BP 9: Postersession I

Topics: Protein Structure and Dynamics (9.1–9.10), Single Molecule Biophysics (9.11–9.20), Biomaterials and Biopolymers (9.21–9.36), Systems Biology & Gene Expression and Signalling (9.37–9.42).

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

BP 9.1 Mon 17:30 Poster A

Internal Dynamics of Unfolded Apo-myoglobin — •Livia Balacescu[1,3], Tobias Erich Schrader[1], Andreas Stadler[2], and Jörg Fitter[2,3] — [1]Jülich Centre for Neutron Science, Forschungszentrum Jülich GmbH, Outstation at MLZ, Garching, Germany — [2]Jülich Centre for Neutron Science JCNS & Institute for Complex Systems ICS, Forschungszentrum Jülich GmbH, Jülich, Germany — [3]1.Physikalisches Institut (IA), RWTH Aachen, Aachen, Germany

As a model for the well-characterized protein systems in different folding states we chose apo-myoglobin.[1,2,3] We investigated internal dynamics of its unfolded and folded form on a time-scale up to several hundred nanoseconds and in the nanometer length-scale using neutron spin echo spectroscopy (NSE) [4]. Aggregation state and center of mass diffusion were monitored in parallel with dynamic light scattering. Our first NSE data show a polymer like behavior of the unfolded protein. This indicates that the powerful polymer models may be used for characterization of protein systems.

[1] J. Phys. Chem. B, 2015, 119 (1), 72 [2] J Mol. Biol., 1996, 263(4), 531 [3] J. Am. Chem. Soc., 2014, 136 (19), 6987 [4] Richter D. et al., 2005, Neutron Spin Echo in Polymer Systems. Advances in Polymer Science, vol 174. Springer, Berlin, Heidelberg

BP 9.2 Mon 17:30 Poster A

Performance of genetically encoded FRET-based biosensors investigated on single molecule level — •Henning Höfig[1,2], Martina Pohl[3], Julia Otten[3], Arnold Boersma[4], and Jörg Fitter[1,2] — [1]RWTH Aachen University, I. Physikalisches Institut (IA), AG Biophysik, Aachen, Germany — [2]Research Centre Juelich, ICS-5, Juelich, Germany — [3]Research Centre Juelich, IGB-1, Juelich, Germany — [4]University of Groningen, Department of Biochemistry, Groningen, Netherlands

Genetically encoded FRET-based biosensors consist of two fluorescent proteins (donor and acceptor) and a sensing domain. The readout of FRET-based biosensors usually utilizes the ratio of fluorescence emission intensities of the donor and the acceptor upon donor excitation. We carried out single-molecule measurements on a confocal microscope for two types of CFP-YFP biosensors, one sensitive to glucose concentration [1] and another one monitors macromolecular crowding [2]. From our measurements we obtained FRET efficiencies histograms dissecting the different subpopulations of the sensor under varying environmental conditions. In order to demonstrate the capability of utilizing transfer efficiency histograms for judging the performance of FRET-based sensor constructs we analyze various glucose sensor constructs. The obtained smFRET histograms display specific fingerprints of the respective sensor properties and provide a valuable basis for a rational design of FRET-based biosensors.

[1] R. Moussa et al., J. Biotechnol., 191, 250-259 (2014); [2] A. J. Boersma et al., Nat. Methods, 12, 227-229 (2015)

BP 9.3 Mon 17:30 Poster A

Dielectric spectroscopy of bovine serum albumin at GHz frequencies — Eva-Maria Laux, Jessica Gibbons, Elena Ermilova, Frank F. Bier, and •Ralph Hölzel — Fraunhofer Institute for Cell Therapy and Immunology, Branch Bioanalytics and Bioprocesses, Potsdam, Germany

In recent years electronic components have become available reaching the upper GHz range. This makes this frequency range accessible for novel biomedical applications. Still, detailed knowledge about the properties of biological materials at these frequencies is missing, and the interaction mechanisms with such electromagnetic fields are often unclear. Here we present an experimental system based on a vector network analyser for the temperature controlled determination of the dielectric properties of biomolecules. The influence of protein concentration, of temperature and of denaturing agents on aqueous solutions of bovine serum albumin (BSA) is presented between 10 MHz and 110 GHz. Further work aims at reducing sample size and improving accuracy.

BP 9.4 Mon 17:30 Poster A

Analysis of dynamics of membrane-protein microdomains in bacteria — Daniella Lucena[1,3], •Marco Mauri[1,2], Felix Schmidt[1,4], Bruno Eckhart[1,4], and Peter L. Graumann[1,3] — [1]SYNMIKRO, Marburg — [2]INRIA Grenoble, France — [3]Department of Chemistry, Philipps University, Marburg — [4]Department of Physics, Philipps University, Marburg

Cell membrane has a remarkably intricate temporal and spatial organization that is central for the maintenance of fundamental processes in bacteria. While early models often envisioned proteins freely and homogeneously diffusing on the membrane, there is nowadays growing evidence in support of lipid microdomains. To date there has been no broad study to evaluate how protein size, number of transmembrane domains, and temperature affect the diffusion of membrane proteins. In this work, we have undertaken a systematic study of the effects of these factors on membrane protein diffusion and investigate the dynamics of membrane organization in live B. subtilis cells by mean of single-molecule tracking, physical modelling and computer aided visualization methods. We found that diffusion coefficients do not correlate with protein molecular weight, but decrease with increased transmembrane radius. Moreover, diffusion coefficients are anomalous and are better described by discriminating diffusion rates into two protein populations. Also, we observed that temperature can influence the spatiotemporal organization of membrane proteins and significantly impact their dynamics. We think that data analysis methods here introduced can be valuable for membrane protein studies in any bacteria.

BP 9.5 Mon 17:30 Poster A

Unraveling the effects of an oscillating electric field on Amyloid-beta (1-40) conformational dynamics using G-PCCA, a generalized Markov state modeling method — •Bernhard Reuter[1], Marcus Weber[2], and Martin E. Garcia[1] — [1]Theoretical Physics II, Institute of Physics, University of Kassel, Kassel, Germany — [2]Zuse Institute Berlin (ZIB), Berlin, Germany

We have studied the influence of a strong oscillating electric field on the Amyloid-beta (1-40) peptide, associated with Alzheimer disease. To this end we conducted extensive molecular dynamics (MD) simulations utilizing the GROMACS v5.1.2 program package. Typically Markov state models (MSMs) are very well suited for the identification and analysis of metastabilities and related kinetics. However, the state-of-the-art methods and tools require the fulfillment of a detailed balance condition, violated in the non-equilibrium case. To date, they are unsuitable to deal with more general dominant data structures including cyclic processes, which are essentially associated with the effects of an oscillating electric field. Instead, for this purpose we utilized a generalization of the common robust Perron cluster cluster analysis (PCCA+) method, termed generalized Perron cluster cluster analysis (G-PCCA). Applying G-PCCA we identified and analyzed, by comparison to equilibrium simulations in the absence of an external electric field, significant non-thermal effects on the conformational dynamics of Amyloid-beta, imposed by the oscillating electric field.

BP 9.6 Mon 17:30 Poster A

Studies of bio-molecular dynamics in aqueous solutions using 147Nd nuclear probe — •Sardool Singh Ghumman — Department of Physics, Sant Longowal Institute of Engineering & Technology, Deemed University, Longowal 148 106 Punjab, India

Conventional perturbed angular correlation technique is employed to investigate molecular dynamics in aqueous solutions of biomolecules of TES (Ntris[hydroxymethyl]methyl 2-Amino ethane sulphonic acid), BSA (Bovine Serum Albumin), Oxine (1,4-Benzodioxane-6-boronic acid pinacol ester) and EDTA (ethylenediaminetetraacetic acid) using 147Nd nuclear probe. In addition to the use of 147Nd radioactive probe that it proves to be helpful tool for perturbed angular correlation studies it also emerges out to understand the dynamics of molecules of bio-molecular compounds in aqueous environments. Considerable decrease in attenuation coefficient with higher molar concentrations is noticed for EDTA complexes while the attenuation effect has been found to be more pronounced for macromolecules of BSA and chelates of Oxine. Applications of this isotope are outlined for future non-bio-

molecular materials too.

BP 9.7 Mon 17:30 Poster A

A computational approach to study signal transduction in coiled-coil structures — •Judit Clopés Llahí[1], Jaeoh Shin[2], Marcus Jahnel[3,4], Stephan Wolfgang Grill[1,3,4], and Vasily Zaburdaev[1] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden, Germany — [2]Department of Chemistry, Rice University, Houston 77005 TX, USA — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, 01307 Dresden, Germany — [4]Biotechnology Center, Technical University Dresden Tatzberg 47/49, 01309 Dresden, Germany

The Early Endosome Antigen 1 (EEA1) is a fibrous protein mediating the tether and fusion of vesicles in the early endosome. Its functionality is related to an allosteric switch between two configurations with different stiffnesses. Recent experiments have shown that the transition from the stiff to the soft state in EEA1 is triggered right after its interaction with Rab5, a small signalling protein that binds to the free end of EEA1. Structurally, the EEA1 folds as a homodimeric coiled-coil in almost its total length, which spans up to 200 nm. In this work, we propose a computational description of the hydrophobic interactions stabilising a coiled-coil structure that could model the underlying mechanism behind the signal transduction of the Rab5:EEA1 interaction. For this, we mapped the hydrophobic interactions by means of a one-dimensional Frenkel-Kontorova model. Using this description, we analyzed how the energy introduced by a register shift in one of the extremes propagates along the chain.

BP 9.8 Mon 17:30 Poster A

Simulating the ADP release of the PKAC cycle with different Magnesium quantities approximated by static charge and dummy-atom models — •Robert C. König, Alexander Lipskij, Bernhard Reuter, and Martin E. Garcia — Theoretische Physik II, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany

The modification of biomolecules by addition of phosphates (phosphorylation/dephosphorylation) is essential for the regulation of vital cell processes as growth, division or morphogenesis. The protein kinase A (PKA) is responsible for important phosphorylation processes. The rate limiting process in the catalytic cycle of PKA is the release of ADP and the so-called Mg2 magnesium ion. The details and actual molecular dynamics of the ADP release are not well resolved. To observe the sub-millisecond behavior of the ADP release, we performed molecular dynamics (MD) simulations utilizing GROMACS v2016.3, with the AMBER03 and AMBER99SB-ILDN force-fields, based on the crystallized structure of PKAC with ADP and Mg2. This structure is already in an intermediate state between the open and the closed conformation, depending on the positions of the Gly-rich loop and C-terminal tail. While simulating the ADP release we investigated the influence of the Mg quantity by running the simulations (i) without any Mg ions, (ii) with one Mg ion and (iii) with two Mg ions, with the second magnesium ion added at the position of the linchpin magnesium ion, termed Mg1. To approximate the effect of the Mg charge we used both a standard static charge and a dummy-atom model, imitating the coordination number of Mg.

BP 9.9 Mon 17:30 Poster A

Scaling rules for vibrational energy transport in proteins — •Luis Valino, Adnan Gulzar, Sebastian Buchenberg, and Gerhard Stock — Biomolekulare Dynamik Physik Uni-Freiburg

Computational studies of vibrational energy flow in biomolecules require the inspection of possible energy pathways on a case by case basis[1]. Though these studies succesfully elucidate the energy flow, the interpretation of the underlying processes driving energy transport is still missing. One alternative to these techniques is a master equation approach that simulates the transfer of energy from one amino acid to another and to the solvent on the basis of transition rates[2]. These transition rates can be determined through the fitting of the master equation to the energy profiles of nonequilibrium MD simulations. The scaling rules arising from this fit reveal a set of simple quantities that govern energy flow in proteins. We apply this model to various systems with different secondary structures and compare the relevant quantities and their scaling rules. Some of the scaling rules are conserved in all cases, whereas some others are dependent on the particular secondary structure.

[1] P. H. Nguyen, S. Park, and G. Stock. Journal of Chemical Physics 132, 025102 (2010)

[2] S. Buchenberg, D. M. Leitner, and G. Stock. J. Phys. Chem. Lett. 7, 25 (2016)

BP 9.10 Mon 17:30 Poster A

Nonequilibrium computational study of vibrational energy transport in proteins — •Adnan Gulzar, Luis Valino Borau, Sebastian Buchenberg, and Gerhard Stock — Biomolekulare Dynamik Physik Uni-Freiburg

Vibrational energy transport is thought to play an important role in numerous processes essential to protein function, including kinetics of ligand binding and dissociation, charge transfer, enzyme kinetics and allosteric mechanisms. Time resolved spectroscopies developed to study vibrational energy flow[1] have elucidated the nature and rate of energy transport through a number of peptides and proteins. To provide a theoretical description of these experiments, extensive nonequilibrium molecular dynamics simulations of the energy transport in various systems, including TrpZip2 and PDZ3, have been performed. To mimic the experimental heating processes we employ computational heating methods such as T-jump- and photo-excitation. These nonequilibrium techniques of introducing energy into the system closely reproduce the observed experimental timescales. Additionally, the high resolution of MD simulations allows an in-depth analysis of vibrational energy transport. As a result, we have found out that energy flows not only through the backbone and β-stabilizing hydrogen bonds, but also through stacking contacts of the peptide with the heater.

[1] V. Botan, E. H. G. Backus, R. Pfister, A. Moretto, M. Crisma, C. Toniolo, P. H. Nguyen, G. Stock, and P. Hamm Energy transport in peptide helices PNAS 2007 104: 12749-12754

BP 9.11 Mon 17:30 Poster A

Ectoine protects biomolecules from ionizing radiation: Molecular mechanisms — •Marc Benjamin Hahn[1,2], Tihomir Solomun[2], Maria-Astrid Schröter[2], Hans-Jörg Kunte[2], Susann Meyer[2], and Heinz Sturm[2,3] — [1]Freie Universität Berlin — [2]Bundesanstalt für Materialforschung und -prüfung — [3]Technische Universitäat Berlin

The compatible solute and osmolyte ectoine is an effective protectant of biomolecules and whole cells against heating, freezing and high salinity. The protection of cells (human Keratinocytes) by ectoine against ultraviolet radiation was also reported by various authors, although the underlying mechanism is not yet understood. We present results[1] on the irradiation of biomolecules (DNA) with ionizing radiation (high energy electrons) in fully aqueous environment in the presence of ectoine and high salt concentrations. The results demonstrate an effective radiation protection of DNA by ectoine against the induction of single strand breaks by ionizing radiation. The effect is explained by an increased in low-energy electron scattering at the enhanced free-vibrational density of states of water due to ectoine, as well as the action of ectoine as an OH-radical scavenger. This was demonstrated by Raman spectroscopy, electron paramagnetic resonance (EPR) and Monte-Carlo simulations (Geant4).

[1] Hahn *et al. Phys. Chem. Chem. Phys.*, 2017, **19**, 25717-25722

BP 9.12 Mon 17:30 Poster A

Preferential binding of urea to single-stranded DNA structures: a molecular dynamics simulation study — •Ewa Anna Oprzeska-Zingrebe and Jens Smiatek — Institute for Computational Physics, University of Stuttgart, Stuttgart, Germany

In nature, a wide range of biological processes, such as transcription termination or intermolecular binding, depend on the formation of specific DNA secondary and tertiary structures. These structures can be both stabilized or destabilized by different co-solutes, coexisting with nucleic acids in the cellular environment. In our molecular dynamics simulation study, we investigate the binding of urea at different concentrations to short 7-nucleotide single-stranded DNA structures in aqueous solution. The local concentration of urea around native DNA hairpin in comparison to an unfolded DNA conformation is analyzed by preferential binding model in the light of Kirkwood-Buff theory. All our findings indicate a pronounced accumulation of urea around DNA, which is driven by a combination of electrostatic and dispersion interactions and accomplished by a significant replacement of water molecules in terms of a dehydration effect. The outcomes of our study can be regarded as a first step into a deeper mechanistic understanding towards co-solute-induced effects on nucleotide structures in general.

BP 9.13 Mon 17:30 Poster A

Dielectrophoretic Immobilization of Nanoobjects as Singles — •Xenia Knigge[1], Christian Wenger[2], Frank F. Bier[1], and

Ralph Hölzel[1] — [1]Fraunhofer Institute for Cell Therapy and Immunology IZI, Branch Bioanalysis and Bioprocesses, Potsdam (IZI-BB), Germany. — [2]IHP GmbH - Leibniz Institute for Innovative Microelectronics, Frankfurt (Oder), Germany.

For the construction of a biosensor the immobilization of the bioreceptor is a key element. Here we demonstrate the immobilization of fluorescently labeled nanospheres as a model system applying dielectrophoresis (DEP). DEP is a phenomenon in which a dipole is induced in a polarizable particle in an inhomogeneous AC electric field. By the right choice of frequency, this particle can be moved and immobilized. Also an alignment of the biomolecules is advantageous to get a strong signal, which is achieved by DEP. The nanoobjects have been immobilized as individual objects on electrodes of a regular array consisting of many thousands of vertical silicon or tungsten based nanoelectrodes. Immobilization and singling is proved by fluorescence microscopy in combination with scanning electron microscopy. Owing to the large number of electrodes being observed simultaneously, occupation numbers of submicroscopical particles could be determined with good statistics applying histograms. Occupation numbers and patterns were determined as a function of particle size (down to 50nm) and electrode diameter (50nm and 500nm).

BP 9.14 Mon 17:30 Poster A

Polymer brushes in motion – measuring flow with nanometre resolution — •Jan Christoph Thiele, Sebastian Isbaner, Narain Karedla, Ingo Gregor, and Jörg Enderlein — III. Institute of Physics – Biophysics, Georg August University Göttingen, Germany

Polymer brushes are a versatile method to tailor surface properties. These include wetting behaviour, friction and interactions with colloids and biomolecules. Coating a surface with polymer brushes changes its hydrodynamic properties in a complex way. Experiments on brush coated capillaries showed an unexpected large flow reduction by the brush, while recent simulations are predicting a backflow within the brush layer.

Our aim is to measure how the brushes impact the flow at the surface and to verify the predicted backflow. For this, we will use fluorescence lifetime correlation spectroscopy (FLCS) in combination with metal induced energy transfer (MIET). FLCS enables a precise and non-invasive measurement of the flow speed, while MIET causes a modulation of the dye's lifetime in close proximity to a gold surface underneath the brush. This modulation allow us to section the volume into different layers based on their lifetime. We will use a fluorescence dye dissolved in the liquid or the brush and measure the movement of the dye molecules and their distance from the gold surface. This way we can obtain a high resolution flow profile in the range of 0 to 100 nm distance to the surface.

BP 9.15 Mon 17:30 Poster A

Organelle-specific density measurements of the V-ATPase using atomic force microscopy — Elisabeth Eilers[2], •Julia Teckentrup[1,2], Katharina Schiller[2], Volker Walhorn[1], Thorsten Seidel[2], Karl-Josef Dietz[2], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanoscience, Bielefeld University, Germany — [2]Plant Biochemistry and Physiology, Bielefeld University, Germany

The V-ATPase functions as a membrane-embedded rotational proton pump, which creates a proton motif force and thus drives secondary active transport of solutes across endomembranes. Therefore, these enzymes are essential for cellular pH- and ion homeostasis.

V-ATPases are located in the endomembranes of the endoplasmic reticulum, the Golgi apparatus as well as the vacuolar membrane in plants, which we could show using molecular biology techniques and fluorescence microscopy. In atomic force microscopy (AFM) images, V-ATPases showed prominent structures with a height of roughly 10 nm corresponding to the hexameric arrangement of their catalytic head. Using AFM we aim to investigate the differences in the number of V-ATPases between different compartments of plant cells. We will further apply AFM-based single molecule force spectroscopy to test the stability of the complexes. The latter is driven by the observation, that the vacuolar enzyme shows a diffuse organization of its stabilizing stalk proteins in the presence of desoxyglucose as observed by FRET-microscopy (Schnitzer et al., 2011, Plant Cell Physiol.).

BP 9.16 Mon 17:30 Poster A

Quantifying the association of the chemotherapeutic drug mitoxantrone to DNA by magnetic tweezers — •Dennis Kreft, Ying Wang, Helene Schellenberg, Katja Tönsing, and Dario Anselmetti — Experimental Biophysics and Applied Nanoscience, Bielefeld Institute for Nanoscience (BINAS), Bielefeld University, Bielefeld, Germany

Chemotherapeutic agents (anti-cancer drugs) are small cytotoxic molecules that often bind to double-stranded DNA (dsDNA) and thus interfere with the cell division process (mitosis). For medical regulation and optimization issues of these pharmaceutical products, it is inevitable to identify/quantify their binding mechanism. Therefore, we investigated the anthraquinone compound mitoxantrone that is used for treating certain cancer types like leukemia and lymphoma. We employed magnetic tweezers (MT) to investigate the association of mitoxantrone with dsDNA and conducted force-extension and rotation-extension experiments with a sensitivity from some piconewtons down to tens of femtonewtons. We found a concentration-dependent bimodal binding behavior, where mitoxantrone associates to dsDNA either as a groove binder at low concentrations and as an intercalator at high concentrations.

BP 9.17 Mon 17:30 Poster A

Investigation of sea cucumber proteoglycans by atomic force microscopy — •Niklas Biere[1], Pierre Piel[1], Volker Walhorn[1], Xavier Fernàndez-Busquets[2], Paulo A. S. Mourão[3], Eduardo Vilanova[3], and Dario Anselmetti[1] — [1]Experimental Biophysics & Applied Nanosciences, University of Bielefeld, Germany — [2]Nanoscience and Nanotechnology Institute (IN2UB), University of Barcelona, Spain — [3]Hospital Universitário Clementino Fraga Filho and Instituto de Bioquímica Médica, Universidade Federal do Rio de Janeiro, Brazil

Sea cucumbers belong to the echinoderm family and are a widely spread marine life form in the world's oceans, yet not all aspects of their biology are well researched. As such, they possess remarkable properties, like the catch connective tissue, whose mechanical stiffness can be adapted without the use of muscles. In this work, we investigate the proteoglycan molecules from the sea cucumber species *Isostichopus badionotus* which make up part of its body wall. These proteoglycans, which exhibit antimalarial and anticoagulant properties, are studied in detail with atomic force microscopy to gain insights in the structure and chemical morphology of their polysaccharide components, namely fucosylated chondroitin sulfates and sulfated fucans. We will discuss their role in maintaining the adaptive elasticity of the tissue and show that this ability is related to the concentration of Ca^{2+} ions, which subsequently influences the tissue's capability to store water.

BP 9.18 Mon 17:30 Poster A

Label-free detection and trapping of individual nanosystems — •Larissa Kohler — KIT, Karlsruhe, Deutschland

The label-free detection of nanosystems provides the opportunity to understand biomolecular dynamics and interactions without undesired modifications of the system. To achieve the high sensitivity required for studying individual nanosystems, we use signal enhancement in a fiber-based Fabry-Perot cavity with high finesse ($F \approx 10^5$), which is integrated in a microfluidic channel. Dispersive interaction between the sample and the cavity field is used to detect the presence and the dynamics of individual nanoobjects. The tight focus of the cavity mode ($w_0 \approx 1\,\mu m$) can be furthermore harnessed to trap individual particles between the fibers far away from surfaces. At the same time, a polarizable particle shifts the resonance frequency and thereby the intracavity laser power, such that particle motion couples back to the trapping potential. In this so-called self-induced back-action regime, trapping of sub-100 nm is predicted to become possible at biocompatible low intensity levels. We show first results on the detection of 150 nm silica nanoparticles and report the current status of the experiment.

BP 9.19 Mon 17:30 Poster A

DNA origami mold-based wires: Synthesis long metallic wires and its temperature dependent charge transport mechanism — •Türkan Bayrak[1,2], Seham Helmi[3], Jingjing Ye[2,3], Jeffrey Kelling[1], Tommy Schönherr[1], Artur Erbe[1,2], and Ralf Seidel[2,3] — [1]Helmholtz-Zentrum Dresden-Rossendorf, Bautzner Landstraße 400, 01328 Dresden,Germany. — [2]Technische Universität Dresden, cfaed, 01062 Dresden, Germany. — [3]Universität Leipzig, Ritterstraße 26, 04109 Leipzig, Germany

The DNA origami method provides a programmable bottom up approach for creating nanostructures of any desired shape, which can be used as scaffolds for nanoelectronics and nanophotonics device fab-

rications. This technique enables the precise positioning of metallic and semiconducting nanoparticles along the DNA nanostructures. In this study, DNA origami nanoMOLDS are used for the fabrication of nanoelectronic devices. To this end, electroless gold deposition is used to grow the AuNPs within the DNA origami nanoMOLDS and create eventually continues nanowires. In order to contact the fabricated nanostructues electrically, a method using electron-beam lithography was developed. Temperature-dependent characterizations for four wires exhibiting different conductance at RT were performed in order to understand the dominant conductance mechanisms from RT to 4.2K. Two of these nanowires showed metallic conductance. The other two wires deviated from pure metallic behavior and they showed thermionic, hopping and tunnelling conductance.

BP 9.20 Mon 17:30 Poster A

Towards video rate imaging of IFT at nanoscale resolution using the Atomic Force Microscope — •Renata Garces and Christoph F. Schmidt — Drittes Physikalisches Institut - Biophysik, Fakultät für Physik, Georg-August-Universität Göttingen

Atomic force microscopy is a powerful tool for characterizing single molecules with nano-scale spatial resolution. The improvement of image acquisition rates render possible to access dynamical processes having place at nano-scale, such as the ones driving the highly dynamic traffic in the cell. Here we present the advances in the implementation of an experimental in vitro model system to study the dynamics of molecular motors involved in Intra Flagellar Traffic (IFT) keeping high spatial resolution. Our system consist of Chlamydomonas reinhardtii axonemes adhered to a hard substrate. Topographic images from the atomic force microscope allows to distinguish doublets of microtubules and tubulin dimers from axoneme surfaces. Adding high concentrations of immobilized dimeric kinesin-1 motor in presence of nonhydrolyzable ATP analog (AMP-PNP) results in fully decorated axoneme surfaces. Addition of ATP at different concentrations results in differentiated motor activity.

BP 9.21 Mon 17:30 Poster A

Smart Gelatin Hydrogels: Modification by Electron Irradiation towards Stimuli-Responsive Elements — •Stefanie Riedel[1,2], Benedikt Heyart[1], Katharina Apel[1], Emilia Wisotzki[1], and Stefan Mayr[1,2] — [1]Leibniz Institute of Surface Engineering (IOM) Leipzig — [2]Felix Bloch Institute, Faculty of Physics and Earth Sciences, University Leipzig

Stimuli responsive materials have attracted considerable interest during the past years due to their potential use in sensor and actuator applications. They are designed to transform small external stimuli e.g. temperature and humidity changes into a significant response. While a large number of alloys or synthetic polymers are well-established at this point, we explore the potential of the biomaterial gelatin to respond to temperature and humidity for possible use as biological active control elements or as switchable scaffolds. To tailor the stimuli responsiveness of gelatin, it is crosslinked by high energy electron irradiation which is nontoxic and thus enables biomedical applications. Thereby, a temperature dependent shape memory is introduced which can be utilized to develop a temperature-responding system. Furthermore, we will show that electron irradiated gelatin has a high potential as a biocompatible and stimuli responsive demonstrator responding to humidity. By adaption of environmental parameters such as irradiation dose, gel concentration, pH-value and salt concentration, the response of the responsive element can be precisely tuned.

BP 9.22 Mon 17:30 Poster A

Uptake and release of proteins in microgels studied on single particle level — •Farzaneh Vaghefikia[1], Julia Kratz[1], Julia Walter[1], Wenjing Xu[2], Andrij Pich[2], and Jörg Fitter[1] — [1]RWTH Aachen University, I. Physikalisches Institut (IA), AG Biophysik, Aachen, Germany — [2]DWI-Leibniz Institut for Interactive Materials, Aachen, Germany

For efficient drug delivery, a smart network of polymers called microgel particles can be used. These particles with an ability to swell and deswell in response to environmental changes, allow uptake and release of drugs in a controlled manner. Their sensitivity to environmental changes along with biocompatibility make it a good candidate for a drug carrier, especially for therapeutic proteins. An impact of environmental conditions on proteins outside the cell often causes protein denaturation and aggregation [1]. We studied the uptake and release of the positively charged cytochrome c, in and from microgel particles. The loading of the microgels took place at pH 8, a value at which microgels are charged negatively [2]. By employing wide-field fluorescence microscopy we made a reliable characterization of single particles, e.g. the maximum loading of the particles, the stability of the loading, and the amount of proteins to be released at the target location.

[1] Antosova et al. Trends Biotechnol. 2009
[2] Ricarda Schröder et al, Macromolecules, 2015.

BP 9.23 Mon 17:30 Poster A

A novel water soluble iron phthalocyanine as a redox mediator integrated to multifunctional hydrogel based graphene nanoplatelet for glucose monitoring — •hadi al-sagur, komathi shanmugasundaram, and aseel hassan — Materials and Engineering Research Institute, Sheffield Hallam University, Sheffield, United Kingdom

Herein, we report a novel sensing platform for glucose biosensor applications. A three-dimensional multifunctional hydrogel interconnected network of water-soluble iron phthalocyanine (FePc) in single-layer graphene nanoplatelet (SLGNPs) for glucose oxidase (GOx) immobilization (PAA-FePc-SLGNPs/PANI /GOx-MFH) has been reported. Structural and morphological studies for (PAA-FePc-SLGNPs/PANI -MFH) were carried out using scanning electron microscopy (SEM), Fourier-Transform Infrared (FTIR), transmission electron microscopy, (TEM), X-ray diffraction (XRD), Raman spectroscopy and UV*Visible absorption spectroscopy. The electrochemical biosensor was fabricated utilizing PAA-FePc-SLGNPs/PANI -MFH as the enzyme immobilizing matrix coated on a screen-printed carbon electrode, and glucose oxidase (GOx) was used as a model enzyme. The electrical conductivity of the detection electrode was studied using electrochemical impedance spectroscopy (EIS). The modified electrodes were studied by amperometry and cyclic voltammetry. The PAA-FePc-SLGNPs/PANI /GOx-MFH was designed towards glucose monitoring with high sensitivity, good selectivity and low detection limit. Our biosensor could potentially be a valuable tool at the clinical uses for monitoring diabetes.

BP 9.24 Mon 17:30 Poster A

Exposure of mesenchymal stromal cells to graphene quantum dots — •Sibel Tezkan[1], Stefan Fasbender[1], Tim Ebbecke[2], Katharina Raba[2], Johannes Fischer[2], and Thomas Heinzel[1] — [1]Experimental Condensed Matter Physics, Heinrich Heine University, Düsseldorf — [2]Transplantation Diagnostics and Cell Therapeutics, University Hospital Düsseldorf

Fluorescent graphene quantum dots (GQDs) are prepared by the slightly modified method of Qu et al. [1] via thermal decomposition of citric acid and diethylenetriamine with subsequent dialysis to obtain a pure GQD solution. The obtained aqueous solution is analyzed with fluorescence spectroscopy. Mesenchymal stromal cells are exposed to GQDs and a high uptake is determined using flow cytometry. The number of incorporated GQDs is estimated by comparing the fluorescence of cells with GQDs and without GQDs. In addition, the uptake of GQDs into exosomes is investigated.

[1] Qu et al., Light: Science & Applications, 2015, 4, e364

BP 9.25 Mon 17:30 Poster A

Effects of changing the Zeta potential of Graphene Quantum Dots for Biological Applications — •Stefanie Berger[1], Stefan Fasbender[1], Sebastian Bauer[2], Stephan Schmidt[2], Laura Hartmann[2], and Thomas Heinzel[1] — [1]Heinrich Heine Universität Düsseldorf, Institut für Experimentelle Physik der kondensierten Materie — [2]Heinrich Heine Universität Düsseldorf, Institut für Organische und Makromolekulare Chemie

Fluorescent graphene quantum dots (GQDs) are prepared by thermal decomposition of citric acid and diethylenetriamine slightly modifying the method of Qu et al. [1]. The concentration dependent fluorescence properties are studied with fluorescence spectroscopy and the Zeta potential is measured using dynamic light scattering. Both is compared to GQDs with modified features. Possible modifications include the binding of a positive charged amide or a slight change of the GQD recipe. In order to analyse the particles' properties for biological applications, their uptake into primary human blood cells and their nucleus is investigated using flow cytometry and visualised via confocal microscopy.

[1] Qu et al., Light: Science & Applications, 2015, 4, e364

BP 9.26 Mon 17:30 Poster A

Cellular uptake of graphene quantum dots into murine precision-cut liver slices and MMTV-PyMT mammary carcinoma cells — •David Kersting[1], Stefan Fasbender[1], Ange-

lika Hallenberger[2], Johanna Naskou[3], Katharina Raba[4], Johannes Fischer[4], Hans Neubauer[3], and Thomas Heinzel[1] — [1]Experimental Condensed Matter Physics, Heinrich-Heine-University Dusseldorf — [2]Institute for Anatomy II, University Hospital Dusseldorf — [3]Department of Obstetrics and Gynecology, University Hospital Duesseldorf — [4]Institute for Transplantation Diagnostics and Cell Therapeutics, University Hospital Dusseldorf

Precision-cut liver slices were produced from outbred C57BL/6 mice liver lobes and incubated under cultural conditions for 1 or 2 days supplementing their growth medium with a defined concentration of N-doped graphene quantum dots (GQDs). The slices were examined using flow cytometry, confocal microscopy and fluorescence spectroscopy clearly indicating a quantum dot uptake into the cultivated tissue, which might decay with increasing penetration depth. These experiments constitute to our knowledge the first incubation of GQDs on precision-cut tissue slices (PCTS), which display a versatile in vitro tool for probing drug effects on cells in a molecular environment close to their in vivo intra-organ situation. In a second approach the GQDs were incubated in two concentrations over a period up to two days on cultured cell lines of the murine MMTV-PyMT mammary carcinoma model. Our first data obtained by flow cytometry hint at a proposed uptake depending linearly on the incubation time.

BP 9.27 Mon 17:30 Poster A

Comparing the properties of graphene quantum dots prepared in a microwave and graphene quantum dots prepared on a hot plate — •Alexandra Steina, Stefan Fasbender, and Thomas Heinzel — Experimental Condensed Matter Physics, Heinrich-Heine-University Dusseldorf

Fluorescent graphene quantum dots (GQDs) are prepared by the method of Wu et al. [1] via hydrothermal treatment (3 hours, 180° C) of citric acid and dicyandiamide on a hot plate (hGQDs). The fluorescence properties of these GQDs (quantum yield: 29 %, emission maximum around 450 nm at 360 nm excitation) are compared to GQDs prepared in a microwave oven (mGQDs) using the same recipe and the same synthesis temperature. The duration of the microwave synthesis is varied and the highest fluorescence quantum yield amounts to 29 % after a synthesis time of 2 minutes. The mGQDs show a nearly identical fluorescence spectrum compared to the hGQDs with the same emission maximum around 450 nm at 360 nm excitation. XPS data reveals that hGQDs are composed of 52 % carbon, 23 % nitrogen and 25 % oxygen whereas mGQDs are composed of 43 % carbon, 26 % nitrogen and 31 % oxygen.

[1] Wu et al., Nanoscale, 2014, 6, 3868

BP 9.28 Mon 17:30 Poster A

Studying the fluorescence properties of graphene quantum dots — •Maren Sakowski[1], Stefan Fasbender[1], Ralf Kühnemuth[2], Bekir Bulat[2], Claus Seidel[2], and Thomas Heinzel[1] — [1]Experimental Condensed Matter Physics, Heinrich-Heine-University Dusseldorf — [2]Molecular Physical Chemistry, Heinrich-Heine-University Dusseldorf

Fluorescent graphene quantum dots (GQDs) are prepared by thermal decomposition of citric acid and diethylentriamine slightly modifying the method of Qu et al. [1]. The particles are purified with HPLC and the fluorescence properties are studied using fluorescence spectroscopy, UV-vis, fluorescence correlation spectroscopy (FCS) and time-correlated single photon counting (TCSPC). The GQDs show an absorption maximum around 360 nm with an emission maximum around 450 nm (25 % quantum yield) and a second absorption maximum around 480 nm with an emission maximum around 560 nm (6 % quantum yield). TCSPC reveals a fluorescence lifetime of 9.92 ns at 360 nm excitation and 1.78 ns at 480 nm excitation. The Stokes radius is identified to be 0.6 nm using FCS.

[1] Qu et al., Light: Science & Applications, 2015, 4, e364

BP 9.29 Mon 17:30 Poster A

Uptake of fluorescent graphene quantum dots into human breast cancer cell lines — •Rabea Pilch[1], Stefan Fasbender[1], André Franken[2], Marina Willibald[2], Katharina Raba[3], Johannes Fischer[3], Hans Neubauer[2], and Thomas Heinzel[1] — [1]Experimental Condensed Matter Physics, Heinrich-Heine-University Dusseldorf — [2]Department of Obstetrics and Gynecology, University Hospital Dusseldorf — [3]Institute for Transplantation Diagnostics and Cell Therapeutics, University Hospital Dusseldorf

Fluorescent graphene quantum dots (GQDs) are prepared by thermal decomposition of citric acid and diethylentriamine referring to the method of Qu et al. [1]. The breast cancer cell lines MCF-7 and MDA-MB-231 and the non-tumor cell line MCF-10A are exposed to various concentrations of GQDs for various times. The MTT viability assay shows a decrease of the viability of all three cell lines to 60 % compared to cells without GQDs, when exposed to a maximum concentration of 1 mg/ml GQDs for 72 hours. Flow cytometry is used to analyse the time dependent uptake of the GQDs into the cells. The number of incorporated GQDs per cell is estimated to be 5 billion for the tumor cell lines (MCF-7 and MDA-MB-231) and 43 billion for the non-tumor cell line (MCF-10A) by measuring the fluorescence intensity of cells exposed to GQDs for 48 hours with fluorescence spectroscopy.

[1] Qu et al., Light: Science & Applications, 2015, 4, e364

BP 9.30 Mon 17:30 Poster A

Secondary structure analysis of xanthan using atomic force microscopy — •Jenny Fjodorova[1], Volker Walhorn[1], Julia Voss[2], Vera Ortseifen[2], Karsten Niehaus[2], and Dario Anselmetti[1] — [1]Experimental Biophysics & Applied Nanoscience, Bielefeld University, Germany — [2]Proteome and Metabolome Research, Bielefeld University, Germany

Xanthan is an extracellular polysaccharide, secreted by the microorganism *Xanthomonas campestris*. Due to its unique viscosifying properties, xanthan has numerous industrial applications. Therefore, the optimization of xanthan production and its rheological properties is of particular interest. Targeted genetic modification of the *Xanthomonas* metabolism can be a powerful tool to optimize shear-thickening potency and to improve the xanthan production efficiency.

Using atomic force microscopy (AFM) imaging and single molecule force spectroscopy (SMFS), we analyzed the structure and the elastic characteristics of single xanthan polymers, which were produced by different *Xanthomonas* strains. We identified structures ranging from single-stranded coiled networks to branched double-strands. Taking into account the varying ability to form double-strands and differences in the bending stiffness, we observed a correlation between the formation of secondary structures and its resulting different viscosifying properties. Our results enable a better understanding of relevant metabolic pathway modifications for an optimized xanthan synthesis.

BP 9.31 Mon 17:30 Poster A

Gas bubbles in thermal gradients accumulate DNA and trigger wet-dry cycles — •Matthias Morasch, Jonathan Liu, Christof Mast, and Dieter Braun — LMU Munich, Amalienstr. 54, 80799 München, Germany

Life has developed in water, but dry steps are essential for many prebiotically plausible syntheses and polymerization processes [1,2]. This posits the question how dry-wet cycles can be combined with an underwater scenario without diluting the reaction products into the ocean. We found that a nonequilibrium system in form of a temperature gradient across a gas bubble in water creates an efficient accumulation setting. In addition to the known thermophoretic trap, molecules hereby strongly accumulate at the water-gas interface [3]. Movements of the gas bubble thereby trigger continuous drying and re-hydration steps, while maintaining high local concentrations of ca. 1000-fold near the interface. Here, we show the underlying mechanisms for the accumulation process at the water-air interface, which also exhibits a length-selectivity e.g. for DNA strands. In addition, we demonstrate the precipitation and redilution of RNA monomers that polymerize only under dry conditions [2]. This mechanism allows reaction pathways such as the formation, phosphorylation, or polymerization of nucleotides that require both aqueous and dry conditions.

[1] Powner et al., (2009) Nature 459:239-242. [2] Morasch et al (2014) ChemBioChem 15:879-883. [3] Braun et al. (in submission)

BP 9.32 Mon 17:30 Poster A

Nanoscale properties of polymer micro-moulds studied by a combination of AFM and SICM — •Annelie Marx, Regina Lange, Ingo Barke, and Sylvia Speller — University of Rostock, Institute of Physics, 18059 Rostock, Germany

PDMS (polydimethylsiloxane) is a versatile material for creating micro-moulds or stamps. We prepared PDMS moulds as test samples for scanning ion conductance microscopy (SICM) and as prospective substrates for cell adhesion experiments. We focus on the achievable level of detail on the nanoscale by producing moulds from dry eched glass structures exhibiting equidistant grids and pillars of different aspect ratios with vertical side walls. We also report on attempts to produce moulds from metallic nanostructures (Fischer samples) and

multichannel plates (MCPs). Both the moulds and the original samples were studied by AFM and SICM. With SICM the topography of a soft sample placed in a (conducting) liquid is measured on the nanoscale, largely avoiding direct forces between the sample and the probe. A decent reproduction quality was obtained on samples with 2 μm deep grooves and unity aspect ratio. We discuss general properties and benefits of PDMS micro-moulds for applications in Biophysics (e.g. with live cells), including the possibility to produce artificial replica by creating a second mould from an initial one.

[1] Y. Xia, G.M. Whitesides, Annu. Rev. Mater. Sci. 28, 153 (1998)

BP 9.33 Mon 17:30 Poster A

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

We report on the trapping of single DNA molecules in liquids with the help of a force-free trapping method utilizing feedback-driven dynamic temperature gradients. These temperature gradients, that are obtained by spatially and temporally vary the temperature at a circular plasmonic nano-structure, induce thermophoretic drift velocities which prevent the randomization of the positions and conformations of the DNA molecules due to Brownian motion. Because of the generated inhomogenous temperature profiles, drift velocities in the outer regions of the thermophoretic trap are larger than those in the center forcing the elongated DNA molecules into more compressed states of their conformation compared to freely diffusing molecules. A model-free statistical tool called principal-components analysis as introduced by Cohen and Moerner [1] is employed to assess these distortions of the DNA's conformation and conformation dynamics.

References

[1] A. E. Cohen, and W. E. Moerner, PNAS 104 (31), 12622-12627 (2007)

BP 9.34 Mon 17:30 Poster A

Dilute molecular crowders enhance activity of ligase ribozyme — •Mrityunjoy Kar, Juan Manuel Iglesias Artola, Oliver Beutel, Alf Honigmann, and Moritz Kreysing — Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

The RNA world hypothesis remains a hallmark in *origin of life* research despite very poor robustness and low reactivity of most model replicators studied so far. A frequently used trick to enhance ribozyme activity is the use of high concentration molecular crowders (M to mM) to increase RNA concentrations by excluded volume effects. Here we show, that excluded volume effect is not strictly required to enhance ribozyme activity using R3C ligase as a model ribozyme and polyethylene glycol (PEG) as a model crowding agent. As observed in other systems before, we find that also for the R3C system reactivity is increased in presence of crowder. However, our data shows higher affinity (lower Km) at lower concentrations of crowder (1% wt/v). This suggests that excluded volume might not be the only effect. If so, enhanced activity should also be seen at even lower concentrations of crowder. Indeed, we find in our experiments a remarkable enhancement of R3C ligase activity at concentrations down to 50ppm (wt/v). With this, we suggest a beneficial role of polymeric crowders (impurities) during the origin of life.

BP 9.35 Mon 17:30 Poster A

Self-Assembled Protein Hybrid Nanofibres — •Christian Helbing[1], Tanja Deckert-Gaudig[2], Gang Wei[3], Volker Deckert[2], and Klaus D. Jandt[1] — [1]Chair of Materials Science, Otto-Schott-Institute of Materials Research, Faculty of Physics and Astronomy, Friedrich Schiller University Jena, Germany — [2]Institute for Photonic Technology, Jena, Germany — [3]Hybrid Materials Interfaces Group, Faculty of Production Engineering, University of Bremen, Germany

Over the last years, the interest in materials consisting of biomolecules arranged in nanofibers increased. There is a special focus on plasma proteins for applications in nanofiber materials because of their high biocompatibility. An easy feasible strategy to create these nanofibers is the self-assembly mechanism of protein molecules. Here we test the hypothesis that novel self-assembled hybrid protein nanofibers (PNF) can consist of two different proteins. In this work, we present self-assembled plasma hybrid PNF consisting of two different plasma proteins. Further, long-time CD-measurements provide information about the fiber formation dynamics. Especially, for the PNNF hybrid it confirmed interactions between both molecules. We confirmed the existence of a novel PNF hybrid by tip enhanced Raman spectroscopy and immunolabeling. Also, differences in the mechanical behaviour were shown by force spectroscopy. These results lay the foundation for a novel biomaterial based on these (h)PNNFs.

BP 9.36 Mon 17:30 Poster A

Peptide heterogeneity enhances genetic identity and fluidity of RNA rich complex coacervates — •Juan M. Iglesias-Artola[1], Mrityunjoy Kar[1], Anatol W. Fritsch[1], Bjorn Drobot[1], Hannes Mutschler[2], Dora Tang[1], and Moritz Kreysing[1] — [1]MPI-CBG, Dresden, Germany — [2]MPIB, Munich, Germany

Complex coacervates have been proposed as a model system for protocells, and we found that they spontaneously assemble in temperature gradients. We have formed complex coacervates from short cationic peptides and an enzymatic RNA molecule. The coacervation process that we observe occurs through the interaction of a positively charged peptide and a negatively charged RNA. As a result, neutral complexes are formed, which phase separate from the surrounding medium to generate droplets. We characterized the physical properties of the RNA inside these compartments. The mobility of the RNA inside these droplets can be tuned by changing the peptide-RNA interaction strength and by the presence of other components in the surrounding medium. These droplets sequester RNA efficiently and can maintain genetic identity for long periods of time. Currently, we are working on rescuing RNA enzymatic activity inside these compartments. Here, we provide evidence on how a rudimentary identity of fluid protocells, necessary for the onset of natural selection, could have arisen when only simple components were available.

BP 9.37 Mon 17:30 Poster A

Modelling the cell-cycle dependent regulation of p21 after DNA damage — •Isabella-Hilda Mendler and Barbara Drossel — TU Darmstadt, Germany

Ionizing radiation causes DNA double strand breaks and hence threatens the successful division or even the survival of a cell. For this reason, cells react to DNA damages by upregulating the tumor suppressor protein p53, which shows multiple pulses after the occurrence of the damage and activates numerous target proteins. One of the most important target proteins of p53 is p21, a potent cyclin-dependent kinase inhibitor that regulates cell-cycle arrest after DNA damage. Recent single-cell experiments showed that the timing and rate of its induction after DNA damage is heterogeneous, with the cell-cycle stage playing a crucial role.

We present a minimalistic nonlinear delay differential equation model for the regulation of p21 by p53 that reproduces the main features of the cell-cycle dependent dynamical behavior of p21 in response to the p53 oscillations following DNA damage. The p53 measurement data are input to the model, and the p21 response is modelled by including cell-cycle dependent protein production and degradation rates. These features enable us to reproduce the observed delay of p21 response in cells that experience the damage in the S phase, as well as the prompt pulse-like response of p21 in cells that are irradiated in G1 and progress to S phase.

BP 9.38 Mon 17:30 Poster A

Clocks and timers in genetic networks. — •Jose Negrete JR[1,2], Ivan M. Lengyel[1,3], Laurel A Rohde[2], Andrew C. Oates[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland — [3]Instituto de Investigación en Biomedicina de Buenos Aires CONICET of, Argentina

Genetic oscillations are noisy and in many cases, as in embryo development, short lived. We present a model of a noisy transcription factor that controls the timing and amplitude of an stochastic genetic oscillator. The transcription factor determines how long the oscillator is on and it is denominated as a timer, while the genetic oscillator is denominated as a clock due to its repetitive nature. The model is given by a single delay differential equation, and we show analytically the set of measurable parameters that characterises it. The predictions of the model were tested by analysing two different cases: self sustained genetic oscillations from cycardian rhythms and in the transient oscillatory gene expression from cells extracted from the presomitic mesoderm of zebrafish embryos.

BP 9.39 Mon 17:30 Poster A

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

Rod cells are responsible for vision in dim light. After the activation of the pigment molecule rhodopsin, a complex signal transduction cascade leads to an electrical signal, which can then be transmitted further through the retina. This phototransduction cascade can be modelled using differential equations for the molecular species involved, mainly with mass-action kinetics [1,2]. The model can reproduce rods' behaviour across a vast range of experiments and mutations.

Rod cells are extremely sensitive: they have a reproducible response to single photons, thus operating at the physical sensing limit [3]. It is astonishing that the response to a single photon is very uniform, since a fluctuating signal would be expected.

To explain the uniformness of the single photon response and investigate which reactions are essential for its reproducibility, we modify the deterministic model of the phototransduction cascade in rods to also include stochasticity and spontaneous activation of the effector. We investigate how the reproducibility of the single photon response comes about and study the effect of multiple phosphorylations of rhodopsin.

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[2] B.M. Invergo et al, Mol. BioSyst. **10** 1481-1489 (2014)
[3] R.D. Hamer et al, J. Gen. Physiol. **122** 419-444 (2003)

BP 9.40 Mon 17:30 Poster A

Time distribution of mRNA delivery mediated by lipoplexes determined from single cell expression onsets — •Anita Reiser[1,2], Neha Mehrotra[1], Rafal Krzyszton[1,2], Daniel Woschée[1], Helmut H. Strey[3], and Joachim O. Rädler[1,2] — [1]Faculty of Physics and Center for NanoScience, Ludwig-Maximilians-University, Munich, Germany — [2]Graduate School of Quantitative Biosciences (QBM), Ludwig-Maximilians-University, Munich, Germany — [3]Department of Biomedical Engineering and Laufer Center for Quantitative Biology, Stony Brook University, Stony Brook, NY, USA

Nucleic acid (NA) based therapies require efficient delivery systems. New Methods are required to assess uptake and release kinetics in living cells in order to improve the internalization of NA carriers. Here we employ automated time-lapse microscopy to study the delivery-time distribution of lipid based mRNA vectors. We determine the protein expression onset-times after transfection from single cell time courses of eGFP reporter fluorescence. We show how maximum likelihood fitting yields best estimates of individual onset times from hundreds of individual time courses in a robust and automated manner. The distribution of delivery dwell-times is found to be log-normal distributed in all cases with the mean depending on the transfection agent. For cationic lipid formulation containing various amounts of cholesterol the delivery timing correlates with efficiency. The profile of delivery timing might be a valuable indicator for the development of nanocarriers with improved uptake activity and endosomal release kinetics.

BP 9.41 Mon 17:30 Poster A

Single-cell kinetics of siRNA-mediated mRNA degradation — •Rafał Krzyszton[1,2], Daniel Woschée[1], Anita Reiser[1,2], Gerlinde Schwake[1], Helmut Strey[3], and Joachim O. Rädler[1,2] — [1]Ludwig-Maximilians-Universität Munich (LMU), Geschwister-Scholl-Platz 1, Munich — [2]Graduate School of Quantitative Biosciences (QBM), Geschwister-Scholl-Platz 1, Munich — [3]Stony Brook University, Stony Brook, NY

RNA interference (RNAi) is a natural mechanism of post-transcriptional gene regulation and is underlying the therapeutic action of small interfering RNA (siRNA) directed against disease-related genes. Quantitative assessment of the siRNA knockdown efficiency is typically carried out at the population level. In contrast, direct measurement of the siRNA induced mRNA degradation requires time-resolved studies. Here we report on life cell imaging of the time-resolved expression and knockdown level after delivery of two mRNA reporter genes (eGFP, CayenneRFP) and delayed delivery of siRNA duplexes. Thousands of single cell time traces were recorded in parallel using micro-pattern assisted time-lapse microscopy (MPA-TLM) combined with automated image analysis. With the help of maximum likelihood fits to a mathematical translation model we yield scatter-plots of individual mRNA life-times and determine the siRNA meditated RISC activity as fold-change of mRNA degradation rate. Time-lapse imaging proves faster (<24hours) and more accurate (+/-1%) measurement of mRNA degradation and hence will allow new sensitive studies of sequence dependence RNAi

BP 9.42 Mon 17:30 Poster A

Network coherences - a universal approach to quantify the match between "omics" data and a biological network — •Piotr Nyczka[1], Marc-Thorsten Hütt[1], Kristina Schlicht[2], Carolin Knecht[2], and Michael Krawczak[2] — [1]Departement of Life Sciences and Chemistry, Jacobs University, Bremen, Germany — [2]Institute of Medical Informatics and Statistics, Christian-Albrechts-University Kiel, Germany

Network-based analyses of "omics" data are a cornerstone of systems medicine. Their goal is to quantify and statistically evaluate the clustering of biological signals (e.g., co-expression of genes) in a network (e.g., a metabolic network or a protein-interaction network). Network coherences are topological indices evaluating the connectivity of subnetworks spanned by the "omics" signal of interest [1,2]. They have been used very successfully to identify scientifically relevant patient subgroups in disease cohorts [2-4].

Here, we aim at a deeper theoretical understanding of network coherence. Using various random walk models on graphs, we test, refine and calibrate this method. In this way, the dependence of a given network coherence upon the number of (e.g., disease-associated) genes, the topology of the underlying biological network or the fragmentation of the functional signal in the network can be studied numerically and compared to analytical predictions.

Our method allows us to detect functional signal even in very noisy data. The main novelty of this approach lies in taking into account collective expression profiles of the whole group of patients and contrast it with individual ones. In order to find relevant signals we "tune" parameters of the collective expression extraction procedure with respect to maximization of the network coherence. This allows us to pick up structures which are not detectable when dealing with individual patients separately.

Based upon our results, we also present a range of applications of (in particular metabolic) network coherence to the analysis of transcriptome profiles in chronic inflammatory diseases. This investigation seems to have huge potential for further development and following applications also outside of this specific field.

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[4] Häsler et al. (2016). Gut, gutjnl-2016-311651.