BP 8: Bioimaging and Biospectroscopy

Time: Monday 14:00–16:30 Location: BPb

BP 8.1 Mon 14:00 BPb

Near Infrared Fluorescence Imaging with Carbon nanotubes and Nanosheets — •Sebastian Kruss — Ruhr-Universität Bochum, Germany

We are interested in 1D and 2D materials that provide novel photophysical properties such as near Infrared (NIR) fluorescence. The NIR range (800-1700 nm) of the spectrum is beneficial for many optical applications because it falls into the tissue transparency window. One example of such a material is semiconducting single-walled carbon nanotubes (SWCNTs). SWCNTs fluoresce in the NIR and their optoelectronic properties are very sensitive to changes in the chemical environment and they are therefore versatile building blocks for fluorescent labels and sensors. In my talk I will show fundamental insights into SWCNT photophysics/surface chemistry and how selectivity of SWCNT-based fluorescent sensors can be enhanced. These sensors can be used for multiscale imaging to resolve single molecules such as kinesin motors in vivo, efflux of neurotransmitters (dopamine, serotonin) from cells, identification of pathogens or stress in whole plants. Furthermore, I introduce a novel class of ultrabright 2D NIR fluorescent silicate nanosheets and demonstrate in vivo particle tracking as well as standoff detection in living plants.

BP 8.2 Mon 14:20 BPb

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

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

BP 8.3 Mon 14:40 BPb

Molecule counts in complex oligomers with single-molecule localization microscopy — Tim Niklas Baldering[1], •Jakob Tómas Bullerjahn[2], Gerhard Hummer[2], Mike Heilemann[1], and Sebastian Malkusch[1] — [1]Institute of Physical and Theoretical Chemistry, Goethe-University Frankfurt, Frankfurt am Main, Germany — [2]Department of Theoretical Biophysics, Max Planck Institute of Biophysics, Frankfurt am Main, Germany

Single-molecule localization microscopy resolves nano-scale protein clusters in cells, and in addition can extract protein copy numbers from within these clusters. A powerful approach for such molecular counting is the analysis of fluorophore blinking using stochastic model functions. Here, we develop a theoretical model for quantitative analysis of photoactivated localization microscopy (PALM) data that accounts for the detection efficiency. By this, we are able to extract populations of different oligomers reliably and in complex mixtures. We demonstrate this approach analyzing simulated PALM data of a photoactivatable fluorescent protein. We generate simulations of blinking data of oligomers and of mixtures of oligomers, and show robust oligomer identification. In addition, we demonstrate this approach for experimental PALM data. https://doi.org/10.1088/1361-6463/ab3b65

BP 8.4 Mon 15:00 BPb

Dissection of Plasmodium falciparum developmental stages with multiple imaging methods — •Katharina Preissinger[1,2], Beáta Vértessy[1,2], István Készmárki[3,4], and Miklós Kellermayer[5] — [1]Department of Applied Biotechnology and Food Sciences, BME, Budapest, Hungary — [2]Institute of Enzymology, Research Center for Natural Sciences, Budapest, Hungary — [3]Department of Physics, BME, Budapest, Hungary — [4]Department of Experimental Physics V, University of Augsburg, Germany — [5]Department of Biophysics and Radiation Biology, Semmelweis University, Budapest, Hungary

Efficient malaria treatment is a global challenge, requiring in-depth insight into the maturation of malaria parasites during the intraerythrocytic cycle. Exploring structural and functional variations of the parasites and their impact on red blood cells (RBCs) is a cornerstone of antimalarial drug development. In order to trace such changes in fine steps of parasite development, we performed an imaging study of RBCs infected by Plasmodium falciparum, using atomic force microscopy (AFM) and total internal reflection fluorescence microscopy (TIRF), further supplemented with bright field microscopy for the direct assignment of the stages. This multifaceted imaging approach allows to reveal correlations of the parasite maturation with morphological and fluorescence properties of the stages. We established identification patterns characteristic to the different parasite stages based on the height profile of infected RBCs which show close correlation with typical fluorescence (TIRF) maps of RBCs.

BP 8.5 Mon 15:20 BPb

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

The endoplasmic reticulum (ER) is a highly dynamic organelle that pervades the entire cell and hosts a variety of vital processes. For example, the exchange of proteins with the secretory pathway occurs at specialized and long-lived membrane domains, called ER exit sites (ERES). In mammalian cells, ERES form protein assemblies that emerge as a lattice-like arrangement of dispersed droplets on the ER membrane. Although ERES were seen to diffuse on short timescales, they appear stationary on longer periods. Notably, their dynamics is different from the cytoskeleton-dependent, shivering motion of ER tubules. To gain insights into the self-organization of ERES patterns, we have studied biochemical perturbations on the morphology of the ER and analyzed the spatial arrangement of ERES by quantitative fluorescence imaging. As a result, we found a significantly changed patterns of ERES components when reducing the amount of curvature-inducing membrane proteins. In contrast, disrupting the ER network into fragments or affecting the cytoskeletons integrity had only mild effects on the ERES patterns. Our findings can be well explained by modelling ER junctions as diffusion barriers for the exchange of ERES protein constituents. Altogether, we provide evidence that the native ERES patterns are the result of a quenched fluctuation-driven two-dimensional demixing process.

BP 8.6 Mon 15:40 BPb

A multisensory interface for exploring nanomechanical tissue properties with human senses — •Robert Magerle, Paul Zech, Martin Dehnert, Alexandra Bendixen, and Andreas Otto — Fakultät für Naturwissenschaften, TU Chemnitz

Tissues display a complex spatial structure and their mechanical properties remain largely unexplored on the nanometer scale. Here we present a multisensory interface that makes nanomechanical tissue properties accessible to human perception and cognition. With a haptic device, we translate the 3D force fields measured with an atomic force microscope (AFM) on the nanometer scale into forces perceivable to humans. This allows human users to explore haptically the specimen's surface shape as well as its local nanomechanical properties while simultaneously employing multiple senses. First tissues studied include native (unfixed), hydrated tendon of sheep, chickens, and mice. AFM imaging in air with controlled humidity preserves the tissue's water content and allows for high-resolution imaging. The force-vs.-distance (FD) data measured with the AFM display a rate-independent hysteresis with return-point memory. A generic hysteresis model that uses FD data collected during one approach-retract cycle predicts the force

(output) for an arbitrary indentation trajectory (input). We implemented this hysteresis model with a haptic device which allows human users to perceive a physically plausible tip–sample interaction. They can discriminate the specimen's local hardness, its elastic response, as well as the energy dissipation due to the rate-independent hysteretic process.

30 min. Meet the Speaker