BP 26: Poster Session II

Time: Thursday 17:00–19:30 Location: Poster B

BP 26.1 Thu 17:00 Poster B

Photokinetics and photostability of fluorescent dyes — •Babette Hinkeldey, Gregor Jung, and Alexander Schmitt — Biophysical Chemistry, Saarland University, Building B2.2, D-66123 Saarbrücken, Germany

In biophysical applications, Fluorescence Correlation Spectroscopy (FCS) has become a well established method to investigate the photokinetics of fluorescent dyes. In combination with fluorescence lifetime measurements calculation of singulet and triplet state parameters is possible.

Yet a quantitative description of the photostability cannot easily be achieved by applying the FCS technique.Therefore a flow cytometric setup is used, where by means of a microcapillary and an electric field the dye molecules are forced into a specific direction. This leads to the possibility to observe the same molecule twice.

We expect to obtain a precise prediction of the average number of excitation cycles before photodegradation in dependence of the excitation intensity. Thus, combination of both techniques allows a more detailed understanding of fluorescence properties.

BP 26.2 Thu 17:00 Poster B

Solvent and lipid self-dynamics of hydrated lipid-bilayers. — •Florian Kargl, Peter Berntsen, Christer Svanberg, and Jan Swenson — Department of Applied Physics, Chalmers University of Technology, SE-41296 Göteborg, Sweden

We report on the microscopic dynamics of a lipid-bilayer system that is hydrated with approximately nine water molecules per lipid molecule. The system was investigated by means of quasielastic neutron scattering (QENS). To independently study the water, the acyl-chain and the polar headgroup motion, selective deuteration was used. We discuss the temperature dependence of the elastic amplitudes measured for motions parallel and perpendicular to the bilayers in the range of 50 K to 310 K. Moreover, the q-dependence of the relaxation processes on time-scales of 10 ps to 100 ps are studied at 290 K, a temperature that is just below the gel to fluid transition. The neutron scattering data is compared to recently performed dielectric measurements that accessed the relaxation dynamics over eight decades in frequency and for a large range of temperatures [1].

[1] P. Berntsen, C. Svanberg, and J. Swenson (in preparation)

BP 26.3 Thu 17:00 Poster B

X-ray radiation-damage studies of regular bacterial surface layers — •Andreas Kade — TU-Dresden, Dresden, Deutschland

We report x-ray radiation-damage investigation of the regular surface layer of Bacillus sphaericus NCTC 9602 using a photoemission electron microscope. The purpose of this work is to provide current perspectives on spectroscopic studies of the simplest biomembranes existing in nature. Here, measurements show the decrease in the C-O and C-N bond density as measured by near-edge x-ray absorption fine structure spectroscopy at the C 1s, N 1s and O 1s excitation thresholds. We found the critical dose for C-O and C-N breaking. The increase in the C-C bond density corresponds to the damage of the other bonds. Furthermore we show the rearrangement of the bond constituents after the radiation damage.

BP 26.4 Thu 17:00 Poster B

Curvature-mediated interactions between membrane-bound particles–analytical results — •Martin Michael Müller[1], Markus Deserno[1], and Jemal Guven[2] — [1]Max Planck Institute for Polymer Research, Ackermannweg 10, D-55128 Mainz, Germany — [2]Instituto de Ciencias Nucleares, UNAM, Apdo. Postal 70-543, 04510 México D. F., Mexico

Membrane-bound particles may interact with each other via the deformations they impose in the lipid bilayer. As the intrinsic nonlinearity of the problem makes it virtually impossible to calculate these interactions analytically, one is typically forced to restrict to linear approximations of the energetics. In some cases this is, however, not necessary.

In this talk, several exact results will be presented that do not rely on any linearizations such as a small gradient assumption. Surface stress and surface torque tensor offer a possibility to determine how the particles interact. Especially for the case of two membrane-bound cylinders (the "1D problem"), that approach can be combined with profile calculations to extract numbers for the strength of interaction.

BP 26.5 Thu 17:00 Poster B

Curvature coupled diffusion of an inclusion in a fluctuating membrane — •Stefan Leitenberger, Ellen Reister-Gottfried, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57/III, 70550 Stuttgart

We analyse the lateral diffusion of an inclusion along a fluctuating membrane. The inclusion interacts with the membrane shape via the local curvature. We derive equations of motion for the membrane dynamics and the projected motion of the inclusion. With these equations and neglecting the influence of the inclusion on the membrane dynamics we calculate the diffusion coefficient of the inclusion. In order to probe the analytical results and to overcome approximations of the analytical calculations, we set up a simulation that also neglects the effects of the inclusion on the membrane dynamics. Comparing the results we find that the diffusion coefficients achieved in the simulations are smaller than the analytical ones. In the calculations it is necessary to average over all possible forces acting on the particle at each lattice site, independently of the actual particle position while the simulations correctly average the force correlations along the particle trajectory. If the diffusing particle remains close to positions on the membrane that are energetically favourable the force correlation function will be reduced compared to the situation when the particle is at some random position. The detailed investigation of the force correlation function indicates that the inclusion generally follows an energy minimum on the membrane. This explains the difference between analytical calculations and simulations.

BP 26.6 Thu 17:00 Poster B

Fluorescence Lifetime Imaging of NAD(P)H in MIN6-cells - Information about cellular metabolism — •Stefan Denicke[1], Raluca Niesner[1], Bülent Peker[1], Ingo Rustenbeck[2], and Karl-Heinz Gericke[1] — [1]Institut. f. Physikalische und Theoretische Chemie, Hans-Sommer-Straße 10, 38106 Braunschweig, Germany — [2]Inst. f. Pharmakologie und Toxikologie, TU Braunschweig, Mendelsohnstraße 1, 38106 Braunschweig, Germany

In recent years Fluorescence Lifetime Imaging (FLIM) has been increasingly applied to biomedical problems since they provide additional information compared to intensity measurements. NADPH and NADH are important indicators for cellular metabolism. Since both are fluorescent molecules, it is possible to use FLIM as a non-invasive, nonlabeling technique. NADPH occurs in a free and a protein-bound state in the cell. Both states display different fluorescence lifetimes. Immortalised pancreatic beta-cells (MIN6-cells) were treated with various glucose concentrations and the ratio of free and metabolised NADPH was determined by analysing the cumulative fluorescence decay via a noniterative biexponential method. The calculation time can be decreased by more than an order of magnitude compared to iterative analyses. All experiments were performed on a two-photon laser scanning microscope with FLIM in the time-domain.

BP 26.7 Thu 17:00 Poster B

Mechanical limits of viral capsids — •Mathias Bünemann and Peter Lenz — Fachbereich Physik, Philipps-Universität Marburg, D-35032 Marburg

Viral shells are extremely stable nano-containers. They are able to sustain internal pressures of $\sim$ 50atm [1] as well as point forces up to $\sim$ 1nN [2]. We have numerically studied the stability of viral capsid in terms of a single dimensionless parameter, the Föppl-von-Kármán (FvK) number γ. We are able to attribute the experimentally observed bimodal distribution of spring constants to the geometry of viral capsids. A criterion for capsid breakage is defined, which explains well the experimentally observed rupture. From our numerics, we find a $\gamma^{2/3}$ dependence of the rupture force for spherical viruses. The influence of internal pressure on the stability of capsids is analyzed. Finally, we suggest a method for determining the spatial distribution of protein binding potentials from the spatial distribution of rupture events.

[1] D.E. Smith et al. Nature 413:748 (2001) [2] I.L.Ivanovka et al., PNAS 101(20):7600 (2003), J.P.Michel et al., PNAS 103(16):6184 (2006)

BP 26.8 Thu 17:00 Poster B

Computational Study on the Formation of Membrane Protrusions by Actin Polymerization — •Mathias Bünemann and Peter Lenz — Fachbereich Physik, Philipps-Universität Marburg, D-35032 Marburg

Actin networks are essential for a living (eukaryotic) cell. They build up the cytoskeleton thus giving the cell structure. Since actin filaments can polymerize and depolymerize these structures are highly dynamical. Their morphology is strongly influenced by interactions with various linking proteins. Actin-polymerization provides a mechanism to deform the cell membrane and to allow the cell to move [1]. In numerical simulations we have analyzed the growth dynamics of actin networks in confining geometries. We are able to calculate the polymerization-induced forces on obstacles. In particular, for filament-induced membrane protrusions we make predictions of the dependence of the growth velocity on polymerization rate and actin concentration.

[1] H. Miyata et al., PNAS 96:2048 (1999), V.C. Abraham et al., Biophys.J. 77:1721 (1999)

BP 26.9 Thu 17:00 Poster B

RNA Unzipping in Nanopores Driven by Variable Forces — •Thomas Schötz[1], Ralf Bundschuh[2], and Ulrich Gerland[3] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for Nanoscience (CenS), LMU München, Germany — [2]Department of Physics, The Ohio State University, Columbus, U.S.A. — [3]Institute for Theoretical Physics, University of Cologne, Köln, Germany

We study a theoretical model for voltage-driven translocation of structured RNA molecules through nanopores so narrow that only single strands can pass through. We focus on the sequence-dependent unzipping behaviour when the applied voltage is increased at a constant loading rate (voltage ramp), as in recent experiments with a single DNA-hairpin [1]. In order to describe the simultaneous, coupled dynamics of translocation and of the base-pairing patterns on each side of the pore, we apply a kinetic Monte Carlo scheme. Within this model, we determine the distribution of translocation times for different loading rates and sequences.

[1] Mathé, J., H. Visram, V. Viasnoff, Y. Rabin, and A. Meller (2004) Nanopore Unzipping of Individual DNA Hairpin Molecules. *Biophys. J.* **87**, 3205–3212.

BP 26.10 Thu 17:00 Poster B

Observation of nanoparticle uptake in living cells by single particle tracking — •Nadia Ruthardt[1], Karla de Bruin[1], Kevin Braeckmans[2], Ernst Wagner[3], and Christoph Bräuchle[1] — [1]Department Chemie und Biochemie and Center for NanoScience (CeNS), Ludwig-Maximilians Universität München, Butenandtstr. 5-13, D-81377 München, Germany — [2]Laboratory of General Biochemistry and Physical Pharmacy, Faculty of Pharmaceutical Sciences, Ghent University, Harelbekestraat 72, B-9000 Ghent, Belgium — [3]Pharmaceutical Biology-Biotechnology, Department of Pharmacy, Ludwig-Maximilians-Universität, Butenandtstr. 5-13, D-81377 München, Germany

Nanoparticles consisting of DNA complexed by cationic polymers (polyplexes) can be used as non-viral vectors for gene transfer into cells and are an important candidate for gene therapy. To enhance cell targeting, PEI polyplexes with a PEG shield were functionalized with EGF (epidermal growth factor) for specific binding to the EGF receptor on the cell surface. By using highly sensitive fluorescence wide-field microscopy, single particle tracking was performed to generate trajectories of the uptake dynamics into living cells. Typically, three types of particle motion were observed: (1) a phase of immobility and slight drift; (2) a diffusive movement in the cytoplasm; and (3) directed motion along microtubules. EGF+ particles are internalized up to 100% within 10-15 minutes whereas PEI particles show internalization to a much lesser extend.

BP 26.11 Thu 17:00 Poster B

EMCCD-based spatially and spectrally resolved fluorescence correlation spectroscopy — •Markus Burkhardt, Jonas Ries, and Petra Schwille — Biophysics/ BIOTEC/ TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

Fluorescence Correlation Spectroscopy (FCS) is based on time dependent fluorescence intensity fluctuations of labeled biomolecules as they enter and leave a diffraction-limited optical detection volume. From simple autocorrelation analysis, concentrations, diffusion and binding coefficients are easily obtained.

Spectral and spatial cross-correlation enhances the sensitivity and accuracy of FCS measurements to determine exact concentrations of interacting partners and to obtain absolute diffusion coefficients, respectively. Both tasks can conveniently be performed employing an electron multiplying CCD camera for detection of the fluorescence signal. Applying different readout modes of the CCD enhances the data acquisition speed and therefore the time resolution needed for FCS.

We demonstrate spatial cross correlation with different focal geometries as well as spectrally resolved FCS using EMCCD-based detection.

BP 26.12 Thu 17:00 Poster B

Molecular motor-induced instabilities and crosslinkers determine biopolymer organization — •David Smith[1], Falko Ziebert[2], Walter Zimmermann[2], and Josef Käs[1] — [1]University of Leipzig, Institute for Soft Matter Physics, Leipzig, Germany — [2]Universität Bayreuth, Theoretische Physik, Bayreuth, Deutschland

All eukaryotic cells rely on the active self-organization of protein filaments to form a responsive intracellular cytoskeleton. The need for motility and reaction to stimuli additionally requires pathways that quickly and reversibly change cytoskeletal organization. While thermally-driven order-disorder transitions are, from the viewpoint of physics, the most obvious method for controlling such organization, the timescales necessary for effective cellular dynamics would require temperatures exceeding the physiologically viable temperature range. We report a mechanism whereby myosin II can cause near-instantaneous order-disorder transitions in reconstituted cytoskeletal actin solutions. When motor-induced filament sliding diminishes, the actin network structure rapidly and reversibly self-organizes into various assemblies. Addition of stable crosslinkers was found to alter the architecture of ordered assemblies. These isothermal transitions between dynamic disorder and self-assembled ordered states illustrate that the interplay between passive crosslinking and molecular motor activity plays a substantial role in dynamic cellular organization.

BP 26.13 Thu 17:00 Poster B

Single molecule studies of eukaryotic transcription using optical tweezers — •Adam Muschielok[1], Joanna Andrecka[1], Florian Brückner[2,1], Patrick Cramer[2,1], and Jens Michaelis[1] — [1]Departement Chemie und Biochemie, Ludwig-Maximilians-Universität München, Deutschland — [2]Gene Center Munich, Ludwig-Maximilians-Universität München, Deutschland

Our goal is to study the molecular mechanisms of the eukaryotic transcription process. Therefore we monitor the activity of single RNA Polymerase II (RNAP) molecules during RNA elongation using optical tweezers. We are interested in the elongation process and in the effects of transcription cofactors on RNAP activity.

We present preliminary data together with simulations to discuss the data analysis.

BP 26.14 Thu 17:00 Poster B

Counterion Dynamics at Charged Polymers: A Study of Electrophoresis — •Sebastian Fischer[1], Ali Naji[1,2], and Roland Netz[1] — [1]Physik Department, Technische Universität München, D-85748 Garching, Germany — [2]Department of Chemistry and Biochemistry, University of California, Santa Barbara, CA 93106-9510, USA

Using the Brownian Dynamics simulation technique, we investigate the electrophoretic response of an infinitely long polyelectrolyte chain and its neutralizing counterions with respect to an external electric field. For large Manning parameters the well-known phenomenon of counterion condensation at long charged polymers tends to decrease the electrophoretic mobility of the polymer chain. In this case we find – as opposed to the common assumption made in theoretical modeling approaches [1] – that there generally is substantial slip between the condensed counterions and the polyelectrolyte. At fixed Manning parameter we observe considerable sensitivity of the electrophoretic mobility to the local chain architecture which we vary through either the charge spacing along the polymer backbone or the monomer-to-counterion size ratio. The influence of local features regarding the electrophoretic response of polyelectrolytes has only recently been pointed out in a capillary electrophoresis study of a synthetic polymer with variable charge spacing [2].

[1] G. S. Manning, J. Phys. Chem. **85**, 1506 (1981)

[2] A. Popov, D. A. Hoagland, J. Polym. Sci. Part B: Polym. Phys. **42**, 3616 (2004)

BP 26.15 Thu 17:00 Poster B

Artificial Chloroplasts from Giant Unilamellar Vesicles —

•Jakob Schweizer and Petra Schwille — Biophysics, Biotec, TU Dresden, Tatzberg 47, 01307 Dresden, Germany

Giant unilamellar vesicles (GUVs) serve as a minimalistic model system for biological cells and especially cell membranes. However, they are also an ideal tool to synthesize sub-cellular structures in order to mimic intracellular processes. Here we present a way to construct a rudimentary artificial chloroplast from purely biological raw materials using merely three main components: lipids, bacteriorhodopsin and F0F1-ATP synthase. Powered by photon absorption bacteriorhodopsin pumps protons into the vesicle, whereas the F0F1-ATP synthase utilizes the emerging proton gradient to produce ATP. The most crucial step is therefore the reconstitution of the functional proteins into the GUVs in the correct orientation. Establishing an artificial chloroplast can provide further insight into the evolution of biological chloroplasts. Moreover, these photo-sensitive systems will also serve as miniature power plants, providing the ATP essential for more complicated cellular model systems.

BP 26.16 Thu 17:00 Poster B

Flow Profile Measurements in a Traveling Wave Micropump with Two-Foci-FCCS — •Wolfgang Staroske[1], Maika Felten[2], and Petra Schwille[1] — [1]Institut für Biophysik, BIOTEC / TU Dresden, Dresden, Germany — [2]Frauenhofer Institute für Biomedizin Technik, Potsdam, Germany

The traveling wave micro-pump is a new technique to transport liquids and particles, for example cells in a micro fluidic chip. The flow in regions of the pump electrodes is highly turbulent and therefor difficult to measure with imaging techniques. We used spatial two-foci Fluorescence Cross-Correlation Spectroscopy to measure flow profiles in different directions inside the micro-pump. First evaluation show reasonable flow profiles. The evaluation also highlighted that the commonly used model for spatial FCCS with flow is not accurate enough for the correct determination of the velocity direction.

BP 26.17 Thu 17:00 Poster B

Stochastic Effects In Drug Transport Through Cell Monolayers (An Analogue To Enzymatic Reactions) — Niko Komin and •Raúl Toral — IMEDEA (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain

The transport processes through multiple cellular membranes is the focus of this work. In the simplest case the system consists of three compartments: an apical and a basolateral volume and the cellular volume in between. The boundaries are the lipid bilayers which (some) molecules can traverse passively, following the concentration gradient. Additionally transporter proteins are integrated into one or both lipid bilayers which actively move molecules from one side to the other (against the concentration gradient, if necessary). Transporter proteins and enzymes can be described by the same equations.

A harmonic approximation of the equations leads to solutions with good accordance to the unsimplified system. From here on we study the source of variability in the measurements. Uncertainties in parameters as well as a small system size (low number of particles) yield uncertainties in the time evolution of the concentrations. The dependences are not lineal.

BP 26.18 Thu 17:00 Poster B

Hydrodynamic flow-induced protein movement on cell surfaces: African trypanosomes as a model — •Eric Stellamanns[1], Niko Heddergott[2], Markus Engstler[2], and Thomas Pfohl[1] — [1]Max PIanck Institute for Dynamics and Self-Organization, Bunsenstr. 10, 37037 Göttingen, Germany — [2]Technical University of Darmstadt, Department of Cellular Dynamics, Schnittspahnstr. 10, 64287 Darmstadt, Germany

African trypanosomes are mammalian bloodstream parasites in e.g. cattle, buffalo, or humans. Therefore, they live in a viscous environment of low Reynolds numbers. Being able to survive the mammalian immune response and to reproduce in such conditions, trypanosomes have evolved effective defense mechanisms combined with highly adapted modes of motility. Using microfluidics in combination with fluorescence and fluorescence resonance energy transfer (FRET) microscopy, we study the motility of trypanosomes relating to protein dynamics on the trypanosome membrane surface. Being able to mimic natural flow conditions with highly defined gradients of proteins, particles, or cells in a spatiotemporal manner, we can illuminate different biophysical aspects of life on the micrometer scale without restricting the mobility of cells.

BP 26.19 Thu 17:00 Poster B

Interaction potential of Lysozyme and Insulin and denaturation properties of Staphylococcal Nuclease - SAXS studies on aqueous solutions at DELTA synchrotron — •Chris Krywka[1], Nadeem Javvid[2], Michael Sulc[2], Vytautas Smirnovas[2], Roland Winter[2], and Metin Tolan[1] — [1]Fachbereich Physik, DELTA, Universität Dortmund, D-44221 Dortmund — [2]Fachbereich Physikalische Chemie, Universität Dortmund, D-44227 Dortmund

The influence of various cosolvents on the native state structure of Lysozyme and Insulin in aqueous solution was studied using small-angle x-ray scattering (SAXS) measurements at beamline BL9 of DELTA synchrotron. A wide range of concentrations of both pure protein and with with added cosolvents (tetrafluoroethylene, sodium chloride, ethanol, trimethylaminoxyd, glycerol) was probed. For the higher concentrated samples information about the intermolecular interaction potential could be obtained from analysis of the structure factor. Unlike Lysozyme and Insulin, Staphylococcal Nuclease can fold and unfold reversibly due to the lack of disulfide bonds or free sulfhydryl groups. This allows to study the intermediate states of unfolding and refolding induced by temperature or pressure, close to the native and denaturated state. SAXS measurements were performed in a wide pressure and temperature range (1 bar to 6 kbar and -10°C to 65°C) in the absence and presence of various cosolvents (tetrafluoroethylene, glycerol, urea, sodium chloride) and the changes in tertiary structure of the different conformational states were analysed.

BP 26.20 Thu 17:00 Poster B

Viscoelastic monitoring mesenchymal stem cells differentiating towards cartilage cells — •Karla Müller[1], Matthias Zscharnack[2], Jörg Galle[3], and Josef Käs[1] — [1]Institute for Soft Matter Physics, University of Leipzig — [2]Cell Techniques and Applied Stem Cell Biology, Center for Biotechnology and Biomedicine, University of Leipzig — [3]Insitiute for Medical Informatics, Statistics and Epedimology, University of Leipzig

The production of cartilage tissue is of enormous medical interest as the replacement of damaged cartilage in knees, for example, nowadays still affords surgical dissection of cartilage tissue close to the damaged site. A new therapeutic approach avoids the dissection of healthy tissue. It uses the fact that mesenchymal stem cells can be differentiated in vitro to form cartilage tissue. This new therapeutic approach is called Multiparametric Monitoring and Steering of Mesenchymal Stem Cell derived Cartilage Formation in 3D Production Systems. We present the mechanical characterization of mesenchymal stem cells on their differentiation path towards cartilage cells. The technique used to noninvasively probe the mechanical properties of suspended cells, is the Optical Stretcher. The elasticity measurements allow us to follow the steps of differentiation without using cell surface markers that would contaminate the cell sample and make it unsuitable for further culture. Adherent stem cells are indented by a modified AFM tip and so they can be characterized even before the first passage.We are furthermore able to determine the single cartilage cell properties and to relate them to the integral properties of cartilage tissue.

BP 26.21 Thu 17:00 Poster B

2c2p excitation and its applications in fluorescence microscopy — •Stefan Quentmeier, Raluca Aura Niesner, and Karl-Heinz Gericke — TU-Braunschweig

We report observation of two-color-two-photon (2c2p) excitation of p-Terphenyl and Furan-2 upon excitation with 400 and 800 nm using the SHG and fundamental wave of a modelocked Ti:Sa femto second laser. This excitation is energetically equivalent to a one photon excitation employing 266 nm light. The fluorescence signal is only visible when both wavelengths are spatially and temporal overlapping. Variation of the delay of the 800 nm puls renderes an cross correlation curve which is in good agreement with the pulse width of our laser. In addition, the fluorescence signal is linear dependent on the intensity of each of the two colors but quadratically on the total incident illumination power of both colors. As background signal we observe one-color-two photon-excitation from the 400 nm light. This background signal can easily be reduced be adjusting the power of the blue light. This results in an increased signal to noise ratio as the 2c2p signal decreases linearly while the 1c2p signal decreases with quadratic dependence on the 400 nm beam. Hence in fluorescence microscopy the use of a combination of intense IR and low intensity blue light as a substitute for UV light for excitation can have numerous advantages. Furthermore the possibility of manipulating the polarisations of both absorbed photons

independently offers information about different transition symmetries and, therefore, allows to distinguish between two molecules absorbing at the same wavelength.

BP 26.22 Thu 17:00 Poster B

Simulation of transport through OmpF channels — •Soroosh Pezeshki, Mathias Winterhalter, and Ulrich Kleinekathöfer — International University Bremen (Jacobs University Bremen as of spring 2007), Campus Ring 1, 28759 Bremen, Germany

The outer membrane protein F (OmpF) trimer is a pore in the outer membrane of *Escherichia coli*. Since the crystal structure of OmpF is known, molecular dynamics simulations are possible [1,2]. Applying a constant electric field, the current caused by potassium and chlorine ions can be determined directly. Good agreement with experimental data is achieved [3]. In the constriction zone, i.e. the narrowest part of the pore, we additionally mutated charged amino acids to neutral ones. With the help of these mutated OmpF structures we investigated the influence of charged and neutral constriction zones on the ionic current. In a second step we are simulating the translocation of antibiotics molecules through the pore.

[1] K. M. Robertson and D. P. Tieleman, FEBS Lett. 528, 53 (2002).
[2] W. Im and B. Roux, J. Mol. Biol. 319, 1177 (2002).
[3] E. M. Nestorovich, C. Danelon, M. Winterhalter, and S. M. Bezrukov, PNAS 99, 9789 (2002).

BP 26.23 Thu 17:00 Poster B

Transfection Statistics from EGFP-Fluorescence Data — •Jan-Timm Kuhr[1,2], Gerlinde Schwake[3], Maria Pamela David[3,4], Eduardo Mendoza[3,4], Joachim Rädler[3], and Erwin Frey[1,2] — [1]Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians-Universität, München — [2]Center for Nano Science, Ludwig-Maximilians-Universität, München — [3]Physics Department, Ludwig-Maximilians-Universität, München — [4]Marine Science Institute, University of the Philippines

We report on the stochastic nature of artificial gene transfer based on high content analysis of single cell fluorescence time courses. Using enhanced green fluorescent protein (EGFP), expression of typically 500-2000 individual cells was monitored. A wide range of expression values was found with typically $10^6 - 10^7$ EGFP molecules per fluorescent cell.

For slowly degrading proteins theoretical analysis predicts that the protein distribution is a superpostion of Poissonians. For large expression factors these overlap only marginally, so the number of proteins per cell is determined by the plasmid content, i.e. variance in maximal expression arises from rare events of successful transfection. Since overlap is small, intrinsic fluctuations of expression can be neglected and the protein distributions is approximately discrete. Assuming a Poisson process for transfection, we find typically $1.3 - 1.4$ plasmids per fluorescent cell and expression factors of $\sim 3 \cdot 10^6$. Hence, we identified variability in protein numbers to arise from stochasticity in the delivery process rather than from cell-to-cell variability in gene expression.

BP 26.24 Thu 17:00 Poster B

Fluorescence-Emission Control of Single CdSe-Nanocrystals using Metal-Modified AFM Tips — •Volker Walhorn, Olaf Schulz, Heinrich Frey, Christoph Pelargus, Dario Anselmetti, and Robert Ros — Experimental Biophysics, Physics Department, Bielefeld University, Germany

The concept of fluorescence switching and modulation due to local energy transfer is of increasing importance in nanobiophysics. Assays taking benefit from fluorescence quenching or fluorescence resonant energy transfer (FRET) between individual nanoobjects are currently evolving and facilitate fascinating possibilities for investigating matter at the nanoscale. We have established a setup combining total internal reflection microscopy (TIRFM) and atomic force microscopy (AFM) in order to do simultaneous laser induced fluorescence imaging and manipulation on the single molecule level [1]. As fluorophores we chose semiconductor nanocrystals (quantum dots) since they show high resistance to photo-bleaching. The quantum dots were addressed with metal functionalized AFM probes while simultaneously measuring the fluorescence-emission. We could not only switch a single fluorophore from the emitting state to the quenched but also observe distance dependent enhancement of fluorescence intensity due to exciton-plasmon coupling. In future force spectroscopy experiments we will use appropriate labeled ligand-receptor complexes, proteins or nucleic acids to reveal supplementary information of inter- or intramolecular dynamics. [1] R. Eckel, V. Walhorn, Ch. Pelargus, J. Martini, J. Enderlein, Th. Nann, D. Anselmetti, and R. Ros; Small (in press).

BP 26.25 Thu 17:00 Poster B

Methods for attaching individual metallic Nanoparticles on AFM Tips — •Olaf Schulz, Volker Walhorn, Christoph Pelargus, Dario Anselmetti, and Robert Ros — Experimental Biophysics, Physics Department, Bielefeld University, Germany

The combination of atomic force microscopy (AFM) and total internal reflection fluorescence microscopy (TIRFM) has proven a valuable tool for analyzing the interaction between single fluorophores and metallic nanoobjects [1]. Since energy transfer effects like fluorescence quenching play an increasing role in the investigation of inter- or intramolecular dynamics it is essential to understand the influence of different quenching agent properties (material, size or geometry) on these effects. Therefore it is crucial to attach single well defined particles to a cantilever tip.

We will discuss different methods of attaching single metallic nanoparticles to the very end of an AFM tip and the possibility to use them for distance controlled fluorescence intensity modulation with our combined AFM-TIRFM Setup.

[1] R. Eckel, V. Walhorn, Ch. Pelargus, J. Martini, J. Enderlein, Th. Nann, D. Anselmetti, and R. Ros; Small (in press).

BP 26.26 Thu 17:00 Poster B

Two-photon imaging and ablation of the mitotic spindle in *S. pombe* — •Nicola Maghelli and Iva Tolic-Norrelykke — MPI-CBG pfotenhauerstrasse 108 01307 DRESDEN

Multiphoton microscopy [1] has become a valuable tool for both in vitro and in vivo analysis of biological samples [2][3]. By focusing a near-infrared fs laser, it is possible to achieve photon densities high enough to exploit non-linear processes. The spatial volume in which such processes take places is around 0.5 μm^3; therefore confocal imaging is possible without the need of a pinhole. By increasing the power of the excitation laser, selective ablation inside living cells can be achieved [4]. We developed a custom-built two-photon microscope and applied it to study the effects of targeted nanosurgery inside the fission yeast *S. pombe*. Simultaneous ablation of the mitotic spindle and 3D imaging help understanding which forces are acting on the spindle during mitosis.

[1] Denk W, Strickler JH, Webb WW Two-photon laser scanning fluorescence microscopy. Science 1990 Apr 6;248(4951):73-6.
[2] Zipfel WR, Williams RM,WebbWWNonlinear magic: multiphoton microscopy in the biosciences. Nat Biotechnol. 2003 Nov;21(11):1369-77. Review.
[3] Squirrell JM, Wokosin DL, White JG, Bavister BD Long-term two-photon fluorescence imaging of mammalian embryos without compromising viability. Nat Biotechnol. 1999 Aug;17(8):763-7.
[4] Sacconi L, Tolic-Norrelykke IM, Antolini R, Pavone FS. Combined intracellular three-dimensional imaging and selective nanosurgery by a nonlinear microscope. J Biomed Opt. 2005 Jan-Feb;10(1):14002.

BP 26.27 Thu 17:00 Poster B

Dynamic Force Spectroscopy Experiments: Bayes and Maximum-Likelihood Approach — •Sebastian Getfert and Peter Reimann — Condensed Matter Theory, Universität Bielefeld, Universitätsstraße 25, 33615 Bielefeld

In dynamic force spectroscopy experiments the distribution of rupture forces is measured at different pulling velocities. An analysis of these distributions allows to draw conclusions about the underlying energy landscape.

In the past years a great amount of work has been spent to improve experiment and theory whereas the methods used to connect theory and experiment are still rather basic. Here we discuss, how the information obtained by dynamic force spectroscopy experiments can be used most efficiently to extract the parameters of interest. A detailed statistical analysis also shows which statements concerning the energy landscape are possible and for which pulling velocities measurements should be performed in order to minimize the statistical uncertainties.

BP 26.28 Thu 17:00 Poster B

Chemically modified chromophore in rhodopsin — •Minoru Sugihara[1], Oliver Weingart[2], Peter Entel[1], and Volker Buss[2] — [1]Theoretical Physics, University of Duisburg-Essen — [2]Theoretical Chemistry, University of Duisburg-Essen

The 11-cis retinal protonated Schiff base is the chromophore of rhodopsin, which is a transmembrane protein in the rod cells of vertebrate eyes. On photo-excitation it isomerizes from a 11-cis to all-trans form. This reaction is the initial step in vision and induces a sequence of biochemical reactions, which eventually lead to the stimulation of

the visual nerve.

The crystal structure of rhodopsin has recently been extended to 2.2 A resolution [1]. Based on this structure we have modeled the retinal chromophore and three chemically modified structures: 13-demethyl-, 10-methyl-13-demethyl- and 10 methyl-retinal with a quantum mechanical/molecular mechanical method [1,2]. Using these structures we were able to study systematically the influence of methyl substitution at 10- and 13-position on geometries and excited state dynamics. We found that the protein environment induces geometrical distortions around the isomerizing region and the initial pre-twist has significant influence on the reaction of the chromophore [3].

[1] T. Okada, M. Sugihara, A.-N. Bondar, et al. J. Mol. Biol. 341(2004) 571. [2] M. Sugihara, J. Hufen, V. Buss, Biochemistry 45 (2006) 801. [3] O. Weingart, I. Schapiro, V. Buss, submitted to J. Phys. Chem. A.

BP 26.29 Thu 17:00 Poster B

Improved data analysis for single molecule force spectroscopy experiments — •Alexander Fuhrmann[1], Sebastian Getfert[2], Dario Anselmetti[1], Peter Reimann[2], and Robert Ros[1] — [1]Experimental Biophysics — [2]Condensed Matter Theory, Physics Department, Bielefeld University, 33615 Bielefeld, Germany

Dynamic force spectroscopy (DFS) is widely used to investigate ligand-receptor interactions on the single molecule level. However, the data analysis is still a challenging task. The framework of the standard theory by Evans and Ritchie [1] has been extended by Raible et al. [2] in order to consistently describe the experimental data by taking into account heterogeneity of chemical bonds via random variations of the force-dependent dissociation rate. An important implication of these theories is that during pulling of the molecules all elastic components must be in equilibrium. Accordingly the force-extension curves before the dissociation of the ligand-receptor complexes must follow a distinct master curve, independently of the particular pulling velocity. Here, we present an analysis method based on the construction of master curves, which significantly increases the consistence of our experimental data with the model of chemical bond heterogeneity. Additionally, analysing the molecular elasticity in relation to the dissociation forces in 2D-histogramms allows a qualitative identification of different binding modes.

[1] E. Evans and K. Ritchie; Biophys.J. 72:1541 (1997) [2] M. Raible, M. Evstigneev, F. W. Bartels, R. Eckel, M. Nguyen-Duong, R. Merkel, R. Ros, D. Anselmetti, and P. Reimann; Biophys.J. 90: 3851 (2006).

BP 26.30 Thu 17:00 Poster B

Investigation on actin binding to various cationic model membranes — •Lydia Woiterski, Josef Käs, and Carsten Selle — Institut für Exp. Physik I, Linnéstr. 5, 04103 Leipzig

The aim of the present work is to study adsorption of a charged polymer at inflexible and flexible charged surfaces under a two-dimensional confinement. As a polymer, we use actin which is one of major components of the cytoskeleton in eukaryotic cells. The filaments form a quasi-two-dimensional network – the so-called actin cortex that plays an important role for cellular functions such as motility or adhesion. It is associated with the inner leaflet of the cell membrane, thus, it is of great interest to elucidate the nature of interaction of polymerized actin and lipids. First, this binding process is studied using giant vesicles prepared from mixtures of neutral lipids, the cationic lipid DODAB and cholesterol. The vesicle is trapped with optical tweezers in a microfluidic chamber. Filamentous actin is injected into the chamber and the properties of binding are investigated in dependence on the ionic strength and the composition of the model membrane using confocal microscopy. Furthermore, different mixed monolayers are studied to establish a system where liquid domains form and provide binding sites for the adsorption of single polymers. The monolayer/polymer system is a good model to mimic the behavior of polymers near lipid interfaces because it allows to manipulate easily the domain size and permits the observation of lateral diffusion within the model membrane in comparison to curved vesicles.

BP 26.31 Thu 17:00 Poster B

Simultaneous Manipulation and Detection of Cell Membrane Dynamics with High Spatial and Temporal Resolution — •Michael Gögler, Timo Betz, and Josef Käs — Soft Matter Physics, Universität Leipzig, Linnéstrasse 5, 04103 Leipzig, Germany

Cell motility is a fundamental process of many phenomena in nature, such as immune response, morphogenesis, and wound healing. In these events, protrusion of the cell membrane at the leading edge is the fundamental step. We use a new laser based technique to study the membrane motion at the leading edge of a cell with high spatial and temporal resolution in the nanometer and microseconds range, respectively. A diffraction limited laser spot is positioned at the leading edge of a cell and the forward scattered light is imaged on a quadrant diode detector which serves as a position sensitive device. We investigated the membrane motion at the leading edge of different cell types, such as fish keratocytes and red blood cells (RBC). We show that this technique can be used to locally manipulate the leading edge of a cell and to detect the movement of the leading edge simultaneously. By increasing the laser intensity we were able to exert a significant force (several pN) on the RBC's leading edge that is strong enough to deform the cell and to change its membrane dynamics. For RBCs it was possible to determine the membrane stiffness and shear modulus. Further capabilities of this technique such as cell imaging are presented.

BP 26.32 Thu 17:00 Poster B

Nonequilibrium mechanics of active cytoskeletal networks — Daisuke Mizuno[1,2], •Catherine Tardin[1], Frederick MacKintosh[1], and Christoph Schmidt[1,2] — [1]Department of Physics and Astronomy, Vrije Universiteit, Amsterdam, The Netherlands — [2]III. Physikalisches Institut, Fakultät f. Physik, Georg-August-Universität, Göttingen, Germany

Cells both actively generate and sensitively react to forces using their mechanical framework, the cytoskeleton, which is a non-equilibrium, composite material including polymers and motor proteins. We measure the dynamics and mechanical properties of a simple three-component model system, consisting of myosin II, actin filaments, and crosslinkers. Stresses arising from motor activity control cytoskeletal network mechanics: both increasing stiffness by a factor of nearly 100 and qualitatively changing the viscoleastic response of the network in an ATP-dependent manner. We present a quantitative theoretical model connecting the large-scale properties of this active gel to molecular force generation.

BP 26.33 Thu 17:00 Poster B

Failure of Viral Shells — William S. Klug[1], Robijn F. Bruinsma[1], Jean-Pilippe Michel[1], Charles M. Knobler[1], Irena L. Ivanovska[2], Gijs J.L. Wuite[2], and •Christoph F. Schmidt[2,3] — [1]University of California, Los Angeles, CA 90095, USA — [2]Department of Physics and Astronomy, Vrije Universiteit, 1081 Amsterdam, — [3]III. Physikalisches Institut, Fakultät für Physik, Georg-August Universität, 37077 Göttingen, Germany

We report a combined theoretical and experimental study of the structural failure of viral shells under mechanical stress. We find that discontinuities in the force-indentation curve associated with failure should appear when the so-called Föppl-von Kármán (FvK) number exceeds a critical value. A nano-indentation study of a viral shell subject to a soft-mode instability, where the stiffness of the shell decreases with increasing pH, confirms the predicted onset of failure as a function of the FvK number.

BP 26.34 Thu 17:00 Poster B

Teeth: a nanostructured multicomponent material — •Christian Zeitz, Frank Müller, Stefan Hüfner, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbrücken, Germany

The enamel of teeth is a complex nanostructured system and is the hardest mineralized tissue in the human body. It contains more than 95 % of mineral, embedded in an organic matrix of enamel proteins and collagen fibers. The aim of our study is the characterization of the structures by means of electron and atomic force microscopy. Furthermore, we are interested in the role of fluorides in reducing the tooth decay. Fluoride ions are incorporated into and stabilize the apatite crystal of teeth, yet the specific type of binding is unclear. We therefore perform photoelectron spectroscopy studies on enamel and artificial enamel surfaces.

BP 26.35 Thu 17:00 Poster B

Stochastic stress response induction in B. *subtilis* — •Ilka Bischofs[1], Denise Wolf[2], and Adam Arkin[1,2] — [1]Department of Bioengineering, University of California at Berkeley, CA 94710, USA — [2]Physical Biosciences Division, Lawrence Berkeley National Lab, Berkeley, CA 94720

There is a growing body of theory and experiments indicating that stress response diversification in microbes can be an adaptive response

to an unpredictably fluctuating environment. B. *subtilis* phenomenologically shows such stress response diversification. When subjected to stressors such as starvations only a portion of the cell population forms an endospore. Here we use a combined experimental and theoretical approach to characterize stochastic sporulation induction in B. *subtilis*. Using fluorescent reporter strains we study population dynamics on the single cell level with quantitative time lapse microscopy and analyze our data with the help of theoretical models. With such quantification of the probabilistic decision making process we are poised to ask questions about the fitness advantage of such stochastic behaviors.

BP 26.36 Thu 17:00 Poster B

In-situ real-time observation of single giant unilamellar vesicle phase behavior under rapid variation of the medium — •Philipp Rauch, Florian Rückerl, Josef Käs, and Carsten Selle — Inst. f. experimentelle Physik, Physik der weichen Materie,Universität Leipzig, Germany

Giant unilamellar vesicles (GUVs) are frequently used as model systems for intracellular and plasma membranes. Phase inhomogeneity corresponding to the appearance of microdomains in biological membranes was postulated to play a key role in triggering and controlling of various intra- and intercellular events like signal processing and absorption or adhesion of foreign matter. The investigation of the phase behavior of lipid systems showing coexistence of two liquid phases at physiological temperatures has moved into the focus of membrane physics. Related temperature-induced phase transitions have been observed and well described since they are easy to follow by fluorescent microscopy (FM) and calorimetry methods. We built a microfluidic flow chamber setup that allows us to manipulate single GUVs via optical tweezers while exposing them to varied media. The dynamics of phase alterations induced by jump-like change of the aqueous medium can be recorded in real-time. We investigated changes induced by increasing pH or ion strength of the surrounding. Our setup provides a compact method to manipulate single GUVs while examining alterations in lipid phase behavior due to arbitrarily modified media. Potentially, data can be obtained allowing conclusions on the role of lipid membranes in the interplay of components in living cells.

BP 26.37 Thu 17:00 Poster B

Unzipping DNA in a biological nanopore — •U. F. Keyser[1,2], N. M. Wennersbusch[1], N. H. Dekker[1], and C. Dekker[1] — [1]Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands — [2]Institut für Experimentelle Physik I, Universität Leipzig, Germany

Biological nanopores like protein toxins from bacteria can be used to analyze the structural properties of nucleic acids like DNA or RNA or proteins. We assemble the alpha-hemolysin nanopore, extracted from staphylococcus aureus, in a artificial lipid membrane. Applying a membrane potential allows driving DNA through the nanopore. Since only single-stranded DNA can pass the pore unhindered we use it to unzip double-stranded DNA constructs consisting of two hybridized strands. Varying the temperature and applied voltage we extract the unzipping time using a simple model. The unzipping time is consistent with values from the literature. We show that the unzipped strand can remain for up to several ms in the hemolysin prepore before it also translocates or leaves the nanopore. Varying the sequence of the DNA has little influence on the results. We discuss different possibilities for interaction between the nanopore and the passing DNA strand.

BP 26.38 Thu 17:00 Poster B

Preparation of horizontal black lipid bilayers incorporated in a microfluidics system for microscopy and industrial parallelization — •Tivadar Mach[1], Claus Fütterer[1], Jürgen Fritz[1], Niels Fertig[2], Catalin Chimerel[1], and Mathias Winterhalter[1] — [1]International University Bremen, Bremen, Germany — [2]Nanion GmbH, München, Germany

A planar black lipid membrane, widely used for electrophysiological studies, is reconstituted on a micron-size glass aperture inside a microfluidic chip, forming a GΩ seal using giant liposome adsorption and rupture. This novel system offers very low noise recordings (under 1 pA RMS at 10 kHz, essentially equal to the open headstage noise in our system), complete control of the measurement environment, access to the bilayer from both sides, the use of μl analyte volumes, and a great potential for automation and parallelization. Minimizing the microfluidics thickness on the lower side of the BLM enables us to approach the bilayer with a 100x objective making concurrent electrophysiological and fluorescence microscopy studies possible.

BP 26.39 Thu 17:00 Poster B

Nanoengineered Polymer Capsules: Tools for Controlled delivery and Site Specific Manipulation — •Raghavendra Palankar, Yannic Ramaye, Sebastian Springer, and Mathias Winterhalter — IUB-Bremen, Campusring 1, 28725 Bremen

Hollow nanometer-sized containers are of increasing interest in nanotechnology, since they can protect proteins, enzymes or drugs from hostile surroundings and provide an optimal microenvironment. Here we report on functionalized nanocapsules as intracellular reporters providing a new tool in cell biology. Cell active molecules, hormones, enzymes or reporter molecules may be hidden from the outside, protected against chemical and biological degradation, targeted to specific compartments inside a cell and released in a controlled manner. To improve the separation of free from encapsulated material we use magnetic liposomes. In a further series we prepared hydrophobic superparamagnetic nanoparticles and entrapped then in the liposomal bilayer. This technique bypasses the step of gel filtration. Further, these magnetoliposomes are coated with alternating polymer polyelectrolyte layers, resulting in magnetoliposome capsules. These capsules are introduced into CHO or Vero cells by either electropermeabilization or microinjection.

BP 26.40 Thu 17:00 Poster B

Planar, freestanding lipid membranes for X-ray structure analysis — •André Beerlink — Institut für Röntgenphysik, Universität Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Since the development of planar, freestanding lipid membranes in the early 1960s by Müller and Rudin, this model membranes have been used for many, especially physiological, experiments. X-ray structure analysis has always been limited to solid supported membrane systems in uni-, bi- or multilamellar phase. For the combination of these two techniques, namely structure analysis of planar, freestanding membranes, improvements of this model membrane system have to be done. We mainly developed the stability of membranes with new types of microstructured apertures and the access for the X-ray beam so that first experiments could be done. Fututre work can open a broad field of simultaneous analysis of physiological and structural information of model membranes.

BP 26.41 Thu 17:00 Poster B

Facilitated permeation through porins — Catalin Chimerel, Tivadar Mach, Helge Weingart, Ulrich Kleinekathöfer, and •Mathias Winterhalter — IUB-Bremen, Campusring 1, 28725 Bremen

The outer cell wall of Escherichia coli contains a number of channel forming proteins called porins. Such channels allow e.g. bacteria to harvest nutrients. We characterise e.g. the transport of antibiotics across such membrane channels on a single molecular level by time resolved ion current. Measureing the ion current fluctuation in presence of different concentrations of penicilins revealed a clear correlation between permeation and biological activity.

BP 26.42 Thu 17:00 Poster B

Diffusion control of proteins within model membrane systems — Florian Rückerl, Philipp Rauch, Josef Käs, and •Carsten Selle — University of Leipzig, Institute for Experimental Physics I, Linnestraße 5, 04103 Leipzig, Germany

Lateral diffusion within membranes plays a major role in biologically important processes as signal transduction.

Diffusion of proteins within inhomogeneous membranes was mimicked by motion of surface-charged fluorescent polystyrene beads in monolayers where two differently ordered phases coexist. Associated to ordered liquid-condensed (LC) domains, dimensionally reduced motion of the model proteins in the liquid-expanded (LE) phase was experimentally found which was caused by dipole-dipole interactions. Monte-Carlo simulations demonstrate that model protein diffusion can be strongly affected by the strength of these interactions and the domain size.

We also studied nanoparticles diffusing on the surface of giant unilamellar vesicles (GUVs) composed of either a single lipid or a mixture of lipids exhibiting fluid coexisting phases. The latter represents an even more similar mimic to cell membranes. The adhesion of the (charged) nanoparticles was found to depend on the surrounding medium.

It seems conceivable that living cells could control protein motion

accomplished by similar mechanisms in order to enhance kinetics of bimolecular enzyme reactions occuring in the membrane.

BP 26.43 Thu 17:00 Poster B

ODMR studies on spin coupling of Nitrogen Vacancy centers to spin labels — Gopalakrishnan Balasubramanian, •Fedor Jelezko, and Jörg Wrachtrup — 3. Physikalisches Institut, Universität Stuttgart , Stuttgart, GERMANY

Spin being a fundamental atomic property; it is often influenced by changes occurring on molecular length scales. Spin images of biomolecules could provide additional perspectives to certain structural and biophysical understanding. A method of using scanning probe microscopy together with optically detected magnetic resonance ODMR was proposed as a possible method towards realizing spin microscope.[1] Single Nitrogen-Vacancy (NV) defect center in diamond has attracted recent interests, primarily because of the possibility to probe and manipulate their spins states.[2] Investigating the coupling of a single NV center spin states to other spins, offers an excellent atomistic spin probe. We present our investigation on ODMR studies of coupling between a single NV center, to a radical spin label-TEMPO (2,2,6,6-Tetramethylpiperidine 1-oxyl). The ability to monitor subtle changes due to the dipolar interaction between the spins makes ODMR of NV centers an ideal probe to offer unprecedented sensitivity and spatial resolution.

[2] B.M.Chernobrod and G.P.Berman, J. Appl. Phys. 97, 014903, (2005). [2] T. Gaebel, M. Domhan, I Popa, C. Wittmann, P. Neumann, F. Jelezko, J.R. Rabeau, N. Stavrias, A.D. Greentree, S. Prawer, J. Meijer, J. Twamley, P.R. Hemmer, and J. Wrachtrup, Nature Physics 2: 408-413 (2006).

BP 26.44 Thu 17:00 Poster B

Lipid Assemblies on Nanostructures — •Jens Kühnle[1,2], Joachim Spatz[1,2], and Ralf Richter[1,2] — [1]Biophysikalische Chemie, University of Heidelberg, Germany — [2]MPI for Metals Research, Stuttgart, Germany

The properties and biological functions of lipid membranes originate from a wealth of different lipid-lipid and lipid-protein interactions. In order to understand the relationship between molecular interactions and the behaviour of the membrane as a whole, simplified model systems have proven useful Here, we propose a new model system that is based on the combination of nanostructured surfaces and supported lipid membranes. Our nanostructuration approach allows for the deposition of arrays of nanometer-sized gold dots with tuneable inter-dot spacings on solid surfaces. We show that supported lipid membranes can be formed on such templates. We characterize the influence of local chemical and geometrical heterogeneities, as presented by the gold dots, on the mobility of lipid molecules by fluorescence recovery after photobleaching (FRAP). The features contained in these model systems might give new insights into the interaction mechanisms that underlie transport and phase separation in lipid membranes.

BP 26.45 Thu 17:00 Poster B

Identifying multidimensional subspaces in multivariate data — •Harold Gutch and Fabian Theis — Max-Planck-Institut für Dynamik und Selbstorganisation, Bunsenstraße 10, 37037 Göttingen, Germany

ICA is the task of recovering n signals $\mathbf{S}$ given only n linear mixings $\mathbf{X}$ of them (so $\mathbf{X} = \mathbf{AS}$) under the additional assumption of stochastical independence of the sources.

However, since we are operating blindly, i.e. we only know $\mathbf{X}$ not $\mathbf{S}$, we cannot verify that $\mathbf{X}$ actually follows the ICA assumptions. We denote the task of recovering the sources $\mathbf{S}$ in the general case, where some dependencies exist between source components as independent subspace analysis (ISA). We call subsets of source components that are jointly stochastically independent of the rest and cannot be factorized nontrivially *irreducible*. Similarly to ICA, we again face the obvious indeterminacies of permutations of any number of irreducible random vectors of the same size, and scaling (which here translates to any linear invertible mixing within a single subspace).

In experiments, extensions of ICA algorithms have been shown to handle this model well, which is a good indicator that ISA gives unique solutions. Under the additional slight assumption of square-integrability of $\mathbf{S}$ (and hence $\mathbf{X}$), we provide a full uniqueness proof in the case where $\mathbf{S}$ consists of two irreducible components. An algorithmic implementation handles the extraction of a single irreducible subspace from arbitrary $\mathbf{X}$ well, and we illustrate how to use this subspace extraction algorithm for dimension reduction.

BP 26.46 Thu 17:00 Poster B

Actin Propelled Colloids: Motility Analysis, Orientation, and Force Measurements — Stephan Schmidt[1], •Maarten Biesheuvel[1], Richard Weinkamer[1], Emmanuèle Helfer[2], Marie-France Carlier[2], and Andreas Fery[1] — [1]Max Planck Institut für Kolloid- und Grenzflächenforschung, Wissenschaftspark Golm, 14424 Potsdam, Germany — [2]Laboratoire d'Enzymologie et Biochimie Structurales, CNRS, 91198 Gif-sur-Yvette, France

The ability to generate forces and move actively is one of the key features of micro-organisms and nature has found various pathways to accomplish it. Many of these processes are driven by actin polymerization were actin filaments grow against the membrane, generating a force and pushing it forward. The molecular scale origin of force generation is still matter of debate. We use a simplified in vitro assay composed of purified proteins on artificial colloidal objects. For example, we can couple actin based motion with coated silica particles or even hollow microcapsules. We have analyzed the motion of colloids, focusing on the curvature of the trajectories of the particles. A simple model explains the curvature distribution and the scaling with velocity. Furthermore, we were able to direct the self propelling colloidal objects along paths on micro-structured substrates. In principle this particle confining setup renders AFM force measurements on the freely moving particles possible. An alternative setup is used for force measurements on the growing actin network directly. Here the growing actin network is clamped between an AFM cantilever and the substrate.

BP 26.47 Thu 17:00 Poster B

Growth pattern of single fission yeast cells: linear, bilinear, or exponential? — •Stephan Baumgärtner and Iva Tolic-Nørrelykke — Max Planck Institute of Molecular Cell Biology and Genetics, Dresden

The exact growth profile of size parameters during the cell cycle is controversial. Linear, exponential and bilinear models are typically considered. Exponential models assume that the rate of growth is proportional to the existing size. However, growth can be linear, or multi-linear, corresponding to different constant rates separated by rate-change points.

The cylindrically shaped fission yeast cells grow in length by extension at the cell ends. The growth pattern of fission yeast cells is currently unclear: a number of models can be well-fitted to the data, due to the relatively low spatial and temporal resolution of the data from literature. We observe single fluorescently labeled cells over a complete cell cycle using confocal microscopy. Our goal is to acquire data of significantly higher quality than the existing data, which will allow for distinguishing between different models of cell growth.

BP 26.48 Thu 17:00 Poster B

Natural cutoff in discrete Fisher waves — •Oskar Hallatschek and David Nelson — Department of Physics, Harvard University

R.A. Fisher introduced some 70 years ago, his famous model for "the spread of an advantageous gene", that has been widely used to describe travelling waves in such diverse fields as ecology, chemistry and QCD. Effects due to the discrete nature of particles have long been ignored, until recently: Brunet and Derrida told us to introduce a cutoff in the growth rate to account for the fact that there is no growth beyond the foremost particle in the front of the wave. To leading order, the ad hoc cutoff theory explains the observed shift in the velocity of discrete Fisher and, more generally, pulled waves. Here, we show that a Hartree-like mean field theory can be fromulated that naturally takes into account the discreteness of particles without the need for an adjustable hard cutoff. For large particle numbers the discreteness correction acts like a soft cutoff in the Fisher equation. We compare this novel mean field theory with simulations and with the heuristic hard cutoff scheme proposed by Brunet and Derrida.

BP 26.49 Thu 17:00 Poster B

Water and salt: physical aspects of biomolecular solvation — •Joachim Dzubiella — Physik Department, TUM, Garching

Aqueous electrolyte solutions are the natural environment for biomolecules, i.e. proteins and enzymes, and thus provide major mechanisms which determine protein structure and stability. The detailed microscopic mechanisms which range from nonspecific phenomena such as hydrophobicity and salt screening to specific structural effects are far from being understood. Here we try to shed some more light on these phenomena by performing atomistic molecular dynamics com-

puter simulations of simple and complex molecules in aqueous electrolyte solutions and show that macroscopic continuum approaches can be extrapolated to microscopic scales and give a partially quantitative description of molecular solvation.