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Overview of Invited Talks and Sessions

(lecture rooms HÜL 186 and ZEU 260, Poster P3 (ZEU 250))

Invited Talks

BP 1.1	Mon	10:15–10:45	HÜL 186	**Taming a Heart Gone Wild** — •Stefan Luther
BP 8.1	Tue	9:30–10:00	HÜL 186	**Robustness and Scaling in Embryonic Development** — •Naama Barkai
BP 8.2	Tue	10:00–10:30	HÜL 186	**The R8 race: Specifying photoreceptor cells in the developing fly eye** — •David Lubensky
BP 10.1	Tue	14:00–14:30	HÜL 186	**Biohydrodynamics of biomimetic and bacterial flagella** — •Holger Stark
BP 12.1	Wed	9:30–10:00	HÜL 186	**Conformational Mechanics of Single Protein Molecules** — •Matthias Rief
BP 12.2	Wed	10:00–10:30	HÜL 186	**Illuminating the way Kinesin-1 walks using FRET between the motor domains** — •Erwin Peterman
BP 14.1	Wed	14:00–14:30	HÜL 186	**Nerve signals as density pulses, conduction events, and the role of anesthetics** — •Thomas Heimburg
BP 18.1	Thu	9:30–10:00	HÜL 186	**Systems biology of yeast cell signaling and response to stress** — •Edda Klipp
BP 18.2	Thu	10:00–10:30	HÜL 186	**Towards an understanding of membrane and protein traffic in living cells** — •Matthias Weiss
BP 20.1	Thu	14:00–14:30	HÜL 186	**Artificial biochemical reaction circuits based on DNA and RNA** — •Friedrich Simmel, Eike Friedrichs, Ralf Jungmann
BP 25.1	Fri	10:15–10:45	HÜL 186	**Role of membrane curvature in membrane trafficking** — •Patricia Bassereau, Benoit Sorre, Andrew Callan-Jones, Gerbrand Koster, Aurélien Roux, Martin Lenz, Jean-François Joanny, Jacques Prost

Invited Talk of the session BP 6 (joint session DY/BP)

DY 4.1	Mon	14:00–14:30	HÜL 386	**Mechanisms of tissue maintenance: a laboratory for statistical physics** — •Benjamin Simons

Invited Talks of the joint symposium SYSO

See SYSO for the full program of the Symposium. Note also in particular the session SYSO IV, Thursday, 11:00-12:30, GÖR 226.

SYSO 1.1	Wed	14:00–14:30	BAR SCHÖ	**Pattern formation in epitaxial growth and ion beam erosion** — •Thomas Michely
SYSO 1.2	Wed	14:30–15:00	BAR SCHÖ	**Patterns and Pathways in Far-from-equilibrium Nanoparticle Assemblies** — •Philip Moriarty, Andrew Stannard, Emmanuelle Pauliac-Vaujour, Matthew Blunt, Chris Martin, Ioan Vancea, Uwe Thiele

SYSO 1.3	Wed	15:00–15:30	BAR SCHÖ	**Block-Copolymer Derived Inorganic Functional Materials** — •Ullrich Steiner
SYSO 2.1	Wed	15:45–16:15	BAR SCHÖ	**Crystallisation of polymers at surfaces and in thin films** — •Günter Reiter
SYSO 2.2	Wed	16:15–16:45	BAR SCHÖ	**Active Organisation of Cell Surface Molecules by Cortical Actin** — Kripa Gowrishankar, Debanjan Goswami, Subhasri Ghosh, Abhishek Chaudhuri, Bhaswati Bhattacharya, Satyajit Mayor, •Madan Rao
SYSO 2.3	Wed	16:45–17:15	BAR SCHÖ	**Phase Behaviour and Dynamics in Lipid Mixtures** — •Peter Olmsted

Invited Talks of the joint symposium SYCS

See SYCS for the full program of the Symposium.

SYCS 1.1	Fri	10:15–11:00	BAR SCHÖ	**Eat, Drink, and Be Merry: The Spread of Health Phenomena in Complex, Longitudinally Resolved Social Networks** — •Nicholas Christakis
SYCS 1.2	Fri	11:00–11:30	BAR SCHÖ	**Transport efficiency and resilience in mycelial networks** — •Mark Fricker, Daniel Bebber, Lynne Boddy
SYCS 1.3	Fri	11:30–12:00	BAR SCHÖ	**From genetic variability between species to the inference of protein-protein interactions** — •Martin Weigt, Robert A. White, Hendrik Szurmant, James A. Hoch, Terrence Hwa
SYCS 1.4	Fri	12:00–12:30	BAR SCHÖ	**Clustering and multiscale structure of graphs** — •Boaz Nadler
SYCS 1.5	Fri	12:30–13:00	BAR SCHÖ	**Clustering, chance, and statistical mechanics** — Marta Luksza, Michael Lässig, •Johannes Berg
SYCS 1.6	Fri	13:00–13:30	BAR SCHÖ	**Physics of recommendation mechanisms** — •Yi-Cheng Zhang

Sessions

BP 1.1–1.10	Mon	10:15–13:15	HÜL 186	**Dynamic Processes and Pattern Formation**
BP 2.1–2.9	Mon	11:00–13:15	ZEU 260	**Biopolymers and Biomaterials (joint session BP/CPP)**
BP 3	Mon	11:00–13:00	ZEU 255	**Statistical Physics in Biological Systems I (joint session DY/BP)**
BP 4.1–4.9	Mon	14:30–17:00	HÜL 186	**Cell Mechanics**
BP 5.1–5.9	Mon	14:30–17:00	ZEU 260	**Proteins**
BP 6	Mon	14:00–16:45	HÜL 386	**Statistical Physics in Biological Systems II (joint session DY/BP)**
BP 7.1–7.62	Mon	17:45–20:00	P3	**Poster I**
BP 8.1–8.11	Tue	9:30–13:00	HÜL 186	**Developmental Processes**
BP 9.1–9.9	Tue	10:45–13:15	ZEU 260	**Actin Dynamics**
BP 10.1–10.9	Tue	14:00–16:30	HÜL 186	**Biofluiddynamics**
BP 11.1–11.8	Tue	14:30–16:30	ZEU 260	**Novel Methods**
BP 12.1–12.12	Wed	9:30–13:15	HÜL 186	**Single Molecules**
BP 13.1–13.9	Wed	10:45–13:15	ZEU 260	**Cell Migration**
BP 14.1–14.11	Wed	14:00–17:15	HÜL 186	**Neuronal and Sensory Systems**
BP 15.1–15.5	Wed	14:30–15:45	ZEU 260	**Motor Proteins**
BP 16.1–16.5	Wed	16:00–17:15	ZEU 260	**Stochastic Processes**
BP 17.1–17.46	Wed	17:15–19:45	P3	**Poster II**
BP 18.1–18.12	Thu	9:30–13:15	HÜL 186	**Regulation and Signaling**
BP 19.1–19.9	Thu	10:45–13:15	ZEU 260	**Cell Adhesion**
BP 20.1–20.11	Thu	14:00–17:15	HÜL 186	**DNA, RNA and Chromatin**
BP 21.1–21.5	Thu	17:30–18:45	HÜL 186	**Population Dynamics and Evolution**
BP 22.1–22.9	Thu	14:30–17:00	ZEU 260	**Transport Processes and Cellular Trafficking**
BP 23.1–23.6	Thu	17:15–18:45	ZEU 260	**Physics of Bacteria and Viruses**
BP 24	Thu	14:30–17:30	ZEU 114	**Biopolymers (joint session CPP/BP)**
BP 25.1–25.10	Fri	10:15–13:15	HÜL 186	**Membranes**
BP 26.1–26.8	Fri	11:00–13:00	ZEU 260	**Photobiophysics**

Annual General Meeting of the Biological Physics Division

Thursday 19:00–20:00 HÜL 186

- Bericht
- Wahl
- Verschiedenes

BP 1: Dynamic Processes and Pattern Formation

Time: Monday 10:15–13:15 Location: HÜL 186

Invited Talk BP 1.1 Mon 10:15 HÜL 186

Taming a Heart Gone Wild — •Stefan Luther — Biomedical Physics Group, Max Planck Insitute for Dynamics and Self-Organization, Bunsenstrasse 10, 37073 Goettingen, Germany

Spatiotemporally chaotic wave dynamics underlie a variety of debilitating crises in extended excitable systems such as heart and brain. It is well known that control of spatiotemporal chaos requires multiple control sites. Creating such sites in living tissue, however, is a long-standing problem. Here we show that natural anatomical heterogeneities within cardiac tissue can provide a large and adjustable number of control sites for low-energy termination of malignant wave dynamics. This allows us to terminate ventricular fibrillation in canine cardiac tissue using small amplitude pulsed electric fields with up to two orders of magnitude lower energies than those used for defibrillating shocks. We quantify the physical mechanism underlying the creation of control sites using fully time resolved high-spatial resolution imaging of wave emission, high-resolution magnetic resonance imaging of cardiac structure, and cell culture experiments. Our method avoids the invasive implantation of multiple electrodes and, more importantly, has the potential to control the tissue where the chaotic state is most susceptible, i.e., at rotating wave cores. This approach promises to significantly enhance current technologies for the termination of life-threatening cardiac arrhythmias, a leading cause of mortality and morbidity in the industrialized world. Moreover, the method should be capable of regulating wave dynamics in other excitable systems, including the nervous system.

BP 1.2 Mon 10:45 HÜL 186

Simulation of wave propagation on moving heart geometry — •Stefan Fruhner[1,2], Steffen Bauer[2], Markus Bär[2], and Harald Engel[1] — [1]TU Berlin, Germany — [2]PTB Berlin, Germany

Cardiac contraction is controlled by electric waves propagating through the heart. Although realistic heart models often include detailed physiological knowledge about ionic dynamics of cardiac cells and accurately account for anatomical details like fibre orientation or heterogeneity of heart tissue, mechanical deformations of the heart during contraction usually is neglected. However, static heart models fail to describe the feedback between propagating waves of electric activity and cardiac contraction which might be essential for understanding the mechanism of cardiac arrhythmias like tachycardia and fibrillation. Based on magneto-resonance images two-dimensional finite-element meshes have been generated to simulate waves of electric activity propagating in a beating human heart. The approach offers the opportunity to calculate the mechanical stresses during cardiac contraction from experimental data without using detailed models on calcium dynamics and stress-activated channels in cardiac myocytes.

BP 1.3 Mon 11:00 HÜL 186

Pattern formation in myxobacteria driven by adventurous motility and cell shape — Fernando Peruani[1,2,3], Jörn Starruss[3], Vladimir Jakovljevic[4], Lotte Sogaard-Andersen[4], •Markus Bär[2], and Andreas Deutsch[3] — [1]ICS Paris, France — [2]Physikalisch-Technische Bundesanstalt, Berlin — [3]ZIH, TU Dresden, Dresden — [4]MPI for Terrestrial Microbiology, Marburg

Bacteria and other microorganisms exhibit a transition to multicellularity which starts with the onset of clustering. We study the combined effects of active, adventurous motion and anisotropic cell shape in assemblies of a mutant strain of myxobacteria that exhibit neither social motility nor so-called C-signalling. We observe a transition to clustering and collective motion, that is presumably caused by simple physical volume-exclusion interactions only. Our results show that in gliding bacteria, the combination of anisotropic cell shape and active motion, leads to an primitive effective alignment mechanism. The transition to clustering is predicted by a mathematical model and verified by comparison of cluster-size statistics predicted by the model with corresponding statistics taken from experimental data.

BP 1.4 Mon 11:15 HÜL 186

Generalized analysis of oscillatory systems in cell biology — •Martin Zumsande and Thilo Gross — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden

We present a generalized approach for the modeling and analysis of oscillatory systems in cell biology. The advantage of this approach is that it does not require detailed knowledge of the functional form of rate laws, which is often not available. Instead, we investigate the system by parameterizing the Jacobian matrices of all steady states that are compatible with a given model structure. We then analyse the bifurcation landscape of the models via statistical sampling methods. This reveals Hopf bifurcations leading to oscillatory dynamics. By computing the first Lyapunov coefficient from a higher order expansion of the dynamics around the steady states we can distinguish between supercritical and subcritical Hopf bifurcations. The latter can lead to a catastrophic loss of stability, while in the former case, the loss of stability is a continuous, and hence reversible, transition. To illustrate our method we show results for small, toy model oscillators and a more complex model of a mammalian circadian oscillator.

15 min. break

BP 1.5 Mon 11:45 HÜL 186

Anti-spiral waves in glycolysis: How molecular enzyme properties determine the resulting spatio-temporal patterns — •Ronny Straube[1] and Ernesto M. Nicola[2] — [1]MPI for Dynamics of Complex Technical Systems, Sandtorstr. 1, 39106 Magdeburg, Germany — [2]MPI for Physics of Complex Systems, Noethnitzer Str. 38, 01187 Dresden, Germany

Spiral waves are probably the most common structure arising in pattern forming systems. Much less common are so called anti-spirals where, in contrast to "normal" spirals, the wave fronts propagate inwardly, i.e. towards the spiral core. Since their first discovery in chemical model systems [1,2] anti-spirals have now been generated in glycolysis using an extract of yeast cells (unpublished results), which represents a biological model system for the energy metabolism. Here, we explore theoretically the conditions for the occurrence of anti-spirals in two well-known glycolytic model systems: The Goldbeter model and the Selkov model. Interestingly, anti-spirals can only emerge in the Goldbeter model provided that the enzyme cooperativity, as measured by the number of enzyme subunits, is sufficiently large. This is in agreement with the observation that under physiological conditions the glycolytic enzyme phosphofructokinase is predominantly found in a tetrameric or octameric conformation.

[1] V. K. Vanag, I. R. Epstein. Science **294**, 835-837 (2001).
[2] X. Shao et.al. Phys. Rev. Lett. **100**, 198304 (2008).

BP 1.6 Mon 12:00 HÜL 186

Mechanically driven reaction-diffusion model for Hydra axis-definition — Jordi Soriano[1], •Sten Rüdiger[2], and Albrecht Ott[3] — [1]Universitat de Barcelona, Spain — [2]Humboldt-Universität zu Berlin, Germany — [3]Universität des Saarlandes, Saarbrücken, Germany

We have studied the relation between morphogenetic processes and mechanical properties during regeneration of the freshwater polyp Hydra. It has been known that the axis-defining step (symmetry-breaking) of regeneration requires mechanical inflation-collapse oscillations of the initial cell ball. We found evidence that axis definition is retarded if these oscillations are slowed down mechanically. We show that a reaction-diffusion mechanism provides a suitable scenario to describe the Hydra symmetry breaking. We employ a model in which the swelling of the initial Hydra cell ball induces changes in the diffusivity rates of activator and inhibitor. The mechanical stress provided by the oscillations drives the system to the Turing unstable regime. Once the organizer is constituted and a chemical gradient is established, the organizer locks and maintains the axis. Analytical considerations of the model show that the symmetry breaking time decreases with increasing swelling rate with the same behavior observed experimentally.

BP 1.7 Mon 12:15 HÜL 186

A Reaction-Diffusion System to Model Symmetry Breaking in C. elegans — •Philipp Khuc Trong[1,2,3], Nathan W. Goehring[2], Ernesto M. Nicola[1], and Stephan W. Grill[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]University of Technology Kaiserslautern, Kaiserslautern, Germany

Prior to the first unequal cell division in the *Caenorhabditis elegans* embryo the PAR proteins become distributed asymmetrically in distinct anterior and posterior domains. Here we present a two-variable, mass conserved reaction-diffusion system in which PAR segregation can be triggered either convectively by cortical flows or spontaneously by random perturbations. We show that the spontaneous symmetry breaking is induced by a mechanism similar to a Turing instability. However, in our model the wavelength of the fastest growing spatial pattern is always equal to the system size. We explore the robustness of this mechanism as a function of the reaction rates and furthermore consider the volume differences between cell cortex and cytoplasm.

BP 1.8 Mon 12:30 HÜL 186

Dynamics of Blood Disorders — •Arne Traulsen[1], Jorge M. Pacheco[2], and David Dingli[3] — [1]Max-Planck-Institute for Evolutionary Biology, 24306 Plön, Germany — [2]App. Theor. Phys.-Group & Centro de Física Teórica e Computacional, Departamento de Física da Faculdade de Ciências, Complexo Interdisciplinar da Universidade de Lisboa, P-1649-003 Lisboa Codex, Portugal — [3]Division of Hematology, Mayo Clinic College of Medicine, Rochester, MN 55905, USA

Blood formation is characterized by a hierarchical architecture, with a small number of stem cells at the highest level. These cells differentiate more and more until they form the huge number of blood cells in the circulating blood. Based on a simple mathematical model for this hierarchy [1], we address the dynamics of different blood disorders. The leads to analytical estimates of the survival time of mutations in the system [2,3]. For chronic myeloid leukemia, the framework allows to describe the origin, development, response to therapy, and relapse after termination of therapy [4]. The resulting dynamics consistent with the available clinical data.

[1] D. Dingli, A. Traulsen, and J.M. Pacheco,PLoS One 2, 345 (2007)
[2] D. Dingli, J.M. Pacheco, and A. Traulsen, PRE 77, 021915 (2008)
[3] A. Traulsen J.M. Pacheco, and D. Dingli, Stem Cells 25, 3081 (2007)
[4] D. Dingli, A. Traulsen, and J.M. Pacheco, Clinical Leukemia 2, 133 (2008)

BP 1.9 Mon 12:45 HÜL 186

Spatiotemporal control of the energy metabolism in a thin layer of yeast cells by oxygen gradients — •Christian Warnke[1], Thomas Mair[2], Mathias Müller[1], Hartmut Witte[1], Marcus J. Hauser[2], and Alois Krost[1] — [1]Otto-von-Guericke-Universität Magdeburg, Inst. Exp. Phys., Abt. Halbleiterepitaxie — [2]Otto-von-Guericke-Universität Magdeburg, Inst. Exp. Phys., Abt. Biophysik

The energy metabolism of cells can work both in absence (anaerobic) and in presence (aerobic) of oxygen. Specially, the anaerobic energy metabolism is represented by glycolysis, a pathway that is characterized by oscillatory behavior. Accordingly, spatiotemporal patterns, resulting from reaction-diffusion coupling, can be observed as well. We present an experimental method to produce spatiotemporal gradients of oxygen in planar yeast cell / Au electrode - interfaces that exhibit glycolytic oscillations. This planar interface allowed a stimulation by electrical pulses of energy metabolism by electrolytic reactions between the blank Au-metal and the electrolytic solution creating oxygen concentration close of the electrodes. The local oxygen pulses are aimed to perturb glycolytic oscillations by a short activation of the aerobic energy metabolism. Additionally, the studies were conducted at different temperatures using a Peltier element connected with the electrode-yeast-interface. We investigated the effect of these local perturbations on the temporal and spatiotemporal dynamics of glycolysis in yeast cells.

BP 1.10 Mon 13:00 HÜL 186

Entrainment in nonlinear oscillator model of insect flight — •Elena Y. Shchekinova[1], Jan Bartussek[2], and Martin Zapotocky[3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Institute of Robotics and Intelligent Systems, ETH Zurich, Zurich, Switzerland — [3]Institute of Physiology, Academy of Science of the Czech Republic, Prague, Czech Republic

In the recent insect flight control experiments the wingbeat frequency transitions and short–time entrainment of the wingbeat cycle to the external stimulus was observed during tethered mechanically stimulated flight. Such an alternation of wing kinematics behavior is achievable due to the changes in the oscillatory combinatorial activity of the flight power and control muscles during flight.

We provide a minimal deterministic description of a synchronous activity of insect flight power and steering muscles. The oscillatory dynamics is modeled by a chain of coupled nonlinear oscillators in the regimes close to the dynamical instability threshold. By introducing small periodic parametric modulation in the model frequency transitions and entrainment to the external driving frequency is achieved. Our results aim to elicit entrainment and frequency transitions in wingbeat regimes observed during mechanically stimulated flight experiment.

BP 2: Biopolymers and Biomaterials (joint session BP/CPP)

Time: Monday 11:00–13:15 Location: ZEU 260

BP 2.1 Mon 11:00 ZEU 260

Radial distribution function for confined semiflexible polymers — •Florian Thüroff, Frederik Wagner, and Erwin Frey — Arnold Sommerfeld Center für theoretische Physik, Ludwig-Maximilians-Universität München

The crowded environment of living cells strongly constrains the conformational degrees of freedom of fluctuating biopolymers. Recent experimental setups achieved to confine single polymers to narrow channels and to directly observe the statistical properties of these chains. We present a theoretical calculation of the radial distribution function of confined semiflexible polymers in the weakly bending limit, for the model case of a parabolic confining potential. Special emphasis has been put on a proper treatment of the boundary conditions. We compare our analytical expressions to numerical data from Monte Carlo simulations and find perfect agreement.

BP 2.2 Mon 11:15 ZEU 260

End-monomer dynamics in semiflexible polymers — •Michael Hinczewski[1,2], Xaver Schlagberger[1], Michael Rubinstein[3], Oleg Krichevsky[4], and Roland R. Netz[1] — [1]Physics Dept., Technical Univ. of Munich, Germany — [2]TUBITAK - Bosphorus Univ. Feza Gürsey Institute, Turkey — [3]Dept. of Chemistry, Univ. of North Carolina, U.S.A. — [4]Physics Dept., Ben-Gurion Univ., Israel

Precise experimental observations over the last few years of end-monomer dynamics in the diffusion of double-stranded DNA have given conflicting results: one study indicated an unexpected Rouse-like scaling of the mean squared displacement (MSD) $\langle r^2(t)\rangle \sim t^{1/2}$ at intermediate times, corresponding to fluctuations at length scales larger than the persistence length but smaller than the coil size; another study claimed the more conventional Zimm scaling $\langle r^2(t)\rangle \sim t^{2/3}$ in the same time range. Spurred by this experimental controversy, we investigate the end-monomer dynamics of semiflexible polymers through Brownian hydrodynamic simulations and dynamic mean-field theory [1]. Both theory and simulation point to a novel intermediate dynamical regime where the effective local exponent of the end-monomer MSD, $\alpha(t) = d\log\langle r^2(t)\rangle/d\log t$, drops below the Zimm value of 2/3 for sufficiently long chains. The deviation from the Zimm prediction increases with chain length, though it does not reach the Rouse limit of 1/2. Anomalously low values of the effective exponent α are explained by hydrodynamic effects related to the slow crossover from dynamics on length scales smaller than the persistence length to dynamics on larger length scales. [1] arXiv:0809.0667, Macromolecules *in press* (2008).

BP 2.3 Mon 11:30 ZEU 260

A liquid state theory for biopolymers — •Jens Glaser and Klaus Kroy — Inst. f. Theoretische Physik, Universität Leipzig, PF 100920, 04009 Leipzig

Solutions of stiff biopolymers, e.g. F-actin, are unique in that the polymers are neither completely rigid nor completely flexible. A successful description of their equilibrium properties is based on the concept that hard-core interactions with the surrounding solution confine each polymer to an effective tube-like cage. The tube radius plays a central role for the phenomenology of stiff polymer solutions. Its scaling behavior with concentration as well as exact prefactors have been derived using

mean-field theory and simulation. Generalizing Onsager's ansatz for hard cylinders, we propose a liquid state theory for stiff polymers and derive the fluctuations of the tube radius itself. We obtain length-dependent corrections to the mean-field result as well as a rigorous result for the second cumulant of the distribution of tube radii. The results compare favorably with new dynamical measurements on F-actin networks, obtained using confocal laser scanning microscopy.

BP 2.4 Mon 11:45 ZEU 260

Active and Passive Microrheology Probes Reconstituted Intermediate Filament Networks — •Sarah Köster[1,2], Yi-Chia Lin[2], Johannes Sutter[2], and David Weitz[2] — [1]Courant Research Centre Physics, University of Göttingen, Germany — [2]Department of Physics and School of Engineering and Applied Sciences, Harvard University, Cambridge, USA

Intermediate filaments (IFs) are one of the major filament systems of the eukaryotic cytoskeleton. Their remarkable tensile strength and biochemical heterogeneity distinguishes IFs from microfilaments and microtubules and identifies them as a key component for cell mechanics. Here, we study in vitro reconstituted vimentin networks by active and passive microrheology. By tracking individual beads we are able to characterize both the overall network properties as well as the degree of heterogeneity and the effect of crosslinking ions on the network structure and mechanics. This also provides a measure of the pore-size distribution in the network. Active microrheology, using magnetic tweezers, allows us to determine the viscoelastic properties of the network. By exposing the network to several sequential cycles of applied force, we observe changes in the response due to network reorganization.

BP 2.5 Mon 12:00 ZEU 260

Non-affine Deformations in Entangled Networks of Semiflexible Polymers — •Hauke Hinsch and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, Ludwigs-Maximilians-Universität, 80333 Munich, Germany

Biopolymers are ubiquitous in nature and play a crucial role for cell mechanics and motility. One prominent example is the semiflexible filamentous actin that constitutes the cytoskeleton by forming large networks with viscoelastic properties that are suited to the cell's need for both rigidity and plasticity.

To characterize these properties we have investigated the modulus of entangled networks of semiflexible polymers. We report on theoretical work and simulation results. While most theoretical descriptions assume the macroscopic deformation to be affinely transmitted to the network constituents, we have developed a model that accounts for local non-affine displacements.

BP 2.6 Mon 12:15 ZEU 260

Fiber Networks: Relationship between Effective Elastic Properties and Morphology — •Susan Sporer[1], Mayhar Madadi[2], Stefan Münster[3], Klaus Mecke[1], Christoph Arns[2], Ben Fabry[3], and Gerd E. Schröder-Turk[1] — [1]Institut für Theoretische Physik, Universität Erlangen-Nürnberg, Germany — [2]Applied Maths, ANU, Canberra, Australia — [3]Center for Medical Physics and Technology, Biophysics Group, Universität Erlangen-Nürnberg, Germany

Elastic properties of disordered 3D fiber networks formed by reconstituted collagen fibers are studied numerically using a two-phase voxel-based finite element method. The fiber network structures are extracted from segmented confocal microscopy image stacks of collagen gels with different concentrations using the medial axis construction [1]. Effective shear moduli are analysed as function of two morphological parameters, fiber thickness and collagen concentration. For these data, the collagen volume fraction is the principal morphological measure that affects the shear modulus, similar to the case of open-cell foam structures. Our quantitative results raise the question if, for the analysis of effective elastic properties, the collagen scaffold can be modelled as a homogeneous body in network shape with locally isotropic elastic moduli – whereas in reality it is a cross-linked network of anisotropic individual fibers.

[1] W. Mickel , S. Münster, L.M. Jawerth, D.A. Vader, D.A. Weitz, A.P. Sheppard, K. Mecke, B. Fabry, G.E. Schröder-Turk, Biophys. J. 95 (12), in print (2008).

BP 2.7 Mon 12:30 ZEU 260

Encapsulation of carbon nanotubes within the microtubules — •Melinda Varga[1,2], Nitesh Ranjan[1], Wolfgang Pompe[1], and Michael Mertig[1] — [1]Institute for Materials Science and Max Bergmann Center of Biomaterials, Dresden University of Technology, D-01062 Dresden, Germany — [2]Institut for Genetics, Dresden University of Technology, D-01062 Dresden, Germany

Manipulation and local defined positioning of carbon nanotubes (CNTs) is one of the main challenges in CNT-based nanotechnology. Here we report the encapsulation of single-walled carbon nanotubes (SWCNT) into the lumen of microtubules with the aim to accomplish a biological functionalization of the CNTs and to elucidate motor-driven active transport of these one-dimensional wires. The encapsulation is obtained by self-assembly of microtubules from tubulin dimers in the presence of CNTs. To this end, a two-step procedure was developed including dispersion of single-walled CNT with tubulin dimers and subsequent polymerization of the protein tubes [1,2]. The obtained products were characterized by various scanning probe and electron microscopy methods. The presence of CNTs within the microtubules was proven by electrostatic force measurements (EFM).

[1] M. Varga, Master thesis: "The interaction of tubulin dimers with carbon nanotubes", Dresden University of Technology (2006). [2] N. Ranjan, Ph.D. thesis: "Dielectrophoretic formation of nanowires and devices", Dresden University of Technology (2008).

BP 2.8 Mon 12:45 ZEU 260

Mineralization kinetics and heterogeneity of mineral content in bone — •Carolin Lukas[1], Harald Engel[2], Peter Fratzl[1], Paul Roschger[3], Klaus Klaushofer[3], and Richard Weinkamer[1] — [1]Max Planck Institute of Colloids and Interfaces, Department of Biomaterials, Potsdam, Germany — [2]TU Berlin, Germany — [3]Ludwig Boltzmann Institute of Osteology, Vienna, Austria

An important factor for the mechanical behaviour of bone at the material level is the amount and the distribution of mineral. The heterogeneous distribution of the bone mineral is due to the continuous remodelling of bone and the consecutive mineralization process. Bone mineralization increases the stiffness of each bone packet by increasing its mineral content. The mineralization kinetics is characterized by the mineralization law which describes the increase in the mineral content in a bone packet as a function of time. Remodelling and mineralization lead to a patchwork of bone elements with different mineral contents. Their frequency distribution, called the bone mineralization density distribution (BMDD), can be measured experimentally and modelled using a continuity equation [1, 2]. Extending the theoretical framework the influence of changes in the mineralization kinetics due to administration of drugs or disease on the BMDD can be described, which is of fundamental interest to medicine. We will present model predictions and compare them to experimental data.

[1] D. Ruffoni et al., Bone, 40(5), 2007.
[2] D. Ruffoni et al., JBMR 2(6), 2008.

BP 2.9 Mon 13:00 ZEU 260

Leg joints of the lobster H. americanus: An example of cuticle modification for specific functions — •Helge Fabritius[1], Torsten Fischer[1], Sabine Hild[1,2], and Dierk Raabe[1] — [1]Max-Planck-Institut fuer Eisenforschung, Duesseldorf , Germany — [2]Institut fuer Polymerwissenschaften; JUK Linz, Austria

The exoskeleton of crustaceans is a structural entity which has to be replaced frequently by the organisms in order to grow. Its various morphologically distinct parts have to fulfill a multitude of different functions like providing mechanical stability to the body, acting as a barrier to the environment, enable movement through the formation of joints and bearing both external loads as well as internal loads caused by attached muscles. To adjust the mechanical properties to the required task, the animals vary the basic cuticle structure through modifications in microstructure like number and thickness of the chitin-protein fibre layers and the amount of incorporated biomaterials as well as the use of different proteins with distinct properties. This study focuses on articulations in the limps of H. americanus, where elaborate joint structures between segments provide mobility to enable locomotion. Joint structures require different mechanical properties than simple load bearing cuticle parts or the soft arthrodial membranes. We chose hinge and pivot joints in the claws to investigate their microstructure, composition and mechanical properties using electron microscopy, Energy-Dispersive X-Ray Analysis, Raman spectroscopy and SFM. The results are compared to previous studies conducted on mineralized cuticle and arthrodial membranes of H. americanus.

BP 3: Statistical Physics in Biological Systems I (joint session DY/BP)

Time: Monday 11:00–13:00 Location: ZEU 255

See program DY 2

BP 4: Cell Mechanics

Time: Monday 14:30–17:00 Location: HÜL 186

BP 4.1 Mon 14:30 HÜL 186

Stem Cell Cytoskeleton Polarization Dictated by Matrix Elasticity - Modelling Cellular Biomechanics with Force Dipoles — •Florian Rehfeldt[1,2], Assaf Zemel[3], Andre E.X. Brown[1], Allison L. Zajac[1], Samuel A. Safran[4], and Dennis E. Discher[1] — [1]University of Pennsylvania, Philadelphia, USA — [2]III. Physikalisches Institut, Georg-August-Universität, Göttingen, Germany — [3]Hebrew University, Jerusalem, Israel — [4]Weizmann Institute of Science, Rehovot, Israel

Biological cells are as responsive to their mechanical environment as they are to biochemical stimuli. As reported recently, human mesenchymal stem cells (hMSCs) plated on collagen-coated gels, differentiated towards the neurogenic, myogenic, and osteogenic lineage, depending on the Young's elastic modulus *E*. We present experimental data and a physical model to explain the non-monotonic dependence of stress-fibre polarization on matrix elasticity. Cytoskeletal organization is analyzed with immunofluorescence images of NMM IIa and actin using an automated segmentation algorithm. The theory generalizes Eshelby's treatment of elastic inclusions in solids to living inclusions (cells) that are capable of building up contractility. Their active polarizability, analogous to the electrical polarizability of non-living matter, results in the feedback of cellular forces that develop in response to matrix stresses. We demonstrate experimentally that matrix rigidity dictates cytoskeletal organization in two and three dimensional environments - a bio-mechanical process yielding different cell shapes that finally leads to lineage specific differentiation.

BP 4.2 Mon 14:45 HÜL 186

Force-induced movement of focal adhesions — •Benedikt Sabass[1,2], Sergey V. Plotnikov[3], Clare Waterman[3], and Ulrich S. Schwarz[1,2] — [1]University of Heidelberg, Bioquant 0013, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [2]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany — [3]National Institutes of Health, Bethesda, Maryland 20892-8019NIH, USA

Adhesion and migration of tissue cells in the extracellular matrix is based on the localization of integrin adhesion receptors into so-called *focal adhesions*, where biochemical and mechanical signals are integrated to determine the cellular response. We have performed high resolution traction force microscopy measurements on fibroblasts to compare the magnitude of transmitted traction with the intensity of the fluorescently labeled cytoplasmic adhesion protein paxillin. We find that the ratio between traction and paxillin fluorescence is highest at the distal side of focal adhesions. The force at focal adhesions can also induce their movement. Analysis of the dynamical behavior of sliding adhesions revealed three characteristic regimes: stationary adhesion, creeping with force transmission and slipping without force transmission. We evoke simple physical models to qualitatively explain these three regimes.

BP 4.3 Mon 15:00 HÜL 186

The compaction of gels by cells: a case of collective mechanical activity — •Pablo Fernandez and Andreas R. Bausch — E27 Zellbiophysik, Technische Universität München, D-85748 Garching, Germany

With our growing understanding of force generation and transduction in biological systems, mechanics is acquiring the status of an organising principle connecting tissue architecture to single cell shape and phenotype. To understand mechanotransduction, purely mechanical phenomena resulting from the crosstalk between contractile cells and their elastic surroundings must be distinguished from adaptive responses to mechanical cues. Here, we revisit the compaction of freely suspended collagen gels by embedded cells (osteoblasts and fibroblasts), an amazing process where a small volume fraction of cells compacts the surrounding matrix by two orders of magnitude. We find it to be crucially determined by mechanical aspects. Gel compaction results from an anisotropic deformation following the mechanical anisotropy at the gel boundaries. The existence of a critical cell density shows the effect to be cooperative, revealing a mechanical interaction between cells. As a consequence of the nonlinear properties of biopolymer gels, the large deformations imposed by the cells irreversibly compact the matrix and render it anisotropic. This intricate interplay between contractility and matrix mechanics provides a robust structure-follows-shape principle with implications for the formation of tissues, and raises questions as to the nature of adaptive cytomechanical responses.

BP 4.4 Mon 15:15 HÜL 186

ATP dependent nonequilibrium mechanics of red blood cells — •Timo Betz, Martin Lenz, Jean-François Joanny, and Cécile Sykes — Institut Curie, UMR CNRS 168, 11 rue Pierre et Marie Curie, 75248 Paris, France

Red blood cells are extremely elastic objects, able to recover their shape even after large deformation as when passing through tight capillaries. The reason for this exceptional properties is found in the composition of the RBC membrane and its interaction with the spectrin cytoskeleton. We investigate the mechanics of the RBC membrane by a novel noninvasive technique that allows for the measurement of the fluctuation amplitudes with μs time and sub nm spatial resolution. This technique was used to determine the internal viscosity and the membrane bending modulus of normal red blood cells. We show that the mechanics do highly depend on the interaction between the membrane and the spectrin cytoskeleton which was altered by inhibition and activation of the 4.1 R proteins that connects the spectrin cytoskeleton with the membrane. Our results show that on short timescales (faster 100ms) the fluctuation are excited exclusively by thermal energy, whereas at timescales longer than 100ms an active energy that we contribute to the ATP consuming phosphorylation of the 4.1R protein can be measured. Hence at high frequencies, RBC membrane fluctuation can be described by thermodynamic equilibrium, whereas at longer timescales an active energy should be considered.

BP 4.5 Mon 15:30 HÜL 186

A Biomechanical Perspective on Cancer: From cell line to primary cells — •Kenechukwu David Nnetu, Franziska Wetzel, and Josef Käs — University of Leipzig, Institute of Experimental Physics I, Leipzig

Cancer being a fatal illness in the case of metastasis has been the subject of considerable scientific research. A vivid understanding of the microscopic changes within a cell leading to the initiation, development and spread of this disease is vital to the diagnosis and treatment of the disease. The cytoskeleton of living cells behaves non-linearly by amplifying microscopic changes within the cells. These cytoskeletal changes affect cellular structures and as a result cellular functions. The cytoskeleton being the main contributor to cell mechanics allows for the probing of cell elasticity with a suitable device such the Microfluidic optical stretcher as in this case.

We therefore, report on the mechanical properties of non-tumorigenic, tumorigenic, metastatic cell lines and primary cells. It was found out that metastatic cell lines were softest while malignant but non-metastatic cell lines were softer compared to non-tumorigenic cell lines. Additionally, cell lines were found to be softer than primary cells. Furthermore, metastatic cell lines were found to be the fastest proliferating cell lines while the malignant but non-metastatic cell lines were faster compared to the non-tumorigenic cell lines. Finally, by using cytochalasin D and jasplakinolide which disrupts and stabilizes actin respectively, the cell lines were found to be softer. The cell lines were also treated with the chemotherapeutic drug taxol.

15 min. break

BP 4.6 Mon 16:00 HÜL 186

Integrin expression increased contractile force generation that regulate cell invasion and tumor outgrowth — •Claudia Mierke[1], Martina Fellner[1], Benjamin Frey[2], and Martin Herrmann[2] — [1]Universität Erlangen, Department für Physik, LS für Physikalisch-Medizinische Technik — [2]Universitätsklinikum Erlangen, Innere Medizin 3, Erlangen, Germany

The process of metastasis formation includes cell invasion that causes malignant progression of tumors. The role of cell mechanics on the malignancy of tumor cells has not been investigated systematically. Highly-invasive tumor cells expressed significantly higher amounts of the a5b1 integrin compared to weakly-invasive. We hypothezise that high-a5b1 expressing cells increase contractile force generation that increased cell invasion into a collagen matrix. Our results show that high a5b1 integrin expression increased cell invasiveness and increased the contractile force generation. Whether the increased contractile force generation is a prerequiste for enhanced cell invasiveness, we inhibited the invasiveness through blocking of the myosin light chain kinase by ML-7 or ROCK kinase by Y27632. Indeed, the reduction of contractile force decreased the cell invasiveness. Furthermore, we analyzed whether high-a5b1 and low-a5b1 cells formed tumor in nude mice. The tumor formation/ growth is impared in high-a5b1 compared to low-a5b1 cells. The integrin a5b1 acts as enhancer of cell invasiveness where contractile forces are necessary to overcome the viscous drag, but as suppressor of primary tumor formation/ growth where increased motility is rather a hindrance for cell clustering to form solid tumors.

BP 4.7 Mon 16:15 HÜL 186

High-Resolution Measurements of Cellular Contractile Forces — •Florian Schlosser[1], Florian Rehfeldt[1], Daisuke Mizuno[2], and Christoph Schmidt[1] — [1]3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen — [2]Organization for the Promotion of Advanced Research, Kyushu Univ., 812-0054, Fukuoka, Japan

Biological cells constantly communicate with their surroundings. Besides their well-characterized biochemical interactions, cells also use physical interactions. Cells sense external forces, and they actively probe the mechanical properties of their environment with contractile forces generated by their actin/myosin cytoskeleton. Using a dual optical trap, we have performed high-resolution measurements of the forces a cell generates between two fibronectin-coated beads. We have monitored the fluctuations of the beads at high spatial and temporal resolution and have analyzed the correlated motions. This approach allows us to measure simultaneously the total force cells generate between the two beads and the fraction of force transmitted to the environment. We present data of different cells attached to beads trapped with different stiffness, demonstrating that the generated forces depend on the elasticity of their environment.

BP 4.8 Mon 16:30 HÜL 186

Contribution of cytoskeletal components to the nonlinear rheology of cells — •Navid Bonakdar[1], Philip Kollmannsberger[1], Karen Kasza[2], and Ben Fabry[1] — [1]Center for Medical Physics and Technology, Biophysics Group, Dept. of Physics, University of Erlangen-Nuremberg, Erlangen, Germany — [2]School of Engineering and Applied Sciences, Harvard University, Cambridge, Mass., USA

The rheology of cells is governed by a creep or stress relaxation response that follows a weak power law over several decades in time, and a highly nonlinear stress-strain relationship, in particular a pronounced stress stiffening. In model cytoskeletal networks, stress stiffening is strongly increased in the presence of filamin A (FLNa), an F-actin crosslinker with the ability to unfold under force. The role of FLNa for the nonlinear rheology of living cells has so far not been characterized. We compared the stiffening response of a FLNa-deficient melanoma cell line (M2) and a variant stably transfected with FLNa (A7). Cell deformations in response to stepwise increasing forces applied to membrane-bound magnetic beads were analyzed using a non-linear superposition model to dissect stress relaxation from stress-stiffening responses. While stiffness and bead binding was reduced in FLNa-deficient cells, there was no difference in the degree of stress stiffening, indicating that contributions from other cytoskeletal components mask the effect of FLNa. The role of actin filaments, microtubules, intermediate filaments and myosin-generated cellular prestress in FLNa expressing and deficient cells was examined by pharmacological interventions.

BP 4.9 Mon 16:45 HÜL 186

Optical Cell Stretching and Cell Squeezing — •Tobias Kiessling, Franziska Wetzel, Karla Müller, Anatol Fritsch, K. David Nnetu, and Josef Käs — University of Leipzig

Rheological measurements on single cells are in general considered to be important for the understanding of living organisms. Determined by the cytoskeleton, the mechanical response provides an insight to the molecular structure and reflects the healthiness of each single cell. For biomechanical measurements, the Optical Cell Stretcher, a tool generating optical surface forces on single cells is of great importance since it provides a noninvasive access to the viscoelastic behavior of about 100 single cells per hour. The induced surface forces tend to stretch the cell and by applying optically induced step-stress experiments on single cells, an intimately relation between deformability and malignancy is revealed. With a slight change of setup paramters optical surface forces can be redistributed leading to a squeezed-like deformation instead of a stretch, and enabling various applications such as frequency dependent single cell rheology.

BP 5: Proteins

Time: Monday 14:30–17:00 Location: ZEU 260

BP 5.1 Mon 14:30 ZEU 260

Self-assembly of peripheral membrane proteins to higher-order structures — •Gernot Guigas and Matthias Weiss — Cellular Biophysics Group, Deutsches Krebsforschungszentrum, Bioquant Center, Im Neuenheimer Feld 267, 69120 Heidelberg

Membrane proteins take part in a plethora of processes that are of vital importance for cells, e.g. signaling, vesicle formation, or protein translocation. In these processes not only transmembrane proteins are of major importance but also peripheral membrane proteins (which are embedded only in one leaflet of the lipid biayer) are involved. Using dissipative particle dynamics (DPD), we have studied generic properties of peripheral membrane proteins. Owing to the local deformation of the leaflets of the bilayer we observed a transient oligomerization of the proteins embedded in the same and/or opposing leaflets. Moreover, the diffusive mobility of these inclusions was slightly increased as compared to transmembrane proteins. Our results may explain the transient formation of gramicidin channels and the eole/function of peripheral membrane proteins in budding events.

BP 5.2 Mon 14:45 ZEU 260

The Kinetics and Structure of Protein Energy Landscapes — Michael Prentiss[1], •David Wales[2], and Peter Wolynes[1] — [1]University of California, San Diego USA — [2]Cambridge University, UK

The complexity of the physical interactions that guides the folding of biomolecules presents a significant challenge for atomistic modeling. Minimal representation protein structure prediction potentials have previously been used to predict protein structure from sequence. The resulting landscapes suggests the actual protein energy landscapes are funneled as predicted from theory. We show how basin-hopping global optimisation can identify low-lying minima for the corresponding mildly frustrated energy landscapes. Further more we calculate several disconnectivity graphs for the folding reaction a protein using a database of minima and transition states. Using these databases we calculate the diffusion of the polypeptide change as a function of an native contacts.

BP 5.3 Mon 15:00 ZEU 260

influence of external electrical fields on the protein folding process — •Ojeda May Pedro and Garcia R. Martin E. — Heinrich-Plett- Strasse 39, 34132 Kassel

We show that an external electric field can be used to modify the fold-

ing path of the peptide V3-loop, Protein Data Bank ID 1NJ0. We employ a force field which includes explicitly the dipole-dipole interactions as an Ising-term [PRL **96**, 078103, 2006]. The external electric field interacts with the dipoles. The density of states (DOS) employed to calculate the thermodynamical properties, is obtained by means of a re-weighted histogram method. In the absence of the field the dipoles can be oriented in any direction and the total free energy is minimized by a β-sheet. On the other hand, in the presence of the field an easy direction is created and the dipoles tend to be parallel to the field giving rise to a helix structure.

BP 5.4 Mon 15:15 ZEU 260

Sequence-specific size, structure, and stability of tight protein knots — •Joachim Dzubiella — Physik, TU München

Approximately 1% of protein structures display knots in their native fold. Nothing however, is known about their function. By using all-atom computer simulations we show that tightened protein knots (TPKs) exhibit a bulky size in quantitative agreement with recent atomic force microscopy (AFM) pulling and a complex stability behavior. TPKs are thus capable of blocking peptide transport through narrow (˜ 2 nm) biological pores in a sequence-dependent way. Hydrophobic side chains shield the knot core from the polar solvent, leading to an exceptionally strong H-bonding and water trapping capability of TPKs. This kinetically arrests knot diffusion along the peptide, and is controllable by the tightening force in special cases. Intriguingly, macroscopic tight knot structures are reproduced microscopically and can be tuned by sequence. Our findings may explain a function of knots in proteins, challenge previous mathematical and physical studies of macromolecular knots, and are readily verifiable in AFM or optical tweezer experiments.

BP 5.5 Mon 15:30 ZEU 260

Hydration and Temperature dependent far-infrared Investigations on Proteins — Christian U. Stehle, Wasim Abuillan, •Bruno Gompf, and Martin Dressel — 1. Physikalisches Institut, Universität Stuttgart

Besides the well studied mid-infrared region with sharp absorption bands, little work has been done on proteins in the far-infrared, where they have several broad absorption bands. Extensive investigations on proteins with a high reproducibility and defined temperature/humidity have been made from 65cm-1 to 690cm-1. Several bands in the spectra of different proteins have been found in comparison to the featureless THz studies, where a protein distinction is not possible up to now. We identified the basic absorption frequencies and found at least one band that seems to be common in all proteins, which is not one of the known amide bands. Via the sorption isotherm equation the protein hydration process could be quantified and compared to the spectra, which show just small hydration dependence. This reveals that protein bound water molecules absorb much less and different than liquid water molecules. The temperature dependence shows a strong over all decrease of absorption with rising temperature. An additional frequency dependent effect especially of the low frequency band around 200cm-1 has been found.

15 min. break

BP 5.6 Mon 16:00 ZEU 260

Investigating The Protein Conducting Channel SecYEb from Methanococcus jannaschii Using Molecular Dynamics Simulation — •Andrew Aird and Jörg Wrachtrup — 3rd Physics Institute, Stuttgart University, D-70569 Stuttgart, Germany

Protein translocation, the transport of a protein through a pore is of great importance for all living organisms. It is essential for cells to have membrane channels which are able to transport proteins to different compartments inside the cell where they are needed. An example for such a channel is the protein conducting channel SecYEb from Methanococcus jannaschii. Molecular dynamics simulations are performed to understand the overall mechanism of protein transport across the membrane and address questions concerning the opening mechanism and sealing of the pore region against water and ions. Translocation processes usually take place on timescales (˜ms) not accessible to standard molecular dynamics simulation. By using steered molecular dynamics simulation to accelerate the opening process together with statistical analysis using fluctuation theorems the potential of mean force for removal of the plug is obtained.

BP 5.7 Mon 16:15 ZEU 260

Influence of solvent particles on molecular recognition — •Johannes Taktikos and Hans Behringer — Fakultät für Physik, Universität Bielefeld, D-33615 Bielefeld

We present a coarse-grained lattice model to study the influence of water on the recognition process of two rigid proteins. The basic model is formulated in terms of the hydrophobic effect. We then investigate several modifications of our basic model showing that the selectivity of the recognition process can be enhanced by considering the explicit influence of single solvent particles. When the number of cavities at the interface of a protein-protein complex is fixed as an intrinsic geometric constraint, there typically exists a characteristic fraction that should be filled with water molecules such that the selectivity exhibits a maximum. In addition the optimum fraction depends on the hydrophobicity of the interface so that one has to distinguish between dry and wet interfaces.

BP 5.8 Mon 16:30 ZEU 260

High Quality Protein Sequence Alignment combining Structural Profile Prediction and Structural Profile Alignment with SABERTOOTH — Florian Teichert[1], •Jonas Minning[1], Ugo Bastolla[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Germany — [2]Centro de Biología Molecular 'Severo Ochoa', CSIC-UAM, Madrid, Spain

To discover evolutionary and functional relationships between proteins by alignment is a major issue in various fields. In many cases, protein structures are not known and one has to rely on aligning protein sequences. Here, we combine (i) a recently developed ansatz to predict structural profiles from sequence with (ii) our structural alignment algorithm SABERTOOTH which is based on structural profiles [1]. Comparing the performance of the resulting sequence alignment algorithm with established tools, we prove a significantly higher quality of the determined alignments evaluated from a structural point of view.
[1] F. Teichert, U. Bastolla, and M. Porto, BMC Bioinformatics **8**, 425 (2007)

BP 5.9 Mon 16:45 ZEU 260

DNA-protein electrostatic recognition: lessons from the Protein Data Bank analysis of DNA-protein complexes — •Andrey Cherstvy — IFF, Theorie-II, FZ Jülich, 52425 Jülich, Germany

We study the details of charge distributions on DNA-binding domains of some DNA-binding proteins. This is a continuation of our research on facilitated protein diffusion on DNA and the mechanism of DNA-protein charge-charge recognition [AC et al., JPCB, 112 4741 (2008)]. We show that relatively large structural proteins of eukaryotes and prokaryotes, which involve DNA wrapping around protein cores and induce severe bends in DNA structure, do obey the theoretical model we proposed. Namely, positively charged protein residues in close proximity of DNA prefer to track the positions of individual DNA negative phosphate charges [AC, submitted to JPCB]. To show this, we have used the computational algorithm for dealing with atomic coordinates of protein amino acids and DNA phosphates available from the Protein Data Bank files for a variety of crystallized DNA-protein complexes. The specificity of amino acid distribution observed contributes to the sequence-specific DNA-protein electrostatic interactions. For the majority of DNA-protein complexes, the latter are however considered in the literature to be rather nonspecific to DNA bp sequence. For many simple/small DNA-protein complexes involving basic motifs of protein binding to DNA, we could not detect any statistical preference in distributions of positive atoms on Arginine and Lysine in DNA vicinity.

BP 6: Statistical Physics in Biological Systems II (joint session DY/BP)

Time: Monday 14:00–16:45 Location: HÜL 386

See program DY 4

BP 7: Poster I

Time: Monday 17:45–20:00 Location: P3

BP 7.1 Mon 17:45 P3

Self Assembled Asymmetric Lipid Bilayers in Microfluidic Channels — •Shashi Thutupalli[1], Ralf Seemann[1,2], and Stephan Herminghaus[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Experimental Physics, Saarland University, Saarbrücken, Germany

Biological lipid membranes are predominantly asymmetric. In the plasma membranes of eukaryotic cells, for example, there is an abundance of phosphatidylcholine and sphingomyelin in the outer leaflet while aminophospholipids are primarily in the cytosolic leaflet. The biological importance of asymmetric lipid bilayers has motivated many studies using model systems, such as planar bilayers, supported bilayers, and vesicles. However, there are numerous experimental difficulties regarding such model asymmetric bilayer systems, in particular studying membrane proteins and ion channels. Here we report a highly robust method to simultaneously form many asymmetric bilayers using gel emulsions generated in a microfluidic channel. Liposomes included inside a droplet of water in an external phase of oil reach the oil-water interface to form a lipid monolayer. Such droplets, comprising different lipid monolayers, are brought together to form asymmetric lipid bilayers at the droplet interfaces. Significant advantages in our system are the monodispersity of the membranes thus formed and the ability to simultaneously form symmetric and asymmetric membranes bounding the same droplet. Further, we present electrical characterization of these membranes and demonstrate ion conduction via the incorporation of the ion channel Gramicidin A into these membranes.

BP 7.2 Mon 17:45 P3

Scanning Fluorescence Correlation Spectroscopy on Membranes — •Jonas Ries, Salvatore Chiantia, Rachel Yu, and Petra Schwille — Biotec, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

When confocal fluorescence correlation spectroscopy (FCS) is applied on membranes, long measurement times are required and instabilities, photobleaching or poor knowledge of the detection area limit the accuracy. Here we present two implementations of scanning FCS (SFCS) to circumvent these problems. Scanning FCS with a scan path perpendicular to the membrane plane is robust against instabilities and allows for very long measurement times, which are required to study slow diffusion. It can be extended to measure calibration-free diffusion constants with scanning two focus FCS and to quantify binding on the membrane with scanning dual color FCS with alternating excitation. We applied this method to study the affinity of the Fgfr1(4) to its ligand Fgf8 in the membranes of living zebra fish embryos. Line-scan FCS with a scan path parallel to the membrane plane greatly increases the statistics by parallel acquisition. It allows for calibration-free diffusion and concentration measurements on membranes within seconds and is virtually not affected by photobleaching. Both approaches can be easily implemented with commercial laser scanning microscopes and allow for quantitative measurements in demanding systems previously not accessible by FCS.

BP 7.3 Mon 17:45 P3

Diffusion of single actin filaments bound to cationic lipid membranes — •Lydia Woiterski, Florian Rückerl, Josef A. Käs, and Carsten Selle — Institut für Exp. Physik I, Linnéstraße 5, 04103 Leipzig

Actin is one major component 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 cell motility. It is associated with the inner leaflet of the cell membrane via protein anchors. Recent studies show that there is a close interplay between the structure of the cytoskeleton and the membrane composition [1]. A model system which mimics the unspecific interactions of cytoskeleton and cellular membranes are actin filaments bound to inhomogeneous lipid membranes. First, the diffusion of single actin filaments adhered to cationic planar membranes will be studied using single polymer tracking. The membranes used are composed of DPPC, DOPC, cholesterol, and the cationic lipid DOTAP and the binding is driven by Manning condensation. Under certain conditions, these liquid membranes show coexistence of ordered and disordered phases. We propose that actin binding can be regulated by the phase state and that preferential binding to one of the coexistent phases occurs due to varied surface charge density. Our aim is a better understanding of how the polymer motion at the membrane can be modulated and the diffusion can be controlled by changing the energy landscape, e.g. by domain sizes and shapes.

1. Kwik, J.et al., PNAS, 2003, 100, p.13964.

BP 7.4 Mon 17:45 P3

Curvature-coupled protein diffusion in a fluctuating model membrane — •Stefan Leitenberger, Ellen Reister-Gottfried, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart

The influence of an interaction between a protein and a fluctuating membrane on the dynamics of the system is analyzed. The energy is given by the Helfrich Hamiltonian in Monge-representation with a correction for the inserted protein. We derive coupled equations of motion for the membrane dynamics and the projected diffusion of the inclusion that are nummerically integrated in our simulation scheme.

In our model the influence of the protein-membrane interaction on the membrane dynamics modifies the height correlation function of the membrane. Two time regimes reflect the different time scale of membrane fluctuations and that of protein diffusion.

The effective lateral diffusion coefficient of the protein is also affected by the curvature-coupling. The resulting coefficient determined by our simulations is smaller than the free diffusion coefficient of the protein. This is in contrast to a previous result that neglects the influence of the particle on membrane fluctuations and shows enhanced diffusion. The analysis of the correlation functions contributing to the mean squared displacement of the protein reveals that the decrease is caused by a strong correlation between the stochastic force on the protein and the response of the membrane to the motion of the protein.

BP 7.5 Mon 17:45 P3

Elucidating structure and domain formation of biomimetic lipid bilayers — •Kristian Boye[1], Gernot Guigas[1], Eszter Molnar[2], Martin Holzer[3], Wolfgang Schamel[2], and Matthias Weiss[1] — [1]DKFZ - German Cancer Research Center, Heidelberg, Germany — [2]Max Planck Institute for Immunobiology, Freiburg, Germany — [3]Institute of Pharmaceutical Sciences, University of Freiburg, Germany

Membrane domains - also known as lipid rafts - are believed to be central to various functions of the cell, including signal transduction, lateral sorting, pathogen recognition and internalization processes. While the nature and stability of these domains in the living cell is still highly controversial, model membrane systems, such as giant unilamellar vesicles (GUVs), allow a direct observation of large, optically resolvable domains that result from the coexistence of two or more lipid phases.

We have used confocal fluorescence microscopy and fluorescence correlation spectroscopy to investigate the spatial and dynamic organization of lipids in artificially produced GUVs with lipid compositions mimicking that of the endoplasmic reticulum and that of the plasma membrane of T cells. In both cases, we observe domain formation and, in part, the formation of buds and tubules. We moreover have evidence that specific transmembrane protein complexes, like the one formed by the T cell receptor, partition into specific lipid subphases.

BP 7.6 Mon 17:45 P3

Influence of Tension on Coarse-Grained Model Membranes — •Jörg M. Neder[1], Beate West[2], Friederike Schmid[2], and Peter Nielaba[1] — [1]Department of Physics, University of Konstanz, 78457 Konstanz — [2]Department of Physics, University of Bielefeld, 33615 Bielefeld

Using a recently developed generic coarse-grained model for lipid bilayers [1] we investigate the effect of an applied tension on these systems at different temperatures. The recorded pressure profiles of the systems are consistent with the external tension. We observe a lowered extensibility of the bilayer in the gel phase compared to the fluid phase. In the region of the phase transition, where our system is in the ripple phase, both regimes of area compressibility are present: the fluid-like behavior for lower tensions and the gel-like decreased extensibility at higher tensions. The effect of laterally lowered pressure on properties of simple model proteins and the surrounding bilayer is examined. Further, the influence of tension on the effective interaction potential of

two cylindrical inclusions (cf. [2]) is analyzed via umbrella sampling. An extension of the elastic theory presented in [3] is used to fit fluctuation spectra of both height and thickness of stressed membranes.

[1] O. Lenz and F. Schmid, *Phys. Rev. Lett.* **98**, 058104 (2007)
[2] B. West et al., *Biophys. J.*, doi:10.1529/biophysj.108.138677 (2009)
[3] G. Brannigan and F. H. L. Brown, *Biophys. J.* **90**, 1501 (2006)

BP 7.7 Mon 17:45 P3

Dynamics of vesicle adhesion through a polymer cushion: role of layer thickness and tension — •Kheya Sengupta[1] and Laurent Limozin[2] — [1]CINAM/CNRS-UPR3118, Marseille, France — [2]INSERM UMR 600 - CNRS UMR 6212, Marseille, France

The adhesion of giant unilamellar phospholipid vesicles to planar substrates coated with extra-cellular matrix mimetic cushions of hyaluronan is studied using quantitative dual wavelength reflection interference contrast microscopy (DW-RICM). The thickness of the cushion is varied in the range of about 50 to 100 nm, by designing various coupling strategies. On bare protein coated substrates, the vesicles spread fast (0.5 sec) and form a uniform adhesion-disc, with the average membrane height about 4 nm. On thick hyaluronan cushions (>80 nm), the vesicle sits on the top of the cushion and spreading is totally prevented. On a thin and inhomogeneous cushion, the adhesion is modified but not totally impeded. The spreading is slow (˜20 sec) compared to the no-cushion case. We show that in addition to the quality of the cushion, the initial tension of the vesicles plays a crucial role in the spreading kinetics. We interpret our experimental results in the light of a theoretical framework which integrates the influence of polymers on the membrane-surface interaction potential on one hand and the role of this potential in the spreading kinetics on the other hand. We conclude that the slow kinetics arises partially from a reduction in the adhesion-strength but the main contribution comes from the increased viscosity in the presence of the polymer.

BP 7.8 Mon 17:45 P3

Artificial Chloroplasts from Giant Unilamellar Vesicles — •Jakob Schweizer and Petra Schwille — Biotechnologisches Zentrum, TU Dresden, Tatzberg 47-51, 01307 Dresden

Giant unilamellar vesicles (GUVs) serve as a minimalistic model system for biological cell membranes. However, they are also an ideal tool to reconstitute membrane-associated sub-cellular structures, in order to mimick intracellular processes under defined conditions. Here we present a way to construct a rudimentary energy-producing active membrane from purely biological raw materials using 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 for which the functionality of both proteins is tested individually. 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 7.9 Mon 17:45 P3

Fast algorithm for determinating the equilibrium configuration of a cable network model describing the actin cytoskeleton — •Karsten Schwarz and Heiko Rieger — Theoretical Physics, Saarland University, D-66041 Saarbrücken

The propagation of mechanical stress through the actin cytoskeleton is studied with a cable network model [1,2]. Cables represent actin filaments connecting two nodes of a network and exerting a specific force F on the two nodes, which depends only on the distance l between them: $F(l) = 0$ for $l \leq l_r$ and $F(l) = c \cdot (\frac{l}{l_r} - 1)$ for $l > lr$ (l_r is the rest-length of the cable). Some of the nodes are fixed, representing focal adhesions, the others arranging themselves according to the resulting force balances into an equlibrium configuration. Typical model networks comprise more than 10^5 nodes making the determination of their equilibrium configuration numerically hard. We map the force balance problem onto a convex optimization problem and present a method to solve this to arbitrary precision in polynomial time. We discuss applications of our method to modelling the migration of adhering cells. [1] Coughlin et al. Biophys.J. 84:1328-1336 (2003) [2] Paul et al. Biophys.J. 94:1470-1482 (2008)

BP 7.10 Mon 17:45 P3

Active chiral gels — •Sebastian Fürthauer, Stephan Grill, and Frank Jülicher — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden, Germany

Many different physical systems display intriguing chiral phenomena, such as the handedness of biomolecules. Here we study consequences of chirality in the actomyosin cortical layer that underlies the membrane of eukaryotic cells. The theory we develop is an extension of the formalism of active polar gels to an active chiral material. We obtain the most general set of linear equations describing the large length and long time-scale dynamics of the gel, by using only conservation laws and symmetries of the system. Finally, we discuss chiral flow and polarity profiles that can emerge spontaneously in such systems.

BP 7.11 Mon 17:45 P3

Cytoskeletal filament length regulation by length-dependent depolymerisation rates — •Christoph Erlenkämper and Karsten Kruse — Theoretical Physics Department, Universität des Saarlandes, Saarbrücken, Germany

In living cells, the length distribution of cytoskeletal filaments often shows a sharp maximum at a finite value. This is in contrast to unregulated polymer growth, which typically leads to exponential distributions. We discuss a simple mechanism by which destabilizing proteins lead to effectively length-dependent disassembly rates. This mechanism produces sharply peaked steady-state distributions.

BP 7.12 Mon 17:45 P3

Dynamics of formin promoted actin polymerization — •Carsten Schuldt, Brian Gentry, Dan Strehle, and Josef A. Käs — Universität Leipzig, Germany

In vivo the semiflexible polymer actin is found as a single filament or is organized in networks and bundles. These structures contribute to the cytoskeleton, whose inherent properties determine the cell's morphology, both mechanically and functionally, and facilitate motility via protrusions and contractions. The assembly of some cytoskeletal actin bundles (contractile ring, filopodia) far from thermodynamic equilibrium is driven by a multi-domain protein called formin. This 'leaky capper' is known to remain bound to the growing ends of filaments and is capable of accelerating the polymerization rate.

We employ an optical tweezer setup in interaction with functionalized microbeads to measure formin's stall force and step size in vitro. Determinig the stall force will yield further insight into formin's ability to produce forces from biochemical energy. In particular, formin may be able to override the force limit of normal actin polymerization. The application of the sophisticated force clamp technique seems to be an apropriate technique to measure step size and examine the behavior of formin with and without external applied tension.

BP 7.13 Mon 17:45 P3

Self-organization of Dynein Motors Generates Meiotic Nuclear Oscillations — Sven Vogel[1], •Nenad Pavin[2,3], Nicola Maghelli[1], Frank Jülicher[2], and Iva Tolic-Norrelykke[1] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden 01307, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden 01187, Germany — [3]Department of Physics, Faculty of Science, University of Zagreb, Zagreb 10002, Croatia

Meiotic nuclear oscillations in the fission yeast Schizosaccharomyces pombe are crucial for proper chromosome pairing and recombination. We report a mechanism of these oscillations based on collective behavior of dynein motors linking the cell cortex and dynamic microtubules that extend from the spindle pole body in opposite directions. By combining quantitative live cell imaging and laser ablation with a theoretical description, we show that dynein dynamically redistributes in the cell in response to load forces, resulting in more dynein attached to the leading than to the trailing microtubules. The redistribution of motors introduces an asymmetry of motor forces pulling in opposite directions, leading to the generation of oscillations. Our work provides the first direct in vivo observation of self-organized dynamic dynein distributions, which, due to the intrinsic motor properties, generate regular large-scale movements in the cell.

BP 7.14 Mon 17:45 P3

Dependence of Eg5Kin force production on monastrol — •André Düselder, Stefan Lakämper, and Christoph Schmidt — 3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen

In the metaphase of mitosis, chromosomes are lined up in the midplane of the cell by the bipolar mitotic spindle. Tetrameric bipolar members

of the Kinesin-5 family of motor proteins play an important role in the establishment of this spindle. We have previously characterized the motile characteristics of Eg5, the Kinesin-5 from Xenopus laevis, using single-molecule fluorescence and optical-trapping experiments. Surprisingly, we observed a novel slip-clutch force sensing mechanism. It remains unclear whether this mechanism is an intrinsic property of the motor domains themselves or if it is due to regulatory domains residing in the stalk or tail domains.

In order to investigate the motile properties of the force-generating units of Eg5 alone, we constructed a stably dimeric chimera, termed Eg5Kin, consisting of the Eg5 motor domain fused to the stalk of D. melanogaster Kinesin-1. In the presence of increasing monastrol concentrations, we observed a reduction in processive run length, but not speed, of single motors.

To date, there has been no data on how monastrol affects Eg5- or Eg5Kin-motility (speed, stallforce, detaching force) under load. Here, we present results from experiments using single-bead optical-trapping interferometry of single Eg5Kin-motors in the presence of increasing monastrol concentrations.

BP 7.15 Mon 17:45 P3

How molecular crowding speeds up mechanotransduction — •Sebastian Sturm[1], Benedikt Obermayer[2], Andrea Kramer[1], and Klaus Kroy[1] — [1]ITP, Universität Leipzig — [2]ASC & CENS, LMU München

No higher forms of life could exist without the ability of biological cells to quickly sense and react to changes in their environment. In general, stimuli excite the cell membrane and have to be transmitted to the nucleus. Mechano-transduction through the cytoskeleton may arguably provide the fastest pathway for mechanical stimuli. Understanding the dynamics of tension propagation through biopolymer networks is thus an important task.

Our approach combines two recent theoretical developments: (i) a systematic theory of tension propagation in single semiflexible polymers [1]; (ii) the glassy wormlike chain model accounting for the influence of a crowded and sticky environment. Extending our previous work, we present (asymptotic) analytical and numerical solutions to the theory and discuss a reinterpretation of the Glassy Wormlike Chain in terms of force transmission through the background medium.

[1] O. Hallatschek, E. Frey and K. Kroy, Phys. Rev. Lett. 94, 077804 (2005)
[2] K. Kroy and J. Glaser, The glassy wormlike chain. New Journal of Physics, 9(416), 2007.

BP 7.16 Mon 17:45 P3

In vitro assembly and characterization of keratin 8/18 intermediate filaments — •Anke Leitner[1], Norbert Mücke[3], Tatjana Wedig[2], Harald Herrmann[2], Michael Beil[4], and Othmar Marti[1] — [1]Department of Experimental Physics, Ulm University, Ulm, Germany — [2]Division of Molecular Genetics, German Cancer Research Center, Heidelberg, Germany — [3]Division Biophysics of Macromolecules, German Cancer Research Center, Heidelberg, Germany — [4]Department of Internal Medicine I, Ulm University, Ulm, Germany

In order to find out more about the mechanical properties of the keratin cytoskeleton it is usefull to have a look on in vitro assembled keratin filaments. In the work presented here we will show nanomechanical properties of the assembled keratin 8/18 filaments. The investigations are done by means of atomic force microscope (AFM). Two different substrates and ways of sample preparation are used. From the 2-dimensional AFM images we calculate the persistence length of the keratin 8/18 filaments with the worm-like-chain model.

BP 7.17 Mon 17:45 P3

Stiff-filament microrheology — Felix Zörgiebel[1], •Marcel Bremerich[1], Frederick C. MacKintosh[2], and Christoph F. Schmidt[1] — [1]3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen — [2]Department of Physics & Astronomy, Vrije Universiteit , 1081 HV Amsterdam

Active and passive microrheology techniques for probing viscoelastic properties of biological samples require the embedding of micron-sized particles. This can give rise to local perturbations and surface interactions. These effects have to be taken into account during data evaluation and form an obstacle for the investigation of living cells.

A way of circumventing these influences is the use of parts of the system itself, such as the microtubules as local probes by observing their thermal bending fluctuations in the surrounding medium. A detailed analysis of the spatial and temporal bending fluctuations can give information about local shear moduli and stress fluctuations in biopolymer networks in the absence of probe artifacts.

We have investigated a network of filamentous actin by attaching nanometer-sized gold particles to embedded microtubules and have measured thermal motions of the gold particles with an optical trap by laser interferometry with high bandwidth.

BP 7.18 Mon 17:45 P3

Hydrodynamic effects in diffusion-controlled reactions of semiflexible polymers — •Yann von Hansen, Michael Hinczewski, and Roland R. Netz — Physics Dept., Technical Univ. of Munich, Germany

We generalize a mean-field theoretical approach (MFT) for the dynamics of semiflexible polymers [1] that provides insight into the scaling regimes of end-monomer mean squared displacement $\langle r^2(t)\rangle$ examined in recent fluorescent miscroscopy experiments on DNA. It also has been shown to closely agree with Brownian hydrodynamics simulations. The resulting analytical Green's function $G(\vec{r},t)$ for individual monomer motion exhibits excellent agreement with simulations, and can be extended to treat the relative motion of freely diffusing particles and the polymer chain. An understanding of this motion is of fundamental importance for a wide spectrum of processes in biology and chemistry, ranging from protein-DNA interaction to polymerization. Using the MFT we analyze a variety of effects which influence the relative motion, including the hydrodynamic coupling of the internal polymer modes as well as the coupling between the polymer and particle. From these we can extract the overall dependence of the protein-DNA association rate as a function of the polymer contour length L and persistence length l_p. [1] M. Hinczewski, X. Schlagberger, M. Rubinstein, O. Krichevsky, R.R. Netz, arXiv:0809.0667, Macromolecules *in press* (2008).

BP 7.19 Mon 17:45 P3

Microtubules inside out — Jan Kleeblat, Christoph F. Schmidt, and •Iwan A. T. Schaap — 3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen, Germany

Microtubules are protein nano-tubes with a diameter of 25 nm which form a crucial part of the cytoskeleton. During the different states of the cell cycle, microtubules have to rapidly assemble and disassemble. To achieve this microtubules are non-equilibrium polymers with complex mechanical properties. We have here used Atomic Force Microscopy and molecular reconstructions to study the inside of microtubules, unfolded on a strongly adhesive substrate. We found evidence for a mechanical instabilty in the shells from the structure of the adhering sheets.

BP 7.20 Mon 17:45 P3

Imaging microtubule modulating proteins with atomic force microscopy — •Karen Hollenberg, Florian Hagene, Iwan A. T. Schaap, and Christoph F. Schmidt — 3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen

Microtubules have the most complex structure of the filaments forming the cytoskeleton and show alternating phases of growth and shrinkage. These microtubule dynamics are regulated by a variety of microtubule stabilizing and destabilizing proteins that allow the cytoskeleton to adapt to the needs of the cell.

We have set out to use atomic force microscopy in buffer to study how and where such stabilizing proteins bind to the microtubule lattice and compare this to the binding patterns of kinesin motor proteins at a single protein resolution.

BP 7.21 Mon 17:45 P3

Atomic force microscopy of collagen — •Nadine Drechsel, Stephanie Röper, Christian Dietz, and Robert Magerle — Chemische Physik, TU Chemnitz, D-09107 Chemnitz

Type I collagen is a protein material which is a basic constituent of all vertebrates. It can be found in various types of biological tissue, e.g., dermal tissue and bone tissue. We investigate purified collagen isolated from bovine hide which is adsorbed on a mica substrate in buffer solution (L-Glycin/KCl, pH 9,2). Collagen in a buffer solution, in moist air and in the dried state is studied with atomic force microscopy (AFM). For measurements in liquid, the sample is rinsed and imaged in buffer solution, for measurements in air collagen is transferred from the buffer solution to a cleaned mica substrate and subsequently either dried or imaged in moist air. In both cases we find the typical D-band with

a repeat distance of 67 nm. We also performed bimodal AFM measurements; the second flexural eigenmode of the cantilever was used for phase imaging while the amplitude of the first eigenmode was used as feedback signal. On a dried specimen we measured the dissipated energy between AFM tip and a collagen fibril. The results on the collagen fibril prepared from bovine hide are compared with measurements on native cortical human bone.

BP 7.22 Mon 17:45 P3

Optical Tweezer: A system for tracking several beads incorporated in the keratin cytoskeleton of pancreatic carcinoma cells — •Tobias Paust[1], Alexander Schmatulla[1], Ulla Nolte[1], Michael Beil[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, University of Ulm, D-89069 Ulm, Germany — [2]Internal Medicine I, University of Ulm, D-89069 Ulm, Germany

The biophysical and viscoelastic properties of the keratin cytoskeleton have an effect on the ability of migration of the pancreatic carcinoma cells in the extracellular environment. Therefore this project handles about the investigation and characterization of these viscoelastic properties of the keratine networks. With the extraction of the cytoplasmatic elements out of the cell the keratin networks are isolated. This ensures that there are no biochemical interrupts of interactions between the network elements. The method of measurement implies the trapping of a polystyrene sphere and the subsequent movement by the laser light of an optical tweezer. In contact with the cytoskeleton it is possible to determine the mechanical properties of the cytoskeleton by analyzing auto- and crosscorrelation of the trapped bead. A high speed camera was incorporated to measure this spatial response by tracking many particles simultaneously with a time resolution better than 1ms. The first measurements depict the dependency of the response of multiple nanometric spheres on the time variable forces of the cytoskeleton.

BP 7.23 Mon 17:45 P3

Strain stiffening and soft glassy rheology in a generalized sliding filament model — •Philip Kollmannsberger, Claus Metzner, and Ben Fabry — Biophysics Group, Department of Physics, University of Erlangen-Nuremberg

Despite their enormous complexity and structural diversity, most biological materials show a remarkably similar viscoelastic phenomenology: nonlinear elasticity, power-law or logarithmic stress relaxation, and plastic length adaptation. We present a simple model based on Huxley's sliding filament model to demonstrate that such behavior can arise from generic structural properties, independent of the actual molecular constituents of the system. The material is represented by an uniaxial arrangement of parallel elastic elements that have a distribution of attachment angles. When the system is sheared or stretched, elements start to align, leading to strain stiffening due to a geometric recruitment of springs. The elastic elements have force-dependent average lifetimes described by energy traps with a broad distribution of energy trap depths. The elements can reattach at random positions and attachment angles after unbinding. Such nanoscale structural rearrangements lead to viscous flow and plastic length adaptation on a macroscopic scale. The model gives quantitative agreement for creep compliance, stress stiffening and plasticity in the case of cell microrheology. These results suggest that recruitment and dynamic unbinding of elastic elements are the common mechanism underlying the mechanical behavior of many complex biological materials from single cells to whole tissues.

BP 7.24 Mon 17:45 P3

Imaging human bone with bimodal scanning force microscopy — •Stephanie Röper[1], Nadine Drechsel[1], Christian Dietz[1], Anke Bernstein[2], and Robert Magerle[1] — [1]Chemische Physik, TU Chemnitz, D-09107 Chemnitz — [2]Experimentelle Orthopädie, Martin-Luther-Universität Halle-Wittenberg, D-06097 Halle/Saale

Biological materials such as bone and teeth are nanocomposites of a soft organic matrix (type I collagen) that is reinforced by a stiff inorganic component (hydroxylapatite). Our study is focused on cortical human bone. The specimen surface was first mechanically grinded and polished, then 10 s etched with formic acid and finally flushed with methanol to stop the etching process. With optical microscopy and tapping mode scanning force microscopy (TM-SFM) a spot on the specimen was chosen for detailed investigation which displays a lamellar structure in the vicinity of a Haversian canal. TM-SFM images measured in air show collagen fibrils with typical D-bands with 67 nm periodicity. For bimodal TM-SFM the second flexural eigenmode of the cantilever was used for phase imaging while the amplitude of the first eigenmode was used as feedback signal. The second eigenmode phase image revealed an enhanced contrast compared to that of the first eigenmode. In addition we measured the energy dissipated between tip and specimen along a collagen fibril. The results obtained on native human bone were compared with measurements on collagen fibrils prepared from purified collagen isolated from bovine hide.

BP 7.25 Mon 17:45 P3

Surface properties relevant for the adhesion of marine microorganisms — •A. Rosenhahn[1], S. Schilp[1], X. Cao[1], F. Wode[1], M.P. Arpa Sancet[1], M. Heydt[1], M.E. Pettit[2], M.E. Callow[2], J.A. Callow[2], and M. Grunze[1] — [1]Applied Physical Chemistry, University of Heidelberg, 69120 Heidelberg, Germany — [2]School of Biosciences, University of Birmingham, Birmingham B15 2TT, UK

The prevention of biofouling is a major challenge for all manmade objects which are in long term contact with seawater. In order to systematically develop non toxic coatings, a fundamental understanding of basic surface properties relevant for adhesion of marine inhabitants is required. To determine the influence of selected surface properties we systematically vary wetting, hydration and charge by self assembly of oligo- and polymers. To obtain well defined morphologies, nanolithography and self assembled multilayers are used. The biological response is determined in settlement and adhesion strength assays using predominantly the green algae Ulva linza, but also barnacle cyprids and marine bacteria. It turned out that contact angles around the Berg limit, hydration of the coatings and micrometer sized structures render surfaces less attractive. Besides static assays we are interested in the time dependent dynamics of biofilm formation. To acquire and analyze the complex, 3D swimming and exploration patterns of algal zoospores, we apply digital in-line laser holography. The influence of surface properties on the motion patterns as well as specific recognition distances will be discussed.

BP 7.26 Mon 17:45 P3

Protein film formation on hydroxy apatite surfaces — •Christian Zeitz, Frank Müller, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbruecken

The composition and the morphology of initial protein films play an important role in the formation of the so-called pellicle, the intraoral biofilm that builds up on tooth surfaces in contact with saliva. Recently, it has been shown on model surfaces that the chemical composition of the uppermost surface layer of a substrate as well as the subsurface composition determines the function of the pellicle and especially the development of the mature biofilm, including bacteria. The aim is to understand the pellicle formation under variable substrate conditions.

The focus of our study lies on the characterization of such protein films on two different kinds of enamel-like surfaces: fluoridated and unfluoridated hydroxyl apatite. It has been shown [1] that the application of acidic amine fluoride agents changes untreated surfaces not only in the uppermost layer but also affects the composition of the bulk material up to a depth of some hundred nanometers. Furthermore, the chemical composition of the (un-) fluoridated samples as a function of depth can be characterized by XPS-ESCA. Both types of surfaces are exposed to protein solutions. Within minutes, the proteins adsorb building up a biofilm, the morphology of which is characterized by AFM.

[1]: Müller et al., arXiv:0806.1425v1 ,2008

BP 7.27 Mon 17:45 P3

Probing the unfolding behavior of SNase mutants by SAXS — •Martin Schroer[1], Christina Krywka[2], Saskia Schmacke[1], Michael Paulus[1], Roland Winter[3], Catherine Royer[4], Bertrand Garcia-Moreno[5], and Metin Tolan[1] — [1]Fakultät Physik/DELTA, Technische Universität Dortmund, D-44221 Dortmund, Germany — [2]Institut für Experimentelle und Angewandte Physik, Christian-Albrechts-Universität zu Kiel, 24118 Kiel, Germany — [3]Physikalische Chemie I, Technische Universität Dortmund, D-44227 Dortmund, Germany — [4]3 CNRS, UMR5048, Centre de Biochimie Structurale, F-34090 Montpellier, France — [5]Department of Biophysics, Johns Hopkins University, 3400 North Charles Street, Baltimore, MD 21218, USA

Investigating the structure of proteins and their stability is of great interest as it is known that destabilization may lead to protein unfolding, misfolding and aggregation. These effects might be first steps for several diseases such as the Alzheimer disease and prion diseases. In

order to get a deeper insight into this process it is thus necessary to determine how the stability and conformation are changed when the protein's amino acid sequence is altered by point mutations.

In our recent SAXS (small angle x-ray scattering) studies we analyzed the unfolding behavior of different mutants of the model protein Staphylococcal Nuclease (SNase) as a function of temperature and pressure. Depending on the physicochemical properties of the particular amino acid exchanged, the stability of the mutants is altered significantly.

BP 7.28 Mon 17:45 P3

Improving protein structure prediction using sequence-derived structure profiles — •Katrin Wolff[1], Andrea Cavalli[2], Michele Vendruscolo[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, TU Darmstadt, Germany — [2]Department of Chemistry, University of Cambridge, Cambridge, UK

A crucial step in the prediction of protein structures is the transition from low- to high-resolution models. There exist various tools that generate candidate sets that contain high-quality, yet coarse-grained, structures. In a subsequent refinement step these structures are improved to all-atom representations and minimized using a high-resolution energy functional. Due to limited computer time it is vital to restrict this refinement step to promising candidates and to identify the best structures. The energy functional used in the structure generation step, however, is only of limited use for the problem of selecting these 'good' structures. We discuss the use of structure profiles for this filtering step. As a proof of principle we show that the exact profile (derived from the native structure) is very reliable in choosing candidates with low RMSD to the native structure and clearly outperforms other filtering methods like filtering by energy or clustering the decoy set. Such structure profiles can be predicted to good accuracy from sequence [1,2]. We therefore explore the use of profiles as predicted from sequence and show that for sufficiently high accuracy this approach is also superior to the other methods of filtering.

[1] A. R. Kinjo *et al.*, BMC Bioinformatics **7**, 401 (2006).
[2] J. Minning, F. Teichert, U. Bastolla, M. Porto, in preparation.

BP 7.29 Mon 17:45 P3

Langevin-Dynamik-Simulation von Peptiden — Uwe Winter und •Tihamér Geyer — Zentrum für Bioinformatik, Universität des Saarlandes, Saarbrücken

Zwischen den Zeit- und Längenskalen, die jeweils mit Molekulardynamik (MD) und Brownscher Dynamik (BD) beschreibbar sind, klafft eine Lücke von etwa zwei Größenordnungen, in denen MD-Simulationen zu aufwändig sind und bei BD-Simulationen die nötige Auflösung nicht erreicht wird. Wir zeigen, wie durch eine explizite Berücksichtigung des Impulses der Gültigkeitsbereich der BD zu kleineren Zeitschritten hin erweitert werden kann und damit realistische ,,Langevin"-Simulationen kleiner flexibler ,,bead-spring"-Peptide möglich werden. Für eine korrekte und stabile Dynamik darf dabei die viskose hydrodynamische Dämpfung durch den Solvens nicht vernachlässigt werden. Wir vergleichen am Beispiel eines kurzen Peptids von 11 Aminosäuren, welches gegen eine MD-Trajektorie parametrisiert wurde, die jeweiligen Schwierigkeiten und Vorteile von BD- und Langevin-Beschreibung.

BP 7.30 Mon 17:45 P3

Oxygenation interactions of the metalloprotein hemocyanin in aqueous solution revealed by core-level spectroscopy — •Daniel Panzer[1], Christian Beck[2], Jochen Maul[1], Nora Bergmann[3], Gerhard Schönhense[1], Heinz Decker[2], and Emad Aziz[4] — [1]Institut für Physik, Staudinger Weg 7, Johannes Gutenberg-Universität, D-55099 Mainz — [2]Institut für Molekulare Biophysik, Welderweg 26, Johannes Gutenberg-Universität, D-55099 Mainz — [3]Max-Delbrück-Center for Molecular Medicine, D-13125 Berlin-Buch — [4]BESSY GmbH, Albert-Einstein-Strasse 15, D-12489 Berlin

Active metal sites play a key role in the biochemistry of oxygen and particularly in oxygen transport. Hemocyanin (Hc) is a widespread respiratory protein in arthropods and molluscs comprehending multiple copper active sites. Observing the binding, interaction and subsequent reactivity of dioxygen at these hemocyanin copper centres is thus essential for understanding its comprehensive chemical and biological functionality.

Here, we use core-level spectroscopy to measure the copper X-ray absorption structure of hemocyanin in aqueous solution and therewith very similar to physiological conditions. We identify the deoxygenated and the oxygenated state of the native Hc molecule by probing the local electronic structure of the oxygen-active metal centres. Our findings demonstrate an X-ray approach to observe the biochemical activity in an intact metalloprotein molecule and open perspectives for X-ray spectroscopy of complex biomolecules under in vivo conditions.

Funded by the DFG (DE 414/12-1 and SCHO 341/7).

BP 7.31 Mon 17:45 P3

Pebble-game rigidity analysis of protein crystal structures is highly sensitive to small structural variations — •Emilio Jimenez, Stephen Wells, and Rudolf Roemer — Department of Physics and Centre for Scientific Computing, University of Warwick, Coventry CV4 7AL, UK

Rigidity analysis using the "pebble game" can usefully be applied to protein crystal structures to obtain information on protein folding, assembly and the structure-function relationship. However, previous work using this technique has not made clear how sensitive rigidity analysis is to small structural variations. We present a comparative study in which pebble-game rigidity analysis is applied to multiple structures, derived from different organisms and different conditions of crystallisation, for each of several different proteins. It appears that the results are highly sensitive to relatively small structural variations.

We find that rigidity analysis is best used as a comparative tool to highlight the effects of structural variation. We advise caution when using pebble-game rigidity analysis as a coarse-graining method in biophysical modelling of proteins. Our comparative use of multiple protein structures brings out a previously unnoticed peculiarity in the rigidity of trypsin.

BP 7.32 Mon 17:45 P3

The mechanisms of lipid membrane-induced IAPP fibrillogenesis and its inhibition — •Sebastian Tiemeyer[1], Florian Evers[1], Christoph G. Jeworrek[2], Michael Paulus[1], Bernd Struth[3], Metin Tolan[1], and Roland Winter[2] — [1]Faculty of Physics / DELTA, TU Dortmund, 44221 Dortmund, Germany — [2]Faculty of Chemistry, TU Dortmund, 44221 Dortmund, Germany — [3]Deutsches Elektronen-Synchrotron, HASYLAB, Notkestr. 85, 22607 Hamburg, Germany

Protein misfolding plays an important role in many diseases like Alzheimer's, Parkinson's or type 2 diabetes mellitus. In the latter case, IAPP is thought to cause the death of insulin-producing beta-cells in the pancreatic islets of Langerhans. Previous experiments propose aggregation of IAPP to amyloid fibrils at beta-cell membranes followed by membrane disruption. X-ray reflectivity (XRR) experiments were performed at the beamline BW1 at HASYLAB in order to investigate the IAPP - lipid membrane interaction in the presence and absence of the red wine compound resveratrol. From the XRR data, we were able to identify the status of nucleation, aggregation and fibrillation of IAPP at the lipid membrane interface. Furthermore, the inhibition of the aggregation process by resveratrol was revealed.

BP 7.33 Mon 17:45 P3

Tip-enhanced single molecule fluorescence near-field microscopy for nanobiophysics — •Heinrich Gotthard Frey, Jan Paskarbeit, and Dario Anselmetti — Experimental Biophysics and Applied Nanoscience, Fakultät für Physik, Universität Bielefeld, Universitätsstraße 25, 33615 Bielefeld

For nanobiophysical applications, scanning near-field optical microscopy (SNOM) of single fluorescent dye molecules must combine high electrical field intensities in the sample near-field with high optical and topographical resolution [1] and the ability to image surface-immobilized biomolecules in aqueous solution. We show, that theses requirements can be satisfied using the electric field enhancement at the tip of far-field illuminated silicon AFM probes in aperture-less SNOM.

Single ATTO-740 dye molecules have been imaged at an optical resolution of 20-25nm (separation of two dye molecules) under ambient conditions and in aqueous solution with commercial silicon AFM probes and sophisticated phase-sensitive single photon counting technology in dynamic AFM mode of operation. Two illumination modes have been tested successfully: a) back-illumination via evanescent fields in a total-internal-reflection-microscopy setup using an oil-immersion objective lens and b) direct top-illumination side. Although both optical setups gave similar results, they differ considerably with respect of potential experimental applications that will be discussed [2].

[1] H.G. Frey et al., Nanotechnology 17, 3105-3110, 2006 [2] H.G. Frey et al., in preparation 2008

BP 7.34 Mon 17:45 P3

Dual-trap optical tweezer for single molecule studies of transcription — •Marcus Jahnel[1,2], Martin Behrndt[1,2], and Stephan W. Grill[1,2] — [1]Max Planck Institut for Molecular Cell Biology and Genetics, Dresden, Germany — [2]Max Planck Institut for the Physics of Complex Systems, Dresden, Germany

The ability to accurately monitor and manipulate individual macromolecules allows the study of key biological processes one molecule at the time. Here, we report the construction of a Brownian noise-limited dual-trap optical tweezer setup to investigate the dynamics of processive nucleic acid-dependent molecular motors. Splitting a 1064 nm solid-state laser beam by polarisation generates two optical traps, each independently manoeuvrable by either a piezo-driven mirror or an acousto-optical deflector. Each trap is capable of holding one end in a bead-molecular motor-nucleic acid-bead "dumbbell-type" experiment. Notably, a careful analysis and subsequent elimination of the cross-talk between the two polarisation states caused by the various optical elements allows the differential distance between the two traps to be determined with very high precision.

Encouraged by feasibility studies of the setup we now address the dynamics of RNA Polymerase during transcription of DNA into RNA, one of the most important cellular processes constituting the first step in transferring genetic information into functional proteins.

BP 7.35 Mon 17:45 P3

Three-bead assay for single molecule ncd study — •Christoph Pieper[1], Li Tao[2], Kerstin von Roden[1], Stefan Lakämper[1], Jonathan Scholey[2], and Christoph Schmidt[1] — [1]3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen — [2]Department of Molecular and Cell Biology, University of California at Davis, Davis, CA 95616

The ncd protein is a dimeric minus-end directed motor of the kinesin family. Previous experiments using optical tweezers and a three-bead, suspended-micotubule assay showed transient microtubule-binding events with a working stroke of about 9 nm at the end of the binding events. Binding events could be detected by the reduction in noise of the suspended microtubule. We have now developed an advanced assay, using a new FPGA board for the rapid online detection of these binding events. The FPGA further controls acousto-optical deflectors for beam steering and trap feedback. With this system feedback can activated on ncd binding to study the behavior of a single ncd motor under a defined load.

BP 7.36 Mon 17:45 P3

Monitoring single membrane proteins in an anti-Brownian electrokinetic (ABEL) trap — •Anastasiya Golovina-Leiker, Nawid Zarrabi, Monika Düser, Rolf Reuter, Jörg Wrachtrup, and Michael Börsch — 3.Physikalisches Institut, Universität Stuttgart, Germany

Brownian motion prevents the observation of one biomolecule for extended periods. Adam E. Cohen and W. E. Moerner have developed an anti-Brownian electrokinetic (ABEL) trap to trap individual protein molecules in free solution, under ambient conditions, without requiring any attachment to beads or surfaces [Cohen and Moerner, PNAS 2006). They also demonstrate trapping and manipulation of single lipid vesicles. We present an extension of their approach to trap membrane proteins reconstituted in lipid vesicles and to simultaneously monitor the conformational changes of the active enzyme by fluorescence resonance energy transfer.

BP 7.37 Mon 17:45 P3

Single Molecule Force Spectroscopy to Study Receptor / Ligand Interactions — Mathias Salomo[1], •Marc Struhalla[2], and Friedrich Kremer[1] — [1]Universität Leipzig, Institut für Experimentelle Physik I, Linnèstraße 5, 04103 Leipig — [2]c-LEcta GmbH, Deutscher Platz 5b, 04103 Leipzig

Optical tweezers (OT) are ideally suited to study the interaction of single receptor-ligand bonds. Here we introduce a newly developed assay using optical tweezers to investigate the interactions between Protein A from Staphylococcus aureus, Protein G from Streptococcus spec. and different immunoglobulins. We demonstrate that the rupture forces depend on the loading rate and on the sodium chloride concentration. The measured loading rate effect is well known in the literature and the data we obtained and which were found to be in good agreement with an already published theoretical model can be used to directly determine interaction parameters like the dissociation rate. The dependence of the rupture forces on the salt concentration demonstrates the influence of hydrophobic interactions on the bond strength. Our experimental setup can probe the interaction between a single receptor and its specific ligand under changing conditions and hence offers manifold applications in single molecule biotechnology.

BP 7.38 Mon 17:45 P3

Monitoring the two rotary motors of a single FoF1-ATP synthase by triple-ALEX-FRET — •Torsten Rendler[1], Stefan Ernst[1], Monika G. Düser[1], Nawid Zarrabi[1], Anastasiya Golovina-Leiker[1], Rolf Reuter[1], Stanley D. Dunn[2], Jörg Wrachtrup[1], and Michael Börsch[1] — [1]3. Physikalisches Institut, Universität Stuttgart, Germany — [2]Department of Biochemistry, University of Western Ontary, London, Canada

Synthesis of ATP from ADP and phosphate is performed by a stepwise internal rotation of subunits of the enzyme FoF1-ATP synthase. The bacterial enzyme also catalyzes ATP hydrolysis. The opposite direction of rotation during ATP synthesis and hydrolysis was confirmed by single-molecule fluorescence resonance energy transfer, FRET, using specific labeling of the rotary subunits γ or ϵ in the F1 motor and the stator subunits. The step size in the F1 motor was 120°. In contrast the step size during proton-driven rotation of the c subunits in the Fo motor was 36° using single-molecule FRET. FRET artifacts could be minimized by 'duty cycle optimized alternating laser excitation'. As the two coupled motors of FoF1-ATP synthase showed apparently different step sizes, this mismatch has to be unraveled by mapping the contributions of rotor and stator subunits for transient energy storage. We present the simultaneous observations of F1 and Fo motor rotations using a single-molecule triple FRET approach, which indicate elastic deformations of the rotor between ϵ and c subunits during ATP hydrolysis as well as synthesis.

BP 7.39 Mon 17:45 P3

Fabrication of metallized solid state nanopores for single molecule experiments — •Ruoshan Wei, Daniel Pedone, Gerhard Abstreiter, and Ulrich Rant — Walter Schottky Institut, Technische Universität München, Deutschland

Nanopores in solid state membranes have emerged as powerful means to study single molecules. In translocation experiments, the trans-pore ionic current is monitored to detect the passage of individual molecules (nucleic acids or proteins). Engineered solid state pores hold considerable advantages over their biological counterparts with respect to stability and adjustability. With the aim of creating an electrically gateable pore which can be used to modulate the biomolecule translocation efficiency, we devised a novel concept where the nanopore is metallized on one side. Here we report on the device fabrication and electrical characterisation in aqueous electrolyte solution. Pores featuring diameters < 30 nm are fabricated in Si3N4 membranes by e-beam lithography. Subsequently, thin (< 20 nm) metal films of Pt or Au are evaporated on Ti adhesion layers. The surface roughness and film morphology are assessed for different deposition methods (e-beam vs. thermal evaporation). The trans-pore current as well as the device capacitances are studied using electrochemical impedance spectroscopy and FFT analysis of high-bandwidth current recordings. Within this framework, we investigate the reduction of current noise by surface passivation using silicone elastomers.

BP 7.40 Mon 17:45 P3

Comprehensive Acquisition and Analysis Software for Optical Tweezers — •Fabian Czerwinski and Lene B. Oddershede — Niels Bohr Institute, Blegdamsvej 17, Copenhagen

Optical tweezers have become a valuable tool in biophysics e.g. for precise detection and manipulation of individual (biological) molecules. We present a comprehensive Labview toolbox for optical tweezers with a photodiode-based detection system. Various incorporated methods allow for calibrating biological objects and optical handles directly [1,2]. Acquisition parameters can be precisely adjusted, leading to reliable feedback modes [3] and minimized noise [4]. Drift and noise are quantified on-the-fly by improved Allan-variance algorithms [5].

The main program is designed in a modular fashion to offer (optionally) independent as well as interconnected control of diode, stage and microfluidics. Further, it also contains support for data-streaming protocols. In order to assure minimal failure and negligible error rates, we utilize programming options such as multicore processing, cache-speed optimization and pipelined register control. The source code is available upon request and under Creative Common License. Future improvements will include an extended readout of image devices to facilitate parallel single-particle tracking and further possibilities for

calibration.

[1] Berg-Sorensen et al., Rev Sci Instr (17)594, 2004. [2] Tolic-Norrelykke et al., Rev Sci Instr (77)103101, 2006. [3] Greenleaf et al., PRL (95)208102, 2005. [4] Gibson et al., Opt Exp (16)5958, 2008. [5] Czerwinski, Matlab Central, 21727, 2008.

BP 7.41 Mon 17:45 P3

Design of a low-cost modular FCS, FRAP and Optical Tweezers setup for educational use — •Thorsten Bloem, Nadine Lang, Philip Kollmannsberger, and Ben Fabry — Biophysics, University of Erlangen, Germany

We demonstrate a flexible yet inexpensive optical setup for undergraduate education which alternately provides Fluorescence Correlation Sprectroscopy (FCS), Fluorescence Recovery after Photobleaching (FRAP) as well as Optical Tweezers (OT) reusing the same components. It is built around a 100x objective with 1,25 NA, two diode lasers (532 nm and 1064 nm) for fluorescence and trapping, a CCD camera and an avalanche photodiode (APD) as detectors, as well as standard optomechanics mounted on a 60x60 cm breadboard. The total price of less than 8 000,- EUR for the basic configuration makes modern imaging and manipulation techniques accessible for undergraduate institutions at a fraction of the cost of high-end research systems. Teaching modules for advanced lab courses are presented to demonstrate the use as an educational platform for modern optics, biological imaging and biophysics.

BP 7.42 Mon 17:45 P3

Phase contrast tomography of human brain using grating interferometry — •Georg Schulz[1], Marco Germann[1], Franz Pfeiffer[2], Timm Weitkamp[3], Christian David[2], and Bert Müller[1] — [1]Biomaterials Science Center, University Basel, Switzerland — [2]Paul Scherrer Institute Villigen, Switzerland — [3]ID19, ESRF Grenoble, France

In order to visualize the human thalamus, which is one of the most ambitious challenges in X-ray tomography, as it exhibits almost no absorption contrast, we use phase contrast tomography which is based on differences of the refraction index. No labelling of the tissue before the measurements is needed in order to segment the vessel tree from the surrounding tissue. In our study we use a grating interferometer consisting of a beam-splitter grating and an analyzer absorption grating. Here we can detect phase shifts in the range of several 10^{-8} *rad*. The presented results derive from measurements at ESRF Grenoble (beamline ID19) at an energy of 26 keV. The resulting voxel sizes range down to 7.5 μm. The examination of the reconstructed tomographic slices implies a measurement sensitivity for the real part of the refractive index of $0.7 \cdot 10^{-10}$, which corresponds to an electron density sensitivity of 0.04 e/nm^3 and a mass density sensitivity of approximately 0.1 mg/cm^3 for aqueous specimens. Blood vessels could be well identified and partially segmented using a simple intensity based segmentation tool. For a complete segmentation more sophisticated tools are needed.

BP 7.43 Mon 17:45 P3

Einfluss der Eigenschaften dielektrischer Schichten auf das Verhalten von Metallelektroden-Zellkultur-Grenzflächen — •Mathias Müller, Christian Warnke, Alexander Franke, Michael Charpentier, Antje Reiher, Kay-Michael Günther, Hartmut Witte, Jürgen Christen und Alois Krost — Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg

Für das elektrische Anregen und Auslesen von Zellkulturen haben sich planare Elektrodenanordnungen (MEAs) etabliert. Bei der Adaption der MEAs an das jeweilige biologische System spielen die elektrischen Übertragungsmechanismen der anregenden Pulse eine wichtige Rolle. Diese Transfervorgänge werden insbesondere durch die Verwendung dielektrischer Schichten auf den Elektroden beeinflusst. Aus diesem Grund haben wir den Einfluss von TaO_x- und SiO_x-Schichten sowie von Photolacken und Polymid auf die elektrischen Übertragungseigenschaften von Au/Ti-Fingerelektroden-Anordnungen untersucht. Die Oberflächen der Elektroden und der dielektrischen Schichten wurden durch Nomarski-Mikroskop und AFM und die elektrischen Eigenschaften mit DC-und AC-Messungen charakterisiert. Mittels Impedanzspektroskopie wurden die Eigenschaften des Überganges Elektrode/Isolatorschicht/Elektrolyt bei verschieden leitfähigen Elektrolytlösungen untersucht. Die Anordnungen wurden schließlich hinsichtlich ihrer Anwendung als Anregungs- sowie Ausleseelektroden für Neuronen- und Hefezellen, charakterisiert. Zusätzlich konnte die elektrolytische Produktion von Gasen in Abhängigkeit von den Schichtparametern der Strukturen nachgewiesen werden.

BP 7.44 Mon 17:45 P3

Competitive Homogeneous Hapten Immunoassay Based on Fluorescence Quenching by Gold Nanoparticles — Benjamin Ehlers[1], Sergiy Mayilo[1], •Meike Kloster[1], Michael Wunderlich[1], Thomas A. Klar[1,2], Hans-Peter Josel[3], Dieter Heindl[3], Alfons Nichtl[3], Konrad Kürzinger[3], and Jochen Feldmann[1] — [1]Photonics and Optoelectronics Group, Department of Physics and CeNS, Ludwig-Maximilians-Universität München, Munich, Germany — [2]Institute of Physics and Institute of Micro- and Nanotechnologies, Technical University of Ilmenau, Ilmenau, Germany — [3]Roche Diagnostics GmbH, Penzberg, Germany

We report on a competitive, homogeneous immunoassay for the detection of the hapten digoxigenin, a drug used to cure atrial fibrillation. The assay consists of gold nanoparticles functionalized with anti-digoxigenin antibodies and fluorescently labelled digoxigenin. Initially, the labelled digoxigenin is bound to the gold nanoparticles and the fluorescence is effectively quenched. Upon the addition of digoxigenin, a competition takes place for the antibodies on the gold nanoparticles leading to labelled digoxigenin free in solution and therefore an increase of fluorescence. By using time-resolved spectroscopy, it is found that the quenching is due to energy transfer from the dye to the gold nanoparticle. The assay is sensitive in the therapeutically relevant concentration range of 0.5 to 3 ng/mL. The method can be applied both in buffer solution and in serum. The same principle of competitive fluorescence quenching can be applied to detect other haptens.

BP 7.45 Mon 17:45 P3

NIR SERS hybrid probes for in vitro and in vivo bioanalytics — •Andrea Matschulat[1,2], Ilona Dörfel[1], Franziska Emmerling[1], and Janina Kneipp[1,2] — [1]Federal Institute of Materialsresearch and Testing (BAM) — [2]Department of Chemistry, Humboldt University, 12489 Berlin, Germany

Raman Spectroscopy, a method with many applications ranging from condensed matter physics to bioanalytical chemistry, offers several advantages such as the rapid and non-destructive study of vibrational fingerprints of chemical and biological compounds. With SERS, scattering efficiencies can be enlarged by a factor of $\sim 10^6$ in bulk samples. This versatile and selective technique provides more sensitive detection, accompanied by high spatial resolution due to local optical near-fields generated by noble metal nanostructures. Our work is concerned with the construction and characterization of Au and Ag nanoparticles whose unique plasmonic properties are tuned for the sensitive NIR-SERS probing of complex biosamples. In our studies, we were successful in detecting spectral fingerprints of various Raman reporter species (DTNB, NT, MBA and PATP) that contrast strongly with commonly used reporter fluorophores due to their larger SERS cross sections. Further, their utilization in multiplex approaches under physiological conditions enables the identification of different types of labelled SERS probes. In first *in vitro* experiments, we have introduced SERS hybrid probes, with which intrinsic information of pollen extracts can be obtained. The role of BSA as a stabilizing agent for nanoparticles and linker for multiple analytes in both will also be discussed.

BP 7.46 Mon 17:45 P3

Biological application of atomic scale magnetometry using single defects in diamond — •Thomas Wolf, Gopalakrishnan Balasubramanian, Roman Kolesov, Fedor Jelezko, and Jörg Wrachtrup — 3. Physikalisches Institut, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

Diamonds contain natural defect centres in their lattice structure known as colour centres. Electron spin states in these colour centres can be changed and measured with optical techniques at room temperature. The potential of locating one of these centres spatially on the nanometer scale with potential for sub-nm precision by using magnetic resonance techniques has been recently shown by our group and collaborators. Using small nanocrystals containing a NV-centre (nitrogen-vacancy) we intend to implement diamond as non-toxic biological marker having potential to overcome the classical resolution limit of light microscopy under physiological conditions.

BP 7.47 Mon 17:45 P3

Sub 300 nm Softlithography with SU8 — •Jörg Käsewieter, Jan Regtmeier, and Darius Anselmetti — Experimental Biophysics & Applied Nanoscience, Faculty of Physics, Bielefeld University, Germany

Softlithograpy is a low-cost strategy to produce micro- and nano devices. Here we demonstrate that the photoresist SU8, which is designed for thick and high aspect ratio application, can also be used to create 3D micro- and nanofluidic channels with dimensions <300 nm. In a multilayer lithography process, a sub 300 nm SU8 film is spincoated and processed, followed by a layer, which is several micron thick. The layers are aligned with a mask aligner allowing for a positioning precision better than 2 micron absolut.

The SU8 multilayers are replicated with Polydimethylsiloxane (PDMS), that is pretreated with an oxygen plasma before assembly to render the surfaces hydrophil. This combination of nano- and microfluidics allows new approaches to bioanalytical lab-on-a-chip devices, which will be discussed.

BP 7.48 Mon 17:45 P3

Deposition of engineered nanoparticles on human lung cells via the air liquid interface — •Andreas Comouth[1,2], Sonja Muelhopt[2], Harald Saathoff[1], Daniel Rzesanke[1], Alicja Panas[3], Carsten Weiss[3], Hanns-Rudolf Paur[2], Silvia Diabate[3], and Thomas Leisner[1] — [1]Institute for Meteorology and Climate Research, Forschungszentrum Karlsruhe, Germany — [2]Institute of Technical Chemistry, Thermal Waste Treatment Division, Forschungszentrum Karlsruhe, Germany — [3]Institute of Toxicology and Genetics, Forschungszentrum Karlsruhe, Germany

Epidemiological studies show a correlation between the concentration of ultrafine particles in the atmosphere and the rate of mortality and morbidity due to respiratory and cardiovascular disease. In order to get quantitative information about the lung toxicity of engineered airborne nanoparticles an in vitro exposure system has been build up and lung specific bioassays have been developed. Unlike submers exposure this set up is more realistic due to the deposition at the air liquid interface of lung cells as it happens in vivo. Further this method enables reproducible deposition conditions by in situ monitoring of particle size distribution and concentration via scanning mobility particle sizing (SMPS) as well as mass dose determination by a quartz crystal microbalance. After exposure at the air liquid interface the cells are analyzed to measure the biological responses such as viability, inflammatory or oxidative stress. In this way it is possible to study the influence of particle properties such as surface area, particle coatings as well as primary particle size and agglomerate size on lung toxicity.

BP 7.49 Mon 17:45 P3

The unwinding mechanism of the hexameric helicase Large Tumor Antigen — •Daniel Klaue and Ralf Seidel — Biotechnology Center, TU Dresden, Germany

Helicases are ATP-driven molecular motors that processively unwind dsDNA by shearing apart the individual strands . The mechanisms by which helicases accomplish strand separation are heavily debated. Two extreme possibilities are either a passive mechanism, in which reannealing of stochastically opened base pairs at the unwinding junction is sterically prevented , or an active mechanism in which the helicase actively ruptures base pairing. Whereas for the latter case the helicase velocity should be force independent, for the first case a strong force dependence is expected. Recently for hexameric helicases from bacteriophages, a largely passive DNA unwinding mechanism has been found. Here we investigate the eukaryotic hexameric helicase Large Tumor Antigen (T-antigen) from Simian Virus 40 on the level of a single molecule using magnetic tweezers, where unwinding of a DNA hairpin can be observed in real time. In contrast to its prokaryotic counter parts we find that within error DNA unwinding by T-antigen is force independent in agreement with an active unwinding mechanism. Interestingly, the refolding of the DNA, when T-Antigen passes the center of the hairpin and translocates on the single strand, occurs faster than unwinding. This suggests that the active unwinding occurs ahead of the unwinding junction which is shielded against applied force. In agreement with an active unwinding mechanism we also find that T-antigen is one of the most processive helicases known so far.

BP 7.50 Mon 17:45 P3

Single-Molecule Studies of DNA Translocating Restriction Enzymes — •Friedrich Schwarz[1], Kara van Aelst[2], Mark Szczelkun[2], and Ralf Seidel[1] — [1]BIOTEC TU-Dresden Germany — [2]University of Bristol, United Kingdom

Restriction enzymes (REs) are the central part of the bacterial defence system against invading viruses. These protein complexes recognize viral DNA by the methylation state of their target sequence and destroy it by cleaving it into pieces. For this, the majority of REs need to interact with two distant target sites. This long-range inter-site communication can be accomplished either by passive 3D diffusive looping or by 1D motion along the DNA contour. Among the different classes of REs, Type I and Type III play a special role due to their helicase domains, which are key to the inter-site communication.

For Type I REs it is established that the helicase domain acts as a dsDNA translocating motor. Cleavage is triggered after a pure 1D communication process, when two translocating motors from distant target sites collide. However details of the actual cleavage-collision process still remain unclear. In comparison, the communication mechanism for Type III REs has not been accurately defined and conflicting models including 3D diffusion and 1D translocation have been proposed. Our recent findings suggest that Type III REs move along DNA by diffusion. In order to explore the cleavage-collision process and to test the diffusion hypothesis we started to track the movement of Type I and III REs along DNA using a setup combining magnetic tweezers with single-molecule fluorescence.

BP 7.51 Mon 17:45 P3

Transport properties of G-quadruplex DNA measured with mechanically controllable break junction electrodes — •Shoupeng Liu[1], Samuel Weisbrod[2], Zhuo Tang[2], Andreas Marx[2], Elke Scheer[1], and Artur Erbe[1] — [1]Physics Department, University of Konstanz, D-78457 Konstanz, Germany — [2]Chemistry Department, University of Konstanz, D-78457 Konstanz, Germany

The conductance properties of G-quadruplex DNA are investigated while stretching the molecules mechanically. Electrodes which are fabricated using a mechanically controllable break junctions (MCBJ) setup enable us to measure the resistance of single or a small number of molecules in various stretching situations. The resistance as a function of the electrode distance, i.e. the so-called open-close curve, shows a plateau, which we associate with the folding and unfolding process of the molecule. From the measured current-voltage characteristics we deduce a semiconductor-like electronic band-structure. The results suggest a comparatively high conductance of the G-quadruplex structure which has promising usage in future nanoelectronics.

BP 7.52 Mon 17:45 P3

Transfer matrix modelling of DNA charge transport with a diagonal-ladder model — •Stephen Wells[1], Chi-Tin Shih[2,3], and Rudolf Roemer[1] — [1]Department of Physics and Centre for Scientific Computing, University of Warwick, Coventry CV4 7AL, UK — [2]Department of Physics, Tunghai University, 40704 Taichung, Taiwan — [3]Physics Division, National Center for Theoretical Sciences, Hsinchu, Taiwan

The structure of DNA, with its stacking of aromatic bases along the axis of the double helix, immediately suggests the possibility of significant charge transport along the molecule. There is increasing evidence that DNA can support a considerable degree of charge transport along the strand by hopping of holes from one base to another, and that this charge transport may be relevant to DNA regulation, damage detection and repair. A surprising amount of insight can be gained from the construction of simple tight-binding models of charge transport, which can be investigated using the transfer-matrix method. We review a set of ladder-like models for DNA charge transport and their extension to include more physically realistic diagonal-hopping terms. There appears to be a correlation between DNA charge-transport properties obtained from these models and the locations and frequency of disease-associated mutations in multiple genes. We present data on genes including p53 (the "guardian of the genome") and genes associated with retinoblastoma and cystic fibrosis.

BP 7.53 Mon 17:45 P3

TmHU-DNA binding studied by atomic force microscopy — •Hergen Brutzer, Mathias Salomo, Friedrich Kremer, and Ulrich Keyser — Institute for Experimental Physics I, Leipzig University, Linnéstraße 5, D-04103 Leipzig, Germany

In contrast to the well-characterized processes of formation and destabilization of complexes from eukaryotic histones with DNA, little is known about interactions between histone-like proteins from prokaryotes and DNA. These proteins also kink and bend DNA leading to chromatin-like structures. The histone-like HU protein is nearly ubiquitous in all bacteria. Especially TmHU from Thermotoga maritima exhibits some extraordinary properties, such as the protection of DNA inside the bacterium against thermal denaturation. Experiments with optical tweezers suggest the existence of a threshold protein concentration for the formation of TmHU-DNA complexes. Here we use atomic

force microscopy to study the concentration dependence by alternative means and minimize influence by external forces. The end-to-end distance and the height of the complexes were measured in dependence of protein concentration (50-5000 nM). With increasing protein concentration the end-to-end distance decreases from 70 to 38 nm while the height increases from 0.7 to 2.2 nm for 250 bp dsDNA, indicative of the formation of a globular structure of the TmHU-DNA complex. Most likely this originates from a secondary organizational level during TmHU-DNA binding observed in optical tweezers experiments.

BP 7.54 Mon 17:45 P3

Buckling Transition during DNA Supercoiling studied by Magnetic Tweezers — •Hergen Brutzer, Daniel Klaue, and Ralf Seidel — DNA motors group, BIOTECnology Center, University of Technology Dresden, D-01062 Dresden

In contrast to its well-characterized stretching and bending behavior, the response of DNA upon twisting is less understood. Initially, under the action of an external force, the molecule extension remains almost constant upon twisting. Once a critical buckling torque is reached a linear decrease in extension with added twist is observed, due to the formation of a superhelical structure. Recent experiments, however, revealed the existence of an abrupt extension change at the buckling transition, i.e. upon superhelix formation. Here we studied this abrupt buckling using magnetic tweezers, in order to elucidate its origin. We recorded the population of the pre and post-buckling states as function of the applied twist with high resolution. Depending on the applied force, the superhelix in the post buckling state comprises considerably more than one turn. Applying a two-state model in which the energy for the first turn of superhelix formation is larger than for the subsequent turns, the observed buckling transition can be explained nearly quantitatively. The model suggests a plectonemic structure with one initial loop of high curvature and a subsequent superhelix with lower DNA curvature. With decreasing salt concentration the appearance of the buckling transition is less pronounced, which is also supported by the model.

BP 7.55 Mon 17:45 P3

Two dimensional semiflexible polymer rings — •Fabian Drube, Karen Alim, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and Center for NanoScience, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstrasse 37, D-80333 München, Germany

The shape of DNA plays a crucial role in many biological processes like protein-DNA interaction. Especially circular DNA shows interesting shape characteristics due to its geometrical constraint. While measuring the three dimensional structure of DNA is not feasible at the moment, recently, circular DNA on a mica surface has been studied experimentally [1]. Comparing these data with the wormlike chain model reveals that topological self-avoidance effects are substantial. We introduce a novel tube-like model of semiflexible polymers to account for excluded volume effects. With extensive Monte-Carlo simulations we quantify the ensuing conformations of circular DNA and compare those with available experimental data.

[1] G. Witz, K. Rechendorff, J. Adamcik, and G. Dietler, Conformation of circular DNA in two dimensions, Phys. Rev. Lett. **101**, 148103 (2008)

BP 7.56 Mon 17:45 P3

A coarse-grained model for RNA tertiary structure formation — •Thomas Schötz and Ulrich Gerland — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

RNA folding is relatively well understood on the secondary structure level, i.e. structure formation in the abstract space of base pairing patterns. However, on the level of the three-dimensional structure in real space, there are hardly any modeling approaches short of full-fletched molecular dynamics simulations, which are challenging even for small RNA molecules. Towards the ultimate goal of filling this gap, we construct a coarse-grained bead-spring type polymer model for RNA, which behaves like a freely jointed rouse chain as long as the bases are unpaired. However, when the short-range sequence-dependent interactions between the bases set in, more complex interactions between adjacent base pairs act to spontaneously create double-helical segments with a non-vanishing bending rigidity and torsion stiffness. We study the rich behavior of this model, including the sequence-dependent folding dynamics as well as static and dynamic properties of the folded tertiary structure, by the use of Brownian dynamics simulation techniques. This approach allows us to examine the dynamic formation and destruction of typical tertiary structure elements, including small pseudo-knotted structures, which play an important role in molecular biology.

BP 7.57 Mon 17:45 P3

Stretching of a DNA/HU-protein complexes in SMD simulations — •Carsten Olbrich and Ulrich Kleinekathöfer — Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany

The protein HU is a member of a family of prokaryotic proteins that interacts with the DNA in a non-specific way [1]. Its major function is the binding, compaction and stabilization of DNA. Steered molecular dynamic (SMD) simulations are applied to DNA which is either bound to the HU protein of the bacteria Anabaena (AHU) or of the Thermotoga maritima (TmHU). Using these all-atom simulations including explicit water and about 80,000 atoms in total, we are able to gain insight into the discrete disruptions events which occur when the DNA releases from the protein body. These disruptions were first observed in experiments performed with optical tweezers [2]. By comparing the unbinding pathways of the complexes, different binding strengths of AHU and TmHU to DNA can be found.

[1] R. Dame and N. Goosen, FEBS Lett. **529**, 151 (2006).
[2] M. Salomo, F. Kremer et al., J. Mol. Biol. **359**, 769 (2006).

BP 7.58 Mon 17:45 P3

Optical tweezers measurements of threading DNA and DNA-ligand-complexes through solid-state nanopores — •Andy Sischka[1], Christoph Kleimann[1], Wiebke Hachmann[2], Marcus M. Schäfer[3], Ina Seuffert[4], Katja Tönsing[1], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanosciences, Bielefeld University, Germany — [2]Molecular and Surface Physics, Bielefeld University, Germany — [3]Center for Nanotechnology (CeNTech), Münster, Germany — [4]Fachbereich Physik, Fach M621, University of Konstanz, Germany

We developed a versatile and high precision 3D optical tweezers setup, capable for force measurements completely based on detection of backscattered light with minimal optical interference to measure forces in the sub-pN regime and to manipulate single molecules. With this novel setup, single dsDNA-molecules were threaded into a solid-state nanopore by applying electrical voltage across the membrane, as the electrostatic force and the ionic current through the pore were measured. Here, individual force steps could be observed for each DNA-molecule entering the nanopore. Active pulling of a single Lambda-DNA-molecule out of the nanopore by linearly increasing the bead-membrane distance induced a force signal with only very weak force oscillations of about 2 pN, until the DNA was completely pulled out of the nanopore. Binding of dedicated protein ligands (peroxiredoxin, and E.coli RNA-polymerase) to dsDNA caused a significant change in the apparent electrostatic forces that are required for threading and unthreading the DNA-ligand-complex through the nanopore.

BP 7.59 Mon 17:45 P3

Force-induced unfolding of G-quadruplex — •Hui Li[1], En-hua Cao[2], and Thomas Gisler[1] — [1]Universität Konstanz, Fachbereich Physik, 78457 Konstanz, Germany — [2]Institute of Biophysics, Chinese Academy of Sciences, Beijing 100101, China

Telomeric DNA sequences can form four-stranded (quadruplex) structures both in vivo and in vitro in presence of cations. However, the folding process of quadruplex is still a mystery and has so far not been accessible with conventional molecular dynamics (MD) simulation. In this publication we study the unfolding of a parallel G-quadruplex from human telomeric DNA by mechanical stretching using steered molecular dynamics (MD) simulation. We find that the force curves and unfolding processes are strongly dependent on the pulling sites. If the stretching springs are connected to the sugar backbone, the force curve shows a single peak and the unfolding can be regarded as a two-state transition. When the stretching springs are connected to the terminal nucleobases, the force curve shows two peaks indicating that unfolding proceeds through an intermediate state. The free energy profile for the base-pulling scenario computed from the force-extension curves using the Jarzinsky equation shows a shoulder which corresponds to the intermediate state. After releasing the force constraint, equilibrium simulations for 8 ns show that the molecule does not refold back to its original structure once it was stretched to the intermediate state. Folding pathways of parallel G-quadruplex are proposed according to the simulated structures.

BP 7.60 Mon 17:45 P3

Probing DNA Tetrahedra — •Alexander Benkstein[1], Iwan A. T. Schaap[1], Christoph M. Erben[2], Andrew J. Turberfield[2], and Christoph F. Schmidt[1] — [1]3. Physikalisches Institut, Fakultät für Physik, Georg-August Universität, 37077 Göttingen — [2]Clarendon Laboratory, Department of Physics, University of Oxford, Parks Road, Oxford OX1 3PU, UK

Well established synthesis procedures and the "programmability" of DNA binding via base pairing makes DNA ideal for the design of nanostructures.

We here investigate the mechanical characteristics of self assembled tetrahedra from DNA oligomers with dimensions smaller than 10nm. For this purpose, the tetrahedra are modified to bind to gold surfaces and are studied by atomic force microscopy in combination with fluorescence microscopy.

BP 7.61 Mon 17:45 P3

AlGaN/GaN-Biosensoren - stabile DNA-Sensoren — •Stefanie Linkohr, Christoph Nebel, Vadim Lebedev, Volker Cimalla und Oliver Ambacher — Fraunhofer Institut für Angewandte Festkörperphysik IAF, Tullastraße 72, 79108 Freiburg

AlGaN/GaN-Sensoren sind hoch sensitive und chemisch stabile Biosensoren, die sowohl für die Detektion von Ionen und Biomolekühlen sowie für die Untersuchungen von biologischen Aktivitäten von Zellen in Flüssigkeiten und Gasen geeignet sind. Weiterhin ermöglichen diese Sensoren durch geeignete Funktionalisierung der GaN-Oberfläche die Untersuchung von DNA-Molekülen. Bei den untersuchten Sensoren handelt es sich um AlGaN/GaN-Heterostrukturen, die mit einer SiO-SiN-PMMA-Multilayer-Passivierung gegen den Kontakt mit Flüssigkeit isoliert sind. Dabei handelt es sich um pH-sensitive-ISFETs dessen Empfindlichkeit bei 59 mV/pH liegt und die in einem pH-Bereich von 4 - 9 eine gute Langzeitstabilität aufweisen. Zur Biofunktionalisierung mit DNA wird das geöffnete Gate mit 10-amino-dec-1-ene Molekülen, funktionalisiert. Unter Benutzung einer hochdruck Halogen UV-Lichtquelle (200 nm) wird die GaN-Oberfläche über 2 bis 8 h beleuchtet. Die Funktionalisierung der GaN-Oberfläche wird mit Hilfe von Rasterkraftmikroskopie, Rastertunnelmikroskopie und röntgeninduzierte Photoelektronenspektroskopie charakterisiert und zeigt das inselartige Wachstum der Olefin-Moleküle. Nach der Funktionalisierung verringert sich die Empfindlichkeit des Transistors, so dass DNA [Ck 20] Hybridisierung und Denaturierung beobachtet werden kann.

BP 7.62 Mon 17:45 P3

Investigating the chemo-mechanical properties of two-dimensional actin networks — •Kai Uhrig[1,2], Rainer Kurre[1,2], Martin Streichfuss[1,2], Friedrich Erbs[1,2], Simon Schulz[1,2], Anabel Clemen[1,2], Tamas Haraszti[1,2], Christian Böhm[1,2], and Joachim Spatz[1,2] — [1]MPI for Metals Research, Dept. Spatz, Heisenbergstr. 3, 70569 Stuttgart — [2]Univ. of Heidelberg, Biophys. Chem. Dept., INF 253, 69120 Heidelberg

The actin cortex, a quasi two-dimensional network of actin, plays an important role in cell stability, motility and viscoelasticity. In vivo, its characteristic properties are controlled by various crosslinkers, such as actin binding proteins or ions. To investigate the influence of a specific crosslinker on the network's behaviour exclusively we create and probe biomimetic models of the actin cortex. This is realized using microbeads trapped by holographic optical tweezers (HOTs) as scaffold for the actin filaments. With this technique we are able to create actin networks in arbitrary geometry and determine the forces exerted by different crosslinkers. Using a special microfluidic flowcell we have full control over the chemical environment in our experiments. The acting forces are measured by highspeed imaging, whereas simultaneous fluorescence microscopy yields information about the structure and density of the actin network. In another approach we use micropillars as framework and measure unzipping forces of crosslinked actin filaments.

BP 8: Developmental Processes

Time: Tuesday 9:30–13:00 Location: HÜL 186

Invited Talk BP 8.1 Tue 9:30 HÜL 186

Robustness and Scaling in Embryonic Development — •Naama Barkai — Department of Physics of Complex Systems, Weizmann Institute of Science, Rehovot 76100, Israel — Department of Molecular Genetics, Weizmann Institute of Science, Rehovot 76100, Israel

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Invited Talk BP 8.2 Tue 10:00 HÜL 186

The R8 race: Specifying photoreceptor cells in the developing fly eye — •David Lubensky — University of Michigan, Ann Arbor, MI, USA

Regular patterns of cell fate appear widely in biology. Such patterns also emerge spontaneously, via a Turing instability, in models of diffusible activators and inhibitors, but it remains unclear to what extent biology takes advantage of this fact. I will discuss a quantitative analysis of Drosophila eye development, focusing on the activator-inhibitor system responsible for spacing the R8 photoreceptors that define the eye's regular ommatidial pattern. The R8 lattice grows by turning on the expression of proneural genes at a moving front to create new columns of R8 cells. I propose a model where R8 fate specification occurs when a bistable genetic switch is flipped in a given cell; a template of inhibitory signals from the existing R8 lattice determines where the switch will be flipped in the new column. A consequence of our model is that transient perturbations of one column can change the pattern in all subsequent columns. Most strikingly, the normal triangular lattice can give way to stripes of R8 cells. These predictions are confirmed experimentally by manipulation of the *Notch* and *scabrous* genes. In our model, the relative timing and strength of signals from the template, rather than competition among neighboring cells, determines the eventual R8. If time allows, I will discuss implications of this picture for other related examples of neural fate specification.

BP 8.3 Tue 10:30 HÜL 186

Quantification of leaf vein patterning — •Karen Alim and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universtät München, Theresienstr. 37, 80333 Munich, Germany

Vein networks are essential in transporting nutrition effectively into all cells of an organism. In plant leaves these vein networks are formed by the opposite transport mechanism, the retraction of the plant hormone auxin. The so formed auxin flow pattern is consistent with the vascular network of the mature leaf. Key factors in the non-uniform transport are the competition of auxin carriers within each cell and the coupling between auxin current and carrier location.

We investigate a microscopic model for the directed auxin transport by carrier proteins performing both computer simulations and analytic calculations. These enable us to identify the relevant biological processes which should be considered for leaf vein patterning. Quantitative results help us to suggest observables and experimental scenarios to measure the kinetic rates governing the active transport.

BP 8.4 Tue 10:45 HÜL 186

Investigating the influence of mechanics on epithelial morphogenesis — •Carina M. Edwards[1], Francesco Pampaloni[2], Ernst H. K. Stelzer[2], and Ulrich S. Schwarz[1,3] — [1]Center for Modelling and Simulation in the Biosciences (BIOMS), University of Heidelberg, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [2]EMBL Heidelberg, Meyerhofstrasse 1, 69117 Heidelberg, Germany — [3]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

Mechanical stress and strain are increasingly being recognized as playing a crucial role in determining tissue size and structure. Because experimentally it is very difficult to measure stress and strain for growing tissues, mathematical modelling is required to correlate stress and strain with biological processes like cytoskeletal remodelling. In order to acquire quantitative data, one needs to combine advanced microscopy techniques with image processing. Here we use light-sheet-based fluorescence microscopy applied to the growth of cysts from Madin-Darby canine kidney (MDCK) cells. Using careful image anal-

ysis we extract time-resolved data on cyst and lumen size, and on the number of cells. These results are used to rule out or validate growth models, including those that incorporate mechanical effects. We are also able to look at the effect of gel stiffness on cyst growth.

BP 8.5 Tue 11:00 HÜL 186

Optimal precision of noisy gene expression domains — •Thorsten Erdmann[1], Martin Howard[2], and Pieter Rein ten Wolde[1] — [1]FOM Institute Amolf, Amsterdam, The Netherlands — [2]John Innes Centre, Norwich, United Kingdom

During early embryonic development, the body plan of the adult fruit fly is laid out by spatial patterns of gene expression. To form a viable organism different domains need to be reliably separated against the adverse influence of stochastic noise. A prominent example is the domain of the Hunchback protein. The production of Hunchback proteins is activated by a fluctuating morphogen gradient. In addition, the rate of protein production is subject to strong fluctuations. We theoretically study the spatial positioning of the Hunchback domain boundary for fluctuating protein concentrations. We find that the interplay between spatial and temporal averaging leads to an optimal precision for the Hunchback boundary as a function of protein lifetime. Moreover, the Hunchback domain boundary can be determined with better accuracy than the noisy input.

15 min. break

BP 8.6 Tue 11:30 HÜL 186

Slowing down of genetic oscillations in vertebrate segmentation — •Saul Ares[1], Luis G. Morelli[1], Andrew C. Oates[2], and Frank Julicher[1] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute of Molecular Cell Biology and Genetics

The subdivision of the vertebrate body axis in a segmented pattern is driven by genetic oscillations in the unsegmented tissue called the Presomitic Mesoderm (PSM). These oscillations form waves of gene expression that start at the posterior of the PSM and move anteriorly to finally stop at an arrest front. In situ snapshots of the PSM display a gene expression pattern of several stripes which are thiner at the anterior. Recently, Gomez et al. [Nature, **454**, 335-339 (2008)] have analyzed experimentally embryos of snake, mouse, chick and zebrafish, measuring the sizes of their PSM and the different number of stripes of cyclic gene expression in each species (from 1 in mouse or chick to up to 9 in snake).

In this contribution we present a Delayed Coupling Theory of vertebrate segmentation that treats the cellular oscillators as phase oscillators coupled with a time delay. Using this theory we analyze the data from Gomez et al. and show for the first time that the way in which oscillators slow down across the PSM is different and characteristic of each species. Together with the PSM size and the collective period of the oscillations, the way in which the oscillator slow down establishes the gene expression pattern setting the number and size of the stripes of cyclic gene expression in the PSM.

BP 8.7 Tue 11:45 HÜL 186

Exploring Fgf8 morphogen gradient in vivo — •Markus Burkhardt, Shuizi Rachel Yu, Matthias Nowak, Jonas Ries, Zdeněk Petrášek, Petra Schwille, and Michael Brand — BIOTEC/ TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

It is widely accepted that tissue differentiation and morphogenesis in multicellular organisms is regulated by tightly controlled concentration gradients of morphogens. How exactly these gradients are formed and maintained, however, is highly controversial. Here, we present a study in living Zebrafish embryos where we directly examine Fgf8 morphogen mobility and concentration by Fluorescence Correlation Spectroscopy (FCS). Our results support a simple mechanism to form an Fgf8 morphogen gradient in Zebrafish embryos. The study shows the potential of FCS as a quantitative method to investigate morphogen gradients at the single molecule level in developing multicellular organisms.

BP 8.8 Tue 12:00 HÜL 186

Early Keratinocyte Differentiation and Epithelial-Tissue Morphogenesis on Micropillar Interfaces — •Simon Schulz[1], Thorsten Steinberg[2], Eva Muessig[2], Jens Ulmer[1], Niels Grabe[3], Gerda Komposch[2], Pascal Tomakidi[2], and Joachim P. Spatz[1] — [1]Biophysical Chemistry, University of Heidelberg, and Max-Planck-Institute for Metals Research, Stuttgart, Germany. — [2]Department of Orthodontics and Dentofacial Orthopedics, Dental School, University of Heidelberg — [3]Department of Medical Informatics, University of Heidelberg

Proliferation and differentiation of keratinocytes play a crucial role in tissue epithelial tissue integrity. Furthermore connective-tissue fibroblasts are pivotal for epithelial-tissue morphogenesis. The combination of material technologies mimicking different tissues with life sciences can lead to the elucidation of fundamental requirements needed for the cells to properly exert tissue specific functions. We fabricated fibronectin covered polydimethylsiloxane (PDMS) micropillar arrays which can be varied in pillar stiffness, diameter and distance. They are applied as a biomechanical microenvironment for immortalized human gingival keratinocytes (IHGKs) and gingival connective-tissue fibroblasts (GCTFs). Qualitative and quantitative differences in expression of the early keratinocyte differentiation markers keratin 1 and 10 could be observed by varying the pillar distances. We show that co-cultures of GCTFs and IHGKs could also be established. Epithelial equivalents of the IHGKs were grown on these topologically defined environments.

BP 8.9 Tue 12:15 HÜL 186

Determinants of Epithelial Morphogenesis Studied in 3D with Light Sheet-Based Fluorescence Microscopy — •Francesco Pampaloni[1], Carina M. Edwards[2], Ulrich S. Schwarz[2,3], and Ernst H.K. Stelzer[1] — [1]EMBL Heidelberg, Meyerhofstr. 1, D-69117 Heidelberg, Germany — [2]Center for Modelling and Simulation in the Biosciences (BIOMS), University of Heidelberg, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [3]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

Understanding how mechanical forces regulate tissue growth is a major issue in biophysics. Since D'Arcy Thompson published his classical work "On Growth and Form" in 1917, it has been recognized that physical interactions with the environment are as essential as chemical cues for an organism's growth, shape, and function. However, these physical aspects can only be understood in a systematic and quantitative approach where biological data is recorded with high reproducibility, high statistics, and minimum perturbation of the sample. New microscopy techniques, such as light-sheet-based fluorescence microscopy (e.g. SPIM) enable to do that by minimizing photodamage and collecting light with high quantum efficiency. We have employed SPIM to study the growth of multicellular MDCK cysts in 3D collagen gel and matrigel (a widespread model of kidney development). We recorded the growth of 50 MDCK cysts with live fluorescence microscopy measuring the increase of volume and the number of cells and have studied how cyst growth depends on the collagen density.

BP 8.10 Tue 12:30 HÜL 186

Morphogen dynamics and growth control during development — •Peer Mumcu[1], Thomas Bittig[1], Ortrud Wartlick[2], Anna Kicheva[2], Marcos González-Gaitán[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, 01187 Dresden — [2]Department of Biochemistry and Department of Molecular Biology, Geneva University, Sciences II, Quai Ernest-Ansermet 30, 1211 Geneva 4, Switzerland

Growing organs in developing animals have the ability to control their size and shape autonomously. Morphogens are a special class of signaling molecules which play a key role in this process. They are secreted from localized sources and spread throughout the growing tissue where they are degraded. They thereby form graded concentration profiles which provide the target tissue with positional information. We present a theoretical study of the transport of morphogens in growing epithelia using a continuum theory and a two-dimensional vertex model. In the vertex model the adherence junctions of the cells are represented as a network of polygons and morphogen transport is described by a diffusion current between neighbouring cells. Within this framework we study the dynamics of the morphogen gradient and we discuss the relationship between the spatio-temporal morphogen levels and the growth rate of the tissue during development. We compare our theory to experimental data from the developing Drosophila wing imaginal disc, a precursor of the fly wing.

BP 8.11 Tue 12:45 HÜL 186

Dynamics of Polar and Hexagonal Order in Developing Epithelia — •Reza Farhadifar[1], Benoit Aigouy[2], Douglas B. Staple[1], Jens Roeper[2], Andreas Sanger[2], Suzanne Eaton[2], and Frank Jülicher[1] — [1]MPI-PKS, Dresden, Germany — [2]MPI-CBG, Dresden, Germany

Planar cell polarity (PCP) is a tissue-level phenomenon that coordinates cell behavior in epithelia, which are two-dimensional tissues. A particular example of planar cell polarity at work is revealed in the orientation pattern of hairs, which form on the wing of the fruit fly Drosophila. Planar polarity is established by a molecular organization that includes an asymmetric distribution of PCP proteins within cells. The distribution of these proteins in a given cell determines of the polarity of neighboring cells. At the end of wing development, a specific pattern of PCP orientational order is established. We present a theoretical study of planar polarity in developing epithelia based on a vertex model, which can account for cell shape and cell mechanics. The distribution of PCP molecules along cell boundaries as well as their interactions with neighboring cells are captured in a coarse grained description. We identify a basic mechanism by which long-range correlations throughout the tissue can be established. We furthermore study the role of quasi-static shear deformations. In the presence of shear, the polarity of the tissue reorients. In addition, hexagonal order emerges under these conditions. These physical mechanisms for ordering can account for the processes observed during development of the Drosophila wing.

BP 9: Actin Dynamics

Time: Tuesday 10:45–13:15 Location: ZEU 260

BP 9.1 Tue 10:45 ZEU 260

Dynamics of the actin cytoskeleton in response to periodic stimuli — •Christian Westendorf[1], Eberhard Bodenschatz[1], and Carsten Beta[1,2] — [1]MPI für Dynamik und Selbstorganisation, Göttingen — [2]Institut für Physik und Astronomie, Universität Potsdam

The dynamic properties of the actin cytoskeleton provide the basis for motility, phagocytosis, and division of eukaryotic cells. Polymerization of actin fibers within the branched cortical network exerts a force at the membrane of the leading edge resulting in the formation of pseudopods and, finally, cell motion. A widely used model system for the study of actin dynamics in vivo is the social amoeba Dictyostelium discoideum. It is the aim of this study to characterize intrinsic time scales of the actin cytoskeleton in chemotactic Dictyostelium cells. We observe filamentous actin using a LimE-GFP construct in an AX-2 background. Microfluidic techniques, including laser-mediated uncaging of caged cAMP, are used to expose single Dictyostelium cells to periodic stimuli of cAMP. Responses of the actin cytoskeleton were recorded by fluorescence imaging of LimE-GFP using confocal laser scanning microscopy. Based on frequency analysis, we find an optimal response regime of the actin system around 20 sec. For longer forcing periods, a frequency doubled resonant response could be observed. For short forcing periods no entrainment was found. We also performed computer automated celltracking on the cells exposed to periodic stimuli.

BP 9.2 Tue 11:00 ZEU 260

Visco-Elasticity of Actively Deformed Actin Bundles — •Dan Strehle[1], Brian Gentry[1], Jörg Schnauss[1], Mark Bathe[2,3], Erwin Frey[2], and Josef Käs[1] — [1]Universität Leipzig — [2]LMU München — [3]MIT Boston

Actin, a highly conserved cellular protein, forms filamentous polymers under physiological conditions. In vivo these are organized into the networks and bundles that comprise the cytoskeleton, which is responsible for the cell*s morphology and is essential for cell locomotion. Cytoskeletal bundles also perform a variety of additional functions. In filopodia, for instance, they probe the extracellular environment and in stereocilia they serve as the signal transducing organelles of hair cells.

Cells can finely tune the mechanical properties of networks for various tasks by choosing from a variety of actin associated proteins to control growth, crosslinking and bundling of filaments. Dynamic crosslinkers such as alpha-actinin or fascin, for instance, create the possibility for a viscoelastic-like response to different stresses encountered in cellular conditions. This behavior is a well-known property of actin networks, but less is known about time-dependent responses of the bundles themselves.

In order to better characterize the mechanical properties of cytoskeletal F-actin bundles, we have actively deformed reconstituted bundles in vitro. We have seen clear evidence of plastic behavior in which bundles maintain their deformed shape after being bent for an extended time. On shorter holding times they response elastically, returning to their undeformed configurations.

BP 9.3 Tue 11:15 ZEU 260

Quantifying athermal fluctuations in active actomyosin complexes — •David Head[1] and Daisuke Mizuno[2] — [1]IFF Theorie II, Forschungszentrum Jülich, GERMANY — [2]Organization for the Promotion of Advanced Research, Kyushu University, Fukuoka, JAPAN

Active gels represent a class of non-equilibrium materials that are currently undergoing vigourous research due to their relevance to a range of important biomechanical processes. The motility, structural and mechanical properties of eukaryotic cells are determined in part by the interaction between protein filaments and motor proteins activated by a reservoir of energy transfer molecules such as ATP. Being athermal in origin, the pN-scale force impulses generated by motor activations violate the fluctuation-dissipation theorem, and first principles modeling is required to relate microscopic processes to macroscopically measurable quantities. Here we present the results of such calculations based on the two-fluid model, in which the active agents are spatially uncorrelated but their stress fields decay algebraically, generating long-range correlations that can and have been measured in 2-particle microrheology experiments. 1-particle results are also derived, and both sets of calculations are supported by zero-frequency elasticity calculations performed in real space. Beyond the obvious advantages of allowing direct comparison to experiment, these results can also be used to speculate about the early-time instability of isotropic networks in the absence of permanent crosslinks, leading to the well-known phenomenon of super-precipitation.

BP 9.4 Tue 11:30 ZEU 260

Filament turnover stabilizes contractile cytoskeletal structures — •Philip Guthardt Torres, Konstantin Doubrovinski, and Karsten Kruse — Universität des Saarlandes, Fachrichtung Theoretische Physik, 66041 Saarbrücken, Germany

Vital cellular processes depend on contractile stresses generated by the actin cytoskeleton. Commonly, the turnover of actin filaments in the corresponding structures is large. We introduce a mesoscopic theoretical description of motor-filament systems that accounts for filament nucleation, growth, and disassembly. To analyze the dynamic equations, we introduce an expansion of the filament densities in terms of generalized Laguerre polynomials. We find that filament turnover significantly stabilizes contractile structures against rupture. Finally, we relate the mesoscopic description to a phenomenological theory of cytoskeletal dynamics.

BP 9.5 Tue 11:45 ZEU 260

Polymerization forces of interacting filaments — •Jaroslaw Krawczyk and Jan Kierfeld — TU Dortmund, Fakultät Physik, 44221 Dortmund

Many cellular processes are driven by polymerization of filamentous proteins. Using stochastic simulations based on the Gillespie algorithm we investigate force-generation by polymerizing groups of filaments or protofilaments and study the influence of an attractive interaction between filaments on the polymerization dynamics. We find that the force-velocity characteristics, the stall force and maximal growth velocity of the filament assembly depend sensitively on the presence of interactions.

15 min. break

BP 9.6 Tue 12:15 ZEU 260

A realistic model for actin driven motility using homogenization techniques — •Karin John[1], Denis Caillerie[2], Philippe Peyla[1], and Chaouqi Misbah[1] — [1]Laboratoire des Spectrométrie Physique, UJF Grenoble I, BP 87 - 38402 Saint-Martin-d'Hères, France — [2]Laboratoire 3SR, INPG, BP 53 - 38041 Grenoble Cedex 9, France

Force generation by actin polymerization is an important step in cellular motility and can induce the motion of organelles or bacteria, which

move inside their host cells by trailing an actin comet behind.

Biomimetic experiments on beads and droplets have identified the biochemical ingredients to induce this motion, which requires a spontaneous symmetry breaking in the absence of external fields.

We had shown previously, that the symmetry-breaking can be captured on the basis of a linear elasticity theory and linear flux-force relationships.

However, a deeper understanding of the process of symmetry-breaking and force generation necessitates a realistic description of the mechanics of the actin gel and its influence on the growth process.

Starting out from the filamentous structure of the actin gel we have derived a set of continuous constitutive equations using homogenization techniques, which takes into account the history of the gel growth.

This description allows us to capture basic phenomena like treadmilling, symmetry-breaking and comet formation without any ad hoc assumptions.

BP 9.7 Tue 12:30 ZEU 260

Cutting viscoelastic materials, the theoretical basis of orientation sensitive stress measurements — •Martin Depken[1], Mirjam Mayer[2], Justin Bois[1], Frank Jülicher[1], and Stephan Grill[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Laser ablation is an important tool to analyze stress distributions in the cell cortex and in the tissues of developing organisms. To describe the response of the cell cortex to such a perturbation, we utilize a hydrodynamic description of active viscoelastic materials. For these materials the initial velocity response is shown to be proportional to the local stress before ablation. This method provides a direction sensitive measure of stress differences, and applying this method to the C. elegans cell cortex we find that the stress can be both anisotropic and inhomogeneous. This constitutes a new tool for the studies of stress in active cellular systems.

BP 9.8 Tue 12:45 ZEU 260

Force Generation of Expanding Actin Gels — •Stephan Schmidt[1], Georg Freund[2], Walter Zimmerman[2], and Andreas Fery[1] — [1]Physikalsiche Chemie II, Universität Bayreuth,Universitätsstr. 30, 95440 Bayreuth Germany — [2]Theoretische Physik I, Universität Bayreuth,Universitätsstr. 30, 95440 Bayreuth Germany

Force generation in actin gels is mainly associated with directed polymerization of actin monomers into branched filaments that extend against the load. Its ability to generate forces by monomer insertion is appealing from a material science point of view. However, while the biochemical processes associated with the actin polymerization are well understood, the molecular scale mechanism of force generation is still matter of debate. We use a simplified in vitro assay composed of purified proteins and artificial colloidal probes to directly study the forces during actin network growth. Force measurements on actin networks are performed using colloidal probe AFM techniques. In our setup the actin gel is compressed between a colloidal probe and a solid substrate while it deflects an AFM cantilever during expansion. Using fluorescence microscopy we observe the gel extension in direct conjunction with the AFM measurement. Furthermore, we vary the actin density and crosslinking via drugs or proteinic constituents like ARP2/3 and gelsolin. Generally, we observe increasing stall forces as the gel density or crosslinking density is increased. Results also suggest that the forces are limited by tensile stress build-up as the gel extends outward. Understanding of the gel behaviour in the framework of linear elasticity theory is subject to ongoing modeling efforts.

BP 9.9 Tue 13:00 ZEU 260

Stress generation and polarity sorting in active filament bundles attached to a membrane — •Marc Neef and Karsten Kruse — Theoretische Physik, Universität des Saarlandes, 66041 Saarbrücken

During the late states of cell division, animal cells are cleaved into two by a contractile ring. It consists of a bundle of actin filaments and molecular motors, where the actin filaments are connected to the plasma membrane. We study the effects of this coupling between filaments and the membrane on the dynamics of the bundle. In our model, we assume that filaments are anchored to the membrane by proteins that are bound to the filament ends. We treat the membrane as a thin film of a viscous fluid and account for hydrodynamic interactions between the anchor proteins. These are included by application of the "method of reflections". Using a stochastic as well as a mean field version of this model, we calculate the stress in the membrane due to interactions between antiparallel filaments. Furthermore, we find polarity sorting within the bundle for sufficiently large interaction strengths. Both effects exist only in the presence of hydrodynamic interactions.

BP 10: Biofluiddynamics

Time: Tuesday 14:00–16:30 Location: HÜL 186

Invited Talk BP 10.1 Tue 14:00 HÜL 186

Biohydrodynamics of biomimetic and bacterial flagella — •Holger Stark — Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstr. 36, D-10623 Berlin, Germany

At the micron scale fluid flow is in the low Reynolds number regime and nature had to be inventive to enable microorganisms to propel themselves in such an environment. Sperm cells, for example, use beating elastic filaments called flagella.

I shortly review our work on modeling a biomimetic flagellum consisting of superparamagnetic beads linked by DNA strands. Attached to a red-blood cell, the first artifical micro swimmer was created actuated by an oscillating magnetic field. The filament can also be attached to a surface in order to explore fluid transport for different beating patterns.

Many types of bacteria propel themselves with the help of a bundle of rotating helical flagella. These flagella can assume different types of helical conformations (polymorphism) depending on temperature, pH value of the solvent and applied external forces or torques as revealed by the tumbling motion of a bacterium. I will talk about our approach to model the flagellar polymorphism on the microscopic level of the flagellin proteins. Then, on a coarse-grained level I will discuss the hydrodynamics of a helical flagellum addressing explicitely the transition between two flagellar polymorphs observed when pulling at the flagellum. The analysis is performed on the basis of a generalized elasticity theory for a helical rod with two helical states. The influence of thermal noise and pulling speed on the force-extension curve is discussed.

BP 10.2 Tue 14:30 HÜL 186

Thermal Nanoparticle Traps: Theory and Experiment — Franz M. Weinert, Philipp Baaske, and •Dieter Braun — Systems Biophysics, Ludwig Maximilians University, Munich, Germany

In the past, we discussed theoretically that thermal gradients in porous rock can accumulate even single nucleic bases more than millionfold in centimeter-sized pore systems [1]. The accumulation is solely driven by a static vertical temperature gradient by convection and thermodiffusion.

We scaled down above mechanism by a factor of 1000. This is possible with light driven microflow [2][3] where the nonlinear combination of thermal expansion with temperature-dependent viscosity drives fluids remotely with a laser scanning microscope. As result we efficiently trap polystyrene beads with diameter of 40nm on the time scale of seconds.

In the future we envisage to combine the trap with the polymerase chain reaction. We previously showed that thermal convection can exponentially replicate DNA by PCR. With above approach we should be able to trap and replicate DNA in the same chamber, opening new possibilities for fast continuous in vitro evolution.

Publications:
[1] PNAS 104, 9346-9351 (2007)
[2] Physical Review Letters 100, 164501 (2008)
[3] Weinert & Braun, Journal of Applied Physics, in press.

BP 10.3 Tue 14:45 HÜL 186

Defined Spatial and Time Resolved Microfluidics for Stimulation of Chemotactic Cells — •Börn Meier, Delphine Arcizet, Joachim Rädler, and Doris Heinrich — Biophysics of Cell Dynam-

ics Group, Fakultät für Physik und Center for Nanoscience (CeNS), Ludwig-Maximilian-Universität München, Geschwister-Scholl-Platz 1, D-80539 München, Germany

The ability of cells to move into the direction of a chemical gradient is an important mechanism involved in physiological responses, like the movement of neutrophils in tissue or for angiogenesis, the development of new blood vessels. In the model organism Dictyostelium discoideum (Dd) it has been shown that the response to chemotactic stimulation occurs within seconds. Therefore it is important to manipulate the chemoattractant concentration on very short timescales, which is possible with the recent developments in microfluidics.

We have built a microfluidic setup to measure the sub-second chemotactic response of single cells, which allows us to expose the cells to defined gradients of chemoattractant, changing directions with switching times down to a few seconds. Consequently we observed a time-dependent directed motion for Dd cells. To study the local protein response to a fast switching gradient by fluorescence imaging, we use knock-out and fluorescently labelled mutants of Dd cells.

We aim at trapping cells by adjusting the switching times of the chemoattractant gradient in a way that the cells repolarise without an actual displacement. Therefore we will be able to perform high precision measurements on immobilised cells.

BP 10.4 Tue 15:00 HÜL 186

Cell surface protein dynamics in microflow — •Eric Stellamanns[1], Sravanti Uppaluri[1], Niko Heddergott[2], Markus Engstler[2], and Thomas Pfohl[1] — [1]Max Planck Institute for Dynamics and Self Organization, Göttingen, Germany — [2]Technical University of Darmstadt, Cellular Dynamics Unit, Darmstadt, Germany

The human bloodstream parasite Trypanosoma brucei has evolved a clever trick to escape its host's immune response. Living in an environment of constant flux, it propels itself with a relative velocity of 20μm/s, washing off any hostile antibody that binds to its variable surface glycoprotein (VSG) coat. Optical tweezers and microfluidic techniques are used to label single VSG dimers of living trypanosomes with quantum dots (Qdots) as antibody mimics. The highly fluorescent Qdots allow us to trace single VSG-Qdot complexes along the cell membrane, thereby we study the effects of flow velocity, fluid viscosity and cell motility on the transport of these "molecular sails". Further we examine hydrodynamic forces on the molecular scale and describe their protein organizing effects in cell membranes.

BP 10.5 Tue 15:15 HÜL 186

Motility Patterns and Structure Formation Dynamics of Physarum Polycephalum — •Christina Oettmeier, Siddharth Deshpande, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

The plasmodium of the slime mold Physarum Polycephalum is a unicellular organism with a large number of nuclei, which can grow several square centimeters in area. The plasmodium develops veins, which cause reversible shuttle streaming of the endoplasm via periodic contractions. We report on the dynamics of this network during formation, growths, and plasmodium extension as a function of environmental conditions. Especially, we are interested in the role of endoplasmic streaming in network formation.

BP 10.6 Tue 15:30 HÜL 186

Steering chiral swimmers along noisy helical paths — •Benjamin M. Friedrich and Frank Julicher — Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden

Helical swimming of microorganisms is ubiquitous in nature and has been observed e.g. for sperm cells, eukaryotic flagellates, and even bacteria. A simple feedback mechanism enables these chiral swimmers to navigate upwards a concentration gradient of a chemoattractant [1]. We characterize the robustness of this chemotaxis strategy in the presence of non-equilibrium fluctuations [2] and derive a formal analogy to the orientation of a dipol in an external field. For an exemplary search problem, we show that search success is maximal for a finite noise level [3]. Different biological swimmers employ various navigational strategies of which chemotaxis along noisy helical paths is just one example. We discuss the availableness of different strategies to a swimmer as a function of the noise level and give biological examples.

[1] B.M.F., F.J.: Proc. Natl. Acad. Sci. USA **104** (2007).
[2] B.M.F., F.J.: New J. Phys., in press.
[3] B.M.F.: Phys. Biol. **5** (2008).

BP 10.7 Tue 15:45 HÜL 186

Theoretical modelling of bacterial motor dynamics — •Eva Baresel and Rudolf Friedrich — Institut für Theoretische Physik, Westfälische Wilhelms-Universität Münster

As a model for bacterial motors we consider the dynamics of an ensemble of swimming objects which are composed of two rigidly connected point vortices. The single objects are able to propel or to tumble depending on the circulations of the single point vortices. We discuss the collective behaviour for several of these objects by means of numerical calculations.

BP 10.8 Tue 16:00 HÜL 186

Investigating cross-linking properties of actin structures with holographic optical tweezers in microfluidic systems — •Kai Uhrig[1,2], Rainer Kurre[1,2], Martin Streichfuss[1,2], Friedrich Erbs[1,2], Simon Schulz[1,2], Anabel Clemen[1,2], Tamas Haraszti[1,2], Christian Böhm[1,2], and Joachim Spatz[1,2] — [1]MPI for Metals Research, Dept. Spatz, Heisenbergstr. 3, 70569 Stuttgart — [2]Univ. of Heidelberg, Biophys. Chem. Dept., INF 253, 69120 Heidelberg

The actin cortex is an adaptive chemo-mechanical polymer network located underneath the cell membrane. A multitude of factors and proteins that induce cross-linking, gelification or bundling of filaments controls its shape and mechanical properties. Recent studies on actin network mechanics were always restricted to three dimensional bulk gels, which are believed to show significantly different mechanic behaviour. We used the combination of holographic optical tweezers (HOT) with microfluidic techniques to create two dimensional network structures on trapped microbeads that could be cross-linked and probed subsequently. High-speed imaging was used to monitor force generation due to contraction of the network at all trapped beads simultaneously whilst fluorescence imaging was implemented to follow structural changes of the actin network. In another approach, HOTs and the combination of optical tweezers with PDMS micropillar substrates are used to investigate cross-linking processes in zipper-like structures between freely suspended actin filaments in detail. Force curves for zipping processes as well as for force induced unzipping could be deduced and correlated to fluorescence micrographs of the zipper structures.

BP 10.9 Tue 16:15 HÜL 186

Hydrodynamic description of cortical dynamics in the *C. elegans* zygote — •Justin Bois[1,2], Martin Depken[1,2], Mirjam Mayer[2], Frank Jülicher[1], and Stephan Grill[1,2] — [1]Max Planck Institute for Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute for Molecular Cell Biology and Genetics, Dresden, Germany

Establishment of cell polarity in the early stages of embryonic development is necessary for unequal cell division and a prerequisite for differentiation in developing organisms. In the zygote of the nematode *Caenorhabditis elegans*, the acto-myosin cortex plays a critical role in polarity establishment. A local down-regulation of myosin activity at the posterior of the zygote triggers directed cortical flow toward the anterior. As the structure and dynamics of the cortex are poorly understood at the microscopic level, we use a coarse hydrodynamic description of the cortex to determine what essential bulk properties are necessary for observed macroscopic flow behavior. We find that on the time scale of the flows, the cortex may be modeled as a viscous fluid that consumes energy through ATP hydrolysis. This simple description gives flow profiles that agree with experimental measurements, suggesting that while they may have other biological significance, more detailed microstructural features are not essential for establishment of cortical flow.

BP 11: Novel Methods

Time: Tuesday 14:30–16:30 Location: ZEU 260

BP 11.1 Tue 14:30 ZEU 260

Fast Dynamics of Cellular Signals Studied With a Novel Miniaturized Multi-Channel Perfusion System — •Claus Fütterer[1], Luru Dai[2], Hans Fried[2], Arne Brombas[2], Arnd Baumann[2], Thomas Gensch[2], and Frank Müller[2] — [1]Forschungszentrum Jülich, IBN-4, 52425 Jülich — [2]Forschungszentrum Jülich, INB-1, 52425 Jülich

In order to study the dynamics of cellular signaling in single cells and ex vivo-tissues, we developed a novel miniaturized fluidic system that allows unparalleled fast and artefact-free solution exchange using multiple inflow channels. To this end, methods of microfabrication and numerical simulations have been involved.

HEK-293 cells were used that expressed octopamine receptors as well as the genetically encoded calcium sensor TN-L15, designed for calcium dependent Fluorescence Resonance Energy Transfer. Switching from octopamine free to octopamine containing solution leads to oscillations of the intracellular calcium concentrationof which the onset and fading out of these oscillations can be controlled with unparalleled temporal resolution.

Further we studied calcium signals in flatmounted retinae of transgenic mice that express TN-L15 in retinal ganglion cells. Cells were activated by switching the perfusion from normal extracellular solution to solution with high K+ concentration to enable the precise measurement of the intracellular calcium concentration. The high temporal resolution achieved in our set-up revealed differences in the response of individual ganglion cells that had not been detected before.

BP 11.2 Tue 14:45 ZEU 260

Giving biomechanics a spin: the Optical Cell Rotator — •Anatol Fritsch[1], Tobias Kiessling[1], Moritz Kreysing[2], Franziska Wetzel[1], and Josef Käs[1] — [1]University of Leipzig, Germany — [2]University of Cambridge, UK

In cell biophysics striking insights have often been connected to new developments of optical microscopy tools enabling a deeper look into the underlying physical principles of cells. We present our newly developed modified divergent dual-beam laser trap, which enables holding and controlled rotation of suspended cells and cell aggregates for high resolution tomographic imaging, called the Optical Cell Rotator.

Showing the possibilities of this technology, we studied the mechanical properties of cells in cell aggregates since it opens the possibility for a deeper understanding of cell-cell interactions in tissues. Malignant tumours are not only agglomerates of homogeneous cells, but rather complex structures containing diverse normal and pathological cells in different stages of aggressiveness. Recent investigations show that the biomechanical properties of benign cells differ from those of cancerous and metastatic cells. However, the optical deformability of primary lung and breast cancer cells compared to their corresponding cell lines show at the first sight an unexpected stiffening behaviour. To elucidate this finding we compare 3D and standard monolayer cultured cells by their mechanical properties with the Optical Stretcher enabling contact-free, whole cell elasticity measurements and the Optical Cell Rotator to connect the findings to the underlying cytoskeletal structure.

BP 11.3 Tue 15:00 ZEU 260

Periodic strain slows down osteoblast proliferation — •Matthias Maier[1], Pablo Fernandez[1], Ludwig Eichinger[2], and Andreas R. Bausch[1] — [1]E27 Zellbiophysik, Technische Universität München, D-85748 Garching, Germany — [2]Institut für Biochemie I, Universität Köln, D-50931 Köln

The quantitative study of mechanotransduction poses a major interdisciplinary challenge. The complex mechanical behaviour of cells demands systematic variation of key mechanical parameters such as strain rate, amplitude and stress, as well as control of adhesive conditions. At the same time the analysis of the cellular response must deal with biological complexity and heterogeneity. Here, we present an experimental setup which combines cell monolayer rheology with DNA microarray technology. By applying shear strain on over 10 million cells simultaneously, we obtain the large amounts of material needed for integral genomics or proteomics characterisation without compromising on a clean, well-defined mechanical perturbation. In a first application, we address the phenomenon that periodic shear at large amplitudes appears to influence osteoblast proliferation. Preliminary results with our setup followed by microarray analysis indeed reveal a down-regulation of genes involved in mitosis, most conspicuously anillin, an essential component of the contractile ring. We speculate on a direct mechanical effect of the external deformation on cytokinesis.

BP 11.4 Tue 15:15 ZEU 260

Label-free bioimaging of living human glioblastoma cells by confocal Raman microscopy — •Alexander M. Gigler[1], Katharina Klein[2], Guido Piontek[2], Thomas Aschenbrenner[3], Wolfram Bunk[3], Gregor Morfill[3], Jürgen Schlegel[2], and Robert W. Stark[1] — [1]Center for Nanoscience (CeNS) and Sect. Crystallography, LMU-München, D-80333 München — [2]Neuropathology, TU-München, Klinikum rechts der Isar, D-81675 München — [3]MPI for Extraterrestrial Physics, D-85748 Garching

Label-free imaging by confocal Raman spectroscopy is becoming a promising alternative to established methods for cell imaging requiring fixation and the use of fluorescent markers. With our setup we are able to image living cells at a high resolution in buffer solution (PBS). Different cellular compartments can be visualized and directly compared to immunofluorescence microscopy (IF). The comparison of Raman and IF image sets allows an assignment of organelles such as nucleus, endoplasmatic reticulum, and mitochondria. From the assigned areas we obtained average spectra of the compartments resulting in an individual spectral fingerprint for each specific region. These fingerprints can in turn be used to define spectral filters for mapping in an iterative procedure. Spectral maps of single cells provide the full set of biochemical information contained in the selected focal plane. To this end, we are using IF staining methods to verify our observations and assignments. On the long run, our aim is to identify specific molecular markers for therapeutic targeting and discriminate between cells of different lines or differentiation states based on spectral information.

BP 11.5 Tue 15:30 ZEU 260

Spatial chemical gradient measurements in microfluidic channels by arrays of nano-gap electrodes — •Enno Kätelhön[1,2], Marcel A. G. Zevenbergen[3], Edgar D. Goluch[3], Serge G. Lemay[3], Andreas Offenhäusser[1,2], and Bernhard Wolfrum[1,2] — [1]IBN-2, Forschungszentrum Jülich GmbH, Germany — [2]JARA- Fundamentals of Future Information Technology — [3]Kavli Institute of Nanoscience, Delft University of Technology, the Netherlands

In recent years, microfluidic devices have received growing attention along with the proceeding miniaturization of electrochemical sensors. In particular regarding biophysical applications, there is an increasing interest due to the potential to establish specific chemical environments inside of microfluidic systems. Since these systems feature a laminar flow trait, they allow setting up highly defined chemical gradient fields that are exclusively based on diffusive mixing. Thus, cell growth characteristics can be investigated concurrently within one experimental setup in different chemical environments.

We present a new method to evaluate the mixing gradient of redox- and non redox-active substances inside of a micro scaled flow. Our system features a set of interdigitated nano-electrode arrays that is incorporated into a PDMS microchannel. By this means, we can record cyclic voltammograms simultaneously at different locations inside of the channel as well as determine the concentration of the redox-active substance at specific spots. Owing to the nano scaled redox cycling approach, our method exhibits a high special resolution and a large current amplification.

BP 11.6 Tue 15:45 ZEU 260

Immunoassay based on long-range fluorescence quenching by gold nanoparticles — •Meike Kloster[1], Sergiy Mayilo[1], Fernando Stefani[1], Michael Wunderlich[1], Thomas A. Klar[1,2], Hans-Peter Josel[3], Dieter Heindl[3], Alfons Nichtl[3], Konrad Kürzinger[3], and Jochen Feldmann[1] — [1]Photonics and Optoelectronics Group, Department of Physics and CeNS, Ludwig-Maximilians-Universität München, Munich, Germany — [2]Institute of Physics and Institute of Micro- and Nanotechnologies, Technical University of Ilmenau, Ilmenau, Germany — [3]Roche Diagnostics GmbH, Penzberg, Germany

Förster energy transfer is a common tool for the detection of biomolecules. However, due to its short-range, the application is limited to small distances. Energy transfer from a dye molecule to a gold nanoparticle (AuNP) is effective over longer distances due to the larger cross-section of the particles and to radiative rate suppression [1]. Here we use the long-range fluorescence quenching by AuNPs to develop a novel immunoassay for a diagnostically relevant example: troponin T (TnT), an indicator of damage to the heart muscle. AuNPs and fluorescent dyes are functionalized with anti-TnT antibodies. In the presence of TnT, the AuNPs and the fluorophores are brought together by their specific interaction leading to fluorescence quenching. By using time-resolved spectroscopy, the contributions of direct energy transfer and radiative decay suppression to fluorescence quenching are quantified.

[1] E. Dulkeith et al., Nano Letters 5, 585 (2005)

BP 11.7 Tue 16:00 ZEU 260

SERS labels for red laser excitation: silica-encapsulated SAM on tunable gold/silver nanoshells — •Magdalena Gellner, Max Schütz, Bernd Küstner, and Sebastian Schlücker — Department of Physics, University of Osnabrück, 49076 Osnabrück

Silica-encapsulated self-assembled monolayers (SAMs) on tunable gold/silver nanoshells for use as surface-enhanced Raman scattering (SERS) labels in bioanalytical and biomedical applications with red laser excitation are presented. [1] This concept combines the spectroscopic advantages due to the maximum surface coverage and uniform molecular orientation of Raman reporter molecules within a SAM together with the high chemical and mechanical stability of a glass shell. The absorption, scattering and extinction spectra of various gold/silver nanoshells were calculated using Mie theory. Quantitative SERS efficiencies based on theoretical scattering intensities are compared with experimental findings. [2] Our improved SERS label design results in $\sim$ 180 times brighter SERS signals compared with existing approaches based on single gold nanospheres.[1] Using SERS-labeled antibodies, the selective localization of prostate-specific antigen (PSA) in the epithelium of prostate tissue specimens by immuno-SERS microscopy with red laser excitation is demonstrated.

[1] B. Küstner, M. Gellner, M. Schütz, F. Schöppler, A. Marx, P. Ströbel, P. Adam, C. Schmuck, S. Schlücker, Angew. Chem. Int. Ed., accepted

[2] M. Gellner, B. Küstner, S. Schlücker, Vib. Spectrosc., 2008, doi:10.1016/j.vibspec.2008.07.011

BP 11.8 Tue 16:15 ZEU 260

Impedance study of AlGaN/GaN HEMT structures in contact with electrolyte solutions — Michael Charpentier, •Hartmut Witte, Christian Warnke, Mathias Müller, Kay-Michael Günther, Armin Dadgar, and Alois Krost — Otto-von-Guericke-University-Magdeburg, Institute of Experimental Physics, 39016 Magdeburg

Planar multi-electrode-arrays (MEA) are widely spread for stimulation and recording of neuron network signals. Besides metal electrodes and Silicon, more and more group-III-nitride devices are used as substrates. For MEA applications the substrate impedance as one of the main signal transfer parameters has to be optimized. In this contribution we investigate the total impedance of AlGaN/GaN high electron mobility structures (HEMT) using impedance spectroscopy between 20 Hz and 2 MHz. The total impedance is composed of the contributions of the two dimensional electron gas (2DEG), the metal contacts and the horizontal and vertical layer material impedances. The impacts of these parts were studied by varying the layer arrangement and applied bias voltages, by using a MESA microstructuring, and by illumination of the samples. All variations significantly change the impedance spectra. Furthermore, samples with different total impedances show disparate signal behavior in contact with electrolyte solutions with varying pH-values and conductivities. Therefore, these investigations are useful for optimization of the device performance for different biosensor applications.

BP 12: Single Molecules

Time: Wednesday 9:30–13:15 Location: HÜL 186

Invited Talk BP 12.1 Wed 9:30 HÜL 186

Conformational Mechanics of Single Protein Molecules — •Matthias Rief — Physikdepartment der TU München, Lehrstuhl für Biophysik E22, 85748 Garching

The development of novel ultrasensitive force probes with high spatial resolution, like AFM and optical tweezers, has allowed us to use mechanical force as a control parameter for bio-molecular conformation. Such single molecule experiments offer new possibilities for understanding the self-organization as well as the mechanical function of bio-molecules. In the talk I will discuss how mechanical forces can be used to explore the complex energy landscape of proteins. Examples will include equilibrium and non-equilibrium folding/unfolding of proteins, as well as force-induced conformational changes of protein-protein complexes.

Invited Talk BP 12.2 Wed 10:00 HÜL 186

Illuminating the way Kinesin-1 walks using FRET between the motor domains — •Erwin Peterman — VU University, Amsterdam, the Netherlands

Kinesin-1 is a motor protein that walks processively along microtubules in a hand-over-hand manner driving intracellular transport of vesicles and organelles. Each step of 8 nm requires the hydrolysis of one ATP and takes about 10 ms at cellular ATP concentrations. Key aspects of kinesin*s walking mechanism are not fully understood. One important question concerns the configuration of the two motor domains during processive motion.

Here, we use a novel assay based on single-molecule confocal fluorescence microscopy to characterize Kinesin-1*s stepping mechanism in vitro. A key advantage of our approach over conventional wide-field methods is that our time resolution is far better, less than 0.1 ms. We apply this approach to kinesin constructs that are labeled with a donor fluorophore on the one motor domain and an acceptor on the other. We follow the distance between the motor domains during stepping with Förster Resonance Energy Transfer. We use four different homodimeric kinesin constructs with dye molecules attached to different sites of the motor domain. With this approach, we can identify an intermediate state in the stepping process that lasts 2-3 ms at saturating ATP concentration. In this intermediate state one motor domain is bound to the microtubule and the other is rotated and substantially less than 8 nm away.

BP 12.3 Wed 10:30 HÜL 186

Single-molecule measurement of protein friction between kinesin and the microtubule surface and its relation to lattice diffusion — Volker Bormuth[1], Vladimir Varga[1], Jonathon Howard[1], and •Erik Schäffer[2] — [1]MPI of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, 01307 Dresden, Germany — [2]Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

Friction within an engine or between a vehicle and its track plays a crucial role in the operation of macroscopic machines. Biological machines such as muscle are also subject to frictional forces. The concept of protein friction has been used in theoretical studies, but experimental studies are scarce. We have developed techniques based on optical tweezers to measure the friction between individual kinesin-8 molecules and microtubules in the presence of ADP. At low speeds we find a friction coefficient of 700 ± 300 nNs/m, which is in good agreement with the diffusion coefficient measured under identical conditions. This confirms the fundamental connection between friction and diffusion. We measured a non-linear dependence of friction on velocity, allowing us to estimate the distance between diffusional hopping steps of 8.0 ± 0.6 nm. This step size was confirmed by direct resolution of step-wise motions as well as a fluctuation analysis; thus kinesin-8 steps between adjacent tubulin dimers. Our experiments therefore confirm the presence of protein friction—an important parameter for active protein locomotion limiting the efficiency.

BP 12.4 Wed 10:45 HÜL 186

Reversible Affinity Switching of a Single Supramolecular Receptor Molecule — •Volker Walhorn[1], Christian Schäfer[2], Tobias Schröder[3], Jochen Mattay[3], and Dario Anselmetti[1] —

[1]Experimental Biophysics and Applied Nanosciences, Bielefeld University — [2]Organic Nanosciences University of Bordeaux 1 — [3]Organic Chemisty Bielefeld University

Photoactivation of single molecules is a common concept in nature. In order to investigate such mechanisms we synthesized a bistable supramolecular complex consisting of a Resorc[4]arene receptor cavity modified with two anthracene moieties. These can be switched between two isoforms either by UV-light or heat [1]. Using atomic force microscope based single molecule force spectroscopy (AFM-SMFS) we investigated the conformation dependent receptor affinity to different ammonium derivates. Our results show that this system can be reversely and repeatedly switched between two different isomeric conformations accompanied by a drastic change of affinity to ammonium ligands. For the "open" high affinity state we could also demonstrate the specificity by competition experiments and estimate associated binding properties like reaction lengths (x_β) and thermal off-rate constants (k_{off}). Robust bistable molecular systems are potential candidates for novel concepts in bio-medical, analytics, directed molecular assembly or controlled drug delivery.

[1] C. Schäfer et. al. J. Am. Chem. Soc. 2007, 129, 1488-1489

BP 12.5 Wed 11:00 HÜL 186

Dual-focus flow detection: Exposing biological heterogeneity one molecule at a time — •Tyler Arbour, Anastasia Loman, and Jörg Enderlein — III. Institut für Physik, Georg-August-Universität Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen

The ability to distinguish between multiple fluorescent species or states in solution at the single-molecule level is an attractive concept. To realize this level of analysis in confocal detection, we must eliminate the uncertainty introduced by random diffusion of the molecule. In other words, we must know the path a molecule takes through the confocal detection volume. In a conventional detection scheme, this translates into directing the fluorescent species through the confocal volume's center using, for example, a microinjection sample capillary surrounded by a continuous sheath fluid flow. This has been successfully demonstrated in the past, first by Richard Keller et al in the sizing of individual dye-labeled DNA fragments.[1] However, such a setup is difficult to build, and the nanometer-scale components are very prone to clogging as well as unwanted fluorophore-capillary interactions; as a result, this idea has been largely abandoned. Here we present a much simpler setup that takes advantage of dual-focus detection in a net fluid flow to achieve precise knowledge of a molecule's path.

1. Goodwin, P.M., et al., Nucleic Acids Research, 1993. 21(4): p. 803-806

BP 12.6 Wed 11:15 HÜL 186

Time resolved three-dimensional orientation of eGFP — •Richard Börner — Universität zu Lübeck, Institut für Physik, Ratzeburger Allee 160, 23568 Lübeck, Germany

Confocal microscopy is a powerful method for single molecule investigation of fluorescent macromolecules. Beside the translatory movement of labeled or autofluorescent molecules rotational dynamics reflect the properties of the macromolecule and its surrounding. In principal the determination of the molecular orientation bases on the defined orientation of the absorption/emission dipole with respect to the molecular frame. Using a method which has been recently proposed by Hohlbein & Hübner [1,2] we demonstrate the time resolved three-dimensional orientation determination for the well known and biological relevant molecule eGFP. By using adapted FCS and TCSPC measurments we observe the orientation on a millisecond down to a nanosecond time scale.

[1] J. Hohlbein & C. G. Hübner, APL, 86, 121104 (2005)
[2] J. Hohlbein & C. G. Hübner, JCP, 129, 094703 (2008)

15 min. break

BP 12.7 Wed 11:45 HÜL 186

Determining the hydrodynamic size and shape of biomolecules by probing single-molecule Brownian motion — •Sandeep Pallikkuth and Andreas Volkmer — 3rd Institute of Physics, University of Stuttgart, Germany

Information regarding the hydrodynamic volume of a fluorescent biomolecule is obtained by monitoring its Brownian motion in solution. While the translational diffusion of a fluorescent biomolecule, occurring on the micro- to millisecond time scale, is conveniently obtained from a conventional fluorescence correlation spectroscopy experiment, the more size-sensitive Brownian rotational dynamics of the molecule, occurring on the pico- and nanosecond time scale, is generally obtained from the measurement of its time-resolved fluorescence anisotropy upon pulsed excitation. The application of the latter technique, however, is limited by its fluorescence lifetime, preventing the accurate measurement of rotational diffusion time when in the order of tens of nanoseconds. Based on recent experimental advances allowing the calculation of second-order correlation function from distinct photon arrival times with picosecond time resolution and applying an exact theoretical model, we demonstrate probing of Brownian rotational diffusion of a biomolecule in free solution at time scales between a picosecond and hundreds of nanoseconds without the need for pulsed excitation. Moreover, the simultaneous measurement of both the translational and rotational diffusion of a biological macromolecule with this technique allows the determination of the hydrodynamic size and shape of the biomolecule.

BP 12.8 Wed 12:00 HÜL 186

Stretching and unfolding titin: Metastability and survival of the fittest — •Douglas B. Staple[1,2], Stephen H. Payne[1], Andrew L. C. Reddin[1], and Hans Jürgen Kreuzer[1] — [1]Dalhousie University, Halifax, Canada — [2]Max-Planck-Institut für Physik komplexer Systeme, Dresden, Germany

Single-molecule manipulation has allowed the forced unfolding of multidomain proteins. Here we outline a theory that not only explains these experiments but also points out a number of difficulties in their interpretation and makes suggestions for further experiments. For titin we reproduce force-extension curves, the dependence of break-force on pulling speed, and break-force distributions and also validate two common experimental views: unfolding titin Ig domains can be explained as stepwise increases in contour length, and increasing force peaks in native Ig sequences represent a hierarchy of bond strengths. Our theory is valid for essentially any molecule that can be unfolded in atomic force microscopy; as a further example, we present force-extension curves for the unfolding of RNA hairpins.

BP 12.9 Wed 12:15 HÜL 186

Dual-Focus Correlation Spectroscopy: Advantages and applications — •Anastasia Loman and Jörg Enderlein — III. Institut für Physik, Georg-August-Universität Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen

Fluorescence correlation spectroscopy (FCS) is a powerful technique for measuring diffusion coefficients of fluorescent molecules at pico- to nanomolar concentrations. A modified version of FCS, dual-focus FCS (2fFCS) shows significantly improvement in the reliability and accuracy of FCS measurements and allows for obtaining not relative but absolute values of diffusion coefficients [1].

The high precision of 2fFCS (absolute accuracy is shown to be better than 5 %) and the simple Stokes-Einstein relation directly coupled hydrodynamic radius and diffusion coefficient allow to monitor interactions of biomolecules - in particular proteins, RNA, DNA - with their environment or reacting to changes in environmental parameters such as pH, temperature, or chemical composition (e.g. protein unfolding) or performing biologically important functions (e.g. enzymatic catalysis).

We demonstrate that this method is sensitive enough to resolve length changes in small peptides of only one amino acis, and size changes of hydrodynamic radii as small as 0.5 nanometers. We used 2fFSC to study conformational changes of proteins such as phosphoglycerate kinase (PGK), α-amylase, and MHC class I complex under different conditions.

1. Dertinger, T. at al., ChemPhysChem 8 (2007) 433.

BP 12.10 Wed 12:30 HÜL 186

Calcium mediated carbohydrate-carbohydrate interactions investigated with single molecule force spectroscopy — •André Körnig[1,2], Iwona Bucior[3], Max M Burger[4], Xavier Fernandèz-Busquets[2], and Dario Anselmetti[1] — [1]Experimental Biophysics, Bielefeld University — [2]Nanobioengineering Group, University of Barcelona — [3]University of California, San Francisco — [4]Friedrich-Miescher-Institute, Basel

Marine sponges associate through species-specific, calcium-mediated carbohydrate-carbohydrate interactions of the g200 glycan found on sponge proteoglycans. A detailed and quantitative single molecule force spectroscopy analysis of g200-g200 binding in Microciona prolifera reveals adhesion forces in the range of 100-250 pN. However, our results indicate that calcium-dependent, macroscopic sponge cell

self-association is only little influenced by the absolute single molecule binding forces but critically rely on the kinetic reaction properties that manifest themselves in Ca^{2+}-mediated bond lifetimes (10 mM Ca^{2+}/ 0 mM Ca^{2+}: 680 s / 3 s) and bond reaction lengths (10 mM Ca^{2+}/ 0 mM Ca^{2+}: 3.47 Å / 2.27 Å). Since cellular association in sponges is a polyvalent process, the observed binding phenomenon has to be analysed with a cooperative adhesion cluster model that distinctively supports the macroscopic observations of mean dissociation lifetimes for sponge multicell integrity in low and high calcium. A potential relation to a more generalized picture of the mid-cambrian explosion of metazoan evolution will be discussed.

BP 12.11 Wed 12:45 HÜL 186

Microfluidic device for polarizability-quantification and fast DNA-separation on single molecule scales — •Lukas Bogunovic[1], Jan Regtmeier[1], Ralf Eichhorn[2], Alexandra Ros[3], and Dario Anselmetti[1] — [1]Experimental Biophysics & Applied Nanoscience, Bielefeld University, Germany — [2]Condensed Matter Theory, Bielefeld University, Germany — [3]Department of Chemistry and Biochemistry, Arizona State University, Tempe, USA

We present a simple and easy to fabricate poly(dimethylsiloxane) (PDMS) microfluidic device, capable of quantifying DNA polarizabilities on a single molecule level. The same system is able to separate long DNA molecules as well as biotechnologically relevant supercoiled plasmid DNA via electrodeless dielectrophoresis in less than 240 seconds.

The device consists of a cross injector and an analysis channel. The latter is structured with a series of conducting posts creating dielectrophoretic (DEP) traps, when a voltage is applied. The quantificaton as well as the separation is consequently based on the size dependent thermally induced esacpes from those DEP traps.

The observed polarizabilities of linear dsDNA demonstrate a length dependence, which has been discussed controversially. This dependence can be described with a simple power law and an exponent for linear DNA from 6 kbp to 164 kbp close to the Flory exponent. In separation mode, separation times of 200s for λ (48.5 kbp)- and T2 (164 kbp)- DNA were achieved with baseline resolution.

BP 12.12 Wed 13:00 HÜL 186

Transport through OmpF channels simulated using molecular dynamics — •Soroosh Pezeshki, Mathias Winterhalter, and Ulrich Kleinekathöfer — Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany

The outer membrane porin OmpF is one of the major porins in E. coli and is the main entrance for small molecules like beta-lactam antibiotics. The narrowest part of the pore, the constriction zone, includes charged residues which have a high but still not well understood influence on the ion permeation. Here different mutations of OmpF are used to study the influence of charged residues on the conductance [1]. The selectivity of the pore can be changed over wide ranges by mutations. In a second step the translocation of antibiotics molecules through the pore is simulated. To speed up the translocation steered molecular dynamics (SMD) is employed. Different pulling strategies are used to get a better understanding of the interaction of pore and antibiotics. The SMD simulations are compared to so-called meta-dynamics simulations for calculating the potential of mean force (PMF) and at the same time used to analyze in vitro experiments [2].

[1] C. Chimerel and L. Movileanu and S. Pezeshki and M. Winterhalter and U. Kleinekathöfer, 2008, Eur. Biophys. J., **38**, 121-125
[2] C. Danelon and E. M. Nestorovich and M. Winterhalter and M. Ceccarelli and S. M. Bezrukov, 2006, Biophys. J., **90**,1617-1617

BP 13: Cell Migration

Time: Wednesday 10:45–13:15 Location: ZEU 260

BP 13.1 Wed 10:45 ZEU 260

Quantitative studies of Dictyostelium discoideum chemotaxis — •Matthias Theves[1], Carsten Beta[1,2], and Eberhard Bodenschatz[1] — [1]Max-Planck Institut für Dynamik und Selbstorganisation, Göttingen — [2]Universität Potsdam

We use microfluidic tools to expose Dictyostelium discoideum amebae, a model organism for eukaryotic chemotaxis, to directional stimuli of cyclic adenosine 3',5' monophosphate (cAMP). We classify the migrational patterns of single cells in stationary linear gradients and quantify the accuracy of directional migration as a function of gradient steepness and varying midpoint concentrations. The results on wild-type chemotaxis serve as a reference to study the altered motility of various cytoskeletal mutants. In particular, we focus on constructs lacking regulators of the Arp2/3 complex, a key player in the formation of a dense cortical actin network at the leading edge of motile cells.

BP 13.2 Wed 11:00 ZEU 260

Force generation in moving fish keratocytes — •Claudia Brunner, Michael Gögler, Daniel Koch, Thomas Fuhs, Allen Ehrlicher, and Josef Käs — Universität Leipzig

A fundamental step in cell migration is the advancement of the cell's leading edge which is hypothesized to be mediated by actin polymerization against the plasma membrane. Our newly established SFM-technique revealed that the force generating mechanism driving this process is indeed actin polymerization. Cells treated with the actin polymerization inhibitor cytochalasin D generated significantly lower forces. Additionally, we directly measured a force associated with the retrograde flow within the lamellipodium, which demonstrates that the protrusion forces are decoupled from the cell body and are generated exclusively at the leading edge. We show that actomyosin interaction is primarily responsible for cell body and traction force generation while myosin II contraction cannot be the dominant force generating mechanism driving retrograde flow in the central lamellipodium.

BP 13.3 Wed 11:15 ZEU 260

Mimicking Cellular Environments: Cells on elastic nanopatterned substrates — •Ilia Louban[1,2], Roberto Fiammengo[1,2], and Joachim Spatz[1,2] — [1]MPI for Metals Research, Dept. of New Materials & Biosystems; Heisenbergstr. 3, D-70569 Stuttgart — [2]Univ. of Heidelberg, Dept. of Biophys. Chemistry; INF 253, D-69120 Heidelberg

The last years, hydrogels based on poly(ethylene glycol) diacrylate (PEG-DA) have been developed to serve as synthetic extracellular matrix analogues with adjustable mechanical and biochemical properties. Their Young's moduli (E) span more than four orders of magnitude (0,6kPa<E<6MPa). Since PEG-DA features protein and consequentially cell repellent properties, the hydrogel surface has to be modified to provide bioactivity. Extended gold nanoparticle arrays, manufactured by block copolymer micellar nanolithography, could be transferred to the hydrogel surface providing single anchor points for biofunctionalization. The interparticle distance (30nm<ΔL<200nm) on the substrate can be varied independently from its rigidity. To promote integrin mediated cell adhesion of rat embryonic fibroblasts, gold nanoparticles were functionalized with a cRGDfK peptide specific for $\alpha V\beta 3$ integrin. The effect of variation of substrate compliance and interparticle distance, tuned at the same time, was investigated. Our experiments reveals a significant decrease in cell spreading area on soft substrates (E<10kPa) and substrate with high interparticle distance (ΔL>70nm) after 6, 12 and 24 hours of adhesion respectively. Additionally we performed atomic force spectroscopy to quantify cellular adhesion to these surfaces.

BP 13.4 Wed 11:30 ZEU 260

Three-dimensional micro scaffolds for single cell experiments — •Joachim Fischer[1], Franziska Klein[2], Clemens Franz[2], Georg von Freymann[1], Martin Bastmeyer[2], and Martin Wegener[1] — [1]Institut für Angewandte Physik, Universität Karlsruhe (TH), 76128 Karlsruhe, Germany — [2]Zoologie I, Universität Karlsruhe (TH), 76128 Karlsruhe, Germany

The extracellular matrix with its specific mechanical and chemical properties has an important influence on eucaryotic cell adhesion, migration and differentiation behaviour. Investigating these cues *in vitro* requires a suitable method to fabricate three-dimensional micro environments with desired geometry, elasticity and functionality. Direct Laser Writing (DLW) allows the highly-reproducible fabrication of nearly arbitrary, three-dimensional polymer-microstructures with

feature sizes between 100 nm and several microns. The structures' mechanical responses to cellular contraction forces can be controlled by using different photoresists or by varying the thickness of individual elements. As a proof-of-principle, we demonstrate that chick cardiomyocytes cultured in these structures can rhythmically deform our elastic 3D-templates. Furthermore, we show a method to characterize the mechanical properties of these structures with an atomic force microscope. In the future, shaping the laser focus via phase- and/or amplitude modulation might allow for bigger and even smaller features and hence make DLW even more versatile for micro scaffold fabrication.

15 min. break

BP 13.5 Wed 12:00 ZEU 260

Single cell motility in tunable environments — •Sravanti Uppaluri[1], Jan Nagler[1], Markus Engstler[2], and Thomas Pfohl[1] — [1]Max Planck Institute for Dynamics and Self Organization — [2]Darmstadt University of Technology

African trypanosomes are parasites that infect a variety of hosts and cause fatal diseases including sleeping sickness in humans. Recent work has shown that trypanosome motility is essential in their evasion of the host immune response [Engstler M et al., Cell 2007]. We investigate the motility of trypanosomes in tunable environments in which we control viscosity (similar to that of blood), physical barriers (ECM-like collagen networks), and nutrient concentration. Despite comparable traveling velocities in all environments, the spread of the parasite, measured by its radius of gyration, is remarkably different among the various environments. In culture medium the trypanosomes move by one of three distinct motility classes: diffusion, directional persistence, and an intermediate class in which they exhibit a combination of both. The distribution of trypanosomes within these classes depends on environmental conditions. We show that the parasites are predominantly directionally persistent in higher viscosities. Analysis of scaling behaviour, corresponding to different motility classes will be presented.

BP 13.6 Wed 12:15 ZEU 260

Stochastic Lamellipodium Dynamics — •Melanie Knorr[1], Daniel Koch[3], Thomas Fuhs[1], Timo Betz[2], Ulrich Behn[1], and Josef Käs[1] — [1]University of Leipzig, Germany — [2]Institute Curie, Paris, France — [3]Georgetown University, Washington

Many processes in the body, such as immune response, wound healing, embryogenesis, and neuronal development rely on both the directed growth and movement of cells. The dynamic behavior of the lamellipodium, a thin veil-like structure at the cell's leading edge, is mainly based on the cytoskeletal processes of actin polymerization and molecular motor-driven retrograde flow. Experimental investigations reveal, that actin polymerization at the leading edge is the driving process of lamellipodial edge fluctuations. Statistical analysis shows that polymerization stochastically switches between "On" and "Off" states, and that both the lifetime of these states and the actin polymerization velocity at the edge determine cell movement. Studying the edge fluctuations of different cell types leads to a classification of cells on the basis of certain parameters that determine the stochastic lamellipodium dynamics. Based on these results we developed a stochastic model that consistently describes the experimentally derived data, including all underlying processes like actin polymerization and retrograde flow.

BP 13.7 Wed 12:30 ZEU 260

Growing Actin Networks Form Lamellipodium and Lamellum by Self-Organization — •Florian Huber, Björn Stuhrmann, and Josef Käs — Universität Leipzig, Linnestr. 5, 04103 Leipzig, Germany

Cell migration is associated with the dynamic protrusion of a thin actin-based cytoskeletal extension at the cell front. This extension has been shown to consist of two different substructures, the lamellipodium and the lamellum, which differ in their kinetic and kinematic properties as well as their molecular composition. While the formation of the lamellipodium is increasingly well understood, organizational principles underlying the emergence of the lamellum are just beginning to be unraveled. We developed a 2D Monte-Carlo simulation and an analytical description that include chemical reaction kinetics, actin monomer diffusion, and filament transport to investigate the formation of growing actin networks in migrating cells. We demonstrate the system*s ability to form two distinct networks by self-organization. We find a characteristic transition in filament lengths and a distinct maximum of depolymerization, both within the leading 1*2 microns of the cell, in agreement with experimental data. We investigate the complex interplay between ADF/cofilin and tropomyosin and propose a mechanism that leads to spatial separation of, respectively, ADF/cofilin- or tropomyosin-dominated compartments. Tropomyosin is found to play an important role in stabilizing the lamellar actin network.. Furthermore, the influence of filament severing and annealing on the network properties is explored. We contribute to a fundamental understanding of how cells organize their molecular components to achieve movement.

BP 13.8 Wed 12:45 ZEU 260

Microtubule-based neuronal growth cone motility — •Thomas Fuhs[1], Allen Ehrlicher[1,2], and Josef Käs[1] — [1]Universität Leipzig, Soft matter physics, Leipzig, Germany — [2]Harvard University, School of Engineering and Applied Sciences, Cambridge, USA

When creating a functional steering aparatus the individual nerve cells in the brain have to form synapses to pass on informations. Prior to the formation of a synapse the nerve cell has to find some other nerve cell to link to, therefore it sends out an exploratory growth cone. The growth cone is connected to the cell body with the microtubule rich axonal stump while on the front it consists mainly of actin, both as a dense network forming lamellipodia or thick actin bundles (filopodia).

This setup suggests an actin polymerization driven type of motility, as is it observed in fibroblasts. But in contrast to fibroblasts we obeserved inverse durotaxis, contradicting the models used for fibroblasts.

So we developed a theoretical model of how actin bundles steer a growth cone by mechanically stabilizing extending microtubules. Simple physics of anisotropic cytoskeleton elasticity and tube-model based ordering show how microtubules must align with stiff actin bundles, while unaligned one get buckled. Hence the side of the growth cone with fewer actin bundles dissipates more elastic energy in bent microtubules, resulting in a pressure pushing the growth cone in the opposite direction. This model also explains the inverse durotaxis, if more acto-myosin energy is dissipated into substrate deformation, less energy is available to deform the exploratory microtubules, resulting in an preferential extension towards softer materials.

BP 13.9 Wed 13:00 ZEU 260

Vinculin exchange dynamics regulates adhesion site turnover and adhesion strength — •Christoph Möhl, Norbert Kirchgessner, Claudia Schäfer, Kevin Küpper, Rudolf Merkel, and Bernd Hoffmann — Institut für Bio- und Nanosysteme 4: Biomechanik, Forschungszentrum Jülich GmbH, 52425 Jülich, Germany

The coordinated formation and release of focal adhesions is a key requirement for effective cell locomotion. New adhesions develop at the cell front and mature over time by changing composition and exchange dynamics of the incorporated proteins. As the cell moves forward, the maturing focal adhesions remain nearly stationary with respect to the substrate. They finally dissolve once the cell's trailing edge comes close. Besides other factors, this adhesion turnover defines the polarization and direction of migration of the cell and is thought to be highly regulated by phosphorylation events.

Here, we analyzed the dynamics of focal adhesions in migrating cells on different time scales. On the long time scale, we measured lifetimes and growth behaviour of focal adhesions, while on the short time scale the exchange dynamics of the focal adhesion protein vinculin was analyzed by FRAP (fluorescence recovery after photobleaching). In parallel, overall focal adhesion phosphorylation was quantified. Additionally, force measurements on moving cells were performed to correlate the maturation state of a focal adhesion with its adhesion strength. Our studies support a direct interplay between phosphorylation, adhesion dynamics and force application.

BP 14: Neuronal and Sensory Systems

Time: Wednesday 14:00–17:15 Location: HÜL 186

Invited Talk BP 14.1 Wed 14:00 HÜL 186

Nerve signals as density pulses, conduction events, and the role of anesthetics — •Thomas Heimburg — Niels Bohr Institute, University of Copenhagen, Denmark

It has long been known that nerve pulses are accompanied by a reversible heat exchange. After a first phase of heat release the heat is practically completely reabsorbed into the nerve membrane. This indicates that the fundamental physical processes underlying nerve action are predominantly of reversible nature. The famous Hodgkin-Huxley model, however, relies on dissipative processes, i.e., on electrical ion currents flowing through resistors (ion channel proteins). Here we show that under physiological conditions there is the possibility of electromechanical soliton generation. This notion is supported by the fact that during nerve pulses various mechanical changes are experimentally observed. The necessary requirement for solitons is a melting transition in the biomenbranes slightly below physiological temperature leading to a nonlinear compressibility. This transition is in fact present in biomembranes. Interestingly, exactly in these transitions one finds quantized ion currents through membranes that are indistinguishable from those reported for ion channel proteins. Anesthetics influence these processes because the induce melting point depression. Thus, they render the pulse excitation more difficult. Again, this is in agreement with data on real nerves. Further, anesthetics are able to "block" the conduction events through membranes.

BP 14.2 Wed 14:30 HÜL 186

Living optical elements in the vertebrate retina — Moritz Kreysing[1], Kristian Franze[1], Boris Joffe[2], Thomas Cremer[2], Leo Peichl[3], Andreas Reichenbach[4], and •Jochen Guck[1] — [1]Cavendish Laboratory, University of Cambridge, GB — [2]Institute of Human Genetics, LMU Munich, Germany — [3]MPI for Brain Research, Frankfurt, Germany — [4]Institute for Brain Research, University of Leipzig, Germany

While cells are mostly transparent they are phase objects that differ in shape and refractive index. Any image that is projected through layers of cells will normally be distorted. Strangely, the retina of the vertebrate eye is inverted and light must pass through several tissue layers before reaching the light-sensitive photoreceptor cells (PRC). Here we report how nature has optimized this apparently unfavourable situation. We investigated the optical properties of retinal tissue, individual Müller glial cells and PRC nuclei. We found that Müller cells act as optical fibers and guide light, which would otherwise be scattered, from the retinal surface to the PRCs. Their parallel arrangement in the retina is reminiscent of fiber-optic plates used for low-distortion image transfer. There is also a specific adaptation of the rod PRC nuclei for improved light transmission through the outer nuclear layer (ONL) of nocturnal animals. These nuclei have an inverted chromatin structure that turns them into micro-lenses channeling the light through the ONL. These findings ascribe a new function to glial cells, demonstrate the first nuclear adaptation for an optical function, and shed new light on the inverted retina as an optical system.

BP 14.3 Wed 14:45 HÜL 186

Eye dominance induces pinwheel crystallization in models of visual cortical development — •Lars Reichl[1], Siegrid Loewel[2], and Fred Wolf[1] — [1]Max-Planck-Institute for Dynamics and Self-Organization, Goettingen — [2]Institute of General Zoology and Animal Physiology, University Jena

The formation of orientation preference maps during the development of the visual cortex is sensitive to visual experience and impulse activity. In models for the activity dependent development of these maps orientation pinwheels initially form in large numbers but subsequently decay during continued refinement of the spatial pattern of cortical selectivities. One attractive hypothesis for the developmental stabilization of orientation pinwheels states that the geometric relationships between different maps, such as the tendency of iso-orientation domains to intersect ocular dominance borders at right angles can prevent extensive orientation map rearrangement and pinwheel decay. We present a analytically tractable model for the coupled development of orientation and ocular dominance maps in the visual cortex. Stationary solutions of this model and their dynamical stability are examined by weakly nonlinear analysis. We find three different basic solutions, pinwheel free orientation stripes, and rhombic and hexagonal pinwheel crystals locked to a hexagonal pattern of ipsilateral eye domains. Using amplitude equations for these patterns, we calculate the complete stability diagram of the model. In addition, we study the kinetics of pinwheel annihilation or preservation using direct numerical simulations of the model.

BP 14.4 Wed 15:00 HÜL 186

Comparison of stochastic integrate-and-fire models — •Benjamin Lindner and Rafael D. Vilela — Max-Planck-Institute for the Physics of Complex Systems, Dresden, Germany

We study three different integrate-and-fire (IF) models, the perfect, leaky, and quadratic IF model driven by white Gaussian noise and present a systematic comparison of their spontaneous and driven firing statistics in terms of power spectra, susceptibilities, and coherence functions. We also look at the correlations induced in the spike trains of two neurons by a common stimulus. Our comparison is based on parameter choices for the different models that make their firing rate and the CV of their interspike intervals equal — a choice that is unique for the three models under investigation as we have recently demonstrated[1]. We find that power spectra are rather similar for all three models while the input-output and the correlation statistics depend on the specific voltage dependence of the model and on the firing regime (combination of rate and CV) considered. Refs: [1] R. D. Vilela and B. Lindner J. Theor. Biol. (in press, 2008).

BP 14.5 Wed 15:15 HÜL 186

From Integrator to Resonator: The effect of dendrites on neuronal excitability — •Christoph Kirst[1], Andreas Herz[2], and Martin Stemmler[2] — [1]Network Dynamics Group, MPI for Dynamics and Self-Organization and BCCN Göttingen, Germany — [2]LMU and BCCN München

Neurons fall into two excitability classes: Type I integrates over synaptic inputs, while type II exhibits a resonance to a particular synaptic frequency [1]. Neuronal excitability is a function not only of the underlying ion-channel kinetics but also of the neuron's spatial structure. For example, the addition of a dendritic tree can change a neuron from a resonator into an integrator [2]. Here we show that the opposite transition can also occur: the presence of dendrites changes a saddle node on limit cycle bifurcation into a Hopf bifurcation, leading to a resonance where there was none before.

In a Morris-Lecar neuron model we show how an increase in the dendritic leak – e.g. by increasing the dendritic membrane surface – induces a change from type I to type II excitability. We analyze the underlying bifurcation structure to reveal the mechanism and the universality of such a transition. Consequences for the dynamics of networks of such neurons are discussed.

[1] G. B. Ermentrout, Neural Comput. 8, 979 (1996); Izhikevich E.M.Dynamical Systems in Neuroscience: The Geometry of Excitability and Bursting. MIT Press (2007).

[2] J. A. Goldberg, C. A. Deister and C. J. Wilson, J. Neurophysiol. 97, 208 (2007).

BP 14.6 Wed 15:30 HÜL 186

Extensive Chaotic Dynamics of Spiking Neuron Networks in the Balanced State — Michael Kreissl[1], •Siegrid Löwel[2], and Fred Wolf[1] — [1]Max Planck Institute for Dynamics and Self-Organization and BCCN in Göttingen, Germany — [2]Friedrich Schiller University and BGCN in Jena, Germany

Based on the calculation of the spectrum of Lyapunov exponents we reveal extensive, spatiotemporal chaos in deterministic neural networks of canonical type I neurons in the balanced state. In the balanced state of cortical networks, neurons are driven by strongly fluctuating inputs that result from balanced recurrent inhibition and excitation. It is the prevailing explanation of asynchronous, irregular firing patterns often observed in vivo. While its robust emergence from the collective dynamics of spiking neuron networks has been shown in several theoretical studies, the precise nature of the network dynamics remains controversial. It depends strongly on the single neuron dynamics. Initially, using binary neurons, Vreeswijk and Sompolinsky found that nearby trajectories diverge faster than exponential. Contrary, using leaky integrate and fire neurons, Zillmer et. al and Jahnke et. al re-

cently showed that nearby trajectories converge. In our study of sparse networks of theta neurons we find conventional chaos with a fat attractor and high entropy production. Because theta neurons exhibit the same type of bifurcation from resting to spiking as real cortical neurons, we expect that this extensive chaotic dynamics is characteristic of the balanced state in biophysically realistic network models.

15 min. break

BP 14.7 Wed 16:00 HÜL 186

First order phase transition to criticality by adaptive interactions — •Anna Levina[1,2], J. Michael Herrmann[1,2,3], and Theo Geisel[1,2] — [1]BCCN-Göttingen, Bunsenstr. 10, 37073 Göttingen — [2]MPI DS, Bunsenstr. 10, 37073 Göttingen — [3]University of Edinburgh, 10 Crichton Street, Edinburgh EH8 9AB, U.K.

The concept of self-organized criticality (SOC) describes a variety of phenomena ranging from plate tectonics, the dynamics of granular media to neural avalanches. In all these cases the dynamics is marginally stable and event sizes obey a characteristic power-law distribution. It was previously shown that an extended critical interval can be obtained in a neural network by incorporation of depressive synapses. In the present study we scrutinize a more realistic dynamics for the synaptic interactions that can be considered as the state-of-the-art in computational modeling of synaptic interaction. Interestingly, the more complex model does not exclude an analytical treatment and it shows a type of stationary state consisting of critical and a subcritical phases. The phases are connected by first- or second-order phase transitions in a cusp bifurcation which is implied by the dynamical equations of the underlying biological model. We present exact analytical results supported by extensive numerical simulations. Although presented in the specific context of a neural model, the dynamical structure of our model is of more general interest. It is the first observation of a system that combines a complex classical bifurcation scenario with a robust critical phase. The system may account not only for SOC behavior, but also for various switching effects observed in the brain.

BP 14.8 Wed 16:15 HÜL 186

Self-organized criticality in a neural network — •Christian Meisel and Thilo Gross — Max-Planck Institut für Physik komplexer Systeme

We evolve a network of excitatory and inhibitory neurons according to two topology-changing rules of synaptic plasticity: spike-time dependent plasticity (STDP) and homeostatic synaptic plasticity (HSP). Both local rules lead to convergence to an average number of synapses per neuron at which the network is at a phase transition. At the evolved connectivity, avalanche sizes for the HSP rule and amplitudes of neuronal activity for the STDP rule are power law distributed. Critical exponents are comparable to those observed in real cortical networks for both power laws. When extrapolated for realistic synaptic strengths, for the STDP rule the evolved average number of synapses per neuron is in the order of the one found in the brain.

BP 14.9 Wed 16:30 HÜL 186

Magnetoreception mechanisms in birds - towards the discovery of the sixth sense — •Ilia Solov'yov and Walter Greiner — Frankfurt Institute for Advanced Studies, Goethe University, Frankfurt am Main, Germany

Many birds are able to orient themselves accurately when the sky is not visible (e.g. covered with clouds). This requires non-visual sources of information. Many studies have established that birds are sensitive to the Earth's magnetic field. European robins, pigeons and other bird species use the geomagnetic field as a compass, and are also sensitive to slight temporal and spatial variation in the magnetic field that is potentially useful for determining location.

We study a putative avian magnetoreception mechanism, which is based on the interaction of two iron minerals (magnetite and maghemite) experimentally observed in subcellular compartments within sensory dendrites of the upper beak of several bird species. The iron minerals in the beak form platelets of crystalline maghemite and clusters of magnetite nanoparticles. We develop a theoretical model [1] to quantitatively describe the interaction between the iron-mineral containing particles, and demonstrate that depending on the external magnetic field the external pull or push to the magnetite clusters may reach a value of 0.4 pN. This might be principally sufficient to excite specific mechanoreceptive membrane channels leading to different nerve signals and causing a certain orientational behavior of the bird.

[1] I. Solov'yov and W. Greiner, Biophys. J. 93, 1493 (2007)

BP 14.10 Wed 16:45 HÜL 186

Enhancement of signal detection by coupling of active hair bundles — •Kai Dierkes, Benjamin Lindner, and Frank Jülicher — Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, 01187 Dresden, Germany

In all vertebrates the hair bundle is the mechano-electrical transducer in both the auditory and the vestibular system. Hair bundles from the sacculus of the bullfrog have been shown to possess the ability to amplify weak periodic stimuli by means of an active process. *In vivo* hair bundles in the sacculus of the bullfrog are attached to an overlying structure that mediates a coupling between them: the otolithic membrane. The same holds true for the hair bundles of outer hair cells in the mammalian cochlea whose tips are connected to the overlying tectorial membrane. Using a stochastic description of hair bundle dynamics we have studied the effect of an elastic coupling of hair bundles. We report that collective effects in systems of coupled hair bundles can e.g. enhance the amplification gain and the sharpness of frequency tuning as compared to the performance of a single hair bundle. Our results thus suggest that coupling of hair bundles could indeed play a significant role for signal detection in inner ear organs.

Reference: Dierkes et al., 2008, *PNAS* 105(48),18669-18674

BP 14.11 Wed 17:00 HÜL 186

Information Filtering by Synaptic Short-Term Plasticity — •Matthias Merkel and Benjamin Lindner — Max-Planck-Institute for the Physics of Complex Systems, Nöthnitzer Strasse 38, 01187 Dresden, Germany

Short-term plasticity (STP) changes the transmission properties of synapses on the scale of 100ms. It is commonly thought to act as a filter for information passing through the synapse. There are two competing effects: synaptic facilitation and depression. They either increase or decrease the postsynaptic amplitude of a presynaptic spike depending on the spike history. We study this filtering process for rate-modulated Poissonian input spike trains and a population of independent synapses. We derive expressions for information-theoretical measures like the spectral coherence in the limit case of pure facilitation and discuss by means of our analytical results conditions for a broadband transmission of information (frequency-independence of the coherence function) which previously has been found numerically [1].

[1] B. Lindner, D. Gangloff, A. Longtin, and J. E. Lewis "Broadband coding with dynamic synapses", (submitted, 2008)

BP 15: Motor Proteins

Time: Wednesday 14:30–15:45 Location: ZEU 260

BP 15.1 Wed 14:30 ZEU 260

Diffusion of yeast kinesin-8 on the microtubule lattice is a random walk with 8-nm steps — •Volker Bormuth[1], Vladimir Varga[1], Jonathon Howard[1], and Erik Schäffer[2] — [1]MPI of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, 01307 Dresden, Germany — [2]Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

The yeast kinesin-8 (Kip3p) walks highly processive towards the plus-end of microtubules in the presence of ATP. In contrast, we found that in the presence of ADP Kip3p diffuses in a one-dimensional manner on the microtubule lattice. Using single molecule fluorescence we measured that the diffusion coefficient was $5400 \pm 1500\,\mathrm{nm}^2/\mathrm{s}$ with an average lifetime on the microtubule lattice of 8 s. The diffusion did not require the highly charged C-termini of tubulin, unlike kinesin-13. We biased the diffusion using optical tweezers and analyzed the time-traces of biased diffusion by means of a fluctuation analysis. We found that Kip3p diffusion is a multi-step process with a physical step size of 8 nm and an average dwell time of 6 ms per step. The step size

was supported by the direct observation of 8 nm motions and a non-linear force-velocity relationship. At high forces the biased diffusion appeared like a one-step process indicating the presence of only one force-dependent step. Our results compared well with Monte Carlo simulations and suggest that Kip3p diffusion is a undirected, hand-over-hand, random walk along the microtubule lattice.

BP 15.2 Wed 14:45 ZEU 260

The Motility of Monomeric and Dimeric Variants of Eg5 studied in the Presence of the Kinesin-5-specific Inhibitor Monastrol — Stefan Lakämper, •Christina Thiede, Stefanie Reiter, Kerstin v. Roden, and Christoph Schmidt — 3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen

The homo-tetrameric motor-protein Eg5 from Xenopus laevis drives relative sliding of anti-parallel microtubules, most likely by the processive action of its two sets of dimeric motor domains at each end. As recently shown by Kwok et al. (NCB 2006) and Kapitein et al. (JCB 2008), tetrameric motors move on a single microtubule in a fashion including diffusional and directional episodes, while motors moving between anti-parallel microtubules act in a highly directional and processive fashion. We have studied the processive behavior of a dimeric chimera (Eg5Kin) carrying the Eg5-motor and neck-linker and the Kinesin-1 neck and stalk. While Eg5Kin displays essentially the same motile properties as a truncated Eg5 (Eg5-513 his, Krysziak et al., JBC 2006, Valentine et al., NCB, 2006) its processivity is 40x increased to about 240 consecutive 8nm-steps on average, at a velocity of 95 nm/s. With increasing monastrol concentrations we find a dose-dependent and cooperative reduction in run length, but not in speed, indicating that two monastrol molecules are required to terminate a processive run. To further study the allosteric effect of monastrol on the motility of Eg5-motors, we generated monomeric and dimeric Eg5-constructs and compared their surface gliding-velocities in the presence of increasing concentrations monastrol.

BP 15.3 Wed 15:00 ZEU 260

Buckling of semiflexible filaments under action of molecular motors — •Krzysztof Baczyński[1], Melanie Müller[1], Reinhard Lipowsky[1], and Jan Kierfeld[1,2] — [1]Max Planck Institute of Colloids and Interfaces, Department of Theory & Bio - Systems, Science Park Golm — [2]TU Dortmund University, Faculty of Physics, D - 44221 Dortmund

In this work we present a model for the buckling of semiflexible filaments under the action of molecular motors. We investigate a system in which a group of motors moves along a clamped filament carrying a second filament as a cargo. The cargo-filament is pushed against the wall and eventually buckles. Depending on boundary conditions we observe different buckling behaviors. For a long cargo-filament the critical Euler force for buckling is much smaller than the stall force of a single molecular motor, which leads to buckling of the cargo-filament. We use an analytical linear approximation of the resulting force-extension relation of the buckled filament [1]. Using Bell-theory for unbinding of a motor and a linear velocity-force relation we obtain a stochastic equation for probability pn(t) that n motors link both filaments at time t. Finally, we calculate the mean first passage time needed for unbinding of linking motors which corresponds also to the transition between buckled and unbuckled state of cargo-filament. Our results show that for sufficiently long filaments the movement of kinesin motors is not affected by the load force generated by the cargo filament. Our numerical solution is confirmed by computer simulations.

1) K. Baczyński, R. Lipowsky, J. Kierfeld, PRE 76, 061914, 2007

BP 15.4 Wed 15:15 ZEU 260

Stochastic simulations of cargo transport by several processive motors — •Christian Korn[1], Stefan Klumpp[2], Reinhard Lipowsky[3], and Ulrich S. Schwarz[1,4] — [1]University of Heidelberg, Bioquant 0013, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [2]Center for Theoretical Biological Physics, University of California, San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0374, USA — [3]Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam, Germany — [4]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

We use stochastic computer simulations to study the transport of a spherical cargo particle along a microtubule-like track by several kinesin-like processive motors. Our adhesive motor dynamics algorithm combines the numerical integration of a Langevin equation for the motion of a sphere with rules for the reaction kinetics of molecular motors. The Langevin part includes diffusive motion, the action of the pulling motors, and hydrodynamic interactions with the planar substrate. The kinetic rules for the motor reactions model binding and unbinding to the filament as well as active motor steps. As a first validation of our model, we show that the simulated mean transport length increases exponentially with the number of bound motors, in good agreement with earlier results. For a fixed number of motors attached to the cargo, the distribution of the number of motors in binding range to the motor track is found to be Poissonian in most cases. We also find that load is equally shared due to a corresponding spatial arrangement of the motors only for unusually long-lived bonds.

BP 15.5 Wed 15:30 ZEU 260

Diffusion of cooperative molecular motors displaying bidirectional motion — •Ernesto M. Nicola and Benjamin Lindner — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

The movement of motor proteins along filaments forming part of the cytoskeleton is usually directional. However, recently it has been observed experimentally that collections of certain motor proteins can move bidirectionally [1]. This bidirectional motion can be described, as proposed by Badoual et al. [2], by a two-state model with many particles attached to a rigid backbone. We contrast this model with a even simpler description based on an active Brownian particle dynamics. This simple description is shown to capture the main features of the more complex ratchet model. In particular, we predict that there should exist a critical force for which the effective diffusion coefficient jumps from very large values to small ones [3]. This critical force applied to the backbone separates a region of giant diffusion from a regime of reliable directed transport.

[1] Endow and Higuchi, Nature **406**, 913 (2000).
[2] Badoual, Jülicher and Prost, Proc. Natl. Acad. Sci. **99** (2002).
[3] Lindner and Nicola, Phys. Rev. Lett. **101**, 190603 (2008).

BP 16: Stochastic Processes

Time: Wednesday 16:00–17:15 Location: ZEU 260

BP 16.1 Wed 16:00 ZEU 260

Anomalous scaling of nano-pore translocation times for structured RNA molecules — Malcolm McCauley[1], Robert Forties[1], •Ulrich Gerland[2], and Ralf Bundschuh[1] — [1]Department of Physics, Ohio State University — [2]Arnold Sommerfeld Center for Theoretical Physics, LMU München

Translocation through a nano-pore is a new single-molecule technique to probe physical properties of biomolecules. A bulk of theoretical and computational work exists on how the main observable, the time to translocate a single molecule, depends on the length of the molecule for unstructured molecules. Here, we study this question for RNA molecules for which the breaking of the secondary structure is the main barrier for translocation. To this end, we calculate the mean translocation time of single-stranded RNA through an idealized nanopore for many randomly chosen RNA sequences. At zero voltage bias, we find that the typical translocation time depends on the sequence length with a power law, the exponent of which changes as a function of temperature and exceeds the naively expected exponent of two for purely diffusive transport at all temperatures. We rationalize this behavior theoretically.

BP 16.2 Wed 16:15 ZEU 260

Optimal protocols in Stochastic Thermodynamics — •Tim Schmiedl[1], Alex Gomez-Marin[2], and Udo Seifert[1] — [1]II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart, Germany — [2]Facultat de Fisica, Universitat de Barcelona, Diagonal 647, 08028 Barcelona, Spain

For systems in an externally controllable time-dependent potential, the

optimal protocol minimizes the mean work spent in a finite-time transition between two given equilibrium states. We consider three different types of dynamics: overdamped Langevin dynamics, underdamped Langevin dynamics, and purely Hamiltonian dynamics. Surprisingly, the optimal protocol involves jumps for overdamped Langevin dynamics and even delta-type singularities for underdamped Langevin dynamics. These optimal protocols significantly improve free energy calculations via the Jarzynski equality.

For purely Hamiltonian dynamics and harmonic potentials, we show that the optimal protocol is highly degenerate and that even in the limit of short transition times, the optimal work is given by the adiabatic work which is substantially smaller than the work for an instantaneous jump. We also perform numerical calculations for purely Hamiltonian dynamics in an anharmonic quartic potential.

[1] T. Schmiedl and U. Seifert, Phys. Rev. Lett 98, 108301 (2007)
[2] A. Gomez-Marin, T. Schmiedl, and U. Seifert, J. Chem. Phys. 129, 024114 (2008)

BP 16.3 Wed 16:30 ZEU 260

Dynamic length regulation in biological transport systems. — •Louis Reese, Anna Melbinger, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München

Microtubules are highly dynamic filaments that perform a variety of tasks in living cells. At the same time they serve as intracellular highways for molecular motors, which are either transported along those tracks or diffuse in the cytosol [1]. Here we examine mechanisms to regulate microtubule-length through the concentration of motors in the cytosol. It is analyzed how the interplay between density-dependent transport on the tracks, and filament polymerization affects the dynamics of filament length [2]. Employing stochastic simulations complemented by analytic calculus we identify three distinct dynamic regimes: (i) steady growth, (ii) bounded growth and (iii) stationary length. The latter shows interesting intermittent dynamics.

[1] A. Parmeggiani, T. Franosch, E. Frey, Phys. Rev. Lett. 90, 086601 (2003).
[2] V. Varga, J. Helenius, K. Tanaka, A. A. Hyman, T. U. Tanaka and J. Howard, Nat. Cell Biol. 8, 957 (2006)

BP 16.4 Wed 16:45 ZEU 260

Polymerization of actin and cooperative ATP hydrolysis — •Xin Li[1], Jan Kierfeld[2], and Reinhard Lipowsky[1] — [1]MPI of Colloids and Interfaces, Science Park Golm, 14424 Potsdam — [2]TU Dortmund, Fakultät Physik, 44221 Dortmund

Actin polymerization plays an important role in many aspects of cell dynamics. Actin polymerization also involves the hydrolysis of ATP molecules, which takes place within an ATP-rich cap and can be spatially separated from the polymer tip. In this study, we theoretically compare different cooperative mechanisms for the coupling between ATP hydrolysis and actin polymerization and describe their effects on experimentally observable quantities, such as cap length, total hydrolysis rate, and actin filament growth rate.

BP 16.5 Wed 17:00 ZEU 260

Optimal potentials for temperature ratchets — •Florian Berger[2], Tim Schmiedl[1], and Udo Seifert[1] — [1]II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart — [2]Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam

Since the introduction by Feynman, temperature ratchets have served as a model for a microscopic heat engine which operates between two heat baths. More generally, directed transport of an overdamped Brownian particle can be induced along a periodic potential in a spatially periodic temperature profile. With a load force applied to the particle, this setup can perform as a heat engine. The dependence of the current on the potential evokes the question: What is the optimal shape of the potential that maximizes the current and thus the power output of the engine for a given load? Using variational calculus, we determine the optimal potential for a sinusoidal temperature profile analytically up to a numerical root search. We discuss the dependence of the optimal potential on scaled model parameters such as the temperature amplitude and the load force.

BP 17: Poster II

Time: Wednesday 17:15–19:45 Location: P3

BP 17.1 Wed 17:15 P3

Elastic properties of human cancer cells — •Carsten Hentschel[1], Hendrik Hölscher[2], Stefan Schneider[2], and Kristina Riehemann[1] — [1]Center for Nanotechnolgy (CeNTech)/University of Münster, Heisenbergstraße 11, 48149 Münster — [2]Affilitation

In the past decade the analysis of biomechanical properties of cancer cells became a tool to determine the invasiveness of a tumor. Atomic force microscope (AFM) has developed to a powerful tool to measure biophysical parameters by using force spectroscopy on living cells in liquid. The force spectroscopy in contact mode can be applied to gain more information about the structure and physical properties (e.g. elasticity) of cells. Different approaches have been shown to get this information [1]. But reproducible results in this area remains to be scarce

We optimized existing methods and showed highly reproducible results demonstrating the elasticity of different celllines strongly correlated to their invasiveness making this methods usefull for clinical applications.

[1] Acta Biomaterialia 3, S. Suresh, 413- 438 (2007)

BP 17.2 Wed 17:15 P3

Force Measurements in Mitotic Spindles — •Aaron Lindner[1], Bastian Rühle[1], Francois Nédelec[2], and Joachim Spatz[1,3] — [1]University of Heidelberg — [2]European Molecular Biology Laboratory, Heidelberg — [3]MPI for Metals Research, Stuttgart

The mitotic spindle is responsible for chromosome alignment and segregation during cell division. It is a complex, microtubule-based assembly of different molecular motors and other proteins. In spite of its essential role in cell proliferation, the mechanics of mitotic spindles is not sufficiently well understood. In this project, the pulling strength of mitotic spindles will be determined experimentally.

Bipolar mitotic spindles can be assembled in vitro around chromatinylated, DNA covered microspheres in a cell-free model system which is gained from Xenopus laevis oocytes. In this work, the DNA covered microspheres are attached on functionalized polymer pillars. This yields a regular pattern of bipolar spindles on a force-sensing material.

Spindle pulling forces are expected to be in the range of one nanonewton, which is for the required geometric parameters below the detection limit of existing polymer pillar technologies. That is why for the first time the pillars were made of hydrogel. The Young's modulus of this hydrogel can be varied by altering the water content during polymerization. So it is possible to adjust the stiffness of the pillars to the experimental needs without changing the geometry. With this method, forces of less than 1nN can be detected by observing the pillar bending.

BP 17.3 Wed 17:15 P3

Towards measuring the centering forces acting on the mitotic spindle in the *C. elegans* embryo — •Horatiu Fantana and Jonathon Howard — MPI of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, 01307 Dresden, Germany

The cytoskeleton is a highly dynamic and adaptable protein scaffold that determines the shape and internal organization of cells. In this project we want to investigate the mechanical properties of the microtubule cytoskeleton by applying forces to a dynamic microtubule array *in vivo* and measuring its displacement.

A prominent example for such an array is the mitotic spindle, which is responsible for chromosome segregation and cleavage plane specification during mitosis. At the beginning of mitosis, the spindle moves to the center of the cell. How does the spindle find the center and what keeps it there? Using magnetic tweezers, we plan to displace the spindle and measure the magnitude of the restoring forces acting on the spindle poles in the one-cell *C. elegans* embryo. Does the restor-

ing force increase in proportion to the displacement? If so, then this tells us that the centering process acts like a spring, supporting some models for centering. Does the centering stiffness depend on whether the displacement is parallel or perpendicular to the long axis of the cell? This may give insight into the molecular mechanism underlying centering. What is the magnitude of the centering force? This will tell us something about the number of force-generating processes involved in centering. The results should provide a good basis for modeling and better understanding the centering process.

BP 17.4 Wed 17:15 P3

Manipulation of stretch-activated calcium channels with the optical stretcher — •Markus Gyger, Christoph Schneider, Susanne Ebert, and Josef Käs — Universität Leipzig, Germany

Cellular response to deforming forces can be measured with the optical stretcher. Cells are trapped by two anti-parallel laser beams. By increasing the laser power the momentum transfered to the cell surface causes visible deformations. This can be used to probe the global mechanical behaviour of single cells in suspension. For low stresses and small deformations most of the cells deform viscoelasticly. However, for higher stretching powers the cells start to counteract the deformations. Sometimes this active response to deformation results in a contraction of the cell relative to its initial, undeformed state. This raises interesting questions regarding the mechanisms by which cells register and respond to the applied forces. Under physiological conditions many cells react to mechanical stimuli. As a prominent example, hair-cells in the Cochlea of vertebrate ears are known to open transmembrane calcium channels upon mechanical stresses. Calcium is one of the most important second messengers and is involved in most of the known mechano-activated cell responses. Since its normal concentration in the cell soma is very low and increases only by influx from outside the cell or release from intracellular calcium stores upon stimulus, the influx can be made visible by appropriate fluorescent dyes. The aim of this work is to investigate the dependence of calcium influx on the forces applied to the cell surface by the optical stretcher in order to gain insight into the mechanisms of active responses to stretching.

BP 17.5 Wed 17:15 P3

Mechanics in Neuronal Development — •Kristian Franze[1], Hanno Svoboda[1], Pouria Moshayedi[1], Andreas Christ[1], James Fawcett[1], Josef Kas[2], Christine Holt[1], and Jochen Guck[1] — [1]University of Cambridge, UK — [2]University of Leipzig, Germany

The neuronal preference for soft substrates and the softness of radial glial cells, along which neurons preferentially grow, strongly point towards a role of mechanics in neuronal guidance. Here we show how neurons detect and avoid stiff substrates and how their mechano-responsiveness is used to guide their axons.

In vitro, neurons continuously probe the mechanical properties of their environment. Growth cones visibly deformed substrates with a compliance commensurate with their own. Externally applied mechanical stress exceeding the threshold of ˜300 Pa caused a calcium influx through mechanosensitive ion channels in the growth cone membrane that triggered neurite retraction. Subsequently, neuronal processes re-extended, thereby enabling exploration of alternative directions. To study the physiological consequences of this mechano-responsiveness, Xenopus eye primordia were cultured on polyacrylamide gels of various compliances. If the outgrowing retinal axons grew either on soft or on stiff substrates, they spread over a wide area. In contrast, on substrates of intermediate compliance they fasciculated and grew into one common direction, resembling an optic nerve. Hence, neurons may actively use mechanics as previously unknown guidance cue. This knowledge may ultimately help in finding new implants that promote axonal regeneration in the injured nervous system.

BP 17.6 Wed 17:15 P3

Modelling control of cellular force distributions by adhesion geometry and rigidity — •Ilka Bischofs[1], Sebastian Schmidt[2], and Ulrich Schwarz[2,3] — [1]Lawrence Berkeley Lab, Berkeley, USA — [2]University of Heidelberg, Heidelberg, Germany — [3]University of Karlsruhe, Karlsruhe, Germany

Adhesion geoemetry and matrix rigidity are important decision factors governing adherent cell morphology and cell differentiation. Both have been shown experimentally to control cellular adhesion forces which affect the status of the cytoskeletal machinery and feed into cell differentiation pathways. Here we present a mechanical contour model based on line and surface tensions that predicts cellular force distributions from the shape and rigidity of the adhesive patterns. For cells constrained to adhesive islands, forces scale with island curvature and preferentially localize to corners. For cells adherent to discrete sites, line tension is the primary force determinant. Forces increase with increasing distance between adhesion sites because surface tension effects result in steeper pulling directions. Substrate compliance counteracts the positive distance effect while the elastic nature of line tension enhances it. The model compares well to experimental observations suggesting that contour forces play an important role in establishing the basic force pattern that might be subsequently amplified by the generation of discrete internal structures such as stress fibers.

BP 17.7 Wed 17:15 P3

Influence of Mn2+ and Mg2+ on the interaction between integrin $\alpha 7\beta 1$ and invasin studied by dynamic force spectroscopy — •Agnieszka Ligezowska[1], Kristian Boye[2], Johannes Eble[3], Bernd Hoffmann[4], Beate Klösgen[2], and Rudolf Merkel[4] — [1]Department of Physics, Jagiellonian University, Cracow, Poland — [2]Memphys Center for Biomembrane Physics, University of Southern Denmark, DK-5230 Odense, Denmark — [3]Institut für Physiologische Chemie und Pathobiochemie, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany — [4]Institut für Bio- und Nanosysteme, Forschungszentrum Jülich, D-52425 Jülich, Germany

The ligand binding function of integrins, a group of transmembrane proteins mediating cell-matrix adhesion in animals, is known to be influenced by divalent cations. We have applied the Biomembrane Force Probe technique to study this phenomenon for a soluble variant of integrin $\alpha 7\beta 1$ and one of its ligands, invasin 497, an outer membrane protein of Yersinia bacteria. In a dynamic force spectroscopy approach, we show that the binding affinity of $\alpha 7\beta 1$ is promoted by divalent manganese and magnesium ions and that these ions work to enforce the binding strength in a synergistic manner. Single bond events could be studied by successive addition of free invasin to the measurement buffer which reduced the number of available binding sites and thus diminished the likelihood of multiply bond formation. Combining force-induced bond dissociation with free ligand binding enabled simultaneous studies of Mn2+ and Mg2+ influence in both, equilibrium and non-equilibrium conditions.

BP 17.8 Wed 17:15 P3

Biomembrane adhesion on micropatterned substrates: A tool for thermal fluctuation analysis — •Cornelia Monzel[1], Susanne Fenz[1], Sabine Dieluweit[1], Kheya Sengupta[2], and Rudolf Merkel[1] — [1]Institute of Bio- and Nanosystems 4: Biomechanics, Research Centre Jülich, Germany — [2]CINAM/CNRS-UPR3118, Luminy, Marseille, France

Cell adhesion is a complex process involving a manifold of forces. Much is known about the specific binding between biomolecules which affect cell adhesion. However, contributions due to generic interactions or repulsive thermal fluctuations are as yet barely understood. Therefore, we developed a simplified model system which permits us to do quantitative analysis of membrane fluctuations. Here, cell adhesion was mimicked by a system consisting of giant unilamellar lipid vesicles, with the specific binding being mediated by the biotin-neutravidin complex. Micropatterns of adhesion-competent and repulsive areas were produced on glass surfaces by microcontact printing. This technique provided us with the means to confine the membrane in a controlled manner. The adhered vesicle exhibited areas of fluctuating and fixed membrane corresponding to the underlying pattern. From Dual-Wavelength Reflection Interference Contrast Microscopy (DW-RICM) analysis, we reconstructed the membrane height distribution and quantified the membrane fluctuations with nano-metric accuracy. We calculated the fluctuation spectrum and the effective potential in which the membrane fluctuates.

BP 17.9 Wed 17:15 P3

Quantification of cell adhesion strength on self assembled monolayers with tuneable surface properties — •Christof Christophis, Michael Grunze, and Axel Rosenhahn — Angewandte Physikalische Chemie, Universität Heidelberg, Im Neuenheimer Feld 253, 69120 Heidelberg

Besides selective receptor interactions, physico-chemical surface properties play an important role in adhesion, proliferation, survival and even differentiation of mammalian cells. Self assembled monolayers are a versatile tool to tune surface properties in a well defined manner and it has been found that cell behavior is directed even by such thin coatings. To obtain quantitative data for cell adhesion on self

assembled monolayers we use time lapse microscopy in combination with microfluidically cultivated cells. Cell adhesion kinetics is determined by image analysis while cell adhesion strength is quantified by application of a well defined liquid flow. The microfluidic system is fabricated in polydimethylsiloxane (PDMS) and integrated in a reusable device where any surface of interest can be used. This experimental design in combination with a well developed preparation protocol allows adhesion strength characterization e.g. for fibroblast cells with high reproducibility and small error bars.We show results on the adhesion of rat embryonic fibroblasts to ethylene glycol terminated self assembled monolayers in dependence of ethylene glycol chain length and end group termination. Interfacial properties including wetting and hydration are thus manipulated in a controlled way and cell response is quantified.

BP 17.10 Wed 17:15 P3

AFM as a chance for studying in situ protein adsorption and bacterial adhesion — •Peter Loskill, Yvonne Schmitt, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbruecken, Germany

The interaction of proteins and of microorganisms with biological or artificial surfaces is a key factor in disease pathogenesis. To reveal the interactions, we follow two pathways: One ansatz is to characterize protein adsorption on a fundamental level via AFM in non-contact mode imaging, another is to directly probe bacterial adhesion by AFM - force spectroscopy. For proteins like amylase we have probed the adsorption kinetics by ellipsometry. Surprisingly, the kinetics is not only depending on surface chemistry, but also on the sub-surface composition [1,2]. In situ AFM scans of protein adsorption reveal the spatial statistics of adsorption sites and allow for a characterization of the mobility of proteins on the surface and the role of protein-protein interactions. Characterizing bacteria/substrate interaction, we use staphylococcus aureus as a model system. S. aureus is known to build complex cell consortia consisting of multilayered organisms, forming a biofilm. Wall-bound and secreted proteins mediate attachment. Since the bacterial cell wall cannot be treated as a homogeneous surface, it is necessary to differentiate between local and global adhesion measurements. To investigate the global adhesion properties of a bacterium in a planktonic state we directly use them as AFM probes.

[1] A. Quinn et al., Europhysics Lett. 81 (2008) 56003
[2] M. Bellion et al., J. Phys.: Condens. Matter 20 (2008) 404226

BP 17.11 Wed 17:15 P3

Cell Adhesion and Cell Detachment Forces on Micro-Nanopatterned Substrates — •Janosch Deeg[1,2], Ilia Louban[1,2], Daniel Aydin[1,2], and Joachim Spatz[1,2] — [1]University of Heidelberg, Dept. of Biophysical Chemistry, Im Neuenheimer Feld 253, D-69120 Heidelberg — [2]Max-Planck-Institute for Metals Research, Dept. of New Materials & Biosystems, Heisenbergstr. 3, D-70569 Stuttgart

Au-nanopatterned substrates, produced by micellar block copolymer nanolithography, are used to make adhesion ligands of a cell be positioned like the quasi-hexagonal ordered Au-nanoparticles on the surface. By tuning the spacing of these biofunctionalized nanoparticles, one is able to control the distance between adjacent binding sites. Former experiments have shown that an interparticle distance of more than 73 nm strongly reduces cell spreading, cell detachment forces and the formation of adhesion clusters. Microstructuring of these patterns divides the surface into regions with and without Au-particles due to vary the global density, meaning in this case binding sites per area, not only by changing the distance between these sites, but by creating entire micrometer sized parts without particles next to nanostructured ones. This diploma thesis is mainly interested in how far the detachment force of adherent cells depends on the amount of available integrin binding sites per area in comparison to their distance. The cell detachment force is measured with an AFM by immobilizing the cell on the functionalized tipless cantilever and subsequently detaching it from the surface. We expect to gain a deeper understanding about the effect of integrin spacing and density on cell adhesion strength.

BP 17.12 Wed 17:15 P3

Cell Motility in Microstructured 3D Topologies — •Sofia Capito, Delphine Arcizet, Joachim Rädler, and Doris Heinrich — Lehrstuhl für Physik weicher Materie und Biophysik, Biophysics of Cell Dynamics, Fakultät für Physik, Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München

Living cells sense mechanical and chemical properties of their environment and especially motile cells react to the surrounding 3D topographical conditions.

Whereas most of the current in vitro experiments are carried out on a flat substrate, we investigate cells in 3D surface topologies with fluorescence microscopy techniques. We fabricate well-defined microstructured substrates, consisting of PDMS pillar arrays with varying properties, such as pillar distance, diameter, and density. We study the influence of the substrate topography on cell velocity, motion persistence, and branching of the cells, and aim at controlling and predicting cellular migration in this model 3D environment. The amoeba Dictyostelium discoideum (Dd) is used as a model organism, exhibiting similar motility to neutrophils.

First results indicate that the substrate topography significantly influences Dd cell motility. The calculated mean square displacement (MSD) of the cell center of mass reveals an overdiffusive cell migration behavior in the pillar field, as opposed to a pure random walk on a flat surface.

Further work will concentrate on identifying the intracellular signaling, which triggers cell reaction to 3D topography.

BP 17.13 Wed 17:15 P3

The first passage problem for diffusion through a cylindrical pore with sticky walls — •Nicholas Licata and Stephan Grill — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

We formulate a simple model to calculate first passage times for diffusion through a cylindrical pore with sticky walls. A particle diffusively explores the interior of the pore through a series of binding and unbinding events with the cylinder wall. Through a diagrammatic expansion we obtain first passage time statistics for the particle's exit from the pore. Connections between the model and nuclear transport are discussed.

BP 17.14 Wed 17:15 P3

Protein diffusion in crowded and charged solutions: A light scattering and neutron spin echo study — •Marcus Hennig[1,2], Felix Roosen-Runge[1,2], Fajun Zhang[1], Stefan Zorn[1], Maximilian Skoda[3], Robert M. J. Jacobs[4], Peter Fouquet[2], Tilo Seydel[2], and Frank Schreiber[1] — [1]Institut für Angewandte Physik, Universität Tübingen, Germany — [2]Institut Laue-Langevin, France — [3]ISIS, Didcot, UK — [4]Chemistry Research Laboratory, Oxford, UK

Globular proteins under physiological conditions occur in crowded solutions with a protein volume fraction attaining up to approximately 40%. A recent finding of reentrant condensation of proteins induced by polyvalent salts underlines the necessity to examine salt-induced charge effects in order to understand the biological function and dynamical behavior of solvated proteins.

We review different existing models to interpret protein diffusion data in "crowded" solutions and we also consider the effect of charges. We discuss these models in the context of a combined light scattering and neutron spin-echo study of the short-range and long-range nanosecond diffusion of the model globular protein bovine serum albumin (BSA) in aqueous solution as a function of the NaCl salt concentration. The interpretation of the data on the BSA model system is put in the context of existing studies on related systems and of the relevance of charges for protein diffusion and protein function under physiological conditions.

BP 17.15 Wed 17:15 P3

Microscopic origins of anomalous diffusion - insights from studies on crowded solutions — •Jedrzej Szymanski and Matthias Weiss — Deutsches Krebsforschungszentrum, Heidelberg, Germany

Subdiffusive motion of macromolecules has been observed in many crowded environments, ranging from polymer and protein solutions to intracellular fluids. A clear understanding of the microscopic origin of the subdiffusive motion, however, has been lacking. To address this point, we have used fluorescence correlation spectroscopy (FCS) to study the diffusion of tracer molecules in crowded solutions with varying composition. We combined this approach with model simulations on percolation-like motion and continuous time random walks (CTRWs). Aiming at discriminating these two fundamentally different processes that may underlie the observed anomalous diffusion in FCS, we compared the experimentally determined distributions of the anomaly degree and the apparent mobility with the simulation data. As a result, the experimental data for crowding-induced subdiffusion are most consistent with a percolation-like motion but deviate strongly from the predictions of a CTRW. Hence, subdiffusion in crowded me-

dia, e.g. in the cytoplasm of living cells, most likely arises due to a stochastic process with a Gaussian-like propagator.

BP 17.16 Wed 17:15 P3

Water diffusion through OmpF channels using molecular dynamics simulations — •Mihai Tomozeiu, Soroosh Pezeshki, and Ulrich Kleinekathöfer — Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany

Outer membrane protein F (OmpF) is one of the most prevalent porins of Escherichia coli. The protein is the main channel for the translocation for small molecules between the interior of the bacteria and its surroundings. One of its main functions is to control the osmotic pressure between the two media. The water diffusion through the channel is studied using molecular dynamics simulations in equilibrium conditions. Temperatures used for the simulations range from a few degrees above the melting point of water up to 363 K. As an additional control parameter, a strong electric field was applied along the channel axis to check if at this level, the electric field has any measurable influence on the water permeation. Due to the charge distribution of the protein the applied voltage drop over the channel was limited to one volt so that membrane and protein are not yet damaged in the simulations.

BP 17.17 Wed 17:15 P3

Theoretical description of endosome dynamics — •Jonathan Edward Dawson[1], Lionel Foret[1,2], Claudio Collinet[3], Yannis Kalaidzidis[3], Lutz Brusch[4], Perla Zerial[4], Andreas Deutsch[4], Marino Zerial[3], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Ecole Normale Supérieure, Laboratoire de Physique Statistique, Paris, France — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [4]ZIH-Technical University Dresden,Germany

We present a theoretical study to describe the collective dynamics of a population of endosomes in a cell. Endosomes are vesicular structures that form networks that sort and transport cargo molecules internalized into the cell by endocytosis. Endosomes undergo fusion and fission thereby changing their size and cargo content. We develop a mean field theory that describes the time evolution of the distribution of endosomal markers or cargo in the network. We calculate these distributions using both analytical and numerical methods. Experimentally these distributions can be determined using fluorescence microscopy. The steady state distribution of total fluorescence intensity of the cargo molecules shows charasteristic and robust features. Our theory is able to quantitatively reproduce the shape of steady state distributions and their time dependence. We determine the kinetic parameters of the early endosomal network in HeLa cells and provide an explanation for observed power law distributions.

BP 17.18 Wed 17:15 P3

Protein translocation across artifical membrane channels — •Stefan Bommer and Patrick Huber — Technische Physik, Universität des Saarlandes, Saarbrücken

Protein translocation across biological membranes is a fundamental process in cell biology. Many qualitative and semi-quantitive aspects of the translocation process have been analyzed over the last 35 years. The bacterial plasma membrane, the membrane of the endoplasmic reticulum, the inner and outer membranes both of mitochondria and chloroplasts all contain protein translocons. They all have one structural feature in common: a narrow aqueous channel as central subunit.

To better understand the collective, physical mechanisms of protein transport across bio-membranes we performed rigorous experimental protein permeation experiments through artificial, tunable channels in solid-state membranes using folded and unfolded cytochrome c supported by Brownian-Dynamics-Simulations that mimic the experimental geometry.

BP 17.19 Wed 17:15 P3

Vesicle Transport in Guided Neuronal Axons — •Carina Pelzl[1,2], Guido Piontek[3], Jürgen Schlegel[3], Joachim Rädler[1,2], and Doris Heinrich[1,2] — [1]Department of Biophysics, Ludwig-Maximilians-Universität München — [2]Center of NanoScience (CeNS) — [3]Institut für Allgemeine Pathologie und Pathologische Anatomie der Technischen Universität München, Klinikum rechts der Isar

Cellular vesicle transport is crucial to many physiological and pathological events. Several neuronal diseases like Amyotrophic Lateral Sclerosis (ALS) and Alzheimer's are caused by disrupted transport along microtubules.

This work focuses on the retrograde transport of vesicles in PC12 cells and primary ALS neurons. These systems are interesting for their geometrical simplicity, since the microtubules in an axon are almost parallel. In order to further reduce the possible parameters, we force the axons in a perfectly 1D geometry by guiding dendrite outgrowth along predefined nanostructures.

To analyze the vesicle motion within an axon, we use a recently developed algorithm [1], based on a time-resolved mean square displacement (MSD) analysis, to distinguish between active and passive phases with a high temporal resolution.

In this way we can compare naturally occuring 1D transport in living cells to theoretical models. Furthermore, we aim at investigating degeneracies in ALS neurons.

[1] Arcizet et al., Temporal Analysis of Active and Passive Transport in Living Cells, Phys.Rev.Let, in press

BP 17.20 Wed 17:15 P3

Influence of a repulsive short-range interaction on the transport properties of a driven two-channel system — •Anna Melbinger[1], Tobias Reichenbach[2], Thomas Franosch[1], and Erwin Frey[1] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC), Center for NanoScience (CeNS), Department of Physics Ludwig-Maximilians-Universität, München, Germany — [2]The Rockefeller University, New York, U.S.A.

We investigate the behavior of a two-channel driven diffusive system where particles on different lanes interact via a repulsive short-range interaction. This system is motivated by biological transport phenomena happening in each cell. The coupling incoperates the effect of large cargos attached to motor proteins which cause an obstruction stemming from the excluded volume. In addition, the model serves as a classical description for spin currents where particles with two internal states are driven through a lattice. Depending on the strength of coupling, the behavior of the system can be divided into three regimes of qualitatively different behavior. While the model can be mapped on a one-channel problem for small and for large potentials, a new and rich phase behavior emerges for an intermediate strength of coupling. In this regime, the transport properties of the system are influenced in a nontrivial way. We rationalize our observations in an analytic approach employing a one-site cluster approximation, and connect the current-density relation with the phase diagrams using the Extremal Current Principle. Our results are confirmed by stochastic simulations.

BP 17.21 Wed 17:15 P3

Rheology and Transport Processes in Living Cells — •Jean Mahowald, Delphine Arcizet, Joachim Oskar Rädler, and Doris Heinrich — Biophysics of Cell Dynamics Group, Lehrstuhl für Physik weicher Materie and Center of NanoScience (CeNS), Fakultät für Physik, Ludwig-Maximilians-Universität München, D-80539 München, Germany

Transport processes play a major role for the viability of cells. Living cells need to continuously uptake nutrients, which are engulfed in lipidic vesicles by endocytosis, and transported towards intracellular compartments. Transport throughout the cell consists of successive phases of diffusion phenomena (Brownian motion, subdiffusion or enhanced diffusion) and active transport along the microtubules by molecular motors.

We investigate the rheology and transport processes in Dictyostelium discoideum cells by magnetic tweezers, which are an interesting model organism due to their cytoskeleton simplicity and the variety of mutant strains available. Super paramagnetic micrometer beads engulfed by the cells are subjected to force pulses of 5 seconds and up to 200 pN. The recorded tracer path is providing real-time information about the transport phenomena. Our home-made algorithm allows us to dissect the bead path into phases of pure diffusion and directed active motion.

We observe that the average duration of diffusive transport events is significantly lowered by the application of an external force. Detailed information about the role of the different cell components in the active processes is obtained by modifying cytoskeleton properties.

BP 17.22 Wed 17:15 P3

Characterisation of Staphylococcus aureus Wall Teichoic Acids and their functional components with Vibrational and Photoemission Spectroscopy in thin films — •Florian Latteyer[1], Timo Birkenstock[2], Heiko Peisert[1], Andreas Peschel[2], and Thomas Chassé[1] — [1]University of Tübingen, Institute for Physical and Theoretical Chemistry, Auf der Morgenstelle 8, D-72076 Tübingen — [2]University of Tübingen, Medical Microbiology

and Hygiene Department, Elfriede-Aulhorn-Str. 6, D-72076 Tübingen

Staphylococcus aureus plays in medical applications a key role. The biofilm formation on surfaces, especially on implants and catheters, is liable for infections in humans. It could be shown in the past that wall teichoic acids, as a part of the bacterial cell wall, are responsible for the initial biofilm formation and hence for the adsorption on surfaces. By genetical manipulation of S. aureus d-Alanine has been removed as part of the wall teichoic acid. After the elimination of d-Alanine no adsorption and biofilm formation on surfaces was monitored. D-alanine is therefore supposed to be as an adsorption anchor. In this work we present IR-, Raman and XPS spectra of wall teichoic acids measured on Si substrates. D-alanine has been identified with his zwitterionic structure in the wall teichoic acid and hence contribute a positive charge to the structure. Thin films of d-Alanine and Glycerolphosphat are prepared and compared with the wall teichoic acid spectra. Structural characteristics of both molecules are investigated and compared with the spectra of the wall teichoic acid. During the investigation of D-alanine with soft x-rays a decomposition was monitored.

BP 17.23 Wed 17:15 P3

Simulating E.coli's Major Efflux Pump: The Extrusion Mechanism for Substrates — •R. Schulz[1], A. Vargiu[2], P. Ruggerone[2], M. Schreiber[3], and U. Kleinekathöfer[1] — [1]Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany — [2]University of Cagliari, 09042 Monserrato (CA), Italy — [3]Technische Universität Chemnitz, 09107 Chemnitz, Germany

Bacteria, such as E. coli, use multidrug efflux pumps to export toxic substrates through their cell membranes. The RND transporter of the AcrAB-TolC efflux pump is able to export structurally and chemically different substrates. This is one reason of the increasing antibiotic resistance of bacteria. The energy is converted in the transmembrane domain and transduced towards the periplasmic part and used there to initiate a three-cyclic peristaltic pumping [1]. The effects of conformational changes on the extrusion of drugs, which have been located into one of the proposed binding pockets, are assessed using different computational methods like targeted molecular dynamics (TMD). The mechanism of pumping is investigated in greater detail than ever before [2]. Within TMD, a linear transition between two conformations is described. To investigate the effect of the conformational changes a feasible substrate, doxorubicin, has been placed into one of the binding pockets. Previously, the conformational changes of TolC which lead to an opening of the aperture have been investigated [3].

[1] M. Seeger et al., Current Drug Targets **9**, 729 (2008)
[2] G. Sennhauser et al., PLoS Biology **5**, 106 (2007)
[3] R. Schulz et al., Biophysical Journal (accepted)

BP 17.24 Wed 17:15 P3

Phenotype Decision in *B. subtilis*: Low Number Fluctuations Enhanced by Non-linear Dynamics — •Jan-Timm Kuhr[1,3], Madeleine Leisner[2,3], Joachim O. Rädler[3], Berenike Maier[2,3], and Erwin Frey[1,3] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), LMU, Germany — [2]Institut für Allgemeine Zoologie und Genetik, Westfälische Wilhelms Universität, Germany — [3]Department für Physik, Ludwig-Maximilians-Universität München, Germany

Clonal populations of the bacterium *B. subtilis* exhibit a variety of phenotypes, depending on the environment. If starved 15-20% of all cells become "competent", gaining the ability to incorporate external DNA into their genome. Competent individuals can adapt quicker to stress conditions than the residual population. Whether to become competent or not is decided on the single cell level.

To elucidate switching to competence we performed single cell experiments and set up a theoretical model incorporating non-linear feedback dynamics and low number fluctuations. Identifying the master regulator protein comK and its corresponding mRNA as the main players, we can describe switching by an effective two-species system: switching is induced by fluctuations and subsequent relaxation to one of two stable fixed points. Deterministic switching, as encountered in mutant strains, is easily explained by disappearance of one fixed point.

Using well-motivated rate constants we quantitatively reproduce our experimental results and give an intuitive picture of stochastic single cell phenotype decision.

BP 17.25 Wed 17:15 P3

Understanding the effect of virus infection on cellular architecture — •Julian Weichsel[1,3], Nikolas Herold[2], Maik Lehmann[2], Hans-Georg Kräusslich[2], and Ulrich S. Schwarz[1,3] — [1]Bioquant, Ruprecht-Karls-University of Heidelberg, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [2]Department of Virology, Universitätsklinikum Heidelberg, Im Neuenheimer Feld 324, 69120 Heidelberg, Germany — [3]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

The filament networks of the cytoskeleton are responsible for a variety of essential cellular processes, including force generation, shape changes and intracellular transport by motor proteins. Therefore even subtle changes in the network architecture are potentially able to affect vital functions of the cell. This fact is exploited by different viruses in different ways. In order to quantify the effect of virus infection on cellular architecture, we have used image processing to compare cells treated with drugs or virus particles to their wildtype analogues. A large number of automated high-throughput fluorescence images have been processed and structure parameters of the actin cytoskeleton have been extracted. This procedure can also be used to parameterize theoretical models for the actin cytoskeleton. We have implemented a random fiber network which is characterized by fiber density and length. In computer simulations we find that small changes in the microscopic parameters can lead to dramatic effects for the transport and mechanical properties of the overall network.

BP 17.26 Wed 17:15 P3

Mechanical properties of non-enveloped viruses — •Bodo D Wilts[1], José L Carrascosa[2], Charles M Knobler[3], Iwan A T Schaap[1], and Christoph F Schmidt[1] — [1]3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen, Germany — [2]Centro Nacional de Biotecnología, CSIC, Campus de la Universidad Autónoma de Madrid, Spain — [3]Department of Chemistry and Biochemistry, University of California, Los Angeles, USA

Non-enveloped viruses protect their genome with a closed protein shell that forms a small and rigid nano-container. The simplest viruses self-assemble in an iscosahedral symmetry that can consist of as few as 60 identical protein subunits.

We have used atomic force microscopy to image, and to probe the mechanical properties of two different viruses by indentation experiments:

i) CCMV (Bromoviridae), a 28 nm diameter plant-infecting virus which has the special ability to change it size under certain conditions. CCMV self-assembles around anionic polymers (such as DNA) and is therefore interesting for nano-technological applications. We have set out to test the variability of the viral mechanics under different buffer conditions.

ii) ϕ29 (Podoviridae), an elongated 42*52 nm bacteriophage with a tail that is used for insertion of the viral DNA into the host bacterium.

Furthermore, we have modeled the measured elastic response of the viruses by finite element methods to compare it with the empirical data.

BP 17.27 Wed 17:15 P3

Optical properties of light-harvesting systems determined by molecular dynamics simulations — •Carsten Olbrich[1], Michael Schreiber[2], and Ulrich Kleinekathöfer[1] — [1]Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany — [2]Technische Universität Chemnitz, Fakultät für Naturwissenschaften, 09107 Chemnitz, Germany

Harvesting sun light to gain energy for life is initially done by light-harvesting antenna complexes containing chlorophyll and carotenoid molecules. Starting from the available crystal structure of the light-harvesting systems 2 (LH2) of purple bacterium, we applied all-atom classical molecular-dynamics (MD) simulations to the LH2 ring embedded in a membrane. Thus obtained thermal fluctuations of the nuclear positions provide the input for quantum chemical calculations. To obtain the energies of the Q_y excited states of the single Bacteriochlorophyll (BChl) molecules, the semi-empirical ZINDO/CIS method is used to be able to analyze longer time series as was previously possible with the CIS method [1]. To include solvent effects to the excited state dynamics, the surrounding atoms of the BChls are treated as classical point charges in the QM calculations. Using the nuclear motion and the obtained energy differences between ground and Q_y excited states with a time-dependent Hamiltonian, we are able to calculate optical properties of the analyzed system.

[1] A. Damjanović, I. Kosztin, U. Kleinekathöfer and K. Schulten, Phys. Rev. E **65**, 031919 (2002).

BP 17.28 Wed 17:15 P3

Novel PSs for PDT: time-resolved detection of $^1O_2$-phosphorescence allows to determine the PS's localisation — •Christoph Feest[1], Annegret Preuss[1], Beate Röder[1], and Ursula Simonis[2] — [1]Institut für Physik, Humboldt-Universität zu Berlin — [2]Department of Chemistry and Biochemistry, San Fransisco State University

Novel photosensitisers (PS) for Photodynamic Therapy (PDT) have been designed to specifically localize at mitochondria as they play a key role in programmed cell-death (apoptosis). The PSs are based on a Tetraphenylporphyrin core and have specific substitutions that modulate their physico-chemical properties and allow for specific intracellular localisation. The photophysical parameters of all compounds were determined in solution. Additionally, the PDT relevant singlet oxygen ($^1O_2$) generation was investigated in vitro using flash-photolysis and time resolved $^1O_2$ luminescence detection. A new setup was successfully used for evaluation of $^1O_2$ consumption during low-dose irradiation of cells. The intracellular localization was investigated *in vitro* using CLSM and FLIM technique. In the future, the combination of these optical methods for investigation of light-induced photosensitized processes may enable us to precisely determine the intracellular site of the photodynamic action.

BP 17.29 Wed 17:15 P3

Theoretical simulation of Protein Kinase C (PKC) membrane translocation — •Mike Bonny, Martin Peglow, Karsten Kruse, and Heiko Rieger — Universität des Saarlandes, Theoretische Physik

Conventional protein kinases C (cPKCs) play an essential role in signal transduction and in gene regulation. PKCα, a member of the cPKC-family, translocates to the plasma membrane after activation via Ca^{2+}-ions in cytoplasm and creates local pattern, so-called local translocation events, with limited spatial spreads ($< 4\mu m$), comprising two groups of lifetimes; brief events ($400-1500$ms) and longlasting events(> 4s).

In our work, we use a mean-field description as well as a three dimensional stochastic reaction-diffusion model. If on assumes interactions among the PKCα molecules in the membrane both models show similar results and are able to explain the two groups of lifetimes and the limited spatial spread of membrane-bound PKCα molecules.

BP 17.30 Wed 17:15 P3

Inflammatory activation of macrophages by specific kinds of nanoparticles — •Kristina Riehemann[1], Kathrin Hardes[1], Stefan Gerbes[2], and Mirko Bukowski[2] — [1]Center for Nanotechnolgy (CeNTech)/University of Münster, Heisenbergstraße 11, 48149 Münster — [2]INM - Leibniz Institute for New Materials, Campus D2 2, 66123 Saarbruecken, Germany

Nanoparticles (NP) find more and more their way to clinical applications. Unfortunately negative side effects may happen e.g. through the activation of the immune system through complementary activation or by generation of autoimmune diseases. Macrophages are involved in the innate immunity of the body. Their reaction on NP is important for further acceptance of the particles by the immune system. We investigated the interaction of NPs with primary cell cultures of macrophages derived from peripheral blood and different kinds of macrophage cell-lines. The synthesised NP we used where SiO2- Particles which differed in size, surface charge and *chemistry. Some particles where modified with polyethyleneglycole(PEG)-chains on their surface. We have shown that dependent on their surface structure NP can activate macrophage as shown by the secretion of inflammation mediators like IL1, iNOS and H2O2.

BP 17.31 Wed 17:15 P3

Quantification of hematopoietic stem cell chemotaxis by microstructured channel systems and ELISA — •Christina Leinweber[1], Rainer Saffrich[2], Wolfgang Wagner[2], Axel Rosenhahn[1], Anthony D. Ho[2], and Michael Grunze[1] — [1]Angewandte Physikalische Chemie, Universität Heidelberg, Germany — [2]Abteilung Innere Medizin V, Universitätsklinikum Heidelberg, Germany

The chemical communication between mesenchymal stromal cells (MSC) and hematopoietic stem cells (HSC), playing an important role in modern leukemia therapy, is not yet understood in detail. It is supposed that HSC migrate towards bone marrow, the so called homing process, guided by a concentration gradient of chemokines which are expressed by marrow cells. We investigate these chemotactic motions of HSC and malignant hematopoietic cell lines using microstructured chip systems. By varying the channel geometries defined concentration gradients are generated that allow to study single parameters, e.g. migration kinetics, thresholds, sensing sensitivity and swarm behaviour. The first migration experiments in microwells and microstructured systems are presented. Stem cell migration is most likely controlled via SDF-1 as chemokine involved in the signalling process. In order to quantify the role of SDF-1 in greater detail we additionally performed ELISA experiments to study the expression of SDF-1 by MSCs. The correlation of migration kinetics and bioanalytical data is an important part of understanding stem cell homing and will be also the basis for mathematical simulations later on.

BP 17.32 Wed 17:15 P3

Controlling cell signalling with magnetic nanoparticles — •Verena Schittler[1,2], Delphine Arcizet[1,2], Yoshihiko Katayama[3,2], Don Lamb[3,2], Stefan Zahler[4], Joachim Rädler[1,2], and Doris Heinrich[1,2] — [1]Department für Physik, Ludwig-Maximilians-Universität, Munich — [2]Center of NanoScience (CeNS) — [3]Department Chemie und Biochemie, Ludwig-Maximilians-Universität, Munich — [4]Department Pharmazie, Ludwig-Maximilians-Universität, Munich

In recent years, numerous biomedical applications for superparamagnetic iron oxide nanoparticles have emerged as targeted drug delivery and magnetic resonance imaging. Labelling these nanoparticles by lipophilic dyes to visualize the nanoparticles via fluorescence microscopy offers new potential for imaging.

Our research is focused on cell control by fluorescent magnetic nanoparticles in living cells and we study the impact of external magnetic forces on transport properties inside the cell and on cell migration as a whole. So far, we investigated the internalisation in Dictyostelium discoideum cells and in human mammary epithelial cells (HMEC) with and without force field. The fluorescence of the particles allows us to visualize this step. To analyse further the intracellular diffusion and active transport by molecular motors of the particles, we use a 3D-tracking setup which offers the possibility to follow the particles online also in the z-direction. We aim at a better understanding of cell migration by stimulating magnetically labelled cells with external magnetic forces and investigate exact mechanisms in magnetotactic response.

BP 17.33 Wed 17:15 P3

Formation of Domains in Bacterial Flagella — •Reinhard Vogel and Holger Stark — TU Berlin

Many types of bacteria swim by rotating a bundle of helical filaments also called flagella. Each filament is driven by a rotatory motor. When its sense of rotation is reversed, the flagellum leaves the bundle and undergoes a sequence of configurations characterised by their pitch, radius and helicity (polymorphism). Finally the flagellum assumes its original form and returns into the bundle.

In general, the helical shape of the bacterial flagellum can assume 11 different configurations depending, e.g., on mechanical loading, temperature, and chemical composition of the solution. In recent optical tweezer experiments, Darnton and Berg [1] pulled at the flagellum and induced transformations between different helical configurations but they also observed the simultaneous occurence of two configurations separated by a transition region. We investigate this domain formation by extending the linear elasticity theory of thin helical rods. We compare two types of elastic free energy with two stable helical states. One is a polynomial of degree four, the other a composition of two harmonic potentials. For realistic parameter values, we discuss the force extension curve for both free energies as a function of pulling speed and explore the influence of thermal noise. Especially for the second free energy, the force extension curve exhibits sharp transitions between two helical configurations reminiscent to experiments.

[1] N.C.Darnton H.C. Berg, Biophys. J. 92, 2230-2236 (2007)

BP 17.34 Wed 17:15 P3

A hydrodynamic model of bacterial motors — •Johannes Greber — Institut für Theoretische Physik WWU Münster

We consider a simple model for bacterial motors moving in two dimensional fluids. The objects are rigidly connected point vortices. We investigate in detail a case of propelling objects and perform an analysis of the collision process between two counterpropagating swimmers.

BP 17.35 Wed 17:15 P3

4D-Tracking of pathogens by digital in-line holography — •Sebastian Weisse[1], Matthias Heydt[1], Niko Heddergott[2], Markus Engstler[2], Michael Grunze[1], and Axel Rosenhahn[1]

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Digital in-line holography is based on the original idea of D. Gabor's 'new microscopic principle'. An interference pattern of the so-called 'source wave' and the so-called 'object wave' is recorded. It contains three dimensional information of the object encoded in phase and amplitude. From a time series of such holograms, three dimensional trajectories of moving microorganisms can be retrieved.

We have built a portable, temperature-controllable digital in-line holographic microscope to study the motion patterns of the blood parasite *Trypanosoma brucei*, the causative agent of African sleeping sickness under physiological conditions. Its cork-screw-like self-propulsion in the bloodstream of a mammalian host is essential for the clearing of immunglobulins from the cell surface by hydrodynamic drag force. Motility is therefore pivotal to evade the host's immune system. So far, the locomotion of the parasite has only been studied in 2D. Using our system parasites were tracked at varying temperatures and viscosities with high spatial and temporal accuracy in 3D. The ability to track different cell strains under varying physical conditions will lead to a deeper understanding of their locomotion and thus their pathogenesis.

BP 17.36 Wed 17:15 P3

Looking at cell motility in blood flow — •Sravanti Uppaluri[1], Eric Stellamanns[1], Dagmar Steinhauser[1], Markus Engstler[2], and Thomas Pfohl[1] — [1]Max Planck Institute for Dynamics and Self Organization — [2]Darmstadt University of Technology

Entry of African trypanosomes, bloodstream parasites responsible for sleeping sickness, into the brain drastically diminishes disease prognosis. With an average swimming speed of 20μm/s, trypanosomes are able to penetrate the blood brain barrier despite significantly higher blood flow rates around the brain. This suggests that trypanosomes may have the ability to preferentially position themselves along the width of a blood vessel even at local flow velocities of up to 1mm/s. Using microfluidic techniques, we emulate blood vessels and thereby study the trypanosome's behaviour in Poiseuille flow. We examine the parasite's position distribution along the width of the 'blood vessel' in increasing flow rates. We demonstrate the trypanosomes' ability to make turns at relatively high flow velocities and penetrate confined gaps. Further, chemical gradients are established within the microfluidic device to investigate the chemotactic response of trypanosomes in flow. These experiments should lead to the development of a microfluidic assay to test for membrane crossing of motile cells.

BP 17.37 Wed 17:15 P3

Survival of heterogenous populations in fluctuating environments — •Florentine Mayer and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

Organisms must rapidly adapt to fluctuating environments to survive. In bacterial populations this is often achieved by phenotypic diversity, where bacteria can switch between different phenotypic states. Survival of the population can increase if each of these phenotypes is adapted to different environmental conditions. We investigate a spatial cellular automaton model for a bacterial biofilm, where each bacterium can take two different phenotypes, whose growth and death rates depend on the environmental conditions. Employing stochastic simulations we explore the spatio-temporal dynamics of the population and the ensuing stationary states. We find a transition between an active and an absorbing state, which is characterized by a probability distribution for extinction times with an anomalous long time tail. Further properties of the stationary states, such as the cluster size and cluster mass distribution are analyzed in detail.

BP 17.38 Wed 17:15 P3

Competition between sexual and asexual reproduction: geographic parthenogenesis in structured resource space — •Yixian Song[1], Irene Ament[3], Stefan Scheu[2], and Barbara Drossel[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Deutschland — [2]Institut für Zoologie, Technische Universität Darmstadt, Deutschland — [3]Institute for Physical Chemistry, Johannes Gutenberg Universität, Mainz, Deutschland

In spite of the twofold cost of sex due to the production of males about 95% of species are sexual. Since the paradox of sexuality was pointed out by Darwin(1859), many explanations were suggested, e.g. Muller's ratchet(1964),Williams' Lottery model(1975), Bell's Tangled Bank(1982), and related models. The recently introduced Scheu-Drossel model(2007) is based on the fundamental fact of limited and structured resources. In this model asexual species win over sexual species only when mortality rates are large, resources regrow fast, many different genotypes are allowed to coexist at the same place, or when resource diversity is small. By adding spatial structure into this model, we obtained a pattern resembling geographic parthenogenesis. "Geographic parthenogenesis"describes the fact that many species reproduce asexually at the boundaries of ranges, i.e. in northern regions, at high elevations, or the transition to deserts. By including a gradient in the rate of mortality or resource diversity in our computer simulations a stable distribution was obtained, with sexuals prevailing in regions of low mortality and high resource diversity, while asexuals prevailing at the boundary, where mortality is high or resource diversity low.

BP 17.39 Wed 17:15 P3

Spatial desynchronization of glycolytic waves as revealed by Karhunen-Loève analysis — Satenik Bagyan[1], Ronny Straube[2], •Marcus J.B. Hauser[1], and Thomas Mair[1] — [1]Otto-von-Guericke University, Institute of Experimental Physics, Biophysics Group, Universitätsplatz 2, 39106 Magdeburg, Germany — [2]Max-Planck-Institute for Dynamics of Complex Technical Systems, Department of Systems

Glycolysis is the central pathways of the energy metabolism in almost all living beings. The dynamics of glycolytic waves in a yeast extract have been investigated in an open spatial reactor. A transition from inwardly moving target patterns to outwardly moving spiral or circular shaped waves has been observed during the course of the experiments. These two phases are separated by a transition phase of more complex spatio-temporal dynamics. The dynamics of the patterns observed at these three intervals was analysed at different spatial scales by means of a Karhunen–Loeve (KL) decomposition. During the initial phase of the experiment the patterns are sufficiently described by the 2 dominant spatially invariant KL modes independently of the spatial scale. However, during the last stage of the experiment this spatial invariance is lost and at least 6 KL modes are required to account for the observed patterns at spatial scales larger than 3 mm while for smaller scales 2 KL modes are still sufficient. This indicates that in the course of the experiment the local glycolytic oscillators become desynchronized at spatial scales larger than 3 mm. We discuss possible reasons for the desynchronization of the glycolytic waves.

BP 17.40 Wed 17:15 P3

Recording of glycolytic oscillations by electrical measurements at planar yeast cell/electrode-interfaces — •Christian Warnke[1], Mathias Müller[1], Michael Charpentier[1], Hartmut Witte[1], Thomas Mair[2], Marcus J. B. Hauser[2], and Alois Krost[1] — [1]Otto-von-Guericke-Universität Magdeburg, Inst. Exp. Phys., Abt. Halbleiterepitaxie — [2]Otto-von-Guericke-Universität Magdeburg, Inst. Exp. Phys., Abt. Biophysik

One example for temporal macroscopic oscillations is glycolysis in yeast cells. For studying and recording the glycolytic oscillations the measurement of the NADH-fluorescence is used as a standard method. An alternative detection method of glycolytic oscillations of yeast cells and yeast extract is the use of impedance measurements by a planar yeast cell/blank electrode interface [1]. This interface was developed further by the isolation of the utilized Ti-Au-electrodes on glass substrates with Ta_2O_5 and SiO_2 layers. As an other alternative approach we used the source-drain-current of an AlGaN/GaN High Electron Mobility Transistor (HEMT) to detect electrical signals from yeast cells. We found oscillations of the electrical measurement parameters with the same temporal dynamics as the glycolytic ones. In order to identify the underlying processes in yeast cells responsible for the electrical signals, we analyzed theses oscillations at different electrical conductivities of the cell membranes.

[1] Reiher, A. et al.: Electrical stimulation of the energy metabolism in yeast cells using planar Ti-Au-Electrode interface, J. Bioenerg. Biomembr. 38 (2006), 143-148.

BP 17.41 Wed 17:15 P3

Modeling of spatio-temporal dynamics in glycolysis with inhomogeneous periodic influx of substrate — •Anastasia Lavrova[1], Eugene Postnikov[2], Thomas Mair[3], and Lutz Schimansky-Geier[1] — [1]Institute of Physics, Humboldt-University at Berlin, Berlin, Germany — [2]Department of Theoretical Physics,

Kursk State University, Kursk, Russia — [3]Institute of Experimental Physics,Otto-von-Guericke-University Magdeburg, Germany

Spatio-temporal dynamics in glycolysis has been observed in the yeast extracts. It has been shown that waves can be induced by local perturbation on the activity of key enzyme, phosphofructokinase (PFK). [Bagyan et al, 2005]. Since the propagation dynamics and shape of traveling reaction-diffusion waves can contain information about the state of the system, it has been suggested that they can play an important role for biological information processing [Mair et al,2000].

In the present work we consider the Selkov model extended with diffusion terms which describes glycolytic phase waves observed in yeast extracts. It has been shown that the slightly non-uniform influx can provide a rich assortment of wave patterns such a traveling waves with a phase reversal, spatial-temporal beats, etc. With the introduction of non-stationary periodic influx it is possible to control the direction and the velocity of waves.

We discuss mechanisms of the waves propagation depending on the inhomogeneous periodic substrate influx.

BP 17.42 Wed 17:15 P3

Network Topology of Physarum Polycephalum — •Siddharth Deshpande, Christina Oettmeier, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

The vein network of the unicellular slime mold Physarum Polycephalum shows a characteristic structure. We study vein creation and network formation. Mainly, we are interested in the distribution of nodes and links as a function of time and growth conditions. Network topology is observed from nanometer to millimeter length scales using Zeiss objectives with various magnifications. Further, we have developed a special macro-observation setup via a Canon digital camera.

BP 17.43 Wed 17:15 P3

Stability analysis and maneuver of gene regulation networks — •Joseph Zhou and Thilo Gross — Max Planck Institute for the Physics of Complex Systems, Noethnitzer Strasse 38, Dresden

A gene regulation network can be viewed as a complex system with the ability to switch back and forth between different gene expression patterns due to a variety of intrinsic or extrinsic perturbation signals. More and more evidences show that malfunctioning cells, such as cancer cells, are not just the accumulation of random delirious gene mutations. Instead, it has an erroneous re-access of proliferating embryonic programs as local attractors which are embedded in the gene regulation network. Could we induce these cells out of these attractors by systematically over-expressing a well-designed combination of genes? For example, the current research of Induced pluripotent stem cell (iPS) is more an art of cell biologists than a well-founded science. The protocol of the combination of different genes, the ratio of these components, the timing and duration of over-expressing these genes is totally dependent on the try-and-error and past know-hows. It is badly needed to perform a systematic gene regulation network study to give some sound guidance for the cell reprogramming. In this research, we emply a general dynamic system model for a cell reprogramming from adult pancreatic exocrine cells to beta-cells to address questions above.

BP 17.44 Wed 17:15 P3

Dynamics of biological networks — •Eva Gehrmann and Barbara Drossel — Institut fur Festkorperphysik, Technische Universitat Darmstadt

We study the dynamical and functional properties of selected biological networks. To this aim, we use the generalized method proposed by Steuer et al. 2006, which does not refer to an explicit set of differential equations, but is based on those quantities that determine the system's Jacobian J. By varying the parameters and the representation of the system, we identify which features are necessary for observing a certain dynamical behaviour.

BP 17.45 Wed 17:15 P3

Extraction of deep sources from human EEG — •Philipp Stern[1], Andreas Galka[2], and Jens Christian Claussen[3,1] — [1]Theor. Phys. & Astrophys., CAU Kiel — [2]Klinik f. Neurologie, Univ.-Klinikum S.-H. — [3]Neuro- und Bioinformatik, U zu Lübeck

Noninvasive brain imaging methods do not allow for a time resolution comparable with EEG or invasive measurements. As many dynamical collective phenomena in the brain are observed in the 0.5-50Hz frequency range, noninvasive methods based on EEG measurements are the standard for clinical and behavioral studies as anaesthesia monitoring, sleep research, and diagnostics of neural disorders as tremor and epilepsy. In this study [1] we employ the Kalman filter method for the inverse problem of EEG measurement [2] to extract time series from localized deep brain regions as the thalamus. We discuss the abilities and limitations of the approach.

[1] Philipp Stern, Diploma thesis, CAU Kiel (2008)
[2] Andreas Galka, Okito Yamashita, Tohru Ozaki, Rolando Biscay, Pedro Valdes-Sosa, NeuroImage 23, 435 (2004)

BP 17.46 Wed 17:15 P3

Clusters of sustained activity in sparse networks - the influence of topology on networks bursts — •Olav Stetter[1], Anna Levina[1,2], and Theo Geisel[1,2] — [1]Max-Planck-Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]BCCN Göttingen, Germany

Recent studies demonstrated the dependence of the avalanche size in neuronal networks on the number and strength of its connections. In different experimental settings a similar dependence of the averaged network activity on the size of an external stimulus has been shown.

Additionally, in these experiments the temporal order of activation is shown to be non-random: There exists a topological hierarchy with a number of neurons that are more likely to take part in an early phase of synchronized network activity ("burst"). Their activity can in fact be used to predict the following network behavior.

Here we ask what characterizes these burst initiation zones. We use a simplified, analytically tractable model and concentrate on relations between the average number of neurons that take part in an avalanche (related to measurements using fluorescent dye imaging) and parameters of the network. We observe that certain classes of topological structures can enable the model network to exhibit sustained activity which then leads to an activation of large parts of the network. The likelihood of such sustained activity depends on characteristics of the network such as the number and strength of connections and the dependence of connection probability on the distance (related to the degree-degree correlation).

BP 18: Regulation and Signaling

Time: Thursday 9:30–13:15 Location: HÜL 186

Invited Talk BP 18.1 Thu 9:30 HÜL 186

Systems biology of yeast cell signaling and response to stress — •Edda Klipp — Humboldt-Universität zu Berlin, Dept. of Biology, Theoretical Biophysics

Life is change. In order to study and understand life, it is necessary, but not sufficient to study genes, proteins or metabolites, and networks thereof in static conditions. Instead, we must handle the dynamic action. Stress and external perturbations are means to study the wiring of biochemical networks or signal transduction pathways and to understand the underlying regulatory principles.

Over the last years, we have studied various signal transduction and regulatory pathways in a model organism, the yeast Saccharomyces cerevisiae, and investigated the response of cells to external perturbations on various levels. To this end, we have established mathematical models, reflecting physical properties such as reaction kinetics, thermodynamic constraints as well as fluxes and forces. They are mainly in form of ordinary differential equation systems. Their structure and parameters are based on publicly available information and new dynamic data measured by our experimental collaborators. Here, I will focus on results with respect to interaction of different signaling and regulatory pathways. Specifically, new aspects in cell cycle regulation and the interaction of stress-activated signaling pathways with cell cycle progression will be discussed. The results indicate that yeast cells have developed different mechanisms for coping with external stress during different periods of their life time.

Invited Talk BP 18.2 Thu 10:00 HÜL 186

Towards an understanding of membrane and protein traffic in living cells — •Matthias Weiss — Cellular Biophysics Group, German Cancer Research Center, Heidelberg, Germany

Sorting of transmembrane proteins is a central task of the secretory pathway in eucaryotic cells. Here, the multitude of transmembrane proteins have to utilize self-organization processes on the molecular scale to decide whether they participate in transport along the secretory pathway or rather reside in their current compartment (e.g. the endoplasmic reticulum, ER, or the Golgi apparatus, GA). Using advanced light microscopy techniques and coarse-grained membrane simulations, we have addressed two of the key issues in membrane and protein trafficking. First, we elucidated the interaction between unfolded proteins and chaperones in the ER. As a result, we found that unfolded proteins show a strongly obstructed diffusion that can be altered to the diffusion behavior of folded proteins, e.g. by blocking the interaction with chaperones. Accompanying simulations indicate that this behavior reflects the obstructed diffusion of a cluster of chaperones and unfolded proteins due to (almost immobile) translocon pores in the ER. Second, we asked for generic mechanisms that support the sorting of folded transmembrane proteins into emerging vesicules at the ER and/or the GA. We showed by means of coarse-grained membrane simulations that hydrophobic mismatching can drive cluster formation of transmembrane proteins and even the demixing of a heterogeneous population of proteins. Based on this result, we propose a generic way to make and fill vesicular carriers with a well-defined cargo of proteins.

BP 18.3 Thu 10:30 HÜL 186

Perfect robust network design of the KaiABC circadian clock — •Christian Brettschneider and Markus Kollmann — Institut für theoretische Biologie, Humboldt Universität zu Berlin

The simple circadian oscillator found in cyanobacteria can be reconstituted in vitro using three proteins - KaiA, KaiB, KaiC. It has been shown that four forms of KaiC differing in their phosphorylation state appear in an ordered pattern. Importantly, it has been revealed that phase, frequency and amplitude of the oscillations do not change under concerted severalfold over- and underexpression of its components. Consequently, the circadian clock is invariant with respect to concerted fluctuations in total protein concentrations of all Kai proteins. This observation is a strong constraint for modeling the circadian clock.

We will present the first quantitative model that includes the ordered pattern of the four KaiC states as well as the measured invariance of concerted variations. The model is systematically developed from intrinsic KaiC autokinase and autophosphatase rates that are modulated by KaiA and KaiB. A formal description shows that the invariance of concerted variations can be achieved by inactivation. In this case, inactivation of KaiA leads to a negative feedback oscillator, that in turn causes synchronization between different KaiC as well as high amplitudes.

BP 18.4 Thu 10:45 HÜL 186

Physical constraints on cooperative transcription factor-DNA interaction — •Nico Geisel[1] and Ulrich Gerland[2] — [1]Departament de Física Fonamental, Universitat de Barcelona — [2]Arnold Sommerfeld Center for Theoretical Physics, LMU München

DNA-binding proteins often interact not only with the genomic DNA, but also with each other. In particular for the case of transcription factors (TFs), cooperative binding is fundamental to the nonlinear and combinatorial control of gene expression. Here, we focus on the simplest case of two TFs binding specifically to two neighboring functional sites, in the background of the quasi-random genomic DNA sequence. Within a coarse-grained theoretical model, we characterize both the equilibrium occupancy of the target sites and the non-equilibrium cooperative search kinetics of the TFs. Based on our model and analysis, we identify physical constraints on the optimal choice of protein-protein and protein-DNA interaction parameters in the context of bacterial gene regulation.

BP 18.5 Thu 11:00 HÜL 186

Influence of chemical modifications on siRNA strand separation and RISC target interaction studied by fluorescence cross-correlation spectroscopy *in vivo* — •Wolfgang Staroske, Thomas Ohrt, and Petra Schwille — Biophysics Group, BIOTEC, TU Dresden, Germany

Short double stranded RNA molecules have emerged as key regulators of gene expression in various organisms, both in the context of controlling developmental programs and as a defence mechanism to protect the genome against viruses and transposons. Short interfering RNAs use Argonaute-containing complexes called RNA-Induced Silencing Complex (RISC) to identify cognate RNA transcripts, whose expression is to be silenced. By combining laser scanning microscopy, fluorescence correlation and cross-correlation spectroscopy (FCS/FCCS) and biochemical methods, we have exploited the interaction of short interfering RNAs with RISC and a target RNA *in vivo*. We used a stable EGFP-Ago2 expressing 293 cell line, with endogenous expression levels suitable for FCS/FCCS measurements and designed a fluorescently labelled RNA, mimicking a target mRNA. By investigating the EGFP-Ago2 cell line and delivered fluorescently labelled siRNAs or targetRNA *in vivo*, we were able to gain new insights into siRNA strand separation, RISC loading and RISC target interactions. Our analysis of various chemical modified and fluorescently labelled siRNAs showed a correlation between chemical modification, passenger strand separation and gene silencing.

15 min. break

BP 18.6 Thu 11:30 HÜL 186

Transfection on the Single Cell Level: Interplay of Stochastic Delivery and Deterministic Expression — •Jan-Timm Kuhr[1,2,3], Gerlinde Schwake[3], Simon Youssef[1,3], Joachim O. Rädler[1,3], and Erwin Frey[1,2,3] — [1]Center for NanoScience (CeNS) — [2]Arnold Sommerfeld Center for Theoretical Physics — [3]Fakultät für Physik, Ludwig-Maximilians-Universität, Muinch, Germany

Non-viral delivery of exogenous genes to cells, known as transfection, is a key technology in gene therapy. To analyze transfection on the single cell level we used complexes of cationic lipids/polymers and fluorophore-encoding plasmids. Statistical analysis of abundant expression curves permits conclusions on key properties of complex delivery.

Expression onset time distributions depict strong cell phase dependence of successful transfection.

Distributions in maximal expression are analyzed within a theoretical model, which describes plasmid delivery as a multi-step stochastic process followed by deterministic gene expression. The model suggests that noise in transfection is primarily caused by small number fluctuations intrinsic to gene delivery. We infer the steady state ratio of proteins per plasmid, the number of activated plasmids per complex, and the average number of delivered complexes from single cell data. Simultaneous transfection with plasmids coding for distinct proteins yields consistent percentages of non-fluorescent, mono- and, dichromatic cells, substantiating our semi-stochastic model of transfection and the resulting distribution of active plasmids per cell.

BP 18.7 Thu 11:45 HÜL 186

Dynamics of receptor-mediated signal transduction in living cells analyzed by correlation spectroscopy — •Steffen Steinert[1], Felix Neugart[1], Andrea Zappe[1], Deborah Buk[2], Lutz Graeve[2], Peter Scheurich[3], and Jörg Wrachtrup[1] — [1]3. Physikalisches Institut, Universität Stuttgart — [2]Biologische Chemie und Ernährungswissenschaften, Universität Hohenheim — [3]Institut für Zellbiologie und Immunologie

Malfunctions of signaling cascades can cause serious diseases such as Alzheimer or Multiple Sclerosis. Thus, it is of high relevance to have an elementary understanding of functionality, stoichiometry and dynamics of signaling processes. However, membrane dynamics of many important hormone and cytokine receptors are still poorly understood. A drawback of biochemical in-vitro techniques is their potential introduction of artifacts due to the analysis of dead cells and the usage of several reagents. Instead, we employ highly sensitive optical methods which are capable of detecting proteins even at the single molecule level in living cells. Among the applied optical techniques are pulsed Total-Internal-Reflection-Fluorescence-microscopy (TIRF), Fluorescence-Correlation-Spectroscopy (FCS) and Fluorescence-Cross-Correlation-Spectroscopy (FCCS). By these optical techniques we can determine spatial and temporal parameters of signaling components in-vivo at physiological concentrations and temperatures. As model systems we are looking particularly into the receptors of Ciliary-Neurotrophic-Factor(CNTF) and Tumor-Necrosis-Factor(TNF).

BP 18.8 Thu 12:00 HÜL 186

Cell stimulation with optically manipulated microsources — •Holger Kress[1], Jin-Gyu Park[1], Cecile Mejean[1], Jason Forster[1], Jason Park[1], Spencer Walse[1,2], Dianqing Wu[1], Orion

Weiner[3], Tarek Fahmy[1], and Eric Dufresne[1] — [1]Yale University, New Haven, USA — [2]US Department of Agriculture, Parlier, USA — [3]UC San Francisco, USA

Many cells can sense spatial and temporal heterogeneities in concentrations of soluble molecules. The cellular signal transduction which forms the basis of this ability consists of signaling cascades and loops whose length and time scales are largely unknown. The systematic investigation of these networks requires control over the chemical microenvironment of cells. We present a novel technique to create molecular concentration patterns that are chemically, spatially and temporally flexible. Our approach uses optically manipulated colloidal particles which act as microsources of soluble molecules. This technique for flexible cell stimulation is combined with quantitative live cell microscopy measurements of cellular responses. We demonstrate the method by inducing chemotaxis in neutrophils. We quantify the intracellular calcium release, actin distribution, shape and motility of single cells. The possibility for quantitative stimulus-response measurements on single cells makes this method applicable to a wide range of cell biological studies.

BP 18.9 Thu 12:15 HÜL 186

Non-optimal microbial response to antibiotics underlies drug interactions — •Tobias Bollenbach and Roy Kishony — Harvard Medical School, Boston, MA, USA

Bacterial cells respond to antibiotic stress by regulating gene expression. Of key importance for survival and growth is the regulation of ribosomal genes, which control the overall cellular translation rate. While ribosome production is known to be tuned to different nutrient conditions to maximize growth, much less is known about the optimality of ribosome production under antibiotic stress. Inhibition of translation by drugs can relieve the inhibitory effect of antibiotics that target DNA synthesis, suggesting a greater-than-optimal expression of ribosomal genes when under DNA stress. Here we test this hypothesis by measuring and manipulating gene expression in *Escherichia coli* under various antibiotic stresses. We find that cells down-regulate ribosomal gene expression in response to antibiotics that inhibit DNA replication. The hallmark of non-optimality is the possibility for improvement: using strains with genetically manipulated ribosomal gene expression, we show that decreased ribosomal expression can increase survival and growth under DNA stress. Further, we find that genetically optimizing ribosomal expression removes the suppression between DNA and protein synthesis inhibitors, demonstrating that these drug interactions result from non-optimal gene regulation. We present a mathematical model which shows how optimal growth rate-dependent regulation of ribosome synthesis can lead to (1) non-optimal regulation in response to antibiotics and (2) suppressive drug interactions.

BP 18.10 Thu 12:30 HÜL 186

Quorum signal integration in the B. subtilis sporulation phosphorelay — •Ilka Bischofs[1], Josh Hug[2], Aiwen Liu[2], Denise Wolf[1], and Adam Arkin[1,2] — [1]Lawrence Berkeley Lab, Berkeley, USA — [2]UC Berkeley, Berkeley, USA

The phosphorelay is a central signal transduction structure in B. subtilis that integrates numerous cues including starvation and cell density signals in order to determine whether to commit to spore formation. Based on a theoretical model we demonstrate that the phosphorelay can act as a computational machine performing a sensitive division operation of inductive kinase encoded signals by instructive quorum modulated phosphatase signals, indicative of cells computing a "food per cell" estimate. In addition, we show experimentally that at least one quorum operon is heterogeneously induced in sporulating microcolonies. Cells delaying sporulation sustain quorum signal expression during periods of active growth, while cells committing to sporulation do not. Together with the model these findings suggest that the phosphorelay normalizes environmental signals by the size of the subpopulation actively competing for nutrients.

BP 18.11 Thu 12:45 HÜL 186

Networks for cell division and their neutral mutants — •Gunnar Boldhaus and Konstantin Klemm — Bioinformatics Group, Department of Computer Science, University of Leipzig, Härtelstraße 16-18, D-04107 Leipzig, Germany

The functioning of a living cell is largely determined by the structure of its regulatory network, comprising complex, typically not pairwise interactions between regulatory genes. An important factor for the stability and evolvability of such regulatory systems is neutrality – typically a large number of alternative structures exhibit the same dynamical behaviour. Here we study the regulatory networks for the cell cycles of the yeast species S. cerevisiae and S. pombe. A coarse-grained Boolean approach allows us to abstract from biochemical details such as precise binding constants and degradation rates.

We exhaustively enumerate all networks performing the same function as the yeast wildtype. For both species, the wildtype is close to optimal with respect to sparse wiring; almost all neutral mutants have more regulatory connections than the wildtype. Furthermore we analyse the reachability of the alternative networks from the wild type. This neutral space of regulatory networks is fragmented under point mutations which establish or delete single interactions.

BP 18.12 Thu 13:00 HÜL 186

Drug absorption in a three-compartment model — •Niko Komin and Raúl Toral — IFISC (UIB-CSIC), Palma de Mallorca, Spain

For the understanding of pharmacological phenomena, a variety of compartment models were and are developed. The concept of interconnected pools, into which the drug is administered, searches solutions for the concentration evolution over time in the different compartments. The connections can be linear or non-linear, the system can be open or closed, concerning its interchange with the environment.

An analytic solution for any of the models would be of great value for understanding experimental data and refining the underlying assumptions. Here we want to present a mathematical way of transforming the system into a different picture and propose an adequate approximation to it. As this is a general approach we will explicitly do that on a closed three-compartment model with a Michaelis-Menten nonlinearity, as a representation of a P-gp limited antibiotic absorption [1], and show how it can be extended to other models.

References:

1. Gonzalez-Alvarez et al (2005) Xenobiotica.

BP 19: Cell Adhesion

Time: Thursday 10:45–13:15 Location: ZEU 260

BP 19.1 Thu 10:45 ZEU 260

Modelling the active mechanical response of stress fibers — •Achim Besser and Ulrich S. Schwarz — University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

Stress fibers are bundles of actin filaments held together by the crosslinker protein α-actinin and actively tensed by the molecular motor protein myosin II. We have developed a model that describes stress fiber dynamics after biochemical or mechanical perturbations. For example, our stress fiber model can be solved analytically for the contraction dynamics after severing the fiber at any point along its length. Experimentally this situation has been realized by laser cutting and our model has been applied to analyze such data. The model equations can also be solved analytically for the case of cyclic boundary forces yielding theoretical predictions for the frequency dependence of the complex modulus of stress fibers. Decomposing it into its real and imaginary parts and using model parameters determined from the laser cutting experiments, we arrive at estimates for the storage and loss moduli. These quantities could be measured in future experiments and then would provide an additional test for our model.

BP 19.2 Thu 11:00 ZEU 260

Adhesion Dynamics of Early Cell Spreading — •Pavel Ryzhkov, Christina Oettmeier, Jac-Simon Kühn, Marcus Prass, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

We report on the adhesion dynamics of spreading mouse embryonic fibroblasts. Advancing membrane edges and adhesions patterns on

two-dimensional substrates are characterized by reflection interference contrast microscopy. We observe spatial-temporal correlations of early spreading events. Adhesion commences via the recurring appearance and disappearance of small patches. These patches grow slowly in size and lifetime until a continuous adhesion patch has formed, which initiates fast cell spreading.

BP 19.3 Thu 11:15 ZEU 260

Influence of bilayer substrate fluidity on cell adhesion and cytoskeleton structure — Daniel Minner[1], •Philipp Rauch[2], Josef Kaes[2], and Christoph Naumann[1] — [1]Indiana University, Indianapolis, USA — [2]University of Leipzig, Germany

Contact and adhesion between cells and their environment (e.g. other cells or the extracellular matrix) play a key role in maintaining cell stability and in all cell motility processes. Transmembrane proteins of the integrin family connect to specific ligands in the extracellular matrix and establish connections e.g. via actinin between the inner cytoskeleton and the extracellular environment. Up to now tethered lipid bilayer model systems mimicking cell surfaces have found limited applications in in vitro studies since they are instable in contact with cells. The novel stacked tethered bilayer substrates developed by D. Minner and C. Naumann at the University of Indiana show good stability and reproducible diffusion properties, adjustable via linker density and number of stacked layers. We used them to investigate the influence of friction and substrate coupling on NIH 3T3 mouse fibroblasts and their cytoskeleton. We find that with increasing fluidity, a rearrangement in the actin cytoskeleton occurs, similar to that observed on gel substrates of different stiffness. This is accompanied by reduced spreading of the cells. First experiments with neuronal cell lines show a contrary effect: On more fluid substrates, dendritic growth seems to be accelerated.

BP 19.4 Thu 11:30 ZEU 260

Dissecting the Impact of Matrix Anchorage and Elasticity in Cell Adhesion — •Tilo Pompe[1], Stefan Glorius[1], Thomas Bischoff[1], Ina Uhlmann[1], Martin Kaufmann[1], Sebastian Brenner[2], and Carsten Werner[1] — [1]Leibniz-Institut für Polymerforschung, Dresden, Germany — [2]Universitätsklinik C.G. Carus, Dresden, Germany

Extracellular matrices determine cellular fate decisions through the regulation of intracellular force and stress. It was anticipated that matrix stiffness and ligand anchorage would have distinct effects on the signalling cascades involved. We now can show how defined non-covalent anchorage of adhesion ligands onto elastic substrates allows the dissection of intracellular adhesion signalling pathways. Fourier transform traction cytometry proved the regulation of cell traction forces by the strength of the non-covalent anchorage of extracellular matrix ligands to the substrate. Using these constrained traction force levels the strain energy exerted by the cell on the substrate was quantitatively described by treating the cell as active force dipoles. Moreover matrix stiffness could be demonstrated to be the dominant exogenous signal of the global mechanical balance in cell adhesion. Besides the decoupling of biophysical signals biochemical signals like phosphorylation of the adhesion signalling protein FAK were distinctively controlled by matrix elasticity but not by varied receptor forces. Furthermore, using the net traction dipole moment of adherent cells our approach revealed a basis for a generalised biophysical treatment of extracellular mechanical signals in cell adhesion.

15 min. break

BP 19.5 Thu 12:00 ZEU 260

Vinculin lipid anchorage influences focal adhesion strength and turnover — •Lang Nadine, Gerold Diez, Thorsten Bloem, Philip Kollmannsberger, Ben Fabry, and Wolfgang Goldmann — Biophysics Group,Departmet of Physics, University of Erlangen-Nuremberg

The focal adhesion protein vinculin links the actin cytoskeleton to other proteins within the focal adhesion complex and plays an important role in cell adhesion and migration. To function properly vinculin needs to bind to the cell lipid membrane but the mechanism is currently not well understood.A lipid-membrane binding site,called lipid anchor, is located at the C-terminus of the vinculin tail. We measured the mechanical behavior of vinculin knock-out mouse embryonic fibroblast cells transfected with EGFP-linked-vinculin deficient of the lipid anchor (vinDeltaC).A magnetic tweezer was used to determine cell stiffness and binding strength.Compared to wildtype and rescue both were reduced in vinDeltaC cells suggesting that lipid binding of vinculin is important for the stability of the focal adhesion complex.Vinculin dynamics in focal adhesions measured with FRAP showed decreased turnover rates of vinDeltaC compared to wild-type vinculin. Because the lipid anchor also contains a c-SRC phosphorylation site we repeated these measurements in cells transfected with full length vinuclin in which either the c-SRC phosphorylation site or the lipid binding sites were scrambled.In both cases we found decreased adhesion strength, suggesting that lipid binding of vinculin and phosphorylation by c-SRC are important for mechanical stability of focal adhesions.

BP 19.6 Thu 12:15 ZEU 260

Correlation of Stress Fibre Pattern and Cell Morphology of Adherent Cells: Experiment and Modelling — •Jörg Meyer, Carsten Werner, and Tilo Pompe — Leibniz Institute of Polymer Research, Dresden, Germany

Cell morphology is known to play a key role in proliferation and differentiation of anchorage dependent cells. In this context the cytoskeleton acts as a mechanical signal transducer for exogenous and endogenous signals. In order to better understand the biophysical processes regulating cell morphology and intracellular stresses we cultured human endothelial cells on micropatterned surfaces. Cell elongation was tuned by adhesion promoting fibronectin stripes of 5 to 40 μm in width. Using autocorrelation image analysis the stress fibre spacing was determined to exhibit a strong discontinuity with a maximum at 15 μm of stripe width. Below this critical value the spacing of actin stress fibres, bundled near the cell edge parallel to the stripe direction, was linearly dependent on stripe width. Above the threshold actin stress fibre spacing mainly remained constant at around 2 μm. Interestingly, we found a similar dependence with a discontinuity at 15 μm of stripe width for the surface area of adherent cells using a finite element model of a liquid drop spreading on adhesive stripes. Total surface area as well as basal contact area of the cell to the stripe correlated to the stress fibre pattern and suggested membrane tension or cell adhesion receptor activation as biochemical triggers for the cytoskeletal arrangement and force distribution inside adherent cells.

BP 19.7 Thu 12:30 ZEU 260

Stochastic dynamics and stability of adhesion sites with different bond arrangements — •Johanna von Treuenfels[1], Christian Korn[1], and Ulrich S. Schwarz[1,2] — [1]University of Heidelberg, Bioquant 0013, Im Neuenheimer Feld 267, 69120 Heidelberg, Germany — [2]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

Adhesive contacts between cells and their environment are organized around a two-dimensional layer of transmembrane adhesion receptors that continuously dissociate and rebind to their extracellular ligands. On the cytoplasmic side, this layer of adhesion bonds is reinforced by additional layers of bonds which on their top side connect to force-generating elements in the cell, mainly the actin cytoskeleton. We introduce a master equation model for adhesion sites which includes these aspects of the spatial organization of the molecular bonds within the adhesion site. We investigate the stochastic dynamics and stability of clusters of bonds connected in series, in parallel and in combinations of these. We consider the mean rupture time as a measure for stability under the disruptive effect of force and find that different configurations are optimal depending on the level of applied force. This suggests that adhesion sites might be organized differently depending on the amount of force they are exposed to.

BP 19.8 Thu 12:45 ZEU 260

Adhesion of bacteria and adsorption of protein: influence of substrate composition — •Yvonne Schmitt, Peter Loskill, and Karin Jacobs — Universität des Saarlandes, Saarbrücken, Germany

The formation of biofilms on substrates that are exposed to a solution containing proteins, sugars, bacteria etc. is a complex process which is still not fully understood. Especially the initial adsorption of proteins and their role in the entire evolution of the biofilm is still unsettled. We focus our recent research on the characterization of the interactions between substrate materials and proteins or bacteria, respectively. Investigations of the adsorption kinetics of proteins like BSA revealed that proteins are sensitive to the composition of the offered substrate [1, 2]. Thus, a manipulation of the adsorption process by tailored substrates is conceivable. Besides, a wide range of methods such as ellipsometry, surface plasmon resonance and x-ray scattering, we use

atomic force microscopy to characterize the dominant forces and parameters involved in the adsorption process and the development of the protein film. Based on the results described above, we study the influence of the substrate material and its composition to the attachment of bacteria. Elasticity measurements on bacteria adsorbed on model surfaces are performed as well as force-distance-measurements with bacteria as probes. These experiments can also be carried out on adsorbed protein films to examine the relevance of a protein layer to the attachment of bacteria.

[1] A. Quinn et al., Europhysics Lett. 81 (2008) 56003
[2] M. Bellion et al., J. Phys.: Condens. Matter 20 (2008) 404226

BP 19.9 Thu 13:00 ZEU 260

Artificial three-dimensional scaffolds for cell adhesion studies — •Thomas Striebel[1], Franziska Klein[2], Martin Wegener[3], Martin Bastmeyer[2], and Ulrich S. Schwarz[1] — [1]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany — [2]University of Karlsruhe, Institute of Zoology, Haid-und-Neu-Strasse 9, 76131 Karlsruhe, Germany — [3]University of Karlsruhe, Institute of Applied Physics, Wolfgang-Gaede-Str. 1, 76131 Karlsruhe, Germany

Adhesion of tissue cells is traditionally studied on two-dimensional culture dishes. In this way, much has been learned how environmental stimuli determine the cellular response, including migration, proliferation and fate. However, much less is known about how tissue cells behave in three-dimensional environments. We have used direct laser writing to design three-dimensional scaffolds for cell adhesion studies with feature sizes down to 100 nm. Our setup can be used to produce structures with many different geometries in a short time and gives highly reproducible results. By applying our procedure to different photoactive materials, we were able to vary the stiffness of the scaffolds and to optimize the system for imaging. Using quantitative image processing, we now can analyze shape, traction and adhesion structures of cells in three dimensions.

BP 20: DNA, RNA and Chromatin

Time: Thursday 14:00–17:15 Location: HÜL 186

Invited Talk BP 20.1 Thu 14:00 HÜL 186

Artificial biochemical reaction circuits based on DNA and RNA — •Friedrich Simmel, Eike Friedrichs, and Ralf Jungmann — Physik Department E14, TU München

Hybridization between complementary sequences of DNA or RNA combined with production and controlled degradation of RNA regulatory molecules can be used for the construction of simplified analogues of naturally occurring biochemical reaction circuits. Such circuits can be used to employ logical decisions, but also interesting dynamical behavior such as oscillations or bistability into biochemical systems. This can be applied, e.g., to control the motion of molecular devices or the synthesis of functional RNA molecules such as RNA aptamers. Experimentally, the dynamical behavior of these reaction networks is studied in bulk solution (in vitro), but also in small reaction compartments such as lipid vesicles or microemulsion droplets. Experiments are supported by numerical studies using deterministic and stochastic models of the networks.

BP 20.2 Thu 14:30 HÜL 186

Self-assembling DNA-caged particles: nanoblocks for hierarchical self-assembly — •Nicholas Licata[1,2] and Alexei Tkachenko[1] — [1]University of Michigan, Ann Arbor, USA — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

DNA is an ideal candidate to organize matter on the nanoscale, primarily due to the specificity and complexity of DNA based interactions. Recent advances in this direction include the self-assembly of colloidal crystals using DNA grafted particles. In this talk we theoretically discuss the self-assembly of DNA-caged particles. These nanoblocks combine DNA grafted particles with more complicated purely DNA based constructs. Geometrically the nanoblock is a sphere (DNA grafted particle) inscribed inside a polyhedron (DNA cage). The faces of the DNA cage are open, and the edges are made from double stranded DNA. The cage vertices are modified DNA junctions. We calculate the equilibrium yield of self-assembled, tetrahedrally caged particles, and discuss their stability with respect to alternative structures. The experimental feasability of the method is discussed. To conclude we indicate the usefulness of DNA-caged particles as nanoblocks in a hierarchical self-assembly strategy.

BP 20.3 Thu 14:45 HÜL 186

Images of Intracellular Kinetics Reveal Accellerated DNA Hybridization — •Ingmar Schön and Dieter Braun — Systems Biophysics, LMU München, Germany

Molecular crowding affects the diffusion properties and the free energies of molecules in densely packed environments. Its impact on reaction kinetics in the relevant context of living cells is still elusive, mainly due to the difficulty of capturing fast kinetics *in vivo*. In this talk, we show spatially resolved measurements of DNA hybridization kinetics in single living cells. HeLa cells were transfected with a FRET labeled dsDNA probe by lipofection. We characterize the reaction kinetics at each image pixel with a kinetic range of $10^{-5} \dots 10^{0}$s by combining laser-driven temperature oscillations, stroboscopic illumination, fluorescence imaging, and frequency-based relaxation analysis. Within individual cells and between different cells, the time constant of the reaction varied according to different DNA concentrations. A quantitative analysis of the concentration dependence revealed that the association rate was considerably enhanced compared to free solution, likely due to molecular crowding effects inside the cell. The imaging modality of our technique facilitates the parallel measurement of different cellular compartments such as the cytoplasm, the nucleoplasm or even the nucleoli. In general, our technique which we call TOOL (Temperature Oscillation Optical Lock-in) microscopy opens up the possibility to map cellular differences in the reaction environment on the micrometer scale and provides quantitative data about intermolecular kinetics for systems biology.

BP 20.4 Thu 15:00 HÜL 186

Promoter proximal transcript secondary structure — •Abigail Klopper and Stephan Grill — Max Planck Institute for the Physics of Complex Systems, Dresden

RNA polymerase transcribes selected parts of the DNA genome into RNA transcripts by advancing processively along a double-stranded DNA template. It melts the DNA into a single-stranded bubble and catalyzes bond formation, which effectively polymerizes the complementary RNA strand. There is evidence to suggest that the nascent RNA forms self-interacting secondary structure elements. These are thought to serve as barriers to an inactive backtracked state, aiding recovery to an active conformation and ensuring the timely production of a functional transcript. We investigate the role of conformational characteristics of the RNA strand in the context of the early stages of transcription, during which the polymerase is prone to premature and irreversible stalling. Specifically, we examine the hypothesis that the absence of long transcripts is the primary cause of stalling in the vicinity of the promoter. Despite prolific attention paid to the conformational statistics of long RNA strands, little is understood about the implications of finite size in shorter strands. With a recursive formulation of the partition function for homogeneous and disordered RNA molecules, we utilize numerical and analytical approaches to calculate the average number of unpaired bases adjacent to the polymerase. We find that the length-dependent equilibrium fold attributed to the nascent strand poses a marked barrier to a backtracking polymerase within length scales commensurate with early stalling events.

BP 20.5 Thu 15:15 HÜL 186

overstretching of DNA duplexes studied with steered molecular dynamics simulations — •hui li and thomas gisler — Universität Konstanz, Fachbereich Physik, 78457 Konstanz, Germany

Single-molecule experiments on long-chain DNA show that the molecule can be overstretched at nearly constant force (65-110 pN) to 60% beyond its relaxed contour length. The origin of this plateau in the force-extension curve is still under debate. Molecular dynamics (MD) simulations of a short DNA duplex with 12 base pairs suggest that it is caused by a transition to a new conformation ("S-DNA") with

inclined base pairs; competing scenarios based on MD simulations of 12-basepair DNA duplexes and thermodynamic considerations suggest the force plateau to arise from a continuous loss of base pairing under external force.

In this contribution we present results from steered MD simulations of a 30-basepair DNA duplex for which a force plateau was recently observed experimentally. We analyzed the pairing between complementary bases and the tilt angles during the stretching. Structure at the force plateau show a coexistence of "S-DNA" segments with "B-DNA" segment which are separated by denatured bases, which has not been seen in stretching simulations of shorter oligomers. In addition, we study the effect of a mismatched base or a gap in backbone on the force plateau and stretched structure. A mismatched base has little effect on the force curves, but the neighbor segments are unwound at the force plateau. A gap in backbone causes the "nicked" region denatured and stretched more than other parts.

BP 20.6 Thu 15:30 HÜL 186

Modeling the BS-transition of DNA under tension — •Thomas Rudolf Einert[1], Douglas Staple[2,3], Hans-Jürgen Kreuzer[2], and Roland Netz[1] — [1]Physik Department, Technische Universität München, 85748 Garching b. München, Germany — [2]Department of Physics and Atmospheric Science, Dalhousie University, Halifax, NS B3H 3J5 Canada — [3]Max-Planck-Institut für Physik komplexer Systeme, 01187 Dresden, Germany

Stretching of double-stranded DNA leads to the denaturation of the molecule. A stretching force $F \approx 65\,\mathrm{pN}$ induces a sharp, structural transition where DNA changes from its native state (B-DNA) to a stretched state (S-DNA). At even higher forces the hydrogen bonds break up and loops start to form giving rise to a second, smoother transition.

We present two statistical mechanics models which exhibit both transitions. To describe the behavior of DNA under tension we use the worm-like chain (WLC) model. Our formulation allows to give arbitrary length-dependent weights for loops. Force-extension curves can be calculated analytically and show excellent agreement with experimental data. In the thermodynamic limit genuine phase transitions are possible depending on the parameterization of the three different states (B-DNA, S-DNA, or loops). The phase transitions are characterized by their order and critical exponents.

15 min. break

BP 20.7 Thu 16:00 HÜL 186

An inter-nucleotide potential for DNA: atomistic and coarse-grained simulations — •Maria Fyta[1,2], Greg Lakatos[1], Simone Melchionna[1], and Efthimios Kaxiras[1] — [1]Department of Physics and School of Engineering and Applied Sciences, Harvard University, Cambridge, MA, USA — [2]Present address: Physics Department, Technical University of Munich, Germany

The structural and dynamical properties of double stranded DNA play a critical role in range of fundamental biological and technological processes. Such processes include DNA translocation through both artificial and nuclear nanopores, the wrapping of DNA around histone proteins, and the use of DNA molecules as nanotethers in a variety of nanoscale devices. To understand the behavior of DNA in these contexts, it is desirable to have a computational model capable of treating oligomers with hundreds to thousands of base pairs, on time scales of microseconds or longer. Utilizing accurate density-functional electronic structure techniques, we are developing a coarse-grained molecular model of double stranded DNA (dsDNA) capable of reproducing the molecule's structural and dynamical properties on these length and time scales. Initial validations of the model indicate that it reproduces a number of experimentally measured structural features of DNA, including the persistence length under physiologic conditions. The model resulting from this study will be used to investigate the behavior of dsDNA during nanopore translocation, and the response of dsDNA to mechanical loads.

BP 20.8 Thu 16:15 HÜL 186

Investigation of the three-dimensional structure of chromatin — •René Stehr[1], Nick Kepper[2], Ramona Ettig[2], Karsten Rippe[2], and Gero Wedemann[1] — [1]Fachhochschule Stralsund, System Engineering and Information Management, 18435 Stralsund, Germany — [2]Deutsches Krebsforschungszentrum & BioQuant, Research Group Genome Organization & Function, 69120 Heidelberg, Germany

We developed a new coarse-grained computer model of chromatin, which enhances the common two-angle model by additional four angles and uses a new nucleosome-nucleosome interaction potential. Based on recent experimental data of native and reconstituted chromatin, three models of chromatin fibers were systematically analyzed by Monte Carlo simulations [1,2]. The results indicate the strong influence of the nucleosome repeat length on the stability of the fiber formation. A model was proposed, in which changes of the chromatin fiber conformation induced by linker histone H1 binding are reproduced by relatively small changes of the local nucleosome geometry. Furthermore, key factors for the control of compaction and higher order folding of the chromatin fiber were identified. We have further developed this approach and are applying it to the analysis of the conformational space of the chromatin fiber, fiber force spectroscopy experiments and atomic force microscopy imaging of chromatin fibers.

[1] Stehr, R., N. Kepper, K. Rippe, and G. Wedemann. Biophys. J. 95:3677 (2008).

[2] Kepper, N., D. Foethke, R. Stehr, G. Wedemann, and K. Rippe. Biophys. J. 95:3692 (2008).

BP 20.9 Thu 16:30 HÜL 186

Structural levels of organization in the TmHU/DNA-complex as studied by optical tweezers assisted force spectroscopy — •Carolin Wagner, Mathias Salomo, and Friedrich Kremer — Universität Leipzig, Germany

The interaction of the histone-like protein TmHU (from Thermotoga maritima) to DNA is analyzed on a single molecule level by use of optical tweezers. This technique provides a nm-resolution in positioning a micron-sized colloid and an accuracy of +/-50 fN in measuring the forces acting on it. As a further refinement, our set-up is now accomplished with a fast feed-back loop (regulation frequency: 30 Hz) which allows to carry out the experiment under conditions of a constant and adjustable force.

The proceeding of the condensation and its dependence on the applied force (2-40 pN) is investigated. At a pre-stretching of 2 pN the length of the DNA is reduced by about 80%. At higher forces, the reaction is disrupted at an incomplete level. The process shows two distinct regimes that can be related to different organizational levels. The condensation also shows a pronounced dependence on the concentration. By stretching the TmHU/DNA-complex, it is possible to disrupt the proteins from the DNA. The length of the smallest event conforms with the results of a simulated rupture.

BP 20.10 Thu 16:45 HÜL 186

Extracting intermolecular forces in protein-DNA complexes from structural data — •Nils Becker and Ralf Everaers — Laboratoire de Physique, École Normale Supérieure, Université de Lyon

It is a standard exercise in mechanical engineering to infer external forces acting on a body, when given its shape and elastic properties. We apply this kind of analysis to distorted double-helical DNA in complexes with proteins, and extract the local *mean* forces and torques acting on each base-pair of bound DNA from high-resolution complex structures. The analysis relies on known elastic potentials and a careful choice of coordinates for the well-established rigid base-pair model of DNA. The results reveal the complex nano-mechanical patterns of interaction between proteins and DNA. An application of this idea to 146bp and 147bp crystal structures of the nucleosome core particle reveals a characteristic force pattern at the well-known DNA contact sites, and leads to an explanation of twist defect placement in the irregular 146bp structure.

BP 20.11 Thu 17:00 HÜL 186

Physical Analysis of Statistical Nucleosome Positioning in the Yeast Genome — •Wolfram Möbius[1,2] and Ulrich Gerland[1,2] — [1]Institute for Theoretical Physics, Universität zu Köln — [2]Arnold Sommerfeld Center and Center for NanoScience, LMU München

Recent experiments determined nucleosome positions in the yeast genome [1-3] and identified two salient features in the spatial organization: (i) nucleosome-free regions upstream of many transcription start sites (TSS), and (ii) an oscillatory nucleosome density downstream. The mechanisms underlying these patterns are less clear. One possible scenario is that the majority of nucleosome positions near the TSS are directly determined by DNA sequence [4], binding competition with other proteins [5], or by active remodelling. An alternative scenario is that only a minority of these nucleosomes is directly positioned by the DNA sequence, forming barriers which strongly constrain the positions of closeby nucleosomes, purely on statistical grounds [3].

Specifically, the nucleosomes might be seen as a one-dimensional gas of rods (Tonks gas) with a few barriers in between. To quantitatively test this scenario, we assess whether the experimentally observed oscillations in nucleosome occupancy are indeed compatible with Tonks gas statistics. Furthermore, we estimate whether biologically reasonable binding specificity suffices to form barriers able to create nucleosome free regions as observed. [1] G.-C. Yuan et al., Science **309**, 626 (2005) [2] W. Lee et al., Nature Genetics **39**, 1235 (2007) [3] T. Mavrich et al., Genome Research **18**, 1073 (2008) [4] E. Segal et al., Nature **442**, 772 (2006) [5] A.V. Morozov et al., arxiv.org:0805.4017v1 (2008)

BP 21: Population Dynamics and Evolution

Time: Thursday 17:30–18:45 Location: HÜL 186

BP 21.1 Thu 17:30 HÜL 186

Determinants of food-web stability — •Lars Rudolf and Thilo Gross — Max Planck Institute for the Physics of Complex System, Nöthnitzer Str.28, 01187 Dresden, Germany

Since the publication of Robert May's seminal work the stability of ecological food webs is a topic of intense research and hot debate. Contrary to many field observations, May showed that large, densely connected food webs are in general unstable. The only way to reconcile May's proof with observation is to find the special properties that lend natural food webs their unusual stability. It has been pointed out that the identification of such stabilizing network properties could have broad implications beyond the field of ecology. Most recent theoretical work focuses on numerical models based on explicit rate equations. These and empirical studies have revealed that weak trophic links may play an important role for stability. However, in contrast to May's abstract random matrix model, numerical constraints limit most simulative studies to the investigation of relatively few instances (approx. 10000) of relatively small food webs (approx. 10 species). Recently, generalized modeling, a novel numerical approach for the analysis of stability in families of nonlinear rate equations, has been proposed. Here we utilize this approach to study several billion instances of food webs of up to 50 species with nonlinear interactions. While we find a stabilizing effect of weak links in small food webs, this stabilization is absent in larger webs. Instead, we identify a universal feature in the distribution of links that is important for stability.

BP 21.2 Thu 17:45 HÜL 186

Life on the Edge: Gene Surfing in Microorganisms — •Oskar Hallatschek[1,2] and David R. Nelson[2] — [1]Max Planck Institut für Dynamik und Selbstorganisation, Bunsenstr. 10, 37073 Göttingen — [2]Lyman Laboratory of Physics, Harvard University, Cambridge, MA 02138

It is widely appreciated that population waves have played a crucial role in the evolutionary history of many species. Genetic footprints of many pioneer species are still recognizable today, and neutral genetic markers can be used to infer information about growth, ancestral population size, colonization pathways, etc. Bacterial growth on a Petri dish can be used to model this phenomenon, using the change of a single amino acid residue in a fluorescent protein encoded on a plasmid as a marker. The frontier of acts as a moving genetic bottleneck, and neutral mutations optimally positioned on the edge of a growing population wave can increase their abundance via a "surfing" phenomenon. Striking patterns of gene segregation and lineage histories are observed for both radial and linear inoculations of populations of bacteria and yeast. Recent experimental and theoretical studies of this effect will be presented, using bacteria and yeast as model systems, including results for surfing of deleterious and favorable mutations during range expansions.[1] O. Hallatschek and D. R. Nelson, http://arxiv.org/abs/0810.0053, and references therein.

BP 21.3 Thu 18:00 HÜL 186

Quasispecies theory with frequency-dependent selection — •Benedikt Obermayer and Erwin Frey — Arnold Sommerfeld Center and Center of NanoScience, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

The Eigen model describes the evolution of macromolecules such as RNA under strong selection and large mutation rates in the limit of infinite population size. For mutation rates below a critical value (the error threshold), its stationary state is characterized by a broad mutant distribution about a fitness peak (the quasispecies). While so far mainly static fitness landscapes have been considered, the fitness of macromolecules depends also on the presence and nature of interaction partners, leading to dynamic and frequency-dependent selection. We analyze quasispecies theory for generic frequency-dependent fitness and obtain qualitatively new analytical and numerical results for the population distribution and the error threshold phenomenon.

BP 21.4 Thu 18:15 HÜL 186

The pace of evolution across fitness valleys — •Chaitanya Gokhale and Arne Traulsen — Max-Planck-Institute for Evolutionary Biology, 24306 Plön, Germany

How fast does a population evolve from one fitness peak to another? We study the dynamics of evolving, asexually reproducing populations in which a certain number of mutations jointly confer a fitness advantage. We consider the time until a population has evolved from one fitness peak to another one with a higher fitness. The order of mutations can either be fixed or random. If the order of mutations is fixed, then the population follows a metaphorical ridge, a single path. If the order of mutations is arbitrary, then there are many ways to evolve to the higher fitness state. In this case, evolution proceeds on a hypercube in d dimensions, where d is the number of required mutations. We address the time required for fixation in such scenarios via analytical expressions for small mutation rates and approximations based on differential equations for higher mutation rates. We also study how the time is affected by the order of mutations, the population size and the fitness values. We also compare a single path, in which the intermediate states have the same fitness values as the initial state, to a hypercube with a fitness valley and ask whether it is faster to cross the fitness landscape via a ridge or a broad fitness valley.

BP 21.5 Thu 18:30 HÜL 186

Estimating the Role of Fluctuations in Evolutionary Games — •Jonas Cremer[1], Tobias Reichenbach[2], and Erwin Frey[1] — [1]Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians Universität München, Germany — [2]Howard Hughes Medical Institute and Laboratory of Sensory Neuroscience, The Rockefeller University New York, NY USA

Evolutionary game theory describes the temporal development of different interacting strategies in a population. Within the standard formulation by replicator equations the dynamical behavior of simple evolutionary games is well known. This description, however, does not take stochasticity into account and thus fails if fluctuations are important. In such a case a stochastic description is required. Having investigated the effects of finite-size fluctuations within the asymmetric two-player game *Battle of the Sexes* [1] we now study the role of stochastic fluctuations within symmetric two-player games. We analyze mean extinction times, i.e. the time until coexistence of an originally mixed population is lost and only one strategy remains, and show that its dependence on the system size is a strong and general applicable concept to reveal the role of fluctuations on the evolutionary dynamics.

[1] Jonas Cremer, Tobias Reichenbach, and Erwin Frey, Eur. Phys. J. B 63 373-380 (2008)

BP 22: Transport Processes and Cellular Trafficking

Time: Thursday 14:30–17:00 Location: ZEU 260

BP 22.1 Thu 14:30 ZEU 260

Modelling anisotropy in protein encounter: a Langevin equation approach with reaction patches — •Jakob Schluttig and Ulrich S. Schwarz — University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

Protein association involves anisotropy for at least two reasons. First the shape of proteins might be non-spherical and thus their diffusion matrix is not necessarily diagonal. Second the association process itself is anisotropic because the binding interfaces are localized at specific positions on their surface. We implemented a Langevin equation approach with reaction patches which allows us to study these two effects [1]. For spherical proteins we find that encounter frequency scales linearly with protein concentration, thus proving that our microscopic model results in a well-defined macroscopic encounter rate. For specific systems of interest and appropriate choices for the size of the reaction patches, encounter rates are obtained within one order of magnitude of the experimentally measured association rates. The number of unsuccessful contacts before encounter decreases with increasing encounter rate and ranges from 20-9000. For spheroids, the principal diffusion coefficients are known analytically and do only sublinearly depend on the ratio ξ of the spatial dimensions. Furthermore the crossover from anisotropic to isotropic diffusion caused by rotational diffusion can be evaluated analytically. These analytical results suggest that the effect of varying ξ on the encounter rate is rather weak, as indeed confirmed by computer simulations.

[1] J. Schluttig et al., J. Chem. Phys. **129**, 155106 (2008).

BP 22.2 Thu 14:45 ZEU 260

Time-resolved analysis of active and passive transport in living cells — •Doris Heinrich[1], Delphine Arcizet[1], Börn Meier[1], Erich Sackmann[2], and Joachim Rädler[1] — [1]Biophysics of Cell Dynamics Group at the Chair of Soft Condensed Matter and Biophysics, Fakultät für Physik und Center for NanoScience (CeNS), Ludwig-Maximilians Universitaet, D-80539 Muenchen, Germany — [2]Physik Department E22, Technische Universitaet Muenchen, D-85748 Garching, Germany

The cellular cytoskeleton is a fascinating active network with exceptional dynamic properties due to the presence of ATP-driven motion. In particular, intracellular transport of cargos is effectively mediated by successive phases of diffusion and active cargo movement along microtubule filaments. We investigated the active and passive intracellular transport phenomena by tracking tracer particles in Dictyostelium discoideum cells and analysing the traces with a novel time-resolved mean-square displacement algorithm [1]. By reliably separating both motion types in a statistical analysis, we were able to determine active velocity distributions as well as diffusion coefficient distributions. The exponential decay of active lifetimes reveals a characteristic life time of cargos on microtubules of t=0.65 s. Further, the active velocity distributions exhibit several peaks, revealing the signature of a finite number of molecular motors working collectively.

[1] D. Arcizet, B. Meier, E. Sackmann, J. Raedler and D. Heinrich. Temporal Analysis of Active and Passive Transport in Living Cells, Phys. Rev. Lett., in press

BP 22.3 Thu 15:00 ZEU 260

Fluorescence correlation analysis of protein dynamics in dividing *C. elegans* embryo — •Zdeněk Petrášek[1], Carsten Hoege[2], Anthony A. Hyman[2], and Petra Schwille[1] — [1]Biophysics group, Biotechnologisches Zentrum, TU Dresden, Germany — [2]Max Planck Institute of Molecular Biology and Genetics, Dresden, Germany

We have combined two-photon fluorescence correlation spectroscopy (FCS), scanning FCS (sFCS) and time-lapse imaging to study the localization and motion of several GFP-labelled proteins involved in the asymmetric first division of *C. elegans* embryo. The diffusion of all investigated proteins in the cytosol, where they are distributed homogeneously on the scale of optical resolution, was measured with a standard FCS, yielding a distribution of diffusion coefficients. The comparison of the protein size and the obtained diffusion coefficients indicates hindered diffusion or formation of larger complexes.

Two of the investigated proteins, known to play an essential role in the first asymmetric division, PAR-2 and NMY-2, are non-uniformly distributed on the embryo cortex. Their motion was characterized by spatio-temporal correlation measured with sFCS. Scanning FCS reduces the effects of dye photobleaching and improves the statistical accuracy, making it possible to study even slow protein dynamics. The PAR-2 cortical pattern is less concentrated into discrete spots and more dynamic than that of NMY-2, indicating predominantly independent localization of the two proteins on the cortex.

BP 22.4 Thu 15:15 ZEU 260

A dynamic model for the morphogenesis of the Golgi apparatus — •Jens Kuehnle[1,2], Julian Shillcock[2], Ole G. Mouritsen[2], and Matthias Weiss[1] — [1]DKFZ, Heidelberg, Germany — [2]Memphys-Center, University of Southern Denmark

While there has been considerable progress in understanding the molecular biology of the secretory pathway of mammalian cells, the fundamental question of how the most prominent and complex organelle of the pathway, the Golgi apparatus, is formed and maintained has remained largely elusive. Using a minimal self-organizing scheme based on incoming transport from the nearby endoplasmic reticulum and aging of Golgi fragments ('cisternal maturation'), we are able to explain the de novo formation of a Golgi apparatus. Moreover, we can determine a region of the models phase space for which secretion rates support the formation of a proper stack of Golgi cisternae. Our simulations are consistent with analytical considerations and agree well with existing experimental data.

BP 22.5 Thu 15:30 ZEU 260

Spot biopolymer motion by NMR — •Michael Kovermann, Martin Schöne, and Jochen Balbach — Institut für Physik/Fachgruppe Biopyhsik, Martin-Luther-Universität Halle-Wittenberg, Betty-Heimann-Straße 7, 06120 Halle/Saale, Germany

The dynamics and the motional behaviour of a protein are important parameters to describe a protein and to understand its function. To learn more about this we characterized the translational motion of various peptides and proteins in solution.

By using a diffusion measurement setup running on an NMR spectrometer we are able to determine the hydrodynamic radius of biopolymers. We compare the correlation times extracted from the diffusion measurements (and known viscosity) with the values from ^{15}N relaxation measurements. From these data we are able to conclude whether the overall tumbling of the biopolymer inside the hydration shell is, on the one hand, caused by the microviscosity or, on the other hand, by the size of the protein.

Additionally we are able to follow a kinetic reaction (fibrillation of the amyloid protein Aβ) which revealed an increase of the hydrodynamic radius by the fibrillation time. This property cannot be observed by using only the signal intensity in the NMR spectrum.

15 min. break

BP 22.6 Thu 16:00 ZEU 260

Elucidating the random process behind crowding-induced subdiffusion — •Marcel Hellmann[1,2], Dieter W. Heermann[2], and Matthias Weiss[1] — [1]German Cancer Research Center, Cellular Biophysics Group (BIOMS), Im Neuenheimer Feld 280, D-69120 Heidelberg — [2]Universität Heidelberg, Institut für Theoretische Physik, Philosophenweg 19, D-69120 Heidelberg

Complex and crowded media are a widespread phenomenon. A prominent example is the cytoplasm of living cells. The presence of filamentous structures and a plethora of embedded macromolecules strongly affect the mobility of tracer particles. Experiments have shown a subdiffusive behavior of tracers with a nonlinear growth of the mean square displacement: $\langle x^2 \rangle \sim t^\alpha$, $\alpha \sim 0.7$ (Weiss *et al.*, Biophys. J.; Guigas *et al.* Biophys J; FEBS Lett.).

Two competing mathematical models have been proposed to rationalize this experimental observation: The continuous time random walk (CTRW) and fractional Brownian motion (fBM). Owing to their distinct propagators (non-Gaussian and Gaussian-like, respectively), these two models make distinct predictions, e.g. concerning the breaking of ergodicity. To explore which of the two models may explain the experimental findings, we have used mesoscopic computer simulations. In particular, we have investigated the diffusion of tracer particles in a crowded environment that mimics the cytoplasm. Our data sug-

gest that crowding-induced subdiffusion relies on (weakly) attractive interactions of the macromolecules.

BP 22.7 Thu 16:15 ZEU 260

Protein diffusion in crowded solutions: A quasi-elastic neutron scattering study — •Felix Roosen-Runge[1,2], Marcus Hennig[1,2], Fajun Zhang[1], Stefan Zorn[1], Maximilian Skoda[3], Robert M.J. Jacobs[4], Tilo Seydel[2], and Frank Schreiber[1] — [1]Institut für Angewandte Physik, Universität Tübingen, Germany — [2]Institut Laue-Langevin, Grenoble, France — [3]ISIS, Didcot, UK — [4]Chemistry Research Laboratory, Oxford, UK

In a typical living cell, proteins function in a relatively crowded cytoplasmic environment where up to 40% of the space is occupied by various biomacromolecules. We present a quasi-elastic neutron scattering (QENS) study of protein dynamics under the condition of "protein crowding" in solution. Using the protein bovine serum albumin (BSA) as model, we studied the protein dynamics as a function of protein concentration, ionic strength and temperature in order to address self-diffusive motions on nanosecond time scales. The dynamics was studied by neutron backscattering scans performed at selected temperatures ranging from 280K up to 325K. The relaxation times and diffusion coefficients extracted from the fits for various states of the BSA solution (temperature, BSA and salt concentration) are analyzed. It was found that salt addition has no significant effect on the relaxation rates on length scales commensurate with protein nearest-neighbor distances, whilst temperature has a strong effect on the diffusive motion of BSA. Charge effects including ionic strength and valence are further addressed by complementary SAXS data.

BP 22.8 Thu 16:30 ZEU 260

Diffusional properties of unfolded proteins — •Nina Malchus and Matthias Weiss — German Cancer Research Center, Heidelberg, Deutschland

The diffusion characteristics of tracer particles in complex systems reveals properties of the surrounding medium and its interaction with the tracer. Using fluorescence correlation spectroscopy (FCS), we have examined the diffusion of folded and unfolded membrane proteins in the endoplasmatic reticulum (ER) of living cells to elucidate the interactions of unfolded proteins with the chaperone machinery. Both, folded and unfolded proteins, show anomalous diffusion with a mean square displacement $\propto t^{\alpha}$, $\alpha < 1$. For unfolded proteins the anomaly was significantly stronger, i.e. α was lower. Disrupting the interaction between chaperones and unfolded proteins resulted in a shift of the anomaly to the values observed for folded proteins. Accompanying computer simulations indicate that obstructed diffusion in the ER and complex formation of chaperones and unfolded proteins are responsible for the observed phenomena. This prediction is well supported by additional experiments.

BP 22.9 Thu 16:45 ZEU 260

Hydrophobic Mismatch: A universal Tool for Clustering, Demixing and Sorting of Transmembrane Proteins — •Ulrich Schmidt, Gernot Guigas, and Matthias Weiss — German Cancer Research Center, Cellular Biophysics Group (BIOMS), Im Neuenheimer Feld 280, D-69120 Heidelberg

Sorting of transmembrane proteins is a central task of eukaryotic cells, in particular in the secretory pathway. Due to a lack of an organizing mastermind, the decision wether a membrane protein participates in secretory transport or not has to be made by a self-organizing process on the molecular scale, e.g. via cluster formation. We show by means of coarse-grained membrane simulations that hydrophobic mismatching can drive cluster formation of transmembrane proteins [1]. Also, proteins with different degrees of hydrophobic mismatching can segregate and form homo-oligomers. In addition, we show that proteins partition into the lipid phase with the smallest hydrophobic mismatch if the membrane has a heterogeneous composition. Our data thus indicate that hydrophobic mismatching may help to organize trafficking along the secretory pathway in living cells.

[1] U. Schmidt, G. Guigas & M. Weiss, Phys. Rev. Lett. 101, 128104 (2008)

BP 23: Physics of Bacteria and Viruses

Time: Thursday 17:15–18:45 Location: ZEU 260

BP 23.1 Thu 17:15 ZEU 260

Membrane fluidity guides bacterial surface motility — •Claudia Holz[1], Berenike Maier[1], Jan Mehlich[2], and Bart Jan Ravoo[2] — [1]Universität Münster, Institut für allgemeine Zoologie und Genetik, Schlossplatz 5, 48149 Münster — [2]Universität Münster, Organisch-Chemisches Institut, Corrensstrasse 40, 48149 Münster

Bacterial surface motility enables bacteria to form microcolonies, colonise human host cells and abiotic surfaces, and is often required for biofilm formation. Twitching motility is powered by polymeric cell appendages called type IV pili. They act as grappling hooks that support motility by a cycle of pilus elongation, surface adhesion and retraction. It is very poorly understood how bacteria control the velocity and direction of twitching.

We investigated twitching motility of the human pathogen Neisseria gonorrhoeae on different surfaces including glass-supported membranes to mimic cell surfaces. We found that bacteria twitch with a velocity of ~1μm/sec and that movement is persistent on a time scale of around 8sec. Velocity and persistence increased with decreasing fluidity of solid supported membranes. On micropatterned surfaces, bacterial movement was confined to the least fluid regions, i.e. we found that motility was guided by surface fluidity. Our experiments reveal an unprecedented physical mechanism for controlling the direction of twitching motility and we hypothesize that this mechanism is involved in formation of microcolonies during infection.

BP 23.2 Thu 17:30 ZEU 260

Min proteins in growing Escherichia coli: from stochastic switching to oscillations — •Elisabeth Fischer-Friedrich[1], Giovanni Meacci[2], Hugues Chate[3], and Karsten Kruse[4] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, 01187 Dresden, Germany — [2]IBM T. J. Watson Research Center, P.O. Box 218, Yorktown Heights, NY 10598 — [3]CEA Service de Physique de l'Etat Condensé, 91191 Gif-sur-Yvette, France — [4]Theoretische Physik, Universität des Saarlandes, Postfach 151150, 66041 Saarbrücken, Germany

Self-organization of proteins in space and time is of crucial importance for the functioning of cellular processes. Often, this organization takes place in the presence of strong fluctuations due to the small numbers of proteins involved. We report on stochastic switching of the localization of Min proteins in short E. coli cells. In longer bacteria, the switching turns into regular oscillations that are required for positioning of the division plane. Considering the intrinsic fluctuations in a simple model reproduces stochastic switching as well as oscillatory behavior. This provides strong evidence for the fact that the macroscopic switching is rooted in the microscopic fluctuations of the molecular processes involved.

BP 23.3 Thu 17:45 ZEU 260

Spatio-Temporal Protein Dynamics in Single Bacteria Cells on Chip — •Dominik Greif[1], Nataliya Pobigaylo[2], Anke Becker[2], Jan Regtmeier[1], and Dario Anselmetti[1] — [1]Experimental Biophysics & Applied Nanoscience, Bielefeld University, Germany — [2]Genetics and Systems Biology of Prokaryotes, Albert-Ludwigs-University Freiburg, Germany

Single cell microscopy of bacterial cells is very challenging due to their small size that differs considerably from eukaryotic cells. In order to investigate subcellular processes in microorganisms we recorded high resolution time lapse fluorescence images (TLFI) for monitoring the dynamics of proteins.
Exemplarily, we present observations of the intracellular protein GcrA as well as the asymmetric localization of the protein DivK in daughter cells of *S.meliloti* over at least two cell divisions. GcrA is a master transcriptional regulator that activates expression of genes participating in DNA replication progression and chromosome partitioning. DivK is part of the phosphorelay system which causes up-regulated expression for proteins required in DNA methylation, septum formation, flagellar synthesis, and chemotaxis. Methodically, a high numerical aperture optical setup with a sensitive CCD camera and a

poly(dimethysiloxane) (PDMS) microfluidic chip, assuring a very good cell viability, was used. For cell immobilization a concentration gradient of polyethyleneimine (PEI) was used. Our approach allows new insight in the control of the bacterial cell cycle in individual cells towards a better understanding of cell proliferation and differentiation.

BP 23.4 Thu 18:00 ZEU 260

In-vitro assembly of Polyoma VP1 — •Henning Seidel — Institute of Physics, Ratzeburger Allee 160, 23538 Lübeck, Germany

One essential element of a virus is its protein shell, the viral capsid, which encloses the viral genome. The murine Polyomavirus is a non-enveloped DNA tumor virus with an icosahedral T=7d structure. Besides the knowledge of the structure, it is of utter importance to understand the process of viral assembly. The assembly reaction of Polyoma VP1 does not show the typical sigmoidal kinetics in light scattering experiments. The apparent kinetics is of fourth order, which appears rather unrealistic. In order to gain knowledge of the capsid composition during assembly beyond ensemble average, we apply methods of single molecule fluorescence, namely fluorescence correlation spectroscopy (FCS), fluorescence-intensity-distribution-analysis (FIDA), and single-particle-imaging (SPI).

These will help to answer the main questions: Is there an initial phase to form a nucleus? Exist pronounced intermediates along the assembly pathway? After building the capsid, is there an exchange of pentameres between capsid (Breathing)?

BP 23.5 Thu 18:15 ZEU 260

Internal Capsid-Pressure Dependence of Viral Infection by Phage λ — •Sarah Köster[1,2], Alex Evilevitch[3], Meerim Jeembaeva[3], and David Weitz[2] — [1]Courant Research Centre Physics, University of Göttingen, Germany — [2]Department of Physics and School of Engineering and Applied Sciences, Harvard University, Cambridge, USA — [3]Department of Biochemistry, Lund University, Sweden

Ejection of the genome from the virus, phage λ, is the initial step in the infection of its host bacterium. In vitro, the ejection depends sensitively on internal pressure within the virus capsid; however, the effect of internal pressure on infection of bacteria is unknown. Here, we use microfluidic devices to produce monodisperse aqueous emulsion droplets in a continuous oil phase. The drops serve as individual, picoliter-sized compartments for cells and viruses and enable us to study organisms on the single cell level while providing valuable statistical information. We monitor individual cells and determine the temporal distribution of lysis due to infection as the capsid pressure is varied. The lysis probability decreases markedly with decreased capsid pressure. Interestingly, the average lysis times remain the same, but the distribution is broadened, as the pressure is lowered.

BP 23.6 Thu 18:30 ZEU 260

Mechanics of the influenza virus are dominated by its lipid bilayer — •Iwan A. T. Schaap, Frederic Eghiaian, John Skehel, and Claudia Veigel — National Institute for Medical Research, Mill Hill, London, UK

The influenza virus protects its RNA genome by a loosely ordered nonsymmetric protein capsid that is enveloped by a lipid bilayer. This membrane contains the various proteins responsible for binding and fusion with the target cell. The composite architecture helps the virus to meet two apparently conflicting demands on its rigidity during its life cycle: 1) it should persist in the often hostile extracellular environment when it transfers from host to host, and 2) it should permit the viral membrane to fuse with the acidic compartments of the target cell to allow infection.

In order to understand how the various parts of the viral structure contribute to its mechanical properties we used atomic force microscopy and finite element modeling to characterize the mechanical performance of influenza virus and compared it to the response of several simplified model systems.

We have found that the elastic properties of the influenza virus are best described by membrane mechanics. In contrast to the symmetrical non-enveloped viruses, the relatively soft influenza virus does not rely on a though protein shell for its survival.

BP 24: Biopolymers (joint session CPP/BP)

Time: Thursday 14:30–17:30 Location: ZEU 114

See program CPP 37

BP 25: Membranes

Time: Friday 10:15–13:15 Location: HÜL 186

Invited Talk BP 25.1 Fri 10:15 HÜL 186

Role of membrane curvature in membrane trafficking — •Patricia Bassereau, Benoit Sorre, Andrew Callan-Jones, Gerbrand Koster, Aurélien Roux, Martin Lenz, Jean-François Joanny, and Jacques Prost — Institut Curie, Lab. PhysicoChimie Curie, Paris, France

Similar to proteins, most membrane lipids are transported by carriers (vesicles or tubules) with typical 50-100nm diameters that bud off from a donor membrane. During budding, sorting occurs: some lipids and proteins are selectively incorporated into these transport intermediates. It has been proposed that components can be dynamically sorted due to membrane curving during coat formation. In order to test this hypothesis, we have pulled membrane nanotubes with controlled diameters (15-500 nm) from Giant Vesicles (GUV). We will show that curvature-induced lipid sorting only occurs if the membrane is close to a demixing point. In addition, for these compositions, lipid sorting is further amplified when even a low fraction of lipids is clustered upon cholera toxin binding, suggesting that lipid-clustering proteins may play an important role in curvature-induced sorting in biological membranes. Another aspect of the role of curvature in membrane trafficking can be studied with these nanotubes. Dynamin is a protein, which assembles in helicoidal structures around the neck of vesicles during budding and induces fission upon GTP hydrolysis. We will show that dynamin assembly can occur only when the neck diameter is below a threshold value. This curvature-dependent polymerization mechanism guaranties a correct timing for carrier budding.

BP 25.2 Fri 10:45 HÜL 186

Multi-Parameter Analysis of Inter-Membrane Adhesion Using Simultaneous Fluorescence and Reflection Interference Contrast Microscopy (RICM) — •Susanne Fenz[1], Rudolph Merkel[1], and Kheya Sengupta[2] — [1]Institute of Bio- and Nanosystems (IBN), Research Centre Jülich, 52425 Jülich, Germany — [2]Centre Interdisciplinaire de Nanosciences de Marseille (CINAM/CNRS-UPR3118), Luminy, Marseille Cedex 9, France

We present a biomimetic model system for cell-cell adhesion consisting of a giant unilamellar vesicle (GUV) adhering via specific biotin-neutravidin interaction to a supported lipid bilayer (SLB). Based on a standard fluorescence microscope, a new set-up was developed that enables simultaneous imaging in RICM and fluorescence microscopy as well as determination of molecular diffusion by continuous photobleaching. GUVs adhering to SLBs were characterized with respect to their inter-membrane distance, adhesion energy density and fluctuation amplitude. Fluorescent imaging and recovery after photobleaching of receptors yielded their distribution, concentration and diffusion constant. We present both static and dynamic analysis of the intermembrane distance and bond ordering for the limiting cases of dense and dilute bonds.

BP 25.3 Fri 11:00 HÜL 186

Specific adhesion of membranes: the role of membrane fluctuations — •Ellen Reister, Ana-Sunčana Smith, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffen-

waldring 57, 70550 Stuttgart, Germany

We analyse adhesion of a membrane to a flat surface via receptor-ligand pairs both in equilibrium and during the adhesion process. The membrane is modeled with the Helfrich energy, while the ligands in the membrane may react with receptors attached to the substrate via springs. The corresponding reaction rate depends on the distance between membrane and substrate. The positions of the ligands in the membrane and the tethers attached to the substrate are kept fixed. For the two coupled dynamic processes in the system - membrane fluctuations and receptor-ligand reactions – we derive equations of motion that are numerically integrated in our novel simulation scheme. To study the influence of thermal membrane shape fluctuations we compare results for a stiff membrane with simulation results. In equilibrium we find that fluctuations make the transition from a bound to an unbound membrane more continuous and that higher binding energies are necessary to maintain the same degree of adhesion. During the dynamic process of adhesion membrane fluctuations are found to increase the adhesion speed. Both in equilibrium and during adhesion observed spatial correlations between bonds indicate that the fluctuating membrane mediates an attractive force between neighboring bonds.

BP 25.4 Fri 11:15 HÜL 186

A solvent-free coarse-grained model for amphiphilic bilayers — •Martin Hömberg and Marcus Müller — Institut für Theoretische Physik, Georg-August-Universität, 37077 Göttingen, Germany

In recent years collective phenomena like membrane fusion or self-assembly of bilayers have attracted tremendous interest. However, atomistic simulations still cannot reach the corresponding time and length scales. Frequently coarse-grained models are employed to save computation time, among them are the solvent-free models, which reduce the amount of interactions to be computed considerably.

Here we present a flexible and computationally efficient bead-spring-model for simulating coarse-grained membranes without explicit solvent. We use a third-order expansion of a free energy functional in the density to describe non-bonded soft interactions, which include the interactions with the solvent implicitly. The expansion coefficients can be related to material properties, such as the molecular density, the compressibility or the incompatibility between the amphiphilic units.

We use DPD simulations with density-dependent forces to investigate the mechanical properties of amphiphilic bilayers, such as the bending rigidity, the area per lipid and diffusion coefficients. These results are compared to experimental data.

BP 25.5 Fri 11:30 HÜL 186

A simulation study of protein-mediated membrane deformations — •Diana Morozova and Matthias Weiss — German Cancer Research Center, Cellular Biophysics Group (BIOMS), Im Neuenheimer Feld 280, D-69120 Heidelberg

Biomembranes assume a variety of function-related shapes, e.g. spherical buds, membrane necks, or tubular protrusions. In virtually all cases membrane proteins are responsible for inducing these shapes. Using dissipative particle dynamics (DPD), a coarse-grained membrane simulation method, we have studied the influence of cone-shaped transmembrane proteins on the shape of a tensionless membrane and the associated membrane-mediated (i.e. bending-induced) interactions between the proteins. We find a clustering of proteins at high densities that is accompanied by a bud formation. The observed clustering not only depends on the protein density but also on the cone angle of the inclusions and the hydrophobic mismatch between the protein's transmembrane portion and the core of the bilayer.

15 min. break

BP 25.6 Fri 12:00 HÜL 186

Pattern formation in membranes by a translocation-diffusion mechanism — Sergio Alonso, •Sebastian Curth, and Markus Baer — Physikalisch-Technische Bundesanstalt, Berlin, Germany

We study the formation of protein patterns in the membranes of living cells by mathematical modelling. The formation of protein domains by electrostatic lipid-protein interactions and the nonequilibrium biochemical reaction cycle of proteins near the membrane give rise to complex dynamics. Here we consider an initially homogeneous membranes where the proteins self-organize into domains due to the competition between their attraction to the membrane and the interaction with different types of enzymes, which translocate the proteins from the membrane to the bulk. We incorporate also the regulation by calcium of the enzymes in the model.

BP 25.7 Fri 12:15 HÜL 186

Interaction of charged colloids and actin filaments with inhomogeneous lipid membranes — •Florian Rückerl, Lydia Woiterski, Josef Käs, and Carsten Selle — Universität Leipzig, Inst. Exp. Phys. I

Lipid bilayers are simple and controllable mimics of cell membranes. The model membranes used in the experiments are composed of ternary mixtures of lipids (DOPC, cholesterol and DPPC or Sphingomyelin). These compositions can form liquid membranes and exhibit an ordered-disordered phase coexistence.

In giant unilamellar lipid vesicles, electrostatic interactions are screened by the surrounding polar liquid and relatively short-ranged. However, even for supposedly neutral membranes, positively charged colloids show a much higher binding affinity to the bilayer than negatively charged colloids. Further, we see a strong influence of the phase boundary on the diffusional properties of the tracer particle, namely a switch from two- to one-dimensional diffusion. This observation is similar to our previous experiments on monolayer systems [1,2].

The negatively charged semiflexible polymer actin readily binds to lipid membranes containing 10% of the cationic DOTAP. There is an interesting interplay between the size of the domains in which the DOTAP partitions into, and the length of the filaments. Our experiments indicate a lower limit for the domain size below which the binding of the filaments does not occur.

[1] Rückerl et al., Langmuir 2008, 24 (7)
[2] Forstner et al., Phys Rev E 2008, 77

BP 25.8 Fri 12:30 HÜL 186

***In vitro* characterization of vinculin's lipid membrane-interacting domain, helix 3** — •Volker Wirth[1], Felix List[2], Gerold Diez[1], Wolfgang H. Ziegler[3], and Wolfgang H. Goldmann[1] — [1]Center for Medical Physics and Technology, Friedrich-Alexander-University of Erlangen-Nuremberg, Germany — [2]Institute of Biophysics and Physical Biochemistry, University of Regensburg, Germany — [3]IZKF, University of Leipzig, Germany

The focal adhesion protein vinculin plays an important role in cell migration and adhesion. Binding of vinculin to lipid membranes ensures these processes. Helix 3 (residues 944 – 972) is one of three potential membrane interaction sites that has been reported on the tail domain. In pull-down assays using artificial lipid membranes it was demonstrated that, when helix 3 is mutated on position K952, K956, R963, R966 to Q, its interaction with acidic phospholipid vesicles is impaired. To date, no data exist on the nature of the interaction.

Using differential scanning calorimetry on wildtype helix 3 we could show that it inserts into lipid vesicles consisting of dimyristoyl-L-a-phosphatidylcholine (DMPC) and negatively-charged dimyristoyl-L-a-phosphatidylserine (DMPS). However, when mutating the four basic residues on helix 3, the insertion into lipid vesicles was reduced. Examining the secondary structure of wildtype helix 3 in the presence and absence of DMPC/DMPS lipid vesicles by CD-spectroscopy showed a conformational shift. These observations indicate that the electrostatic interaction of the basic residues on helix 3 induce the insertion into the hydrophobic core.

BP 25.9 Fri 12:45 HÜL 186

Long-Range Motion of Phospholipids on a Picosecond Timescale as Seen with Quasielastic Neutron Scattering — •Sebastian Busch[1], Christoph Smuda[1], Luis Carlos Pardo Soto[2], and Tobias Unruh[1] — [1]Physik Department E13 and Forschungsneutronenquelle Heinz Maier-Leibnitz (FRM II), Technische Universität München, Lichtenbergstraße 1, D-85747 Garching bei München — [2]Grup de Caracterització de Materials, ETSEIB, Universitat Politècnica de Catalunya, E-08028 Barcelona

Phospholipids are not only interesting because of their ubiquity and importance for every living being, but also because they can be used in a variety of technological applications, e.g. as stabilizers of lipid nanoparticles for drug delivery. We aim to understand the diffusional dynamics of phospholipids on a molecular scale, the difference in dynamics of monolayers compared to bilayers, the influence of coemulsifiers, and the correlation of these microscopic parameters to macroscopic physicochemical quantities.

On a long timescale, the free volume theory can describe the long-range diffusive motions of phospholipids satisfactorily. Molecular dynamics simulations have observed that on a short time scale, collective, flow-like motions become important.

We studied liquid crystals, vesicles, and emulsions with DMPC using quasielastic neutron scattering at the time-of-flight spectrometer TOFTOF at FRM II. Experimental evidence was found that the long-range motion on a picosecond time range indeed has a flow-like character.

BP 25.10 Fri 13:00 HÜL 186

Radial density profile and size distribution of synaptic vesicles determined by small angle x-ray scattering — •Simon Castorph[1], Matthew Holt[2], Michael Sztucki[3], Reinhard Jahn[2], and Tim Salditt[1] — [1]Institute for X-ray Physics, Göttingen, Germany — [2]Max Planck Institute for Biophysical Chemistry, Göttingen, Germany — [3]European Synchrotron Radiation Facility, Grenoble, France

The release of neurotransmitters from neurons, in response to stimulation, forms the basis of communication in the nervous system. Neurotransmitters are stored in small membraneous organelles, synaptic vesicles, within the presynaptic terminal. These vesicles undergo an elaborate cycle of fusion with the plasma membrane (releasing neurotransmitter), followed by retrieval and reformation and transport back to the plasma membrane for further rounds of fusion.

In recent years there has been enormous progress in our knowledge of the molecular composition and structure of synaptic vesicles. However, we still lack a detailed view of the physical properties of this trafficking organelle as it proceeds through its life-cycle.

Small angle x-ray scattering is used to find the average structural properties of synaptic vesicles form rat brain. Quantitative fitting of the x-ray scattering curves reveals the width of the size distribution and details of the radial scattering length profile of the vesicle structure. We obtain representative values for the inner and outer radii and the size polydispersity, as well as the density and width of the inner and outer protein layers.

BP 26: Photobiophysics

Time: Friday 11:00–13:00 Location: ZEU 260

BP 26.1 Fri 11:00 ZEU 260

Photon statistics in the fluorescence from single light-harvesting complexes — •Gregor Hehl, Sandeep Pallikkuth, and Andreas Volkmer — 3rd Insitute of Physics, University of Stuttgart

The photosynthetic apparatus of purple bacteria contains pigment-protein complexes that are optimized for efficient energy transfer, such as the light-harvesting complex (LH2) with bacteriochlorophyll a (BChla) pigments arranged in ring-like structures. Strong electronic interaction among the BChla governs their excited state properties, which are theoretically described in terms of excitonic wave functions. In contrast to prior fluorescence excitation/emission single-molecule spectroscopy, here we report on the photon statistics in the fluorescence of individual LH2 complexes at room-temperature that provides information about photo-physical processes ranging from picoseconds to milliseconds. The fluorescence of individual LH2 complexes is investigated by means of their photon arrival times, and analyzed in terms of interphoton time distributions and second-order correlation functions. These measurements revealed photon antibunching at short times, indicating sub-Poissonian photon statistics and singlet-singlet annihilation, and an excitation power-dependent photon bunching effect at longer times.

BP 26.2 Fri 11:15 ZEU 260

Absorption and Fluorescence Spectroscopic Characterisation of the Circadian Blue-Light Photoreceptor Cryptochrome from Drosophila melanogaster (dCry) — •Javid Shirdel[1,3], Peyman Zirak[1], Alfons Penzkofer[1], Helena Breitkreuz[2], and Eva Wolf[2] — [1]Institut II-Physik, Universität Regensburg, D-93053 Regensburg, Germany — [2]Max-Planck-Institute of Molecular Physiology, D-44227 Dortmund, Germany — [3]Institut für Physik, Carl Von Ossietzky Universität Oldenburg, D-26129 Oldenburg, Germany

Cryptochromes are blue-light sensitive flavoproteins that are related to photolyases, but do not have the DNA repair mechanism of photolyases. They regulate growth and development in plants, regulate circadian rhythms in plants and animals, act as chemical magneto receptors in migratory birds, and are functioning in bacteria and algae. Here we report the absorption and fluorescence behaviour of the circadian blue-light photoreceptor cryptochrome from Drosophila melanogaster (dCry) in a pH 8 aqueous buffer solution. The flavin adenine dinucleotide (FAD) cofactor of dCry is identified to be present in its oxidized form, and the 5,10-methenyltetrahydrofolate (MTHF) cofactor is found to be hydrolyzed and oxidized to 10-formyldihydrofolate (10-FDHF). Photo-excitation of oxidized FAD in dCry causes a reductive electron transfer to the formation of anionic FAD semiquinone, and photo-excitation of the generated anionic FAD semiquinone causes an oxidative electron transfer to the back formation of oxidized FAD.

BP 26.3 Fri 11:30 ZEU 260

Analysis of pigment-protein-complexes by hole burning- and time resolved fluorescence spectroscopy — •Elmar Hassan Hubrich[1], Franz-Josef Schmitt[1], Jörg Pieper[2], Hans Joachim Eichler[1], and Gernot Renger[2] — [1]Institut für Optik und Atomare Physik — [2]Max-Volmer-Laboratorium, Technische Universität Berlin, Strasse des 17. Juni 135, 10623 Berlin

The water-soluble chlorophyll-binding protein (WSCP) found in plants is primarily expressed under stress conditions (drought, heat). The precise function is still not clearified. In contrast to other photosynthetic pigment-protein complexes WSCP binds a maximum number of one molecule chlorophyll (Chl *a* or *b*) per subunit and does not contain carotenoids. WSCP forms tetrameric complexes, with two strongly excitonically coupled chlorophylls in an "open sandwich" geometry. Chl bound to WSCP shows a drastically reduced formation of reactive singlet oxygen in comparison to Chl in solution. WSCP is an excellent minimal model system to investigate pigment-pigment and pigment-protein interactions. We applied the complementary techniques of picosecond fluorescence spectroscopy (time- and wavelength-correlated single photon counting) and hole-burning spectroscopy. A fluorescence rise kinetics was found with a characteristic lifetime of 80 ps at 10 K, noticeably shorter lifetime and markedly reduced amplitude at 160 K and a time constant below the detection limit at higher temperatures. Hole burning and temperature dependent absorption spectroscopy were used to determine the spectral positions of the exciton states and to characterize their coupling to protein vibrations.

BP 26.4 Fri 11:45 ZEU 260

Polarisation-dependent Raman measurements of crystallized photosystem II — •Katharina Brose[1], Athina Zouni[2], Peter Hildebrandt[2], Christian Thomsen[1], and Janina Maultzsch[1] — [1]Institut für Festkoerperphysik, Technische Universität Berlin, Hardenbergstrasse 36, 10623 Berlin — [2]Institut für Chemie, Technische Universität Berlin, Strasse des 17. Juni 135, 10623 Berlin

Raman spectroscopy is one of the standard methods to analyse the structural and vibrational properties of molecules and solids. In photosynthesis, the energy of light is converted into a separation of charge in the photosystem II reaction center. Using the newest photosystem II (PSII) dimer crystal structure (3.0 Å resolution), in which 11 β-carotene molecules (Car) and 14 lipids are visible in the PSII per monomer [1]. In the reaction center two Car molecules Car_{D1} and Car_{D2} are assigned, which are oriented perpendicular to each other. The function of these two carotene molecules in the photosynthesis process is still under debate. Polarisation-dependent Raman measurements are expected to give deeper insights in the structure-function relationship of these two Car molecules in the reaction centre of PSII. In this talk, we will present polarisation dependent Raman measurements on single PSII crystals of PSII.

[1] Loll, B., Kern, J., Saenger, W. Zouni, A., Biesiadka, J. (2005). Towards complete cofactor arrangement in the 3.0 Å resolution structure of photosystem II. Nature 438, 1040-1044.

BP 26.5 Fri 12:00 ZEU 260

Dynamics of light induced charge separation in PS II Core Complexes from thermophilic cyanobacteria (Thermosynechococcus elongatus) and higher plants (spinach) — •Rachel Olliges[1], Franz-Josef Schmitt[1], Athina Zouni[2], and Gernot Renger[2] — [1]Institut für Optik und Atomare Physik — [2]Max Volmer

Laboratorium TU Berlin, Straße des 17.Juni 135, 10623 Berlin

The key steps of solar energy exploitation through photosynthetic water splitting take place in Photosystem II (PS II) of cyanobacteria, alga and higher plants. The light absorbed by antenna systems generates excited singlet-states that are efficiently funnelled to the photoactive pigment P680 of the reaction-center (RC) where the transformation takes place leading to the radical ion pair $P680^{+\bullet}$ $Q_A^{-\bullet}$. The rate of these processes can be gathered from measurements of the time resolved fluorescence decay and model based data evaluation. At present two basically different types of models are discussed: a) radicalpair/exciton equilibrium (REE) model and b) transfer to the trap limited (TTL) model (diffusion limited model).

Time resolved fluorescence-spectroscopy was performed on PS II core complexes (PS IICC) from thermophilic cyanobacteria (Thermosynechococcus elongatus) and higher plants (spinach) by using single photon counting techniques providing a time resolution of about 10 ps. The data shows that the widely used REE model is not able to describe the dynamics completely.

BP 26.6 Fri 12:15 ZEU 260

Multidimensional Optical Probes of Electronic Correlations and Exciton Dynamics in Photosynthetic Complexes — •Dmitri V. Voronine[1], Darius Abramavicius[2], and Shaul Mukamel[2] — [1]Institut für Physikalische Chemie, Am Hubland, Universität Würzburg, Würzburg, Germany — [2]Department of Chemistry, University of California, Irvine, USA

We simulate the multidimensional electronic chirality-induced (2D ECI) signals of excitons in the photosynthetic Fenna-Matthews-Olson (FMO) complexes from two species of green sulfur bacteria Chlorobium tepidum (C.t.) and Prosthecochloris aestuarii (P.a.). The spectra provide sensitive probes of local protein environment of the constituent bacteriochlorophyll a chromophores and reflect electronic structure variations (site energies and couplings) of the two complexes. Pulse polarization configurations are designed which can separate the coherent and incoherent exciton dynamics. Two main energy transfer pathways are revealed by varying the middle time delay in t2-dependent electronic 2D ECI spectra of FMO. Using coherent control we demonstrate optimal laser polarization configurations which enhance chirality-sensitive spectral features, revealing a slow energy transfer pathway which was not resolved in the non-chiral spectra. We show that coherent control can be used to optimize the resolution of cross-peaks and corresponding energy transfer pathways in 2D optical spectroscopy.

BP 26.7 Fri 12:30 ZEU 260

Resolution limits in nanobiophotonics — •Franz-Josef Schmitt — Institut für Optik und Atomare Physik, Technische Universität Berlin, Strasse des 17. Juni 135, 10623 Berlin

According to recent progress in high resolved fluorescence microscopy literature presents new relations for the spatial resolution limit suggesting a principally infinite resolution of fluorescing pigments. We show that similar relations would also be found for the time resolution and present examples where time- and space-correlated single photon (TSCSPC) counting is used to determine sub-nm distances and sub-ps energy transfer and exciton relaxation processes in biophysical pigment-protein complexes (e.g. plant proteins containing chlorophyll). Up today TSCSPC still did not reach an unbreakable limitation of the resolution. We show results of 24 h measurements which are limited by the long time stability of the sample and the long time stability of the measurement setup. The possible refinements of these both stability problems are shortly discussed (e.g. by correction of thermal drift, deep temperature measurements to reduce photobleaching). Even in a principal approach without respect to sample and setup stability one will find that an infinite resolution is not possible although fluorescence spectroscopy might be still far away from the principal lower bound of resolution for arbitrary big and arbitrary stable systems.

BP 26.8 Fri 12:45 ZEU 260

Evolutionäre Bestimmung kinetischer Parameter für Simulationen metabolischer Systeme — •Tihamér Geyer, Xavier Mol und Volkhard Helms — Zentrum für Bioinformatik, Universität des Saarlandes, Saarbrücken

Sollen für ein metabolisches System die Raten für die individuellen Reaktionen bestimmt werden, so stellt sich oft das Problem, daß die Antwort des Systems von einer Reihe von Raten bestimmt wird, die experimentell nicht unabhängig gemessen werden können. Wir zeigen am Beispiel des photosynthetischen Apparats des Purpurbakteriums *Rhodobacter sphaeriodes*, wie mit einem evolutionären Algorithmus die Parameter für eine stochastische Simulation so angepasst werden können, daß ein Satz zeitabhängiger Experimente möglichst gut reproduziert wird. Für die Photosynthese wurden etwa zwei Drittel der Parameter in die Optimierung, die mit publizierten Experimenten durchgeführt wurde, einbezogen. Werden die Experimente auf die Optimierung abgestimmt, sollten auf diese Weise auch für andere Systeme fast alle Parameter durch den Fit bestimmbar sein.