohrbach — University of Freiburg, Department of Microsystems Engineering - IMTEK, Laboratory for Bio- and Nano-Photonics, Georges-Köhler-Allee 102, 79110 Freiburg, Germany

Fluorescence techniques dominate the field of live-cell microscopy, but bleaching and motion blur from too long integration times limit dynamic investigations of small objects. High contrast, label-free life-cell imaging of thousands of acquisitions at 150nm and 200 Hz is possible

by Rotating Coherent Scattering (ROCS) microscopy, where intensity speckle patterns from all azimuthal illumination directions are added up within a few milliseconds. However, ROCS lacks the important imaging feature of specificity. We address this deficiency by using different absorption markers, characterized by their different complex valued refractive indices to achieve a difference in image contrast in the observed structures. We demonstrate how different gray values in the image are obtained from interferences between scattered and unscattered light, resulting from material dependent phase shifts of the scattered light. Absorption-based specificity in ROCS imaging may open new fields of applications, adding on top of its high spatio-temporal resolution.

BP 7.46 Mon 18:00 P1

Novel concepts in scanned light-sheet microscopy to improve speed, contrast and resolution — •Yatish Yatish[1,2,3] and Alexander Rohrbach[1,2] — [1]Laboratory for Bio- and Nano-Photonics, Department of Microsystems Engineering-IMTEK, University of Freiburg, 79110 Freiburg, Germany — [2]CIBSS - Centre for Integrative Biological Signalling Studies, Freiburg, Germany — [3]Spemann Graduate School of Biology and Medicine (SGBM), University of Freiburg, Freiburg, Germany

Light-sheet microscopy (LSM) enables fast 3D, high contrast imaging offering effective sectioning and low photo-toxicity. LSM allows to investigate the issue of light scattering in both the illumination and detections, and to better understand the complex image formation. Switchable computer holograms can generate special Bessel beams that are scanned through the object offering increased penetration depths due to their self-reconstruction capability. These beams generate images with better contrast and resolution, when combined with confocal line detection. A future challenge will be to automatically adapt the illumination beam dimensions to the specific structure of object to enhance the 3D image quality. We have investigated the propagation of different beams through classes of spheres. All experiments were performed in combination with advanced computer simulations to better understand the effects of scattering. This includes the loss in quality of bead images along the optical illumination and detection axes through bead clusters, but also the position dependent scattering and absorbing of illumination and fluorescence light in cancer cell clusters.