BIOLOGICAL PHYSICS

BIOLOGISCHE PHYSIK (AKB)

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OVERVIEW OF INVITED TALKS AND SESSIONS

(lecture rooms ZEU 255, ZEU 260)

Invited Talks

AKB 1.1	Mon	09:45	(ZEU 255)	**Biophysics of Cells: Active Matter in Motion**, Frank Jülicher
AKB 3.1	Mon	11:30	(ZEU 255)	**Symmetry Breaking and Elastic Deformations drive Actin-Based Movement**, Ewa Paluch, Jasper van der Gucht, Jean-François Joanny, Cécile Sykes
AKB 5.1	Mon	14:00	(ZEU 255)	**Cell motility as persistent random motion: theories from experiments**, Henrik Flyvbjerg, David Selmeczi, Stephan Mosler, Peter H. Hagedorn, Niels B. Larsen
AKB 7.1	Tue	09:45	(ZEU 255)	**Cytoskeletal Polymerization Motors**, Marileen Dogterom
AKB 10.1	Tue	11:30	(ZEU 255)	**Synaptic Plasticity and Memory from an Optimality Viewpoint**, Wulfram Gerstner, Taro Toyoizumi, Jean-Pascal Pfister, Kazuyuki Aihara
AKB 12.1	Tue	14:00	(ZEU 255)	**Transport and Reaction-Diffusion Phenomena in Soft-Matter Nanofluidic Devices**, Owe Orwar
AKB 14.1	Tue	16:00	(ZEU 255)	**Single-molecules at work - Deciphering the mechanism of a molecular motor**, Jens Michaelis, Yann Chemla, K. Aathavan, Thorsten Hugel, Carlos Bustamante
AKB 16.1	Wed	14:00	(ZEU 255)	**Biological Networks: Design Principles of Robust Information Processing**, Markus Kollmann
AKB 18.1	Wed	15:30	(ZEU 255)	**Synthetic Analogues of Biological Voltage-Gated Channels, Fabrication of Ion-Current Rectifiers and Protein Sensors**, Zuzanna Siwy
AKB 20.1	Thu	09:45	(ZEU 255)	**DNA self-assembly: nanostructures and molecular machines**, Andrew Turberfield
AKB 20.2	Thu	10:15	(ZEU 255)	**Synthesis, properties and perspectives of complex nanocrystal structures**, Liberato Manna
AKB 22.1	Thu	14:30	(ZEU 255)	**Signal processing by clusters of membrane receptors**, T.A.J. Duke, I. Graham
AKB 26.1	Fri	11:00	(ZEU 255)	**The physics of cellular computation**, Pieter Rein ten Wolde

Sessions

AKB 1	**Cellular Processes**	Mon 09:45–11:30	ZEU 255	AKB 1.1–1.5
AKB 2	**Membranes: Conformations and Dynamics**	Mon 10:30–11:30	ZEU 260	AKB 2.1–2.4
AKB 3	**Cell Motility I**	Mon 11:30–13:15	ZEU 255	AKB 3.1–3.6
AKB 4	**Membranes: Phase Behavior and Dynamics**	Mon 12:00–13:15	ZEU 260	AKB 4.1–4.5
AKB 5	**Cell Motility II**	Mon 14:00–15:45	ZEU 255	AKB 5.1–5.6
AKB 6	**DNA Mechanics**	Mon 14:30–16:00	ZEU 260	AKB 6.1–6.6
AKB 7	**Biopolymers I**	Tue 09:45–11:30	ZEU 255	AKB 7.1–7.6

AKB 8	**Cell Motility: Neuronal Growth**	Tue	10:15–11:00	ZEU 260	AKB 8.1–8.3
AKB 9	**Chemical Bonds and Adsorption**	Tue	11:00–12:00	ZEU 260	AKB 9.1–9.4
AKB 10	**Neuroscience**	Tue	11:30–13:30	ZEU 255	AKB 10.1–10.7
AKB 11	**Cell Adhesion I**	Tue	12:00–13:00	ZEU 260	AKB 11.1–11.4
AKB 12	**Soft-Matter Nanofluidic Devices**	Tue	14:00–16:00	ZEU 255	AKB 12.1–12.7
AKB 13	**Cell Adhesion II**	Tue	14:30–15:45	ZEU 260	AKB 13.1–13.5
AKB 14	**Molecular Motors**	Tue	16:00–18:30	ZEU 255	AKB 14.1–14.9
AKB 15	**Biopolymers II**	Tue	16:30–18:30	ZEU 260	AKB 15.1–15.8
AKB 16	**Biological Networks**	Wed	14:00–15:15	ZEU 255	AKB 16.1–16.4
AKB 17	**Population Dynamics**	Wed	14:30–15:30	ZEU 260	AKB 17.1–17.4
AKB 18	**Ion Channels and Nanopores**	Wed	15:30–16:45	ZEU 255	AKB 18.1–18.4
AKB 19	**Proteins**	Wed	16:00–16:45	ZEU 260	AKB 19.1–19.3
AKB 20	**Nano-Biomaterials and Devices**	Thu	09:45–12:45	ZEU 255	AKB 20.1–20.10
AKB 21	**Intracellular Transport**	Thu	10:45–12:30	ZEU 260	AKB 21.1–21.7
AKB 22	**Sensory Biophysics and Signal Transduction**	Thu	14:30–16:15	ZEU 255	AKB 22.1–22.6
AKB 23	**Photo-Biophysics**	Thu	16:15–17:15	ZEU 255	AKB 23.1–23.4
AKB 24	**Brownian Motion and Fluctuation Theorems**	Thu	17:15–18:00	ZEU 255	AKB 24.1–24.3
AKB 25	**Cell Mechanics I**	Thu	15:00–18:00	ZEU 260	AKB 25.1–25.12
AKB 26	**Cellular Computation and Gene Regulation**	Fri	11:00–12:00	ZEU 255	AKB 26.1–26.3
AKB 27	**Cell Mechanics II**	Fri	11:30–13:00	ZEU 260	AKB 27.1–27.6
AKB 28	**Single Molecule Probes**	Fri	12:00–13:00	ZEU 255	AKB 28.1–28.4
AKB 30	**Poster Session I**	Mon	15:30–18:00	P1	AKB 30.1–30.40
AKB 40	**Poster Session II**	Wed	16:30–19:30	P3	AKB 40.1–40.69

Annual General Meeting of the Section Biological physics

Thu 18:30–20:00 ZEU 255

Programmplanung 2007 - Themenschwerpunkte - Fachinterne Symposien - Fachuebergreifende Symposien

Sessions

– Invited, Contributed Talks and Posters –

AKB 1 Cellular Processes

Time: Monday 09:45–11:30 Room: ZEU 255

Prize Talk AKB 1.1 Mon 09:45 ZEU 255

Biophysics of Cells: Active Matter in Motion — •Frank Jülicher — Max Planck Institut für Physik komplexer Systeme, Dresden — Träger des Robert-Wichard-Pohl-Preises

A fascinating feature of living cells is their inherently dynamic nature which is exemplified by the ability to generate spontaneous motion. A prototype system to study dynamics and active processes in cells is the cytoskeleton, a complex gel-like filament network which governs the material properties of cells. Complex cellular dynamics is driven by active processes on the molecular scale, for example the action of motor molecules. On the cellular scale, this activity can result in new material properties, emergent collective modes and spontaneous movements which play an important role for processes such as cell locomotion and cell division. Active cellular processes are also directly involved in the amplification of mechanical vibrations by sensory cells of our ear. The nonlinear and active properties of this cellular amplifier are essential to endow the ear with its exquisite abilities to detect sound.

AKB 1.2 Mon 10:30 ZEU 255

Mechanics and dynamics of actin ring constriction during cytokinesis: The role of filament polymerization — •Alexander Zumdieck, Karsten Kruse, and Frank Jülicher — MPI-PKS, Nöthnitzer Str. 38, Dresden

The cytoskeleton is a complex network of protein filaments. Driven by active processes such as filament polymerization and depolymerization and the action of molecular motors it represents an active, soft material. It is intrinsically dynamic and able to generate mechanical stress and flow of filaments.

We present a theoretical description of the dynamics and mechanics of contractile actin rings, important cytoskeletal structures, which constrict cells during cytokinesis. Quantitative comparison of experimental data together with a phenomenological description of ring contraction allows us to estimate the essential parameters characterizing mechanics and dynamics of a contracting ring. We discuss in particular the cell elastic modulus, the mechanical stress generated by the ring as well as the filament density in the ring and the rates of filament turnover.

Using a more microscopic description of filament interactions in the ring, we identify physical mechanisms of ring contraction driven by motors and filament turnover. In particular we discuss how filament bundles may generate tension in the absence of molecular motors.

AKB 1.3 Mon 10:45 ZEU 255

Spatio-temporal protein dynamics in rod-shaped bacteria — •Elisabeth Fischer, Giovanni Meacci, and Karsten Kruse — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str.38, 01187 Dresden

In the bacterium E.coli, positioning of the division plane involves oscillations of the Min-proteins form one cell pole to the opposite. We study a possible mechanism underlying the oscillations by usage of a coarse-grained description in terms of partial differential equations. The analysis of the dynamics in a three-dimensional geometry akin to the bacterial shape shows oscillations that are reminiscent of the oscillations observed experimentally. In addition, we find several other dynamic states including traveling waves. Furthermore, we discuss the influence of noise on the oscillation pattern and compare our results to experiments.

AKB 1.4 Mon 11:00 ZEU 255

By chance or by the clock: How do concentrations in cells oscillate? — •Martin Falcke and Alexander Skupin — Abteilung Theorie SF5, Hahn Meitner Institut, Berlin

Intracellular concentration oscillations can be deterministic limit cycle oscillations or can be driven by fluctuations in a non-oscillatory dynamic regime. The cause of oscillations of intracellular Ca^{2+} concentrations was discussed on theoretical grounds in the last 2-4 years. We present experimental data very much in favor of one of the mechanisms and substantiate them with theoretical results.

AKB 1.5 Mon 11:15 ZEU 255

The precision of genetic oscillators and clocks — •Luis G. Morelli and Frank Jülicher — Max Planck Institut für Physik komplexer Systeme, Nöthnitzer Str. 38 (01187) Dresden, Germany

Genetic oscillations play a major role in different cellular processes, for example in circadian clocks, during the cell cycle, and patterning in developing embryos. Due to the stochastic nature of gene expression, the period of these oscillations is subject to fluctuations. The precision of the oscillator can be characterized by the quality factor. We study the precision of genetic oscillators in a simple but general stochastic feedback system. We show that high quality is possible for certain parameter ranges even when the number of molecules is low and amplitude fluctuations are large. We relate our results to circadian clocks in bacteria, where high quality oscillations have been observed in single cell experiments.

AKB 2 Membranes: Conformations and Dynamics

Time: Monday 10:30–11:30 Room: ZEU 260

AKB 2.1 Mon 10:30 ZEU 260

Stresses and torques in biological fluid membranes — •Martin Michael Müller[1], Markus Deserno[1], and Jemal Guven[2] — [1]Max Planck Institute for Polymer Research, Ackermannweg 10, D-55128 Mainz, Germany — [2]Instituto de Ciencias Nucleares, UNAM, Apdo. Postal 70-543, 04510 México D.F., Mexico

Forces in fluid membranes can be described with the help of the covariant surface stress tensor, in analogy to classical elasticity theory. Additionally, torques can be written in terms of the surface torque tensor.

In the context of interface mediated interactions, such as the interaction between protein inclusions in a lipid membrane, it has proven advantageous to use this approach: nonlinear expressions for the force and, in some cases, also the sign of the interaction could be derived [1]. The condition of torque balance imposes further restrictions on the solution. Other complications, such as a pressure difference between the two sides of the membrane or a lipid tilt, are readily included in the formalism.

[1] M. M. Müller, M. Deserno, and J. Guven, Europhys. Lett. **69**, 482 (2005).

AKB 2.2 Mon 10:45 ZEU 260

Studying the Curvature Elasticity of Biomembranes Through Numerical Simulations — •VAGELIS HARMANDARIS and MARKUS DESERNO — Max-Planck-Institute for Polymer Research, Ackermannweg 10, D-55128 Mainz, Germany

Biological membranes have been extensively studied in the past using both experimental techniques and simulations [1]. The latter have the advantage of being able to relate the membrane properties with structure and composition at the molecular level. One of the main aspects that can be directly studied this way is the curvature elasticity of membranes. A well known way to do this is from the spectrum of equilibrium membrane fluctuations [2].

Here we propose an alternative methodology for studying the curvature elasticity of membranes. The basic idea is to impose a deformation of the membrane and measure the force required to hold it in the deformed state. We apply this method to a new solvent-free coarse-grained model proposed recently [3]. Specifically we stretch a cylindrical vesicle and measure the force needed for such an extension. Results are presented

about the force acting on the stretching cylindrical vesicle, as well as about the bending modulus, and are compared with the predictions from the analysis of the spectrum of equilibrium membrane fluctuations.

\Zitat{1}{Structure and Dynamics of Membranes, R. Lipowsky and E. Sackmann (Eds.), Elsevier, Amsterdam, 1995.} \Zitat{2}{U. Seifert, Adv. Phys. 46, 13 (1997).} \Zitat{3}{I.R. Cooke, K. Kremer and M. Deserno, Phys. Rev. E 72, 011506 (2005).}

AKB 2.3 Mon 11:00 ZEU 260

Collective dynamics of lipid membranes studied by inelastic-neutron scattering — •Maikel C. Rheinstädter[1], Tilo Seydel[1], Wolfgang Häussler[2], and Tim Salditt[3] — [1]Institut Laue-Langevin,B.P. 156,6 rue JulesHorowitz,38042 Grenoble,France — [2]FRM-II,Technische Universität München,85747Garching,Germany — [3]Institut für Röntgenphysik,Friedrich-Hund-Platz1,37077 Göttingen,Germany

While most spectroscopic techniques, as ,e.g., nuclear magnetic resonance or dielectric spectroscopy probe macroscopic responses, neutron and within some restrictions also x-ray scattering experiments give the unique access to microscopic dynamics at length scales of intermolecular distances. Only recently, it has become possible to study collective dynamics, ,i.e., the dispersion relations in the gel and fluid phases of planar lipid bilayers using neutron spectroscopy techniques[1]. By combining neutron three-axis, backscattering and spin-echo spectroscopy, we present measurements of short and long wavelength collective fluctuations in a biological model membrane in a large range in momentum and energy transfer, covering time scales from about 0.1 ps to almost 1 μs and length scales from 3 Å to about 1000 Å. Neutron backscattering technique thereby gives information about molecular dynamics of lipid acyl chains and the water molecules in between the stacked bilayers [2]. The dispersion relation of the long wavelength undulation modes has been determined by quasielastic reflectometry using spin-echo spectrometers.

[1] M.C. Rheinstädter *et al.*, Phys. Rev. Lett. 93, 108107 (2004).
[2] Maikel C. Rheinstädter *et al.*, Phys. Rev. E 71, 061908 (2005).

AKB 2.4 Mon 11:15 ZEU 260

Forced Crumpling of Self-Avoiding Elastic Sheets — •Vliegenthart Gerrit and Gompper Gerhard — IFF, Forschungszentrum Jülich

Thin elastic sheets are important materials across length scales ranging from mesoscopic (polymerized membranes, clay platelets, virus capsids) to macroscopic (paper, metal foils). The crumpling of such sheets by external forces is characterized by the formation of a complex pattern of folds. We have investigated the role of self-avoidance — the fact that the sheets cannot self-intersect — for the crumpling process by computer simulations. The force-compression relations of crumpled sheets for both self-avoiding and phantom sheets are found to obey universal power-law behaviors. However, self-avoiding sheets are much stiffer than phantom sheets, and they develop many more folds. Moreover, self-avoidance is relevant already at very small volume fractions. The fold-length distribution for crumpled sheets is determined and found to be well described by a log-normal distribution. The stiffening due to self-avoidance is reflected in the changing nature of the sheet-to-sheet contacts from line-like to two-dimensionally extended with increasing compression.

AKB 3 Cell Motility I

Time: Monday 11:30–13:15 Room: ZEU 255

Invited Talk AKB 3.1 Mon 11:30 ZEU 255

Symmetry Breaking and Elastic Deformations drive Actin-Based Movement — •Ewa Paluch[1,2], Jasper van der Gucht[1], Jean-François Joanny[1], and Cécile Sykes[1] — [1]Institut Curie/CNRS, UMR 168, 26 rue d'Ulm, 75005 Paris, France — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, 01307 Dresden, Germany

Cells move and change shape by means of the cytoskeleton, an active gel made of polar filaments such as actin. The filaments themselves are highly dynamic and continuously polymerize and depolymerize using chemical energy. Bacterial pathogens such as Listeria monocytogenes have been shown to hijack the actin polymerization machinery inside cells in order to propel themselves forward. This mechanism is often studied using beads, which polymerize on their surface an actin gel that spontaneously polarizes and gives rise to an actin comet that propels the bead forward.

We use a simple assay composed of purified commercial proteins to study the symmetry breaking event that precedes movement. We show that gel breakage results from a release of elastic energy and propose a model based on the theory of fracture in polymer gels. Moreover we provide direct evidence that the actin gel in the comet continues to deform even after symmetry breaking. We propose a model that accounts for these deformations, where the comet is considered as an elastic fluid.

AKB 3.2 Mon 12:00 ZEU 255

Dynamics of Cilia and Flagella — •Andreas Hilfinger[1], Ingmar Riedel[2], Amit Chattopadhyay[3], Karsten Kruse[1], Jonathon Howard[2], and Frank Jülicher[1] — [1]Max-Planck-Institute for the Physics of Complex Systems, Dresden — [2]Max-Planck-Institute of Molecular Cell Biology and Genetics, Dresden — [3]Mathematics Institute, University of Warwick, UK

Directed motion on the level of single cells is in many cases achieved through the beating of whip like appendages (cilia or flagella). These organelles contain a highly conserved structure called the axoneme, whose characteristic architecture is based on a cylindrical arrangement of elastic filaments (microtubules). In the presence of ATP, molecular motors (dynein) exert shear forces between neighbouring microtubules, leading to a bending of the axoneme through structural constraints.
We present a theoretical description of such an elastic cylinder, driven by internally generated stresses and show that self-organised bending waves emerge from a non-oscillatory state via a dynamic instability. The corresponding beat patterns are solutions to a non-linear wave equation with appropriate boundary conditions. We discuss three-dimensional beat patterns that resemble the vortical motion of nodal cilia, which play an important role in establishing the left-right axis of embryos in many vertebrate species.

AKB 3.3 Mon 12:15 ZEU 255

Biomimetic flagella and cilia — •Holger Stark and Erik Gauger — Universität Konstanz, Fachbereich Physik, D-78457 Konstanz

In biological systems, small organisms move in a Newtonian fluid and fluid itself is transported with the help of beating filaments (cilia) or rotating flagella. The motion is governed by small Reynolds numbers, i.e., by a regime where inertial effects can be neglected. Thus directed motion can only occur in systems where time-reversal symmetry is broken.

Recently, Dreyfus *et al.* realized a one-armed swimmer [1] that fulfills these requirements. It is based on an elastic filament formed by superparamagnetic particles that are hold together by chemical linkers. Whereas real flagella or cilia are driven by internal machinery, the artificial filament is actuated by an external field. We simulate the filament using a discretized elastic-rod model where the particles also interact via dipolar and hydrodynamic interactions. We discuss two characteristic quantities, i.e., the swimming velocity and its efficiency. Furthermore, we demonstrate how the biomimetic cilium when attached to a bounding surface can be used to transport fluid.

[1] R. Dreyfus, J. Baudry, M. L. Roper, M. Fermigier, H. A. Stone, and J. Bibette, Nature **437**, 862 (2005).

AKB 3.4 Mon 12:30 ZEU 255

Hydrodynamic flow patterns and synchronization of beating cilia — •Andrej Vilfan[1] and Frank Jülicher[2] — [1]J. Stefan Institute, Jamova 39, 1000 Ljubljana, Slovenia — [2]MPIPKS, Nöthnitzer Str. 38, 01187 Dresden, Germany

We study the dynamics of hydrodynamically interacting cilia by means of a minimal physical model, representing cilia as particles on tilted elliptical trajectories. We first calculate the hydrodynamic flow field generated far from a cilium which is attached to a surface and beats periodically. In the case of two beating cilia, we show that hydrodynamic interactions can lead to synchronization of the cilia. We present a state diagram where synchronized states occur as a function of distance of cilia and the relative orientation of their beat. Synchronized states occur with different relative phases. In addition, asynchronous solutions exist. Our model provides a basis for the explanation of metachronal waves in microorganisms and ciliated tissues.

AKB 3.5 Mon 12:45 ZEU 255

A self-organized simple swimmer driven by molecular motors — •Stefan Guenther and Karsten Kruse — Max-Planck-Institut für Physik komplexer Systeme, 01187 Dresden, Germany

Microorganisms often use flagella or cilia to move in an aqueous environment. In eukaryotes these hair-like appendages are internally driven by molecular motors. Spontaneous oscillations of the motors lead to two- or three-dimensional beating patterns of the appendage, which propels the organism. Due to the complicated structure of cilia and flagella our understanding of the swimming mechanism is still far from complete.

Here, we study a simple self-organized swimmer, that is based on elements thought to be important for the beating of flagella. The swimmer consists of three spheres arranged in a line. Two adjacent spheres are coupled by an active joint containing molecular motors. These joints are similar to sarcomeres, the elementary contractile units of muscle, and can oscillate spontaneously. Taking the hydrodynamic interactions between the spheres into account, the system moves directionally along its long axis. We calculate the swimming speed as a function of the fluid's viscosity and find a critical value above which there is no net motion. For parameters appropriate for sarcomeres, swimming speeds are in the order of μm/min and should be experimentally observable.

AKB 3.6 Mon 13:00 ZEU 255

Collective effects in ciliar arrays — •Andrey Ryskin and Peter Lenz — Fachbereich Physik, Philipps-Universität Marburg, D-35032 Marburg

Collective effects in ciliar arrays are studied analytically and numerically. A new phase oscillator description for ciliar motion is introduced which depends only on a single parameter. It allows to systematically study hydrodynamic interactions between cilia exhibiting arbitrary beating patterns. It is shown that under suitable conditions hydrodynamic interactions lead to synchronization of ciliar beating and formation of metachronal waves. The stability of these dynamical states is discussed.

AKB 4 Membranes: Phase Behavior and Dynamics

Time: Monday 12:00–13:15 Room: ZEU 260

AKB 4.1 Mon 12:00 ZEU 260

Dynamic simulations of lateral diffusion in fluctuating membranes — •Ellen Reister-Gottfried and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart

When regarding lateral diffusion it is important to remember, that the membrane is flexible and subject to thermal fluctuations. Therefore the Langevin (or Smolouchovski) equation governing the dynamics of a protein diffusing in the membrane becomes a function of the membrane shape. In our novel simulation algorithm we combine the simulation of the membrane dynamics with the simulation of the protein movement. The membrane dynamics follows from the membrane Hamiltonian and a hydrodynamic coupling of the membrane to the surrounding fluid. The movement of the inclusion is calculated by numerically integrating the appropriate Langevin equation, that uses the instantaneous membrane shape. This simulation method allows for studies on large length and time scales and is easily extendable to include various protein-membrane interactions or external potentials acting on the membrane. We use this scheme to calculate diffusion coefficients projected on a flat plane, because this is the quantity, that is typically measured in experiments. In previous work we analytically calculated the difference between the projected and the actual intramembrane diffusion coefficient in the limit that membrane fluctuations are faster than protein diffusion. These results are compared with results achieved with the new simulation method.

AKB 4.2 Mon 12:15 ZEU 260

Coarse-grained simulations of internal phases in lipid membranes — •Friederike Schmid and Olaf Lenz — Universität Bielefeld

We study internal membrane phase transitions by Monte Carlo simulation of a simple coarse-grained model system. Lipids are modeled as single spring-bead chains. They are forced to self-assemble by a surrounding fluid of "phantom" solvents, which only interact with the lipids, but not with one another. The solvent is thus very cheap from a computational point of view, and the model can be simulated very efficiently. Depending on the model parameters, it exhibits a fluid state, tilted and untilted gel states, and an interdigitated state. In the "pretransition" region between the tilted gel state and the fluid state, two types of undulated rippled structures are observed: an asymmetric structure with a sawtooth profile and a period of roughly 15-20 lipid diameters, and a symmetric structure with a period twice as long. Both structures have been reported in experiments, and their molecular structure is still under debate. The structure of our asymmetric ripple state agrees with that found recently by de Vries et al (PNAS 102, 5392, 2005) in an atomistic simulation of a Lecithin bilayer. Moreover, our simulations suggest a structural model for the structure of the symmetric ripple state.

AKB 4.3 Mon 12:30 ZEU 260

Alternative mechanisms of structuring biomembranes — •Markus Bär [1] and Karin John[2] — [1]Physikalisch-Technische Bundesanstalt, Abbestr. 2-12, 10587 Berlin — [2]Max-Planck-Institut für Physik komplexer Systeme, Noethnitzer Str. 38, 01187 Dresden

Cell membranes are composed of a mixture of lipids. Many biological processes re-quire the formation of spatial domains in the lipid distribution of the plasma membrane. In a first step, we study two mechanisms for the formation of protein patterns near membranes of living cells by mathematical modelling. Self-assembly of protein domains by electrostatic lipid-protein interactions is contrasted with self-organization due to a nonequilibrium biochemical reaction cycle of proteins near the membrane. While both processes lead eventually to quite similar patterns, their evolution occurs on very different length and time scales. Self-assembly produces periodic protein patterns on a spatial scale below 0.1 μm in a few seconds followed by extremely slow coarsening, whereas self-organization results in a pattern wavelength comparable to the typical cell size of 100 μm within a few minutes [1].

[1] K. John and M. Bär, Phys. Rev. Lett. 95, 198101 (2005).

AKB 4.4 Mon 12:45 ZEU 260

Ordered domains control membrane diffusion in model membranes — •Carsten Selle, Florian Rückerl, and Josef Käs — University of Leipzig, Insitute for Experimental Physics I, Soft Matter Physics, Linnestr 5, 04103 Leipzig, Germany

We investigate the diffusion properties of biological membrane components by a Single-Particle-Tracking (SPT) technique employing monolayers at the air/water interface as two-dimensional membrane mimetics. Protein diffusion within inhomogeneous membranes was mimicked by motion of surface-charged fluorescent polystyrene beads in monolayers where two differently ordered phases coexist. Associated to ordered liquid-condensed (LC) domains, dimensionally reduced motion of the model proteins in the liquid-expanded (LE) phase was observed. We assume that dipole-dipole interactions between the diffusing beads and LC domains give rise to an attractive potential resulting in a strikingly modified bead diffusion in the LC domain neighborhood. This view point is supported by suitable Monte-Carlo simulations. The simulations demonstrate that model protein diffusion can be strongly affected by both potential depth and also by the domain size. It seems conceivable that living cells could make use of diffusion control accomplished by similar mechanisms in order to enhance kinetics of bimolecular enzyme reactions occuring in the membrane. In recent experiments performed in our lab, giant unilamellar vesicles interacting with fluorescent polystyrene beads have been employed to study the behavior of model proteins at curved sufaces. First results are presented.

AKB 4.5 Mon 13:00 ZEU 260

Phase transition induced morphological changes in lipid vesicles — •Christian Leirer, Achim Wixforth , and Matthias Schneider — Institut für Physik (Biophysik), Universtät Augsburg, Universitätsstraße 1, D-86159 Augsburg

Phase transition in lipid membranes are accompanied by dramatic changes in the area per molecule and their elastic properties. Using Micropipett aspiration, AFM, fluorescence and light microscopy we studied basic phenomena in membranes, that depend strongly on the phase state and explain them in the theoretical framework of membrane elasticity. A variety of effects showing strong similarities to biological systems are dicussed.

AKB 5 Cell Motility II

Time: Monday 14:00–15:45 Room: ZEU 255

Invited Talk AKB 5.1 Mon 14:00 ZEU 255

Cell motility as persistent random motion: theories from experiments — •Henrik Flyvbjerg[1,2], David Selmeczi[2,3], Stephan Mosler[2], Peter H. Hagedorn[1], and Niels B. Larsen[1,2] — [1]Biosystems Department, Risø National Laboratory, DK-4000 Roskilde, Denmark — [2]Danish Polymer Centre, Risø National Laboratory, DK-4000 Roskilde, Denmark — [3]Department of Biological Physics, Eötvös Loránd University, H-1117 Budapest, Hungary

Cell migration is essential in many physiological and pathological processes and in emerging medical technologies that depend on it for colonization of biomaterials. Quantitative migration studies rely on motility models for data interpretation. Finding no model in the literature that captures the nature of our data, we used the data to capture the nature of suitable models. An analysis of trajectories followed by motile human keratinocytes and fibroblasts lead to cell-type-specific motility models. These models show that cells have memory, and apparently reflect the cells' different roles in the organism. The method of analysis is general and may be applied to other motile cell-types and organisms.

AKB 5.2 Mon 14:30 ZEU 255

A biomimetic model system shedding light on active lamellipodial biomechanics — •Björn Stuhrmann[1], Florian Huber[1], Thomas Rudolph[2], Klaus Zimmer[2], and Josef Käs[1] — [1]Institute for Soft Matter Physics, University of Leipzig, Linnéstr. 5, 04103 Leipzig, Germany — [2]Leibniz-Institut für Oberflächenmodifizierung e.V., Permoserstr. 15, 04303 Leipzig, Germany

In cells displaying crawling motility, cell boundary advancement is governed by the assembly of actin protein, tightly regulated by a wealth of accessory proteins. The key molecular players involved in these processes have been identified [1] and are used in this project to build a minimal model system of the cell lamellipodium. A polymerizing actin gel representing the lamellipodium is generated in nanostructured, cell-sized chambers. System confinement to cellular volumes is a crucial step towards cellular conditions and distinguishes our approach from existing assays. In the presence of ATP, the emerging gel represents for the first time a self-sustaining, polymerizing machine mimicking the cell lamellipodium *in vitro*. Offering the possibility to selectively change biochemical and physical parameters and to study the system's response in terms of its structural, dynamical and rheological properties, this model system presents a novel means to explore biomechanical mechanisms underlying cell motility.

[1] Loisel TP, Boujemaa R, Pantaloni D, Carlier MF. Nature. 1999 Oct 7;401(6753):613-6.

AKB 5.3 Mon 14:45 ZEU 255

Measuring protrusion forces of locomoting cells — •Marcus Prass[1], Ken Jacobson[2], and Manfred Radmacher[1] — [1]Institute of Biophysics, University of Bremen, 28359 Bremen, Germany — [2]Dept. of Anatomy and Cell Biology, University of North Carolina, Chapel Hill, USA

Cell migration is very important for cellular processes like wound healing or metastasis. Although much is known from the biological point of view on the actin-myosin machinery involved in cell migration, the exact mechanism of force generation is still unclear. One possible mechanism of force generation is the polymerization ratchet model. Here, thermal fluctuations of actin filaments are necessary for polymerization of actin filaments. Since this process effectively converts chemical energy in mechanical energy a protrusive force is generated. We have designed a cantilever-based instrument to measure directly protrusion forces at the leading edge of migrating cells. An AFM-cantilever oriented perpendicular to the substrate is deflected by a migrating keratocyte (epithelial cell prepared from trout scales). The deflection could be measured by video microscopy or at better temporal and spatial resolution using a position sensitive detector. The distance between cantilever and substrate was approximately 80 nm to guarantee that the leading edge of the lamellipodium was investigated. We will show first experimental results and discuss them in the context of existing theories.

AKB 5.4 Mon 15:00 ZEU 255

Investigation and Manipulation of Membrane Dynamics by an Optical Tweezers Technique — •Michael Goegler, Timo Betz, and Josef Käs — Institute for Soft Matter Physics, University of Leipzig, Linnéstrasse 5, 04103 Leipzig, Germany

Cell migration is essential in various cellular activities, such as morphogenesis, wound healing, and metastasis. In these events, protrusion of the cell membrane at the leading edge is the fundamental step, and the mechanism driving this movement is likely associated with the elongation of polymerizing actin filaments or with molecular motors, such as myosin. To elucidate the mechanism of protrusion, we use a new laser based technique to study membrane motion with high spatial and temporal resolution in the nanometer and microseconds range, respectively. A diffraction limited laser spot is positioned at the leading edge of a cell and the forward scattered light is imaged on a quadrant diode detector which serves as a position sensitive device. We investigated the membrane motion at the leading edge of different cell types, such as fibroblasts and erythrocytes. The new technique has the potential to reveal relative contributions to the membrane fluctuations based on its frequency spectrum, and to measure physical properties, such as the bending rigidity of the membrane. By increasing the laser intensity we were able to exert a significant force on the cell's leading edge that is strong enough to deform the cell and change its membrane dynamics. We present the capabilities of the technique and show that it provides the opportunity to measure rheological properties of cells.

AKB 5.5 Mon 15:15 ZEU 255

Protrusion Forces Driving Rapidly Translocating Cells — •Michael Goegler[1], Claudia Brunner[1], Allen Ehrlicher[1], Bernd Kohlstrunk[1], Detlef Knebel[2], and Josef Käs[1] — [1]Institute for Soft Matter Physics, University of Leipzig, Linnéstrasse 5, 04103 Leipzig, Germany — [2]JPK Instruments AG, Bouchéstrasse 12, 12435 Berlin, Germany

Cell motility is a fundamental process of many phenomena in nature, such as immune response, wound healing, and metastasis. Mechanisms of force generation for cell migration have been described in various hypotheses requiring actin polymerization and/or molecular motors, but quantitative force measurements to date have focused on traction forces. Here we present a direct measurement of the forward force generated at the leading edge of the lamellipodium and at the cell body of a translocating fish keratocyte. We positioned an elastic spring, the cantilever of a scanning force microscope (SFM), in front of a moving cell, which pushed the cantilever out of its path. The forward force was calculated using the detected vertical deflection of the cantilever in an "elastic wedge model", which considers cellular deformation. We measured forward forces between 1-8 nN without visibly affecting the cells. At stronger opposing forces up to at least 15 nN the lamellipodium of the cell retracted locally whereas the overall movement of the cell remained unaffected. Measurements with steadily increasing applied force were carried out to determine a load dependence behaviour. We investigated the effect of cytochalasin D in force measurements to elucidate the importance of actin polymerization in cellular protrusion.

AKB 5.6 Mon 15:30 ZEU 255

Lateral Membrane Waves Constitute a Universal Dynamic Pattern of Motile Cells within the Animal Kingdom — •H.-G. Döbereiner[1,2], B. J. Dubin-Thaler[1], J. Hofman[3], H. S. Xenias[1], T. N. Sims[4], G. Giannone[1], M. L. Dustin[4], C. Wiggins[3], and M. P. Sheetz[1] — [1]Biological Sciences, Columbia University, New York — [2]Physics, Columbia University, New York — [3]Applied Physics, Columbia University, New York — [4]Skirball Institute, New York University School of Medicine, New York

Cell motility is driven by actin polymerization and myosin motor activity. We have monitored active movements of the cell circumference using quantitative differential interference contrast and total internal reflection fluorescence microscopy. Spreading and motility essays were done on specifically adhesive substrates for a variety of cells including mouse embryonic fibroblasts and T-cells, as well as wing disk cells from drosophila melanogaster. Despite their functional diversity, all those cell types exhibit similar dynamic patterns in their normal membrane velocity. In particular, we found that protrusion and retraction activity is organized

in lateral waves running along the cell circumference with speeds on the order of 100 nm/s. These wave patterns show both spatial and temporal long-range periodic correlations reflecting a corresponding organization of the actomyosin gel. These lateral waves seem to be quite a general phenomenon, since we found them in two different cell types of the mouse, a mammal, and in one cell type of the common fruit fly, an insect. Thus, we encounter a universal motility pattern across different phyla within the animal kingdom.

AKB 6 DNA Mechanics

Time: Monday 14:30–16:00 Room: ZEU 260

AKB 6.1 Mon 14:30 ZEU 260

Bubble Nucleation and Cooperativity in DNA Melting — •Saul Ares[1], Nikolaos K. Voulgarakis[2], Kim Ø. Rasmussen[3], and Alan R. Bishop[3] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden — [2]Center for Nonlinear Studies, Los Alamos National Laboratory, Los Alamos, New Mexico 87545, USA — [3]Theoretical Division and Center for Nonlinear Studies, Los Alamos National Laboratory, Los Alamos, New Mexico 87545, USA

The onset of intermediate states (denaturation bubbles) and their role during the melting transition of DNA are studied using the Peyrard-Bishop-Dauxois model by Monte Carlo simulations with no adjustable parameters. Comparison is made with previously published experimental results that used a novel bubble quenching technique based in the possibility of hairpin formation on single strands of DNA. An excellent agreement is found between our theoretical predictions and experimental results. Melting curves, critical DNA segment length for stability of bubbles, and the possibility of a two-state transition are studied. The content of this contribution is published in Physical Review Letters 94, 035504 (2005).

AKB 6.2 Mon 14:45 ZEU 260

An Intermediate Phase in DNA Melting — •Richard A. Neher and Ulrich Gerland — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoSciene (CeNS), LMU München

We predict a novel temperature-driven phase transition of DNA below the melting transition. The additional, intermediate phase exists for repetitive sequences, when the two strands have different lengths. In this phase, the longer strand is completely absorbed onto the shorter strand. The excess bases form mobile bulge loops inside the helical region. Below the transition temperature, more and more of these bulge loops condense into overhanging single stranded ends. We calculate the partition sum of such DNA exactly and find, that this transition is continuous and in many aspects analogous to Bose-Einstein condensation. When the periodicity of the sequence is destroyed by rare point mutations, the transition becomes discontinous. Furthermore, we find that the order of the melting transition of repetitive DNA differs from that of ordinary DNA.

[1] R.A. Neher and U. Gerland, qbio.BM/0509015

AKB 6.3 Mon 15:00 ZEU 260

Tracking of Type I restriction enzymes along DNA — •Ralf Seidel[1,2], Joost G. P. Bloom[1], Carsten van der Scheer[1], Nynke H. Dekker[1], Mark D. Szczelkun[3], and Cees Dekker[1] — [1]Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands — [2]Biotechnolgisches Zentrum, TU Dresden, Germany — [3]Department of Biochemistry, University of Bristol, UK

Type I restriction enzymes are complex cellular machines that cleave foreign, viral DNA using two DNA translocating motor subunits. During the translocation process the core unit of the enzyme complex stays bound to the DNA whilst the motors translocate adjacent DNA and thus pull it towards the enzyme, which results in the formation of large DNA loops. Using magnetic tweezers, we investigated on the level of a single enzyme how the DNA motors track along their DNA template. We found that the motor subunits follow directly the helical pitch of the DNA. Due to the attachment of the motors to the core unit of the enzyme, their rotation around the DNA is inhibited and torsional stress is not released. In this way the DNA gets threaded through the enzyme complex leading to an almost complete untwisting of the DNA in the extruding loop and strongly positively supercoiled DNA in front of the motor. Probing both the translocated distance on the DNA and the amount of generated supercoils, we found that the enzyme translocates 11 $\pm$ 2 bp per generated supercoil, which strongly suggests tracking of the DNA helical pitch. We furthermore found that the motors track along the 3'-5' strand by investigating how small single strand gaps are overcome.

AKB 6.4 Mon 15:15 ZEU 260

The effect of semiflexibility on the dynamics of DNA in nucleosomes — •Wolfram Möbius, Richard A. Neher, and Ulrich Gerland — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for Nanoscience (CeNS), LMU München

Even though the DNA in eukaryotic cells is tightly packed with the help of histones, it must be accessible for passively binding regulatory proteins. According to the *site exposure mechanism* [1], these proteins can temporarily gain access to a buried DNA site during conformational fluctuations of nucleosomes, the fundamental packing units consisting of about 150 base pairs of DNA wrapped around a histone complex. Recently, the dynamics of spontaneous partial DNA unwrapping was observed directly, using optical single molecule techniques [2,3]. Here, we study this dynamics within a mesoscopic model of the nucleosome, using Brownian dynamics simulations and theoretical analysis of simplified toy models. We find that the internal polymer dynamics of the semiflexible DNA has a strong impact on the dynamics of our nucleosome model. We characterize this effect in detail and discuss a number of experimentally relevant predictions of our model.

[1] Polach and Widom, Journal of Molecular Biology **254**, 130 (1995)
[2] Li *et al.*, Nature Structural & Molecular Biology **12**, 46 (2005)
[3] Tomschik *et al.*, PNAS **102**, 3278 (2005)

AKB 6.5 Mon 15:30 ZEU 260

Electrostatic interactions of DNA can quantize azimuthal orientations of nucleosome core particles in bilayers — •Andrey Cherstvy and Ralf Everaers — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Germany

We propose that DNA charge distribution can affect electrostatic interactions of nucleosome core particles (NCP) in bilayers and crystals. The bilayers of NCPs are formed by densely packed columns of NCPs, stacked on top of each other with axes nearly parallel to columnar axis. We suggest that mutual azimuthal orientations of NCPs in neighboring columns across the NCP bilayer are quantized with the angle of about 45 degrees. The reason for that is the helical symmetry of DNA charge distribution, with its phosphates and cations adsorbed in the grooves. This results in azimuthal charge "oscillations" on outer circumference of NCPs, along a "ring" of wrapped DNA. When two NCPs are close to each other, these charge patterns can establish an electrostatic zipper, similarly as for two parallel DNA molecules [1]. Our predictions can be tested experimentally, provided a better statistics and resolution of cryoelectron micrographs [2] will be achieved. This can provide new information about inter-nucleosomal electrostatic interactions that influence DNA compactification in chromatin fibers, the phenomenon which is still poorly understood. [1] A. G. Cherstvy, A. A. Kornyshev, and S. Leikin, J. Phys. Chem. B, 106, 13362 (2002); ibid., 108, 6508 (2004) and references therein [2] A. Leforestier, J. Dubochet, and F. Livolant, Biophys. J., 81 2414 (2001).

AKB 6.6 Mon 15:45 ZEU 260

Single Molecule FRET detects sequence dependent Bending and Kinks in DNA — •Filipp Oesterhelt — Heinrich Heine Universität Düsseldorf, Universitätsstrasse 1, Geb. 26.32.02.30, 40225 Düsseldorf

Fluorescence Resonance Energy Transfer (FRET) is a universal tool to measure distances in the range of a few nanometers. This makes FRET ideally suited to analyse distances and distance changes between and within single biomolecules. In the principle accuracy in distance changes is in the sub nanometer range. But the calculation of absolute distances is difficult due to systematic errors. We applied the method of Multiparameter Fluorescence Detection to single DNA doublestrands, internally labelled with a donor and an acceptor fluorophore at various positions. The comparison of the measured energy transfer efficiencies with the fluorophore positions modelled by molecular dynamic simulations revealed that the fluorophore positional and orientational variability has to be

taken into account. The absolute distances calculated from our FRET measurements did not only show the helicity of the DNA duplex, but also a sequence dependent bending which was in good agreement with values calculated earlier by NMR and other techniques. We also applied our high precision FRET measurements to the analysis of kinked DNA containing adenosine bulges. From our data we could reconstruct the 3D structure of the kink, revealing the angle, the relative rotation of the helical arms and the offset between their helix axes.

AKB 7 Biopolymers I

Time: Tuesday 09:45–11:30 Room: ZEU 255

Invited Talk AKB 7.1 Tue 09:45 ZEU 255

Cytoskeletal Polymerization Motors — •Marileen Dogterom — FOM Institute AMOLF, Amsterdam, Netherlands

Dynamic cytoskeletal polymers such as microtubules and actin filaments provide forces for various types of cellular and intracellular motility. To understand how these polymerization motors work we use optical tweezers-based techniques and microfabricated barriers that allow us to study both actin and microtubule force generation at a single polymer level. We can measure force-velocity relations and monitor how the polymer assembly dynamics responds to force, both in the absence and presence of relevant binding proteins. In addition, we use microfabricated devices to mimic the physical confinement of living cells and study, for example, the role of microtubule-based force generation in the positioning of microtubule organizing centers. In cells, this positioning results from a complex interplay between dynamic, force-generating microtubules, the cell cortex, the cell geometry, and regulatory proteins. In microfabricated chambers, we have previously shown that in simple cases the pushing of the growing microtubules on the chamber walls is enough to center the organizing center. We have now refined this type of experiment by adding specific biochemical activity to the chamber walls. This allows us to study the effect of localized motor proteins and cortical regulatory proteins on microtubule organization and the positioning of microtubule organizing centers.

AKB 7.2 Tue 10:15 ZEU 255

Polymers in Axially Symmetric Confining Geometries — •Frederik Wagner[1], Gianluca Lattanzi[2], and Erwin Frey[1] — [1]Arnold Sommerfeld Center and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München, Germany — [2]Department of Medical Biochemistry, Biology and Physics, TIRES-Center and INFN, Università di Bari, Piazza Giulio Cesare 11, 70124 Bari, Italy

The growing interest in understanding the constituents of the cell demands a rigorous analysis of its main structural components: polymers of different flexibilities (e.g. DNA, actin, microtubules) confined to a micrometer scale. In additon, confinement of polymers on micro- and nano-scales plays an important role in developing new devices for the visualization and manipulation of polymers. These recent advances require a careful analysis of the relevant accessible quantities and their dependence on the two main parameters of the system: the persistence length ℓ_p which entails the flexibility of the chain, and the Odijk deflection length l_d, which provides a measure of the confinement. We developed a Monte Carlo simulation to investigate the general features of the wormlike chain model in axially confining geometries. In particular, we have studied the case of harmonic potentials, which is amenable to analytic approximations. Our simulations critically assess the approximations used in analytical calculations, extend the range of parameters and the quantities that can be compared with experimental observables, and provide a deeper insight on scaling relations, the influence of boundary conditions and the details of the confining geometry.

AKB 7.3 Tue 10:30 ZEU 255

Actin Filaments Confined in Microchannels — •Patrick Levi and Klaus Mecke — Institut fuer Theoretische Physik I, Universitaet Erlangen-Nuernberg, Staudtstrasse 7, 91058 Erlangen, Germany

The statistical physics of semiflexible polymers in confined geometries faces the problem of treating bending modes in non-parabolic potentials. We present an analytic expression for the distribution of the end-to-end distance in a parabolic potential. Our result is in good agreement with experimental data for hard wall confinement in rectangularly shaped microchannels. For non-parabolic potentials we developed a selfconsistent ansatz for mapping the wall distance of a rectangular channel to an effective parabolic potential strength. Deviations from the Odijk result for the correlation function in a parabolic potential are discussed. The selfconsistent approach is also used to calculate forces on the filaments in inhomogeneous channel geometries.

AKB 7.4 Tue 10:45 ZEU 255

Entropic forces generated by grafted semiflexible polymers — •Azam Gholami[1], Jan Wilhelm[2], and Erwin Frey[2] — [1]Hahn-Meitner-Institut, Abteilung Theorie, Glienicker Str. 100, D-14109 Berlin, Germany — [2]Arnold Sommerfeld Center for Theoritical Physics and CeNS, Department of Physics, Ludwig-Maximilian-Universität München, Theresienstrasse 37, D-80333 München, Germany

We compute both numerically and by Monte Carlo simulations the average force exerted by a fluctuating grafted semi-flexible polymer upon a rigid smooth wall as well as the corresponding free energy. Both quantities are thought to be of interest for understanding the physics of actin-polymerization driven cell motility and movement of bacteria like Listeria monocytogenes. Depending on the angle between the constraining wall and the direction of the graft, two asymptotic regimes with different dependence of the force on the position of the wall can be discerned. The angle determining the position of the crossover varies as the square root of the ratio of the polymer's length to its persistence length. For angles larger than the critical angle, previous expressions are qualitatively valid but for smaller angles different behavior is found.

AKB 7.5 Tue 11:00 ZEU 255

The flexural rigidity of microtubules relates to a limited compliance of inter-protofilaments bonds — •Francesco Pampaloni[1], Gianluca Lattanzi[2], and Davide Marenduzzo[3] — [1]EMBL Heidelberg - Cell Biology and Biophysics Programme - Heidelberg (Germany) — [2]University of Bari - Faculty of Medicine (Italy) — [3]Mathematics Institute - University of Warwick (UK)

The structure of microtubules (MT) is highly optimized to a maximum of mechanical performance: the hollow tube shape allows high strength and stiffness combined with a minimum of structural elements (tubulin dimers). Moreover, MTs are anisotropic in their elastic properties: they are softer on basal plane than along the axial direction. Such unusual properties of MTs - light, flexible, stiff - make them very similar to composite materials designed by engineers. Remarkably, tiny structural variations in the MT lattice, like protofilaments torsion and shifting, are not confined locally, but propagate in a concerted way along the whole MT length. It is likely that the energy required by this deformation is very low, of the order of the thermal fluctuations. Sub-nanometer deformations of the lateral bonds produce a slight relative shift between protofilaments, that introduces a significant shear component to MTs deflection. Consequently, for MTs the shear modulus is small enough to produce a length dependence of the bending stiffness. We present a multi-scale approach to investigate the elastic properties of MTs based on Monte Carlo simulation and conformational analysis of tubulin dimers in typical MTs architecture and we provide an useful framework for the interpretation of experimental data.

AKB 7.6 Tue 11:15 ZEU 255

Elastic response, buckling and rupture of microtubules under radial indentation — •Iwan A.T. Schaap[1], Carolina Carrasco[2], Pedro J. de Pablo [2], Frederick C. MackIntosh[1], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Departamento de Física de la Materia Condensada C-III, Universidad Autónoma de Madrid

We have tested the mechanical properties of single microtubules by lateral indentation with the tip of an atomic force microscope. Indentations up to ˜3.6 nm, i.e. 15 % of the microtubule diameter resulted in an approximately linear elastic response, and indentations were reversible without hysteresis. At an indentation force of around 0.3 nN we observed an instability corresponding to a ˜1 nm indentation step in the taxol-stabilized microtubules, which could be due to partial or complete rupture of a relatively small number of lateral or axial tubulin-tubulin bonds. These indentations were reversible with hysteresis when the tip was retracted and no trace of damage was observed in subsequent high-resolution images. Higher forces caused substantial damage to the

microtubules, which either led to depolymerization or, occasionally, to slowly reannealing holes in the microtubule wall. We have modeled the experimental results using finite element methods and find that the simple assumption of a homogeneous isotropic material, albeit structured with the characteristic protofilament corrugations, is sufficient.

AKB 8 Cell Motility: Neuronal Growth

Time: Tuesday 10:15–11:00 Room: ZEU 260

AKB 8.1 Tue 10:15 ZEU 260

Optical Neuron Guidance and Growth Cone Motility — •Daniel Koch, Timo Betz, Allen Ehrlicher, Michael Gögler, Björn Stuhrmann, and Josef Käs — Institut for Soft Matter Physics, University of Leipzig, Linnestr. 5, 04103 Leipzig, Germany

Understanding and controlling neuronal growth is a main research focus in the life sciences. All molecular stimuli for neuronal growth eventually address the polymeric cytoskeleton of the growth cone, a highly motile structure at the tip of an advancing neurite. However, the detailed molecular mechanisms underlying growth cone motility still need to be resolved. We have shown that optical forces induced by a highly focused infrared laser beam influence the motility of a growth cone by biasing the polymerization-driven intracellular machinery. In actively extending growth cones, a laser spot placed at specific areas of the neurite's leading edge affects the direction taken by a growth cone. In an optical tweezers setup simultaneous phase contrast and fluorescence imaging, real-time shape detection, and automated laser irradiation are combined to control growth cone motility. Additionally we use high resolution edge detection in combination with a cross-correlation algorithm to extract the actin cytoskeletal dynamics in a growth cone in order to shed light on the mechanisms underlying optical neuron guidance. These novel techniques allow the investigation and manipulation of a natural biological process, the cytoskeleton driven morphological changes in a growth cone, with potential applications in the formation of neuronal networks and in understanding growth cone motility.

AKB 8.2 Tue 10:30 ZEU 260

Filopodia orientation determines neurite turning — •Allen Ehrlicher, Timo Betz, Michael Gögler, Daniel Koch, Björn Stuhrmann, and Josef Käs — University of Leipzig, Linnéstr. 5 Abt PWM 04103 Leipzig Germany

Neurons must migrate through a complex array of tissues, chemical signals, and mechanical stimuli to form the connections necessary for life. At the leading edge of neuronal extensions are highly dynamic structures called growth cones, which navigate through the body, interpreting the myriad of signals into appropriate attractive or repulsive responses. Extending beyond the growth cone are spike-like bundles of actin known as filopodia, which communicate many of these environmental cues to the cell, and probe the immediate area of the cell for the best path. We have observed that the orientation of these filopodia strongly predicts growth cone turn behavior. Furthermore, using optical tweezers we directly manipulate the position and orientation of filopodia, and thus are able to induce growth cone turning. All of a cell's movements are generated by its polymeric cytoskeleton, which is composed principally by actin, microtubules, and motor proteins such as myosin, though the relevance of each constituent is yet unclear. Our observations strengthen the hypothesis that microtubule extension into the growth cone's peripheral region along filopodia is the dominating factor for neurite turning, and not asymmetry in the polymerizing actin meshwork.

AKB 8.3 Tue 10:45 ZEU 260

Quantifying the Dynamic Actin Gel and its Active Forces in Neuronal Growth — •Timo Betz, Daniel Koch, Daryl Lim, Miriam Wisehart, Allen Ehrlicher, and Josef Käs — Institut for Soft Matter Physics, University of Leipzig, Linnestr. 5, 04103 Leipzig, Germany

The neuronal wiring of a developing organism is performed by the highly motile structures at the tips of growing neurites, called growth cones. The locomotion of these structures is largely driven by the dynamics of an active actin gel in the lamellipodium, similar to other motile cells. We developed an experimental assay to measure the neuronal actin dynamics by tracking prominent structures in the lamellipodium of GFP-actin transfected neuronal cells. This is used to quantify the active movement of the actin gel in the neuronal growth cones, a process called retrograde flow. It is currently believed that the growth cone exerts forces onto the substrate by coupling the retrograde flow of the active actin gel to the substrate. To further investigate this, we additionally measure the substrate forces directly by detecting the deformation of an elastic substrate, allowing us to correlate retrograde flow with traction forces. With this assay we have established a method to simultaneously measure all the forces and dynamics necessary to test recently proposed theoretical models for cell motility. We present a detailed analysis of the actin dynamics, substrate forces and local friction constants used by neuronal growth cones as they migrate through the body to correctly wire complex neuronal networks during development.

AKB 9 Chemical Bonds and Adsorption

Time: Tuesday 11:00–12:00 Room: ZEU 260

AKB 9.1 Tue 11:00 ZEU 260

Polymer and peptide adsorption to attractive substrates — •Michael Bachmann and Wolfhard Janke — Institut für Theoretische Physik, Universität Leipzig, Augustusplatz 10/11, 04109 Leipzig, Germany

The interest in understanding polymer adsorption at substrates has grown quite recently with the development of high-resolution experimental equipment allowing for studying the technologically important problem of substrate-binding specificity of synthetic peptides. In our study of simple hybrid models [1,2], we investigate how solubility of the surrounding solvent and temperature influence the substrate-binding of nongrafted polymers in a cavity with an attractive surface. Applying a suitably adapted variant of the multicanonical chain-growth algorithm [3] for self-avoiding walks, we performed simulations of lattice polymers with up to 200 monomers and obtained the entire temperature-solubility pseudo-phase diagram of the hybrid system within a single simulation. We clearly separated expected thermodynamically stable phases dominated by the respective adsorbed and desorbed collapsed and random-coil conformations. Another central aspect of our study is the discussion of pseudo-phases that specifically depend on finite-size properties such as the precise number of monomers or, for peptides, the sequence of residues.

[1] M. Bachmann and W. Janke, Phys. Rev. Lett. **95**, 058102 (2005).
[2] M. Bachmann and W. Janke, to be published.
[3] M. Bachmann and W. Janke, Phys. Rev. Lett. **91**, 208105 (2003).

AKB 9.2 Tue 11:15 ZEU 260

Analysis of Adsorbed Protein Patterns at Surfaces — •Armin Nagel[1], Hubert Mantz[1], Christof Weitenberg[1], Anthony Quinn[2], Markus Bellion[3], Ludger Santen[3], and Karin Jacobs[1] — [1]FR 7.2 Experimental Physics - Soft Matter, Saarland University, D-66123 Saarbrücken — [2]Department of Chemical and Biomolecular Engineering, University of Melbourne, Australia — [3]FR 7.1 Theoretical Physics - Statistical Physics of Nonequilibrium and Disordered Systems, Saarland University, D-66123 Saarbrücken

The aim of this project is to identify the mechanisms for salivary protein adsorption at solid-liquid interfaces, with the intention of optimising the biocompatibility of dental replacement materials.

The methodology involves the characterisation of protein adsorption on surfaces that have been specifically tailored to have differing interaction potentials by varying the short and long range forces. The composition and topography of these tailored surfaces is carefully controlled and characterised via AFM and wettability analysis, enabling the structural and interfacial tension components to be identified.

AFM scans of the protein layers, both ex situ (in air) and in situ (in a buffer solution) are compared to ellipsometry measurements of the ki-

netics. The resulting complex patterns were analysed by image analysis methods (Minkowski Measures), so that tendencies during the adsorption process could be identified.

We compare the experimental protein patterns with patterns obtained by Monte-Carlo simulations of the protein adsorption process.

AKB 9.3 Tue 11:30 ZEU 260

Characteristics of Protein Adsorption at Solid-Liquid Interfaces — •Hubert Mantz[1], Armin Nagel[1], Anthony Quinn[2], and Karin Jacobs[1] — [1]FR 7.2 Experimental Physics - Soft Matter, Saarland University, D-66123 Saarbrücken — [2]Department of Chemical and Biomolecular Engineering, University of Melbourne, Australia

Adsorption of proteins occurs instantly whenever a protein solution (e.g. any body fluid) gets in touch with a surface (biomaterials or medical devices) and thereby is of crucial importance to all kinds of biomedical technologies. Adsorption is a very complex process and is not yet fully understood. The adsorbed amount and the structure of the adsorbed layer depend on many factors including properties of the surface, the surrounding medium and the protein itself.

In this study, the in situ adsorption kinetics of some selected saliva proteins (amylase and lysozyme) in liquid environment has been studied by ellipsometry. Through judicious choice and modification of the substrates, the influence of short- and long-range forces on the adsorption process could be separated. The ellipsometry measurements were compared with AFM images of the resulting topographies.

The experimentally observed adsorption kinetics does not follow any standard adsorption model. We compare our results with Monte-Carlo simulations (cf. contribution of Bellion et al.), assuming conformational changes of the proteins upon increasing surface coverage.

AKB 9.4 Tue 11:45 ZEU 260

Kinetics of Protein Adsorption at liquid/solid interfaces: A Monte Carlo study — •Markus Bellion and Ludger Santen — Fachrichtung Theoretische Physik, Universität des Saarlandes, 66041 Saarbrücken

We investigate by means of extensive Monte Carlo simulations the protein adsorption at liquid/solid interfaces. Proteins are modelled as colloidal particles. The particle-particle and the particle-surface interactions are described in the framework of the DLVO theory, which considers steric repulsion, electrostatic and van der Waals interactions. In order to investigate the time evolution of the surface coverage in agreement with the experimental setup (see contribution of H. Mantz, A. Quinn, A. Nagel and K. Jacobs for comparison), we use a layered three dimensional simulation box. In the upper layer a grandcanonical ensemble is applied, which controls the concentration of proteins in the solution. In contrast, the particle number is conserved in proximity to the liquid/solid interface.

In agreement with the experimental results we find the aggregation of a protein monolayer. If we include the possibility of conformational changes, we are able to reproduce the experimentally observed three stepped kinetics: a fast linear increase of the adsorbed amount for low coverages is followed by a second linear regime before saturation of the surface coverage sets in. The second linear regime can be understood as a collective transition from a conformation which is stable on the single-particle level to a conformation that optimizes adsorbed amount at the surface.

AKB 10 Neuroscience

Time: Tuesday 11:30–13:30 Room: ZEU 255

Invited Talk AKB 10.1 Tue 11:30 ZEU 255

Synaptic Plasticity and Memory from an Optimality Viewpoint — •Wulfram Gerstner[1], Taro Toyoizumi[1,2], Jean-Pascal Pfister[1], and Kazuyuki Aihara[2] — [1]Ecole Polytechnique Federale de Lausanne, EPFL — [2]University of Tokyo

Connections between neurons change and these changes (potentiation and depression of synapses) are thought to be the basis of learning and memory. Despite a diversity of experimental facts, we believe that the rule controlling changes of synapses should be simple. More precisely, we studied the hypothesis that synaptic dynamics is controlled by three basic principles:

(A) Synapses adapt their efficacies so that neurons can effectively transmit information;

(B) homeostatic processes stabilize the mean firing rate of the postsynaptic neuron; and

(C) weak synapses adapt more slowly than strong ones while maintenance of strong synapses is costly.

Our results show that a synaptic update rule derived from these principles depends on spike timing, is sensitive to correlations in the input, and is useful for synaptic memory.

AKB 10.2 Tue 12:00 ZEU 255

The role of inhibitory feedback for information processing in thalamocortical circuits — •Jörg Mayer, Heinz Georg Schuster, and Jens Christian Claussen — Institut für Theoretische Physik und Astrophysik, Christian-Albrechts Universität, Olshausenstraße 40, 24098 Kiel, Germany

The information transfer in the thalamus is blocked dynamically during sleep or deep anaesthesia, in conjunction with the occurence of spindle waves. We analyze two modeling approaches for a recent experiment by Le Masson *et al.* on the thalamocortical loop. In a first step, we use a conductance-based neuron model to reproduce the experiment computationally. In a second step, we model the same system by using an extended Hindmarsh-Rose model, and compare the results with the conductance-based model. In the framework of both models, we investigate the influence of inhibitory feedback on the information transfer in a typical thalamocortical oscillator. We find that the extended Hindmarsh-Rose neuron reproduces the experiment better than the conductance-based model. Further, inhibitory feedback leads to stable self-sustained oscillations which mask the incoming input, and thereby reduce the information transfer significantly.[1]

[1] Jörg Mayer, Heinz Georg Schuster, and Jens Christian Claussen, The role of inhibitory feedback for information processing in thalamocortical circuits, arxiv.org e-print q-bio/0510040

AKB 10.3 Tue 12:15 ZEU 255

Electrical field parameters for the electrical stimulation of isolated neurons on wide planar interfaces — •A. Reiher[1], H. Witte[1], A. Krtschil[1], S. Günther[1], A. Krost[1], A. de Lima[2], and T. Voigt[2] — [1]Inst. of Experimental Physics, University of Magdeburg, PO Box 4120, 39016 Magdeburg — [2]Inst. of Physiology, University of Magdeburg, Leipziger Str. 44, 39120 Magdeburg

Embryonal neocortical neurons form physiologically active, synaptically interconnected networks after two weeks in vitro. In order to stimulate larger groups of neurons we developed an interdigitated electrode structure for electrical stimulation of the whole network. This interface consists of a planar finger structure of gold on a 5 nm thin Ti-undercoating with a gap of 300 μm between the electrodes exhibiting an overall electrode thickness of 55 nm. Stimulation conditions leading to synchronous network activity were analyzed in [1]. Here we show that the network activity generated by previous stimulation parameters is not due to the direct activation of single neurons, but depends on widespread synaptic interactions. The parameters for the stimulation of single neurons independent from synaptic interactions were analyzed either by inhibiting glutamate and $GABA_A$ receptors in synaptically interconnected networks, or in immature networks with still non-interconnected neurons. The electrical field strength distribution for the interface is calculated with the finite-elements-method. These results are compared with a position dependent analysis of separated firing neurons in order to determine the critical electrical field strength for single neuron stimulation.

[1] A. Reiher, et al., Appl. Phys. Lett. 86, 103901 (2005)

AKB 10.4 Tue 12:30 ZEU 255

Analytical approach to correlation- and feedback-induced oscillations in biological neural networks — •Benjamin Lindner[1,2], Brent Doiron[2], and Andre Longtin[2] — [1]MPI fuer Physik komplexer Systeme, Noethnitzer Str. 38, 01187 Dresden — [2]Department of*Physics, University of Ottawa, 150 Louis Pasteur, Ottawa, Canada*K1N-6N5

A network of leaky integrate-and-fire neurons with global inhibitory feedback and under the influence of spatially correlated noise is studied. We calculate the spectral statistics of the network (power spectrum of the population activity, cross spectrum between spike trains of different neurons) as well as of a single neuron (power spectrum of spike train, cross spectrum between external noise and spike train) within the network. As shown by comparison with numerical simulations, our theory works well for arbitrary network size if the feedback is weak and the amount of external noise does not exceed that of the internal noise. By means of our analytical results we discuss the quality of the correlation-induced oscillation in a large network as a function of the transmission delay and the internal noise intensity. It is shown that the strongest oscillation is obtained in a system with zero internal noise and adiabatically long delay (i.e. the delay period is longer than any other time scale in the system).

REFS.: Doiron, Lindner, Longtin, Maler, Bastian Phys. Rev. Lett. 93, 048101 (2004), Lindner, Doiron, Longtin Phys. Rev. E (2005, in press)

AKB 10.5 Tue 12:45 ZEU 255

Postsynaptic signaling at the Drosophila neuromuscular junction during development — •Thomas Bittig[1], Veronica Dudu[2], Eugeni Entchev[2], Anna Kicheva[2], Marcos González-Gaitán[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Noethnitzer Strasse 38, 01187 Dresden, Germany — [2]Max Planck Institute for Molecular Cell Biology and Genetics, Pfotenhauer Strasse 108, 01307 Dresden, Germany

Cellular signaling systems play an important role during development to determine cell fates and regulate cellular properties. Muscle development is affected by cell-to-cell communication at the synapse which involves the TGF-beta signaling pathway. Synaptic plasticity and the role of growth factors can be studied in the Drosophila neuromuscular junction (NMJ), which is formed during embryogenesis and grows during larval stages to adjust itself to the growth of the muscle. There TGF-beta signaling is transduced by the phosphorylation of transcription factors in the cytosol, which causes their accumulation in the nucleus where they activate gene expression.

We use a simple kinetic model to describe cytoplasmic and nuclear pools of phosphorylated and non-phosphorylated transcription factors that mediate TGF-beta signaling in the muscle cells. This model is used to interpret the time dependence of the concentrations of these molecules as observed in FRAP (Fluorescence Recovery after Photobleaching) experiments. We determine several rate constants of intracellular signaling and show that synaptic signaling via neural action potentials modulates the developmental signaling via growth factors.

AKB 10.6 Tue 13:00 ZEU 255

Analysis of the Neuron-Silicon Interface with a 2D Transistor Array — •Ralf Zeitler[1], Armin Lambacher[1], Roland Thewes[2], and Peter Fromherz[1] — [1]Max Planck Institute for Biochemistry, Department of Membrane and Neurophysics, Martinsried/München — [2]Infineon Technologies, Corporate Research, München

A twodimensional transistor array with a pitch of $7.8\mu m$ is used to study the electrical interfacing of neurons and silicon chips. The 128x128 array is implemented in extended CMOS technology. The open gates of the sensor transistors are insulated by titaniumdioxide. Identified neurons from Lymnaea stagnalis are cultured on the chip. The extracellular voltage in the cell-chip junction is recorded as it is induced by action potentials. The response is not homogeneous in the cell-chip contact, but exhibits dramatic variation in shape and amplitude.

For an interpretation we modelled the ionic membrane current on the basis of literature data and own patch-clamp measurements. Computed action potential shapes agree well with experimental intracellular records. The electrolyte in the narrow cleft between cell and chip was described by a two-dimensional Nernst-Planck equation. By comparing computed extracellular voltage patterns with experimental data it is possible to draw conclusions about the distribution of ion channels in the adhesion membrane.

AKB 10.7 Tue 13:15 ZEU 255

Capacitive Stimulation of Neurons on Silicon Chips: Discrimination of Channel Opening and Electroporation — •Frank Wallrapp and Peter Fromherz — Department of Membrane and Neurophysics, Max Planck Institute for Biochemistry, Martinsried, Germany

The implementation of neuroelectronic systems requires a stimulation of neurons from silicon chips by capacitive interaction. The displacement current through a dielectric layer may give rise to extracellular and intracellular voltages that enhance the membrane conductance. Two mechanisms are feasible: (i) Opening of ion channels. (ii) Transient electroporation. Here, we show that both processes can be induced capacitively and discriminated with proper protocols of the applied voltage. In the model experiments, we use HEK293 cells, stably transfected with the K^+ channel Kv1.3. We cultured them on TiO_2-insulated silicon chips. By applying voltage ramps to the chip, we induce an extracellular voltage in the narrow cleft between cell and chip. For a given amplitude of negative voltage ramps, membrane current is solely due to K^+ channels if the slope is beneath a certain threshold. The selectivity is checked with a toxin for Kv1.3. Above the threshold, a current component appears that is not blocked by the toxin. It is also observed for positive voltage ramps above a threshold of the slope. We assign it to electroporation. With respect to neuronal stimulation we conclude that rectangular voltage pulses applied to a capacitor inevitably elicit reversible electroporation. Selective activation of ion channels is achieved with slower voltage ramps of long duration that require a large amplitude and large capacitance.

AKB 11 Cell Adhesion I

Time: Tuesday 12:00–13:00 Room: ZEU 260

AKB 11.1 Tue 12:00 ZEU 260

Cellular Unbinding Forces on Biofunctionalized Nanostructured Substrates — •Christine Selhuber[1], Nadine Walter[1], and Joachim P. Spatz[1,2] — [1]University of Heidelberg, Biophysical Chemistry, INF 253, D - 69120 Heidelberg — [2]Max-Planck-Institute for Metals Research, Heisenbergstrasse 3, D-70569 Stuttgart

The adhesion of cells to substrates is a highly complex biological process and a fundamental step for many cell activities. To explore integrin mediated adhesion we investigate cell adhesion as a function of defined ligand distances.

To generate ligand patterns, we apply a nanolithographical technique that is based on the self-assembly of diblock copolymers. The result is a pattern of hexagonally arranged gold dots, where the separation of the dots is controlled over a wide length scale. The gold dots are functionalized with an RGD peptide to create adhesive patches for cellular integrin receptors. Cell culture experiments have shown that a dot separation of more than 73 nm restricts cell adhesion, cell spreading and focal contact formation.

To quantify the regulation of cell adhesion by specific nanostructures, we study unbinding forces of cells both during initial and long-term adhesion. The unbinding forces are measured with magnetic tweezers and AFM, respectively. For both adhesion periods the experiments reveal a strong dependence of unbinding forces on ligand distance.

The results indicate that characterizing adhesion forces is a suitable method for probing cell adhesion properties as a function of substrate preparation.

AKB 11.2 Tue 12:15 ZEU 260

Impact of receptor-ligand distance on adhesion cluster stability — •Thorsten Erdmann and Ulrich S. Schwarz — Center for Modelling and Simulation in the Biosciences (BIOMS), Universität Heidelberg, Im Neuenheimer Feld 293, 69120 Heidelberg, Germany

Cells adhere to substrates through two-dimensional clusters of weak adhesion bonds, which open and close stochastically. In many common receptor-ligand systems, the ligands are tethered to the substrate via polymeric spacers. Binding of tethered ligands depends crucially on

receptor-ligand distance because it requires stretching of the polymers. Experimentally, the distance-dependent interplay of rupture and rebinding in adhesion clusters can be studied *in vitro*, e.g. in the surface forces apparatus. We study this effect theoretically using a one-step master equation for the stochastic dynamics of parallel bonds. The force exerted by stretched tethers is balanced by the elastic stiffness of the force transducer. The force accelerates rupture of ligands but it is shared equally by all closed bonds. Formation of new bonds reduces the receptor-ligand distance and increases the probability for further binding. Receptor-ligand binding in adhesion clusters is thus a cooperative and self-reinforcing process. A bifurcation analysis of the deterministic differential equation for the average number of closed bonds reveals the existence of a bistable region in which bound and unbound clusters coexist. Stochastically, the system fluctuates continuously between these two macrostates.

AKB 11.3 Tue 12:30 ZEU 260

Theoretical and experimental studies of force induced growth of focal adhesions — •Achim Besser[1], Patrick Heil[2], Joachim P. Spatz[2], and Samuel A. Safran[3] — [1]Center for Modelling and Simulation in the Biosciences, University of Heidelberg, INF 293, 69120 Heidelberg, Germany — [2]Dept. Biophysical Chemistry, University of Heidelberg, INF 253, 69120 Heidelberg, Germany — [3]Dept. Materials and Interfaces, The Weizmann Institute of Science, 76100 Rehovot, Israel

Focal adhesions are μm-sized protein aggregates that connect the actin cytoskeleton to the extracellular matrix, a network of macro-molecules surrounding tissue cells. Experiments show that as the force acting through the actin cytoskeleton is increased, focal adhesions grow in size and in the direction of the force. We consider a model for the adsorption of adhesion proteins from the cytoplasm to the adhesion site and the resulting force-sensitive anisotropic growth. The theory couples the mechanical forces to the adsorption dynamics. We derive the velocity of both the front and back of the adhesion as a function of the applied force. In addition, our results show that the relative motion of the front and back of the adhesion is asymmetric and in different ranges of forces, the adhesion shrinks or grows in the direction of the force.

These force-induced shape adaptations of focal adhesions are visualized in our experiments by means of fluorescence microscopy. The application of a micro-mechanical device allows the exertion of forces in the nN regime on the cell and thereby controlled stimulation of adhesion growth. The obtained experimental data is in line with the qualitative predictions of our model.

AKB 11.4 Tue 12:45 ZEU 260

Experiment and Modelling of Pattern Development during Fibronectin Nanofibril Formation — •Tilo Pompe[1,2], Jörn Starruss[3], Manfred Bobeth[4], Wolfgang Pompe[4,2], and Carsten Werner[1,2] — [1]Leibniz Institute of Polymer Research Dresden, Hohe Str. 6, 01069 Dresden, Germany — [2]Max Bergmann Center of Biomaterials Dresden — [3]Institut für Lebensmittel- und Bioverfahrenstechnik, Technische Universität Dresden, 01062 Dresden, Germany — [4]Institut für Materialwissenschaft, Technische Universität Dresden, 01062 Dresden, Germany

Adherent endothelial cells reorganize fibronectin molecules in the extracellular space into an ordered fibrillar network with characteristic patterns on the microscale as well as on the nanoscale. Cell culture experiments on polymer substrates with a gradated physicochemistry yield a dependence of fibronectin fibril pattern on the modulated anchorage strength of fibronectin to the substrates. The distinct spacing of fibronectin fibrils observed on the nanometer scale by scanning force microscopy can be correlated to the force sensitivity of the adhesion apparatus of the cell and the inner structure of the actin stress fibres [1].

To support this idea a stochastic model has been developed to explain the nanoscale observation of paired nanofibrils as a result of diffusion-controlled aggregation and myosin-driven transport of fibronectin-integrin complexes. The evolving patterns of fibronectin clusters and fibrils can be summarized in a morphological diagram as a function of fibronectin-substrate and fibronectin-fibronectin interaction energies.

[1] Pompe T, Renner L, Werner C (2005) Biophys. J. 88:527-534.

AKB 12 Soft-Matter Nanofluidic Devices

Time: Tuesday 14:00–16:00 Room: ZEU 255

Invited Talk AKB 12.1 Tue 14:00 ZEU 255

Transport and Reaction-Diffusion Phenomena in Soft-Matter Nanofluidic Devices — •Owe Orwar — Department of Chemistry and Biotechnology, Chalmers University of Technology, SE-412 96 G*teborg, Sweden

Methods for the construction of fluid state lipid bilayer networks consisting of nanotube-conjugated vesicles are presented. Unilamellar vesicles (5-25 μm in diameter) can be connected with nanotubes (30-300 nm in diameter) in a controlled fashion using both self-organization, and forced shape transformations, allowing design of nanofluidic networks of particular geometries and topologies[1-4]. The membrane composition (e.g. lipids, transporters, receptors, and catalytic sites) and container contents (e.g. catalytic particles, organelles, and reactants) can be controlled on the single-container level allowing complex chemical programming of networks [5].

Transport in nanotubes and materials exchange between conjugated containers can be obtained by using three different methods. 1. Marangoni flows where transport is modulated by changes in membrane tension[6-9], 2. electrophoresis [10] where an electric field is applied across nanotubes using Ag/AgCl electrodes inside gel-plugged pipettes, and 3. by diffusional relaxation from systems with pre-programmed chemical potential. All these transport modes can be combined with confocal microscopy and sensitive APD detectors, for single-molecule interrogation. For example, electrophoretic transport and single-molecule detection of large DNA molecules while confined in the lipid nanotube was achieved [10].

Thus, networks of nanotubes and vesicles serve as a platform to build nanofluidic devices operating with single molecules and particles and offers new opportunities to study chemistry in confined biomimetic compartments. As an example, we demonstrate that a transition from a compact geometry (sphere) to a structured geometry (several spheres connected by nanoconduits) induces an ordinary enzyme-catalyzed reaction to display wave-like properties. The reaction dynamics can be directly controlled by the geometry of the network and such networks can be used to generate various wave-like patterns in product formation. The results have bearing for understanding catalytic reactions in biological systems as well as for designing emerging wet chemical nanotechnological devices.

[1.] Karlsson M, Nolkrantz K, Davidson MJ, Stroemberg A, Ryttsen F, Akerman B, Orwar O. Electroinjection of colloid particles and biopolymers into single unilamellar liposomes and cells for bioanalytical applications. Analytical Chemistry (2000) 72, 5857-5862. [2.] Karlsson A, Karlsson R, Karlsson M, Cans A-S, Stroemberg A, Ryttsen F, Orwar O. Molecular engineering - Networks of nanotubes and containers. Nature (2001) 409, 150-152. [3.] Karlsson M, Sott K, Cans A-S, Karlsson A, Karlsson R, Orwar O. Micropipette-assisted formation of microscopic networks of unilamellar lipid bilayer nanotubes and containers. Langmuir (2001) 17, 6754-6758. [4.] Karlsson M, Sott K, Davidson M, Cans A-S, Linderholm P, Chiu D, Orwar O. Formation of geometrically complex lipid nanotube-vesicle networks of higher-order topologies. Proc. Natnl. Acad. Sci. USA (2002) 99, 11573-11578. [5.] Davidson M, Karlsson M, Sinclair J, Sott K, Orwar O. Nanotube-vesicle networks with functionalized membranes and interiors. Journal of the American Chemical Society (2003) 125, 374-378. [6.] Karlsson R, Karlsson M, Karlsson A, Cans A-S, Bergenholtz J, Akerman B, Ewing AG, Voinova M, Orwar O. Moving-wall-driven flows in nanofluidic systems. Langmuir (2002) 18, 4186-4190. [7.] Karlsson A, Karlsson M, Karlsson R, Sott K, Lundqvist A, Tokarz M, Orwar O. Nanofluidic networks based on surfactant membrane technology. Analytical Chemistry (2003) 75, 2529-2537. [8.] Davidson M, Dommersnes P, Markstroem M, Joanny J-F, Karlsson M, Orwar O. Fluid mixing in growing microscale vesicles conjugated by surfactant nanotubes. Journal of the American Chemical Society (2005) 127, 1251-1257. [9.] Karlsson R, Karlsson A, Orwar O. Formation and transport of nanotube-integrated vesicles in a lipid bilayer network. Journal of Physical Chemistry B (2003) 107, 11201-11207. [10.] Tokarz M, Akerman B, Olofsson J, Joanny J-F, Dommersnes P, Orwar O. Single-file electrophoretic transport and counting of individual DNA molecules in surfactant nanotube Proc. Natnl. Acad. Sci. USA 102, 9127-9132.

AKB 12.2 Tue 14:30 ZEU 255

Microaligned collagen matrices by hydrodynamic focusing — •Sarah Köster[1,2], Jennie Leach[2,3], Bernd Struth[4], Joyce Wong[2], and Thomas Pfohl[1] — [1]Max Planck Institute for Dynamics and Self-Organisation, Bunsenstraße 10, 37073 Göttingen, Germany — [2]Department of Biomedical Engineering, Boston University, Boston, MA, USA — [3]University of Maryland Baltimore County, Chemical and Biochemical Engineering, Baltimore, MD, USA — [4]European Synchrotron Radiation Facitlity, 6 rue Horovitz, B. P. 220, 38043 Grenoble Cedex, France

The hierarchical structure of type I collagen fibrils is a key contributor to the mechanical properties of the extracellular matrix (ECM). To date, there are few methods available for precisely controlling and investigating collagen fibril assembly. The objective of this work was to create highly aligned collagen substrata to systematically determine the effects of microscale collagen alignment on cellular behavior. We use a microfluidic diffusive mixing device to create a defined pH gradient, which in turn initiates the self-assembly and concurrent alignment of soluble collagen. Our method enables us to investigate collagen assembly using polarized light microscopy and x-ray microdiffraction. Finite element method simulations of the hydrodynamic and diffusive phenomena predicted feasible operating conditions for tuning collagen fibrillogenesis and were verified experimentally. Furthermore, substrates prepared by using this technique can be used as scaffolds for cell growth. Anisotropic collagen induces alignment of the cytoskeleton and may facilitate the study of its interactions with the ECM.

AKB 12.3 Tue 14:45 ZEU 255

Evolution of DNA compaction in microchannels — •Rolf Dootz[1], Alexander Otten[2], Sarah Köster[1], Bernd Struth[3], and Thomas Pfohl[1] — [1]Max Planck Institute for Dynamics and Self-Organization, Bunsenstraße 10, 37073 Göttingen, Germany — [2]Applied Physics Department, University of Ulm, Albert-Einstein-Allee 11, 89069 Ulm, Germany — [3]European Synchrotron Radiation Facility, 6 rue Horovitz, BP 220, 38043 Grenoble, France

Combining microfluidics with X-ray microdiffraction and Raman microscopy, the dynamic behaviour of soft matter in specific consideration of the molecular structure can be investigated. Owing to the generated elongational flow, alignment of the investigated materials is induced which allows for an improved structural characterisation. Here, the dynamics of the compaction of DNA by polyimine dendrimers is studied. Due to the laminar flow inside the microchannels, a highly defined, diffusion controlled compaction of the DNA occurs enabling the study of different states of the reaction during one measurement by varying the observation position in the channels. The evolution of a columnar mesophase with an in-plane square symmetry is monitored by X-ray microdiffraction and the molecular interaction between the two reactants is traced using Raman microscopy leading to a more profound comprehension of the condensation reaction.

AKB 12.4 Tue 15:00 ZEU 255

Vesicle deformation in shear and capillary flows — •Hiroshi Noguchi and Gerhard Gompper — Institut fuer Forstkoeperforschung, Forschungszentrum Juelich 52425 Juelich, Germany

We study the dynamics of vesicles in shear flow and in micro-channels. A new simulation technique is presented, which combines a three-dimensional mesoscale simulation technique, multi-particle collision dynamics[1] for the solvent with a dynamically-triangulated surface membrane model. The deformation of vesicles is an important subject not only of fundamental research but also in medical applications. For example, in microcirculation, the deformation of red blood cells reduces the flow resistance of microvessels. We focus the effects of membrane viscosity in shear flow [2,3] and the effects of the shear elasticity and bending modulus of membrane in capillary flow [4]. We have found several shape transtions. In capillary flow, an elastic vesicle (red-blood-cell model) transits from a discocyte to parachute-like shape, while the fluid vesicle transits into prolate with increasing flow rate. In both cases, the shape transitions reduce the flow resistance.

[1] A. Malevanets and R. Kapral, J. Chem. Phys. 110, 8605 (1999)
[2] H. Noguchi and G. Gompper, Phys. Rev. Lett. 93, 258102 (2004)
[3] H. Noguchi and G. Gompper, Phys. Rev. E 72, 011901 (2005)
[4] H. Noguchi and G. Gompper, Proc. Nat. Acad. Sci. USA 102, 1415993 (2005)

AKB 12.5 Tue 15:15 ZEU 255

High-Throughput Microfluidic Delivery of Suspended Cells for Marker-Free Deformability Measurement — •Bryan Lincoln — Institute for Soft Matter Physics, University of Leipzig, Linne'strasse 5, 04317 Leipzig

Microfluidic channels typically have the advantage of being laminar flow systems, meaning that are both reversible and linear. This enables their use as an efficient method of cellular transport. By incorporating a dual-beam laser trap, or optical stretcher, into a capillary-based microfluidic chamber, suspended cells can be serially delivered to the trap location where they undergo a step-stress deformation experiment. This deformability is a sensitive, quantitative measure of a cell's global cytoskeletal organization and can be used to track cytoskeletal alterations during both physiological and pathological changes. Applications include the study of the progression of cancer, the differentiation of stem cells, the effects of cell culture conditions and cell cycle, and the evolution of primary cells in culture. This is a marker-free technique with potential for efficient sorting with minimal damage.

AKB 12.6 Tue 15:30 ZEU 255

Heating effects in dual beam laser traps — •Susanne Ebert, Kort Travis, and Jochen Guck — Universität Leipzig, Department of Soft Matter Physics, Linnéstr. 5, 04103 Leipzig, Germany

Dual beam laser traps in a microfluidic environment are a very useful tool for noninvasive handling and manipulation of cells and similar objects. Due to the low energy density of the divergent trapping beams, heating effects are expected to be rather small but cannot be generally excluded.

We applied a fluorescence intensity ratio technique using rhodamineB and rhodamine110 to measure spatial temperature profiles in a microfluidic setup with a confocal laser scanning microscope. The data, taken for two different wavelengths (1064 nm and 780 nm), will be compared to theoretical models and to measurements taken with a thermosensitive camera.

AKB 12.7 Tue 15:45 ZEU 255

Hydrodynamics of Sperm Motion near Hard Walls — •Jens Elgeti and Gerhard Gompper — Forschungszentrum Jülich, Institut für Festkörperforschung, 52425 Jülich

Sperm cells are propelled in a fluid by an active, snake-like motion of its tail, the flagellum. It is already known for some time experimentally that cells accumulate at a wall, swimming always in clockwise circles.

We investigate the sperm motion in a film geometry theoretically. The sperm tail is modelled as a semi-flexible polymer, which is subjected to a sinusoidal bending force. The sperm head is modeled as a sphere, asymmetrically displaced from the beat plane of the tail. Hydrodynamic interactions, which are responsible for the directed motion of the cell, are taken into account by a particle-based, mesoscopic simulation technique (multi-particle collision dynamics).

We show that this highly simplified model captures the basic features of cell motion described above. This shows that hydrodynamic interactions are responsible for the effective attraction to a wall.

Tuning the asymmetry, we find three different types of motion, which are characterized by different radii of curvature, different distance distributions from the wall, and different angles between the beat plane and the wall. Finally, we compare our results with experimental data.

AKB 13 Cell Adhesion II

Time: Tuesday 14:30–15:45 Room: ZEU 260

AKB 13.1 Tue 14:30 ZEU 260

Redistributing intracellular stress with biofunctionalized PDMS pillars to investigate the force induced growth of Focal Adhesions — •Patrick Heil[1,2], Achim Besser[1,2], and Joachim Spatz[1,2] — [1]Max-Planck-Institute for Metals Research, Heisenbergstr. 3, 70569 Stuttgart, Germany — [2]Dept. Biophysical Chemistry, University of Heidelberg, INF 253, 69120 Heidelberg, Germany

Focal contacts (FCs) are important adhesion sites between eukaryotic cells and the extracellular matrix. The development of FCs is substrate dependent: they grow more favorably on stiffer substrates than on soft ones. A deeper insight into this observed cellular mechanosensitivity is crucial to understand the role of FCs in cell adhesion and motility. To quantitatively study this mechanosensitivity and the stimulation of FC growth, microfabricated arrays of elastic polymer pillars are used to manipulate the FC assembly of rat fibroblasts: We use cell-attached micropillars to apply lateral force to the Focal Adhesion sites.

The micropillars are specifically biofunctionalized with ligands such as fibronectin that are known to stimulate cell adhesion. Furthermore, they can be used as force sensors to monitor the applied lateral force in real time. The cells, fibroblasts transfected to express YFP-labeled Paxilin, are maintained in favorable conditions, allowing live imaging of FCs over extended periods of time. Thus, the resultant growth rate of FCs versus applied force can be systematically measured.

We also present a theoretical model to explain force dependent growth of FCs. This model is based on the interplay between an elastic equation for the plaque of FC proteins and the dynamics of protein adsorption.

AKB 13.2 Tue 14:45 ZEU 260

The Electrical Noise of Cell-Substrate-Junctions: A New Method to Probe Cell Adhesion — •Moritz Voelker and Peter Fromherz — Max-Planck-Institut für Biochemie, Martinsried

The junction between cultured cell and substrates is filled with electrolyte. The aqueous cleft between membrane and solid has a width of typically 50 nm and a sheet resistance in the order of several Mohm-square. As every electrical resistance, the junction resistance must exhibit Johnson noise in the form of fluctuations of the local voltage with respect to the bulk electrolyte. We report on a measurement of these voltage fluctuations for rat hippocampus neurons on silicon dioxide, using electrolyte-oxide-silicon field-effect-transistors with a particularly low intrinsic noise. We evaluate the spectral power density of the junction noise by subtracting the noise of open transistors from the total noise of covered transistors. In a first approximation, the resulting net power spectrum is fitted with a Lorentz spectrum for an RC equivalent circuit of the cell-chip junction. The novel technique is non-invasive, does not rely on molecular probes and does not require any intra or extracellular stimulation. It allows to detect variations of cell adhesion in real time as induced by external chemical stimuli.

AKB 13.3 Tue 15:00 ZEU 260

Adhesion of microcapsules — •Peter Graf and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57/III, D-70550 Stuttgart

We describe the adhesion and deformation of an initially spherical capsule on a flat surface due to an attractive contact potential. The model includes the Helfrich bending energy, the energy of the elastic deformations, and the energy of the contact potential. Given the elastic constants of the capsule's material and the strength of the contact potential we calculate the axially symmetric shape of the adhered capsule. Above a critical adhesion strength a contact area forms. For the radius of this contact area we find a power law. Its prefactor depends on the elastic constants and can be expressed in scaling form. We discuss this elastic case in relation to adhesion of fluid vesicles and compare our model with recent experimental results (N. Elsner, F. Dubreuil, and A. Fery, Phys. Rev. E 69, 031802 (2004)) with good agreement.

AKB 13.4 Tue 15:15 ZEU 260

Cell Adhesion by Atomic Force Measurements — •Julia Schmitz[1], Martin Benoit[1], Jenia Manevich[2], Ronen Alon[2], and Kay-Eberhard Gottschalk[1] — [1]LMU Munich — [2]Weizmann Institute

Integrins are involved in many fundamental cellular processes. They act in concert with other receptors and are the starting point of intracellular signalling networks. Since integrins are force transducing proteins, atomic force spectroscopy is an ideal tool to investigate these receptors in their native environment. The here examined VLA-4 integrin of white blood cells plays an important role in the immune response. Its natural ligand is the vascular cell adhesion molecule, VCAM. First, we are testing VLA-4 mediated interactions of the resting cell with immobilized VCAM. By doing force measurements under different immobilized VCAM densities, we obtain insight into on- and off-rates of two non-soluble proteins, one being immobilized on a surface and and the other being in the outer membrane of a living cell. Additionally, the mechanical properties of the anchoring cell membrane are probed. These measurements will serve as a baseline for the characterization of the cell behaviour under a variety of conditions. We are now characterizing the influence of divalent cations as well as of chemokines. Initial results demonstrate that the information we are obtaining by means of AFM is extremely detailed and complementary to flow-chamber and other measurements, so that a combination of different tools will be very valuable for a better characterization of cell adhesion properties.

AKB 13.5 Tue 15:30 ZEU 260

How Mechanical Forces Controll Cell Adhesion — •Matthias F. Schneider[1], Stefan W. Schneider[2], and Achim Wixforth[1] — [1]Biophysics Group, Universität Augsburg, Universitätsstr. 1, D-86135 Augsburg, ermany — [2]Deptartment of Dermatology, University of Muenster, Von-Esmarch-Str. 58, D-48149 Muenster, Germany

Proteins and cells are exposed to a variety of flow conditions when traveling through our vascular system. Shear rates range between 1 to 10000 1/s. The impact of such high shear forces on the protein's function and its controll of adhesion is being investigated in the present study. Therefore we designed a novel acoustically driven microfluidic device (few microliters) to mimick blood flow szenarios on a chip. We found that von willebrand factor (VWF) - the key protein in the first steps of platelet adhesion- is a shear flow and hence mechanically activated protein. At a critical shear rate the protein undergoes a discontinous conformation from a compact coil to an elongated fiber. Only when elongated the protein binds to the surface and is able to mediate blood platelet adhesion.

This is an excellent example how mechanicall forces controll cellular functions. As an example it is discussed how the described effect is able to explain the onset of arteriosclerosis in narrow arteries.

AKB 14 Molecular Motors

Time: Tuesday 16:00–18:30 Room: ZEU 255

Invited Talk AKB 14.1 Tue 16:00 ZEU 255

Single-molecules at work - Deciphering the mechanism of a molecular motor — •Jens Michaelis[1,2], Yann Chemla[3], K. Aathavan[3], Thorsten Hugel[2,4], and Carlos Bustamante[3] — [1]LMU München, Department Chemie und Biochemie, 81377 München — [2]Center for Nanoscience, CeNS, LMU München, 80539 München — [3]UC Berkeley, Physics Department, Berkeley, USA — [4]TU München, Zentralinstitut für Medizintechnik, 85748 Garching

Molecular motors are extremely complex and highly evolved nanometer-sized machineries that couple the free energy liberated by a chemical reaction to provide mechanical work. Details about this so called mechano-chemical coupling will not only further our understanding of biological phenomena, but also provide clues for constructing highly efficient nano-machines.

Here, we present our recent data from a viral protein-complex that drives the translocation of DNA into a protein shell, as part of the viral life-cycle.1 Single-molecule force spectroscopy allowed us to elucidate de-

tails of the mechano-chemical cycle and identify movement steps and coupling mechanism for this motor-complex. On the other hand, structure-function relationships can be tested using single-molecule fluorescence techniques.

1 Y. Chemla, K. Aathavan, J. Michaelis, S. Grimes, P. Jardine, D. Anderson und C. Bustamante, Mechanism of force generation of a viral DNA packaging motor, Cell 122, (2005), 683-692.

AKB 14.2 Tue 16:30 ZEU 255

Measurement of the distance that walking kinesin holds its cargo away from the microtubule surface — •Jacob Kerssemakers[1], Jonathon Howard[1], Henry Hess[2], and Stefan Diez[1] — [1]MPI of Molecular Cell Biology and Genetics, Dresden, Germany — [2]University of Florida, Gainesville, USA

While much has been learnt about how the heads of kinesin step along a microtubule, little is known about the role that the rod and tail domains play in motility. The tail is thought to be involved in cargo-binding and in generating a compact, autoinhibited conformation, but the role of the rod is not known. Here, we have investigated the extension of the rod during active transport by measuring the height at which microtubules glide over a kinesin-coated surface in the presence of ATP. To perform height measurements with nanometer-precision we utilized fluorescence-interference-contrast (FLIC) microscopy, the principle of which is based on high-resolution interference effects if fluorescent objects are imaged in the vicinity of a reflecting surface. Utilizing a self-calibrating method, we determined the distance by which kinesin molecules lift gliding microtubules above the surface to be 19.3+/-0.8 nm (95% confidence). While significantly shorter than the contour length of the motor molecule, this value is consistent with the segmented structure of the molecule. We propose that the function of the rod is to hold cargo sufficiently far away from the surface of the microtubule so that transport is not interfered with by proteins bound to the microtubules or the organelles.

AKB 14.3 Tue 16:45 ZEU 255

The mitotic kinesin Eg5 is processive and chemical inhibitors can modulate its speed and run length — •Lukas C. Kapitein[1], Benjamin H. Kwok[2], Jeffrey H. Kim[2], Erwin J.G. Peterman[1], Tarun M. Kapoor[2], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Laboratory of Chemistry and Cell Biology, The Rockefeller University, New York, NY 10021, USA

Small molecule inhibitors of kinesin-5, a protein essential for eukaryotic mitosis, represent important alternatives to anti-mitotic agents that target tubulin, a protein needed in dividing and non-dividing cells. Kinesin-5 inhibitors, like monastrol, are the only known specific inhibitors for microtubule-based motor proteins, and act through poorly understood allosteric mechanisms distinct from those utilized by ATP-derivatives. Moreover, the microscopic mechanism of kinesin-5 motility is not known. Here we characterize the motile properties of a vertebrate kinesin-5 (Eg5) in the absence and presence of monastrol, using a GFP-fusion protein in single-molecule fluorescence assays. We find that Eg5, against common belief, is a processive motor like conventional kinesin. Unlike conventional kinesin, its motility is discontinuous, switching between pause and run states. Monastrol inhibition prolongs the pause states and decreases Eg5*s speed and run length. Our data on the modulation of Eg5's mechano-chemical cycle by a cell-permeable inhibitor provide essential input for the inhibitor's use as a mechanistic probe and for its development as a chemotherapeutic agent.

AKB 14.4 Tue 17:00 ZEU 255

Application of semiconductor nanocrystals to explore molecular motors — •Bert Nitzsche, Cecile Leduc, Jacob Kerssemakers, Felix Ruhnow, Yannis Kalaidzidis, and Stefan Diez — Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, 01307 Dresden

Employing single molecule fluorescence microscopy and nanometer tracking, recent years have seen great progress in understanding cytoskeletal motors like kinesin or myosin. The used fluorescent labels were either fluorescent proteins or chemical dyes, which both exhibit only moderate brightness and suffer from photobleaching. As a result, temporal resolution and/or observation time can be very limited. Here we attached semiconductor nanocrystals - a new class of sophisticated fluorescent labels that is also called quantum dots (QDs) - to molecular motor systems. Due to their superior photophysical properties (spectacular brightness and high photostability) they have proven ideally suited to study biological (sub)systems such as motor proteins walking along cytoskeletal filaments. We demonstrate that we can combine high temporal and spatial resolution with long observation durations. Beyond this, we show new findings on the trajectories of cytoskeletal motors using QDs, which gives further insights into working mechanisms and functions of molecular motors.

AKB 14.5 Tue 17:15 ZEU 255

Force dependence of motor protein mediated filament depolymerisation — •Gernot Klein, Karsten Kruse, and Frank Jülicher — Max Planck Institute for the Physics of Complex Systems Nöthnitzerstr. 38 01187 Dresden

Many active processes in cells are driven by highly specialised motor proteins, which interact with filaments of the cytoskeleton. Members of the KIN-13 kinesin subfamily are able to induce depolymerisation of the filaments ends[1]. In the mitotic spindle, certain members of the KIN-13 subfamily, which are linked to chromosomes, facilitate pole ward-movement of chromosomes by depolymerising spindle microtubules. In this situation, motors are mechanically coupled and remove subunits under the influence of external forces. Recently we have developed a general description of motor protein induced filament depolymerisation[2]. Based on this description, we study the collective behaviour of depolymerising motor proteins, which are mechanically linked to a common anchoring point, e.g. a bead, and examine the influence of an externally-applied force on motor-induced filament depolymerisation. We find that the depolymerisation velocity can increase as well as decrease for an increasing external force before motors detach from the filament. This behaviour depends on the processivity of the motors during depolymerisation. We compare results obtained in mean-field description with discrete stochastic simulations. The situation studied in our work could be realised by in vitro experiments in which KIN-13 family members are attached to a bead and interact with a filament end. [1] A.W. Hunter, et al., Mol. Cell 11, 445 (2003) [2] G.A. Klein, et al. Phys.Rev.Lett. 94, 108102 (2005)

AKB 14.6 Tue 17:30 ZEU 255

Motor-induced filament interactions in active gels — •Karsten Kruse and Frank Jülicher — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden

Motivated by active dynamic properties of the cytoskeleton, we develop a general framework for describing the dynamics of systems consisting of polar filaments and active cross-links. In the cytoskeleton, active cross-links are formed by motor proteins that are able to induce relative motion between filaments. The framework is based on an analysis of the momentum flux in the system and allows to calculate the stresses in the filament network generated by the action of motor proteins. We relate the dynamics to continuum theories of active polar gels and show that instabilities occur for sufficiently strong motor activity. We show that the instability can be either in the filament orientation or the filament density, depending on the relative values of the filaments' longitudinal and transversal friction coefficient. Finally, we relate our results to in vitro experiments.

AKB 14.7 Tue 17:45 ZEU 255

Enhanced ordering of interacting filaments by molecular motors — •Jan Kierfeld, Pavel Kraikivski, and Reinhard Lipowsky — Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam

We theoretically study the cooperative behavior of cytoskeletal filaments in motility assays in which immobilized motor proteins bind the filaments to substrate surfaces and actively pull them along these surfaces. Because of the mutual exclusion of the filaments, the coupled dynamics of filaments, motor heads, and motor tails leads to a nonequilibrium phase transition which generalizes the nematic-isotropic phase transition of the corresponding equilibrium system, the hard-rod fluid. Langevin dynamics simulations show that the motor activity enhances the tendency for nematic ordering. We develop a quantitative theory for the location of the phase boundary as a function of motor density. At high detachment forces of motors, we also observe filament clusters arising from blocking effects.

AKB 14.8 Tue 18:00 ZEU 255

The interplay between crosslinkers and dynamic molecular motor-induced instabilities in the moderation of biopolymer organization — •David Smith[1,2], David Humphrey[2], Falko Ziebert[3], Walter Zimmermann[3], and Josef Käs[1,2] — [1]Institute for Soft Matter Physics, Universität Leipzig, Linné Str. 5, D-04103 Leipzig Deutschland — [2]Center for Nonlinear Dynamics, University of Texas at Austin, Texas 78712, USA — [3]Physikalisches Institut, Universität Bayreuth, D-95440 Bayreuth Deutschland

Structure and function of biological cells rely on the highly-dynamic self-organization of protein filaments to an intracellular cytoskeleton responsive to mechanical and chemical stimuli. While dissolving these complex cellular structures through Brownian motion is inherently slow (tens of minutes), changes in the activity of the molecular motor myosin II cause rapid order-disorder transitions within 1-2 minutes in reconstituted cytoskeletal actin networks. When motor-induced filament sliding decreases, actin network structure rapidly and reversibly self-organizes into various assemblies triggered by a nonlinear instability. Modulation of static crosslinker concentrations allow for a wide phase space of order ranging from nematics to compact asters & dense packing of motor-filament clusters. The observed isothermal transitions between disorder and self-organization illustrate that molecular motors can substantially contribute to dynamic cellular organization.

AKB 14.9 Tue 18:15 ZEU 255

Biotemplated generation of motor protein nanotracks for the directed motion of microtubule transporters — •Cordula Reuther[1], Robert Tucker[2], and Stefan Diez[1] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]University of Florida, Gainsville, FL, USA

Biological machines have recently found an increasing number of applications in hybrid bionanodevices, where they fulfill tasks of biomolecular transport and manipulation in engineered environments. For example, microtubule-based gliding motility assays have been used to transport micro- and nanometer-sized objects. Spatial control of motility is a crucial criterion for the successful implementation of these nanoscale transport systems. So far, topographic channels with selective surface chemistry have proven to yield the most efficient guiding. However, the fabrication of such structures is labour-intensive and costly, and the channel width might limit the possible size of transported cargo.

Here, we present a method to deposit submicrometer-wide tracks of motor proteins (nanotracks) on unstructured surfaces. We use microtubules themselves as biological templates for the stamping and alignment of motor proteins. Compared to other soft lithography techniques like microcontact printing our approach circumvents protein denaturation due to drying and conformational changes caused by mechanical stress. The generated structures prove very efficient for the guiding of microtubules without topographical barriers. Furthermore, our assay comprises a novel means to study biologically relevant mechanical functions (such as microtubule-microtubule sliding) in vitro.

AKB 15 Biopolymers II

Time: Tuesday 16:30–18:30 Room: ZEU 260

AKB 15.1 Tue 16:30 ZEU 260

Apparent Persistence Length Renormalization of Bent DNA — •Helmut Schiessel[1], Igor M. Kulic[2], Herve Mohrbach[3], and Rochish Thaokar[4] — [1]Instituut-Lorentz, Universiteit Leiden, The Netherlands — [2]Dept. of Physics and Astronomy, University of Pennsylvania, Philadelphia, USA — [3]LPMC, Metz University, France — [4]Dept. of Chemical Engineering, IIT, Bombay, India

We derive the single molecule equation of state (force-extension relation) for DNA molecules bearing sliding loops and deflection defects. Analytical results are obtained in the large force limit by employing an analogy with instantons in quantum mechanical tunneling problems. The results reveal a remarkable feature of sliding loops - an apparent strong reduction of the persistence length. We generalize these results to several other experimentally interesting situations ranging from rigid DNA-protein loops to the problem of anchoring deflections in AFM stretching of semiflexible polymers. Expressions relating the force-extension measurements to the underlying loop/boundary deflection geometry are provided and applied to the case of the GalR-loop complex.

AKB 15.2 Tue 16:45 ZEU 260

Hydrodynamic interactions for stiff polymers — •Jens Glaser[1], Oskar Hallatschek[2], and Klaus Kroy[1] — [1]Institut für theoretische Physik, Universität Leipzig, PF 100 920, 04009 Leipzig — [2]Harvard University, Lyman Laboratory, Cambridge MA 02138

The minimal model for the statics and dynamics of stiff polymers such as the polymers of the cytoskeleton is the wormlike chain. For quantitative predictions of wormlike chain dynamics non-local hydrodynamic interactions (HI) have to be taken into account. The importance of a correct treatment of HI is discussed for the short- and long-time limits of the dynamic structure factor. The results are compared with those of recent dynamic light scattering experiments, e.g. for actin. For extracting consistent and reliable values of the model parameters (persistence length and the backbone thickness) inclusion of HI on the Rotne-Prager level is found to be necessary and sufficient. As another example, a stiff polymer under the influence of a constant external force field, e.g. gravity, is discussed. HI induces a spontaneous symmetry breaking. The corresponding conformational dynamics is analyzed analytically.

AKB 15.3 Tue 17:00 ZEU 260

Dynamics of single semiflexible polymers under force — •Benedikt Obermayer[1], Oskar Hallatschek[2], Klaus Kroy[1], and Erwin Frey[3] — [1]Institut für Theoretische Physik, Universität Leipzig, Augustusplatz 10-11, 04109 Leipzig — [2]Lyman Laboratory of Physics 426, Harvard University, Cambridge, MA 02138 — [3]Arnold Sommerfeld Center for Theoretical Physics, LMU München, Theresienstr. 37, 80333 München

The wormlike chain model gives an accurate theoretical description for many important semiflexible biopolymers. While their static equilibrium properties are well known, the dynamics under external forces is not yet completely understood. We have analyzed the response to forces acting in longitudinal and transverse direction for single chains under thermal conditions in the weakly-bending limit. Since the longitudinal dynamics is closely related to backbone tension, a unified description of its propagation and relaxation behavior provides both a rigorous formalism as well as an intuitive understanding of the dominant relaxation mechanisms; hence we can systematically substantiate and restrict previous heuristic approaches. We present our results in terms of asymptotic scaling laws and by means of crossover solutions computed numerically, and we point out experimental implications.

AKB 15.4 Tue 17:15 ZEU 260

Vibrational imaging of single type I collagen fibrils by multiplex CARS microscopy — •Adam Muschielok, Marina Kovaleva, Alexander Kovalev, and Andreas Volkmer — 3rd Institute of Physics, University of Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

Collagen, one of the most abundant proteins in the extracellular matrix of animals, is important for the stability of tissues. Furthermore, because of its ability to self-assemble into fibrils, it is used as a model system for the formation of biopolymer structures. We have employed coherent anti-Stokes Raman scattering (CARS) microscopy in order to study the vibrational properties of individual in-vitro grown type I collagen fibrils. CARS microscopy allows the non-invasive imaging of collagen fibrils with high sensitivity, with three-dimensional sectioning capability, and with high spatial resolution. Beyond imaging, a multiplex CARS scheme was employed for the fast acquisition of CARS spectra in the region of the C-H stretching vibration. A detailed spectral analysis will be presented, which yields a representation of characteristic Raman line shape parameters in space, directly revealing the chemical and physical properties of a single collagen fibril in solution.

AKB 15.5 Tue 17:30 ZEU 260

Diffusion and intramolecular dynamics of double-stranded DNA in solution — •Eugene P. Petrov[1], Thomas Ohrt[1], Roland G. Winkler[2], and Petra Schwille[1] — [1]Institute of Biophysics / BIOTEC, TU Dresden, Tatzberg 47-51, 01307 Dresden — [2]IFF, Forschungszentrum Jülich, 52425 Jülich

We present results of an experimental investigation of diffusional motion and intramolecular dynamics of double-stranded DNA molecules in solution at the room temperature. Dynamics of single-end fluorescently labeled lambda-DNA fragments with lengths covering the range of 10^2 to 10^4 base pairs were studied by means of fluorescence correlation spectroscopy (FCS). Mean-square displacement of the fluorescently labeled end obtained from FCS data scales at short times as $t^{2/3}$, thus indicating the Zimm-type dynamics of the DNA polymer in solution. The experimental data are in a good agreement with the predictions of the theory of semiflexible polymers [1], which allows to extract diffusion coefficients and intramolecular relaxation times of DNA in solution from FCS measurements.

[1] L. Harnau, R.G. Winkler, P. Reineker, J. Chem. Phys. **104**, 6355 (1996).

AKB 15.6 Tue 17:45 ZEU 260

Characterizing Formin: A Step-By-Step Approach — •Brian Gentry — Institute for Soft Matter Physics, Uni-Leipzig, Linnéstr. 5 04103 Leipzig

The actin cytoskeleton in Eukaryotic cells is a complex system capable of dynamic reorganization during motility processes. Many actin-binding proteins are involved in the reorganization, including motors, cappers and molecules which nucleate and branch filaments. Formin is an end-binding molecular engine which is capable of nucleating and driving the polymerization of actin polymers in vivo. It is involved in the formation of long, unbranched massive actin fibers, such as those found in filipodia. We are currently studying formin and its ability to drive polymerization in vitro using laser tweezers. Using this state-of-the-art method we are investigating the force produced as well as the stepsize of the motor and hope to gain insight into the underlying dynamics of its operation. This method will allow us to directly measure polymerization forces in a controlled manner.

AKB 15.7 Tue 18:00 ZEU 260

Thermophoresis is Entropophoresis — •Stefan Duhr and Dieter Braun — Noether Group on Dissipative Microsystems, Applied Physics, Ludwig Maximilians Universität München, Amalienstr. 54, 80799 München, Germany

Molecules move along temperature gradients, a phenomenon known from experiments for 150. The effect is called thermophoresis, Soret-effect or thermal diffusion. Here we present experiments which back a unifying theoretical explanation. Measurements span a wide range of molecule types and sizes, possible by the use of a novel fluorescence technique which measures thermophoresis in 10 picoliter microfluidics. Optically imposed temperature patterns are shown to manipulate molecules in solution on the micron scale. Our experiments demonstrate that thermophoresis is driven by the entropy of solvation. In water, two solvation entropies counteract. Entropy of ionic shielding leads to thermophobic depletion. Entropy of hydration results in thermophilic accumulation at low overall temperatures. The theory predicts thermophoresis of polystyrene beads and DNA with 10 % accuracy without free parameters. It allows the determination of the effective charge and hydration entropy over a wide molecule size range not measurable with electrophoresis. With this theoretical foundation, thermophoresis can be used for all-optical quantitative biomolecule analysis.

AKB 15.8 Tue 18:15 ZEU 260

Microtubule Dynamic Instability analyzed in 3D over time with Selective Plane Illumination Microscopy — •Philipp Keller, Francesco Pampaloni, Klaus Greger, and Ernst Stelzer — EMBL Heidelberg, Cell Biology and Biophysics Unit, Meyerhofstraße 1, 69117 Heidelberg

Microtubules (MTs) are highly dynamic cytoskeletal filaments that continuously undergo stages of growth and shrinkage (dynamic instability). MTs radiate from a MT organizing center, forming starshaped MTs asters. In our studies of MT asters, we transfer the two-dimensional experiments of MT dynamic instability performed between two closely-spaced glass flats, to a three-dimensional environment and use the SPIM for imaging. Experiments are performed in vitro using Xenopus laevis egg extracts, providing us with a physiological yet biochemically easily modifiable system. Three-dimensional sample preparation ensures a minimal area of artificial surfaces and an unconstrained development of the asters in three dimensions. Apart from addressing the fundamental questions of MT dynamics, this approach allows us to phrase questions that specifically focus on three-dimensional aspects of MT structural dynamics. In our SPIM data sets, the evaluation of three-dimensional MT length distributions over time takes basically all of the asters' MTs into account. This provides us with a very good statistical basis to test and improve theoretical models of dynamic instability.

AKB 16 Biological Networks

Time: Wednesday 14:00–15:15 Room: ZEU 255

Invited Talk AKB 16.1 Wed 14:00 ZEU 255

Biological Networks: Design Principles of Robust Information Processing — •Markus Kollmann — University of Freiburg, Institute of Physics, Hermann-Herder-Str. 3, 79104 Freiburg

Cellular biochemical networks have to function in a noisy environment using imperfect components. In particular, networks involved in gene regulation or signal transduction allow only for small output tolerances and the underlying network structures can be expected to have undergone evolution for inherent robustness against perturbations. We combined theoretical and experimental analysis to investigate an optimal design for the signalling network of bacterial chemotaxis, one of the most thoroughly studied signalling networks in biology. We experimentally determined the extent of intercellular variations in expression levels of chemotaxis proteins and use computer simulations to quantify the robustness of several hypothetical chemotaxis pathway topologies to such gene expression noise. We demonstrate that the experimentally established topology of the chemotaxis network in Escherichia coli is one of the smallest sufficiently robust structures, allowing accurate chemotactic response for almost all individuals within a population. Our results suggest that this pathway has evolved to show an optimal chemotactic performance while minimising the cost of resources associated with high levels of protein expression. Moreover, the underlying topological design principles compensating for intercellular variations seem to be highly conserved among bacterial chemosensory systems.

\Zitat{1}{M. Kollmann, L. Lovdok, K. Bartholome, J. Timmer, and V. Sourjik, Nature, in press }

AKB 16.2 Wed 14:30 ZEU 255

Locating overlapping dense subgraphs in gene association networks and identifying novel functional units among these groups — •Illes J. Farkas, Gergely Palla, Imre Derenyi, and Tamas Vicsek — Biol. Phys. Res. Group of HAS and Dept. of Biol. Phys., Eotvos Univ., H-1117 Budapest, Pazmany P. stny. 1A, Hungary

The identification of the groups of proteins performing the diverse tasks in a cell is crucial to our understanding of cellular networks. In the yeast, *S. cerevisiae*, known physically interacting groups of proteins (complexes) strongly overlap. The total number of proteins in them by far underestimates their total size (from Refs. [1,2] the ratio is 2750/8932 and 1355/2676), thus, all functional groups of proteins, both physically interacting and other, are likely to share many of their members with other groups. However, most current community search methods exclude overlaps. With the aim to *discover* both novel *functions of individual proteins* and novel *functional units* in gene association networks we combine (*i*) a search for overlapping dense subgraphs based on the Clique Percolation Method (CPM) [3,4], which explicitly allows overlaps among the groups, and (*ii*) the verification and characterization of the identified groups of nodes (genes) by annotation tools listing known functions [5].

[1] Guldener, U., *et.al. Nucl. Acids Res.* **33**, D364-368 (2005).
[2] Gavin, A. C., *et.al. Nature* **415**, 141-147 (2002).
[3] Derenyi, I., *et.al. Phys. Rev. Lett.* **94**, 160202 (2005).
[4] Palla, G., *et.al. Nature* **435**, 814-818 (2005),
http://angel.elte.hu/clustering .
[5] The Gene Ontology Consortium. *Nature Genetics* **25**, 25-29 (2000).

AKB 16.3 Wed 14:45 ZEU 255

Architecture of Randomly Evolving Idiotypic Networks — •Holger Schmidtchen and Ulrich Behn — Institut für Theoretische Physik, Universität Leipzig, POB 100 920, 04009 Leipzig

B-Lymphocytes express on their surface receptors (antibodies) of a given specifity (idiotype). Crosslinking these receptors by complementary structures, antigens or antibodies, stimulates the lymphocyte. Thus a large functional network of interacting lymphocytes, the idiotypic network, emerges. Idiotypic networks conceived by Niels Jerne 30 years ago, experience a renewed interest, e.g. in the context of autoimmune diseases. In a previously proposed minimalistic model [1] idiotypes are represented by bitstrings. The population dynamics of the idiotype clones is reduced to a zero–one scheme. An idiotype survives only if it meets enough but not too much complementary structures. We investigate the random evolution of the network towards a highly organized functional architecture which is driven by the influx of new idiotypes, randomly generated in the bone marrow. The vertices can be classified into different groups, which are clearly distinguished, e.g., by the mean life time of the occupied vertices. They include densely connected core groups and peripheral groups of isolated vertices, resembling central and peripheral part of the biological network. We found the building principles of the observed patterns and propose a description of their architecture, which are easily transferable to other patterns and applicable to different system sizes.

[1] M. Brede, U. Behn, Patterns in randomly evolving networks: Idiotypic networks, Phys. Rev. E **67**, 031920 (2003)

AKB 16.4 Wed 15:00 ZEU 255

Robustness and evolvability of genetic networks — •Stefan Braunewell and Stefan Bornholdt — Institute for Theoretical Physics, University of Bremen, Otto-Hahn-Allee, 28359 Bremen, Germany

The molecular biological networks that control the processes of a living cell are required to be robust: They simply have to be stable against perturbations to ensure the survival of the organism [1]. On the other hand, organisms are highly evolvable and have proven quite flexible in the course of biological evolution. Therefore, also the genetic control networks should be flexible under evolution [2]. Is robustness evolvable and does network robustness affect evolvability? We here study these questions in the framework of a simple discrete dynamical network model. We develop a new method for modeling noise in genetic networks and use a non-stochastic approach that allows for exact results.

[1] K. Klemm and S. Bornholdt, Topology of biological networks and reliability of information processing, Proc. Natl. Acad. Sci. USA (2005), in press.

[2] S. Bornholdt and K. Sneppen, Neutral mutations and punctuated equilibrium in evolving genetic networks, Phys. Rev. Lett. 81 (1998) 236.

AKB 17 Population Dynamics

Time: Wednesday 14:30–15:30 Room: ZEU 260

AKB 17.1 Wed 14:30 ZEU 260

Swarm formation of anisotropic self-propelled particles — •Fernando Peruani[1,2], Markus Baer[3], and Andreas Deutsch[2] — [1]Max-Planck Institute for the Physics of Complex Systems — [2]ZIH, Technische Universität Dresden — [3]Physikalisch-Technische Bundesanstalt

We study clustering (swarming) in biologically motivated systems of asymmetric self-propelled particles interacting through volume exclusion. Through simulations, we give numerical evidence of a transition to swarming. At the same time, we show that clustering effects can be captured by a mean field approach. We find that clustering is controlled by the particle aspect ratio κ and the packing fraction η. We report a transition from unimodal to bimodal cluster size distribution which is triggered by a critical κ_c. We show κ_c is a function of the packing fraction η. The applicability of these finding to bacterial swarming is also discussed.

AKB 17.2 Wed 14:45 ZEU 260

Coevolutionary dynamics: From finite to infinite populations — •Jens Christian Claussen[1], Arne Traulsen[2], and Christoph Hauert[2] — [1]Institut für Theoretische Physik und Astrophysik, Universität Kiel, Germany — [2]Center for Evolutionary Dynamics, Harvard

Traditionally, frequency dependent evolutionary dynamics is described by deterministic replicator dynamics assuming implicitly infinite population sizes. Only recently, stochastic processes have been introduced to study evolutionary dynamics in finite populations. However, the relationship between deterministic and stochastic approaches remained unclear. Here we solve this problem by explicitely considering the limit of infinite populations. In particular, we identify different microscopic stochastic processes that lead to the standard or the adjusted replicator dynamics. Moreover, differences on the individual level can lead to qualitatively different dynamics in asymmetric conflicts and, depending on the population size, can even invert the direction of the evolutionary process.

[1] J.C. Claussen & A. Traulsen, Phys. Rev. E 71, 025101(R)

[2] Arne Traulsen, Jens Christian Claussen, Christoph Hauert, Phys. Rev. Lett (2005, in print; arXiv.org e-print cond-mat/0409655)

AKB 17.3 Wed 15:00 ZEU 260

Vicious walkers in one-body potentials — •Karen Winkler[1] and Alan J. Bray[2] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center of Nanoscience (CeNS), LMU München — [2]Department of Physics and Astronomy, University of Manchester, Manchester M13 9PL, U.K.

Vicious walkers are short-ranged interacting random walkers which annihilate each other on meeting. The backward Fokker-Planck equation is an elegant tool to derive the asymptotic behavior of the probability that all N vicious walkers have survived. We introduce a method to compute the survival probability of N vicious walkers in general one-body potentials. Using this method we are able to give results for N vicious walkers on a semi-infinite line with reflecting boundary at the origin [1].
We also derive explicit results for three vicious walkers in an inverted harmonic potential, which can be interpreted as a new predator-prey problem [2].

[1] A.J. Bray and K. Winkler, J. Phys. A **37**,5493 (2004)
[2] K. Winkler and A.J. Bray, J. Stat. Mech.(2005) PO2005

AKB 17.4 Wed 15:15 ZEU 260

Phase Transitions and Fluctuations in Stochastic Lattice Lotka-Volterra Models — •Mauro Mobilia[1,2], Ivan T Georgiev[2], and Uwe C Taeuber[2] — [1]Arnold Sommerfeld Center for Theoretical Physics, Ludwig-Maximilians-Universität München — [2]Virginia Polytechnic Institute and State University, Blacksburg, USA

Modeling dynamics of interacting species has received considerable attention in the fields of biology and ecology since Lotka and Volterra's pioneering work. In this contribution we report on the general properties of stochastic two-species competing populations with Lotka-Volterra type interactions defined on a d-dimensional lattice.

Introducing spatial degrees of freedom and allowing for stochastic fluctuations generically invalidates the classical, deterministic mean-field picture. Already within mean-field theory, however, spatial constraints, modeling locally limited resources, lead to the emergence of a continuous phase transition. Field-theoretic arguments, supported by numerical results, indicate that this transition, which represents an extinction threshold for the predator population, is governed by the directed percolation universality class. In the active state, where predators and prey coexist, the classical center singularities with associated population cycles are replaced by either nodes or foci. In the vicinity of the stable nodes, the system is characterized by clusters of predators in a sea of prey. Near the stable foci, however, the stochastic lattice Lotka-Volterra system displays complex spatio-temporal patterns. We discuss the irregular oscillations of the population densities associated to spatial fluctuations and the robustness of the overall scenario.

AKB 18 Ion Channels and Nanopores

Time: Wednesday 15:30–16:45 Room: ZEU 255

Invited Talk AKB 18.1 Wed 15:30 ZEU 255

Synthetic Analogues of Biological Voltage-Gated Channels, Fabrication of Ion-Current Rectifiers and Protein Sensors — •Zuzanna Siwy — Department of Physics and Astronomy, University of California, Irvine, USA

We have fabricated a single asymmetric nanopore that mimics behavior of biological voltage-gated channels. The single pores have been prepared by the track-etching technique. The pores are conical in shape with diameter of the small opening down to several nm and the big opening in the micrometer range. We have designed two nanotube systems, which exhibit ion current rectification through two distinct mechanisms (i) through asymmetric potential energy profile for an ion inside the pore, and (ii) electro-mechanical gate placed at the entrance of the conical pore.

We have also designed single nanopore system, which produces voltage-dependent ion current fluctuations with the kinetics of opening and closing similar to voltage-gated biochannels.

I will also discuss application of synthetic voltage-gated nanopores as platforms in biosensing. The internal surfaces of the nanopores have been modified with a specific biochemical molecular-recognition agent (the *capture* agent, e.g., an antibody) which interacts specifically with a given biomolecule (the analyte) brought into contact with the nanotube. The binding interaction between the nanotube-bound capture agent and the solution-phase analyte is transduced as a change in the ion current that flows through the nanotube. We have demonstrated operation of the sensor for detection of ricin and immunoglobins.

AKB 18.2 Wed 16:00 ZEU 255

Gating charge effects in excitable membranes — •Gerhard Schmid, Igor Goychuk, and Peter Hänggi — Institut für Physik, Universität Augsburg

Voltage dependent ion channels mainly determine the electric properties of axonal cell membranes. The ion channels thereby do not only allow the passage of ions trough the cell membrane but they also contribute to the additional charging of the cell membrane resulting in the so-called capacitance loading. The switching of the channel gates between an open and a closed configuration is always connected with movement of gating charge within the cell membrane. At the beginning of an action potential the gating current is opposite to the direction of the ion current through the membrane. Therefore the excitability is reduced due to capacitance loading. Our stochastic Hodgkin-Huxley modelling takes into account both, channel noise – the fluctuations of the number of open ion channels [1] – and the capacitance fluctuations due to gating charge. We investigate the spiking dynamics of small membrane patches and analyze the statistics of the spontaneous spiking. In doing so, we find that such gating charge effects yield a drastic reduction of the spontaneous spiking rate. This work is supported by DFG (SFB 486).

[1] G. Schmid, I. Goychuk, P. Hänggi, Europhys. Lett. **56**, 22-28 (2001).

AKB 18.3 Wed 16:15 ZEU 255

Direct force measurements on DNA in a solid-state nanopore — •U. F. Keyser, B. N. Koeleman, D. Krapf, R. M. M. Smeets, S. G. Lemay, N. H. Dekker, and C. Dekker — Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands

Amongst the variety of roles for nanopores in biology, an important one is enabling polymer transport, for example in gene transfer between bacteria and transport of RNA through the nuclear membrane. Recently, this has inspired the use of protein and solid-state nanopores as single-molecule sensors for the detection and structural analysis of DNA and RNA by voltage-driven translocation. The magnitude of the force involved is of fundamental importance in understanding and exploiting this translocation mechanism, yet so far has remained unknown. Here, we demonstrate the first measurements of the force on a single DNA molecule in a solid-state nanopore by combining optical tweezers with ionic current detection. The opposing force exerted by the optical tweezers can be used to slow down and even arrest the translocation of the DNA molecules. We obtain a value of 0.24*0.02 pN/mV for the force on a single DNA molecule, independent of salt concentration. Our data allow the first direct quantitative determination of its effective charge of 0.53*0.05 electrons per base pair, corresponding to a 73% reduction of the bare DNA charge. Our novel single-molecule technique further is a major step forward in biotechnology (towards rapid DNA sequencing) and biophysics (study of unfolding of RNA or DNA-protein binding).

AKB 18.4 Wed 16:30 ZEU 255

Antibiotic translocation through OmpF — •Tivadar Mach[1], Karin Türk[1], Luminita Damian[1], Sergei M Bezrukov[2], and Mathias Winterhalter[1] — [1]International University Bremen, Germany — [2]National Institutes of Health, Bethesda, MD, USA

The first step for antibiotics to reach their target in gram-negative bacteria is crossing the outer membrane. Several studies have concluded that general diffusion porin OmpF plays an important role in the uptake of some antibiotics, and that this uptake can often be considered the limiting step in their functionality. We use the analysis of the ion current through a single trimeric OmpF porin reconstituted into a planar lipid bilayer to study binding and translocation of fluoroquinolone antibiotics of different structure and hydrophobicity. Because the size of the antibiotic molecules is close to the size of the constriction zone in the OmpF pore, longer residence times of the fluoroquinolones in the channel cause random transient blockages in the ion current. Analysing these fluctuations we calculate chemical binding constants, affinity, and transfer probability. Our findings complete and corroborate earlier indications and indirect measurements of pathways of entry, providing a test-case for a direct, controlled measurement method also to be expanded to other antibiotic structures.

AKB 19 Proteins

Time: Wednesday 16:00–16:45 Room: ZEU 260

AKB 19.1 Wed 16:00 ZEU 260

Origin of the twisting in β-sheet structures — •Joel Ireta and Matthias Scheffler — Fritz-Haber-Institut der Max-Planck-Gesellschaft, Faradayweg 4-6, D-14195, Berlin

The potential-energy surface of a single-strand β-sheet is studied using density-functional theory in the Perdew, Burke, and Ernzerhof approximation to the exchange-correlation functional. Infinite polyalanine and polyglycine chains are used to model the single-strand β-sheet structure. The potential-energy surface of polyalanine is found to be asymmetric with respect to twisting. This leads to a left-handed twist of few degrees in the structure. However for polyglycine, the potential-energy surface is found to be symmetric. We find that the asymmetry in the potential-energy surface of polyalanine can not be solely attributed to repulsive interactions between the side group, which is absent in polyglycine, and the helix backbone but to the pyramidalization of the nitrogen atom in the peptide bond. Symmetry with respect to twisting in the potential-energy surface of polyalanine is induced when nitrogen pyramidalization is avoided. In a survey throughout the crystallized structures of proteins listed in the protein data bank, we find indeed a left-handed twisting in the β-sheet conformations.

AKB 19.2 Wed 16:15 ZEU 260

On the balance of the enthalpic and the entropic contributions to the stability of the helix: A DFT-GGA study — •Lars Ismer[1], Joel Ireta[1], Matthias Scheffler[1], and Jörg Neugebauer[2] — [1]Fritz-Haber-Insitut der Max-Planck-Gesellschaft, Faradayweg 4-6, D-14195 Berlin — [2]Max-Planck-Institut für Eisenforschung, Max-Planck-Strasse 1, D-40237 Düsseldorf

Accurate theoretical studies of the thermodynamic stability of isolated peptide chains may serve as a reliable reference to understand the stability of the secondary structure of proteins. We have therefore calculated the free energy difference needed to fold the fully extended structure (FES) of isolated, infinite polyalanine (Ala) and -glycine (Gly) chains into various helical conformations such as the 3_{10}-, α-, and π-helix. The calculations were done by employing DFT-GGA, plane waves, pseudopotentials and the quasi-harmonic approximation to estimate the finite tem-

perature effects. We find that entropic contributions to the free energy strongly reduce the enthalpic stability of the helices at elevated temperatures, leading to a transition to the FES at $T_c \sim 460$ K for Ala and $T_c \sim 400$ K for Gly. Below T_c the α-helix is the conformation with the lowest free energy. The π-helix shows the strongest temperature dependence resulting in a significant destabilization with respect to the α- and 3_{10}-helix for $T > 0$ K. A detailed analysis showed these thermodynamic trends to be *intrinsic* features of the specific hydrogen bonding network formed by the various helices and to be largely independent of the specific amino acid.

AKB 19.3 Wed 16:30 ZEU 260

Protein structure comparison based on a vectorial structure representation — •Florian Teichert and Markus Porto — Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstr. 8, 64289 Darmstadt, Germany

A vectorial structure representation has recently been proposed as an equivalent description of globular protein folds. We develop suitable similarity measures for this vectorial structure representation, incoorporating the proper treatment of gaps, based on which we divise a scheme to align protein structures which is conceptually different from existing schemes.

[1]˜F.˜Teichert and M.˜Porto (in preparation)

AKB 20 Nano-Biomaterials and Devices

Time: Thursday 09:45–12:45 Room: ZEU 255

Invited Talk

AKB 20.1 Thu 09:45 ZEU 255

DNA self-assembly: nanostructures and molecular machines — •Andrew Turberfield — University of Oxford, Department of Physics, Clarendon Laboratory, Parks Road, Oxford OX1 3PU, United Kingdom

DNA is a wonderful material for nanoscale construction. It is a structural material whose self-assembly can be programmed by making use of its information-carrying capability; its hybridization can also be used as an energy source for molecular devices. I shall describe our recent work on three-dimensional nanofabrication and molecular machinery, including progress towards the construction of a free-running synthetic molecular motor.

Invited Talk

AKB 20.2 Thu 10:15 ZEU 255

Synthesis, properties and perspectives of complex nanocrystal structures — •Liberato Manna — National Nanotechnology Laboratory of CNR-INFM, Distretto Tecnologico - Isufi, Via Arnesano Km 5, 73100 Lecce, ITALY

Research on colloidal nanocrystals has moved from the synthesis of simple structures, such as spherical nanoparticles, to more elaborate shapes such as rods,[1-3] stars, discs, branched nanocrystals [1,4] and recently to nanoparticles based on inorganic sections interconnected without the need of organic linkers.[5-8] Nanocrystal heterostructures represent a convenient approach to the development of nanoscale building blocks, as they group inorganic sections with different functionalities in the same particle. The present talk will give an overview of the synthetic strategies to complex nanocrystals and will highlight their structural properties, as well as the perspectives in this field.

[1] Manna, L.; Scher, E. C.; Alivisatos, A. P., Synthesis of soluble and processable rod-, arrow-, teardrop-, and tetrapod-shaped CdSe nanocrystals. Journal of the American Chemical Society 2000, 122, (51), 12700-12706.

[2] Peng, X. G.; Manna, L.; Yang, W. D.; Wickham, J.; Scher, E.; Kadavanich, A.; Alivisatos, A. P., Shape control of CdSe nanocrystals. Nature 2000, 404, (6773), 59-61.

[3] Hu, J. T.; Li, L. S.; Yang, W. D.; Manna, L.; Wang, L. W.; Alivisatos, A. P., Linearly polarized emission from colloidal semiconductor quantum rods. Science 2001, 292, (5524), 2060-2063.

[4] Manna, L.; Milliron, D. J.; Meisel, A.; Scher, E. C.; Alivisatos, A. P., Controlled growth of tetrapod-branched inorganic nanocrystals. Nature Materials 2003, 2, (6), 382-385.

[5] Milliron, D. J.; Hughes, S. M.; Cui, Y.; Manna, L.; Li, J. B.; Wang, L. W.; Alivisatos, A. P., Colloidal nanocrystal heterostructures with linear and branched topology. Nature 2004, 430, (6996), 190-195.

[6] Kudera, S.; Carbone, L.; Casula, M. F.; Cingolani, R.; Falqui, A.; Snoeck, E.; Parak, W. J.; Manna, L., Selective growth of PbSe on one or on both tips of colloidal semiconductor nanorods. Nano Letters 2005, 5, (3), 445-449.

[7] Mokari, T.; Rothenberg, E.; Popov, I.; Costi, R.; Banin, U., Selective growth of metal tips onto semiconductor quantum rods and tetrapods. Science 2004, 304, (5678), 1787-1790.

[8] Gu, H. W.; Zheng, R. K.; Zhang, X. X.; Xu, B., Facile one-pot synthesis of bifunctional heterodimers of nanoparticles: A conjugate of quantum dot and magnetic nanoparticles. Journal of the American Chemical Society 2004, 126, (18), 5664-5665.

AKB 20.3 Thu 10:45 ZEU 255

DNA-switchable hybrid structures — •Andreas Reuter, Michael Olapinski, Tim Liedl, and Friedrich Simmel — Department für Physik, Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 München

Programmable self-assembly with DNA molecules has been previously used for the construction of a variety of nanoscale structures as well as for the realization of simple machine-like molecular devices. These devices were capable of performing nanoscale movements such as stretching, rotation and even translocation. In combination with functional nucleic acids such as aptamers or ribozymes, functional DNA devices could be realized which can bind or release molecules, compute and respond autonomously to environmental inputs. We here demonstrate that also hybrid devices can be realized which are composed of an inorganic part such as a nanoparticle or a microstrucured electrode on a surface and a DNA actuating component. The DNA actuator part can be used to reversibly and selectively change the distance between organic components of the hybrid devices (such as fluorescent dyes) and the inorganic components. The conformational changes can be characterized by monitoring energy transfer between fluorophores and metallic device components. Such structures may find use in sensors and actuators where the transduction of a biomolecular recognition event to an electronic or optical signal is desired. On a more fundamental level, the ability to tailor and reversibly change the distance between nanoscale components can be used to study distance-dependent interaction phenomena between these components.

AKB 20.4 Thu 11:00 ZEU 255

Driving a DNA conformational switch with a pH oscillator — •Tim Liedl and Friedrich Simmel — Department für Physik, Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 München

DNA conformational changes occuring in artificially generated DNA structures can be used to produce motion on the nanometer scale. Such DNA-based nanodevices are either driven by hybridization events between complementary strands of DNA or by buffer-induced conformational changes. One prominent example of such a conformational change is the formation of the so-called i-motif, which is a folded four-stranded DNA structure characterized by noncanonical hemiprotonated cytosine-cytosine base-pairs. The transition of DNA strands prone to fold into the i-motif occurs in the pH range between 5 and 7. Usually, DNA devices are driven by the manual addition of fuel molecules or by the periodic variation of buffer conditions. In an attempt to produce self-running nanodevices which do not require intervention by an external operator, we here show that a DNA switch based on the i-motif can also be driven autonomously within a continuously stirred flow reactor in which periodic pH oscillations are generated by a nonequilibrium chemical process. The conformational changes are monitored simultaneously with the pH value in fluorescence resonance energy transfer experiments.

AKB 20.5 Thu 11:15 ZEU 255

Fundamental Hemostasis Investigations in Microdevices — •Heather Evans, Stephan Herminghaus, and Thomas Pfohl — Max Planck Institut für Dynamik und Selbstorganisation, Göttingen, Germany 37073

Fibrin is a prominent protein in the complex process of hemostasis, or blood clotting. This protein aggregates at a site of injury when monomers

of fibrinogen assemble into fibers of fibrin via enzyme catalysis. The biodegradable nature and good tissue tolerance of fibrin networks have already been demonstrated in terms of commercially available wound covering agents, and this protein has been implicated in medical conditions such as artherosclerosis, cancer, and multiple sclerosis. Our studies aim to elucidate mechanisms of fibrin assembly while utilizing the spatio-temporal resolution and confinement induced by microchannel structures. Microchannel devices require less reagent, resulting in a more efficient and cheaper experimental design, and enable investigations of the evolution of biomolecular interactions in ambient conditions. Small angle X-ray microdiffraction and microscopy studies have been conducted on fibrin formed within microchannels. In our experimental system, the addition of enzyme and subsequent formation of fibrin can be carefully controlled by adjusting parameters such as concentration, flow rate, and channel geometry. To this end, network densities and fibrin bundle sizes of structures formed within microchannels will be discussed.

AKB 20.6 Thu 11:30 ZEU 255

Light-induced Manipulation of DNA on Amorphous Silicon Surfaces — •M. Höb, S. Gatz, M. Stutzmann, and M. Brandt — Walter Schottky Institut, Technische Universität München, D-85748 Garching, Germany

Lab-on-a-chip devices depend on methods, which ideally are non-mechanical, to move, dispense, sort or mix (bio)chemical substances such as DNA. Electrokinetics is ideally suited to perform such functions, as the movement is induced and controlled by electric fields. We report a novel technique to manipulate DNA based on light-induced dielectrophoresis on hydrogenated amorphous silicon surfaces (a-Si:H), in which the coupling of an inhomogeneous ac electric field to the induced dipole moment of DNA allows the manipulation of the macromolecules. An otherwise unstructured a-Si:H/ZnO-layer sequence, which is locally illuminated, serves as a light-controlled 'virtual electrode' to create the non-uniform electric field necessary in the electrolyte. Light-induced positive dielectrophoresis of the DNA molecules to the virtual electrode is observed by fluorescence microscopy. The attraction to the illuminated spot is studied as a function of frequency and amplitude of the applied ac voltage as well as the power density of the illumination.

AKB 20.7 Thu 11:45 ZEU 255

Rapid Chiral Synthesis of Rigid DNA Building Blocks for Molecular Nanofabrication — •Catherine F. Tardin[1], Russell P. Goodman[2], Iwan A.T. Schaap[1], C. M. Erben[2], Richard M. Berry[2], Andrew J. Turberfield[2], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Clarendon Laboratory, Department of Physics, University of Oxford, Parks Road, Oxford OX1 3PU, UK

The programmability of base-pairing interactions makes DNA an ideal molecule for construction by self-assembly. Practical components for 3D molecular nanofabrication must be simple to produce, stereopure, rigid and adaptable. We report a family of DNA tetrahedra, less than 10nm in size, that can be made in seconds with near-quantitative yield. Their triangulated architecture allows them to support a compressive load: by compressing a DNA tetrahedron by little more than 1 nm with an AFM we have measured the axial compressibility of DNA and have observed the buckling of the double helix under high loads.

AKB 20.8 Thu 12:00 ZEU 255

Raman Sensors using Photonic Crystal Fibers for Chemical and Biological Applications — •John Erland Østergaard[1], Stig Christensen[2], Kasper Jørgensen[2], Søren Hassing[2], Thomas Søndergaard[3], Stefan Banke Ovesen[1], and Karsten Rottwitt[4] — [1]University of Southern Denmark, Fysisk Institut, Campusvej 55, DK-5230 Odense M — [2]Engineering College of Odense, Niels Bohrs Alle 1, DK-5230 Odense M — [3]Aalborg University, Institute of Physics and Nanotechnology, DK-9220 Aalborg Øst — [4]Technical University of Denmark, COM, DK-2800 Kgs. Lyngby

The recent development in photonic-crystal-fibers (PCF) is currently explored for new types of optical sensors taking advantage of introducing a liquid in the PCF for enhanced sensitivity for Raman signals generated from the liquid. For a Raman sensor, a large air-core PCF with air-holes running along the fiber is considered. It is possible to guide light strongly localized to the large central air-hole via the Bragg effect[1,2]. In our calculations for holes filled with water (n=1.33 compared to silica n=1.45), it is also possible to guide light confined to the core region of the fiber due to the band gap properties of the cladding material. Three frequency ranges for Raman sensing are identified where light is guided well in the core region. In the case where the liquid has a larger refractive index than glass, the PCF supports a mode localized to the liquid-filled core region of the fiber above a cut-off frequency, as for standard fibers. Experimental examples of Raman generation in the PCF for different light propagation regimes is discussed. [1] R.F. Cregan et al, Science, 285, 1537 (1999). [2] Broeng et al., Opt. Lett. 25, 96 (2000).

AKB 20.9 Thu 12:15 ZEU 255

A Novel Method to Fabricate Continuous Surface Tethered Membranes — •Christian Daniel[1], Luisa Andruzzi[2], Kirstin Seidel[2], Joachim Rädler[2], Erich Sackmann[1], and Bert Nickel[2] — [1]Techn. Univ. Munich, Physics Dep. E22, James-Franck-Str. 1, 85748 Garching — [2]L. M. Universität, Dep. f. Physik LS J. Rädler, Geschw.-Scholl-Pl. 1, 80539 München

Functionalization of solid surfaces (semiconductors, metal coated supports, electrooptical devices) with polymer supported lipid membranes provides a promising strategy to generate bio-analogue interfaces between inorganic and biological materials for scientific and practical applications. This work reports a new method for the generation of lipid bilayers separated from the surface by an ultra-thin soft polymer cushion mimicking the role of e.g. actin cortices of cell envelopes. The stratified films are fabricated by covalent anchorage of lipids on the solid surface and passivation of the uncovered surface with hydrophilic polymer films of different thickness. Spreading of vesicles on these activated surfaces results in the formation of supported membranes which are continuous over large areas and are characterized by very high long range mobility of constituents. Structural studies of the supported membranes by synchrotron x-ray reflectivity allow the determination of the thicknesses of the different interfacial films with sub-nanometer resolution. The major advantage of the tethered membranes is the reproducibility of the bilayer deposition procedure, which is expected to greatly facilitate the investigation of specific lipid-protein interaction mechanisms and their role for the self assembly and function of biological membranes.

AKB 20.10 Thu 12:30 ZEU 255

Silicon-on-insulator based nanogap structures for bio-molecular electronics — •Sebastian Strobel[1], Allan Hansen[1], Kenji Arinaga[1,2], and Marc Tornow[1] — [1]Walter Schottky Institut, TU München, 85748 Garching, Germany — [2]Fujitsu Laboratories Ltd., 10-1 Morinosato-Wakamiya, Atsugi 243-0197, Japan

The starting point for electrical transport measurements on bio-molecular "wires" such as DNA oligonucleotides is the preparation of suitable nanogap - electrodes that serve as contact to the molecules. Here, one necessary requirement are biocompatible substrates with sufficient stability in aqueous solutions, such as silicon and silicon oxide.

We pursue a new strategy to prepare nanogap structures of predetermined electrode distance based on silicon-on-insulator substrates. The combination of reactive ion etching and selective wet oxide etching allows for the fabrication of 10-20 nm wide trenches, which act as template for a subsequent metal thin film evaporation step.

We successfully verified the electrical functionality of 20 nm devices by bridging the electrodes with electrically trapped gold nanoparticles. First transport measurements after functionalisation with DNA oligonucleotides will be presented.

AKB 21 Intracellular Transport

Time: Thursday 10:45–12:30 Room: ZEU 260

AKB 21.1 Thu 10:45 ZEU 260

A stochastic model for intra-cellular transport of single-headed molecular motors — •Andreas Schadschneider[1], Philip Greulich[1], Katsuhiro Nishinari[2], Yasushi Okada[3], and Debashish Chowdhury[4] — [1]Institut für Theoretische Physik, Universität zu Köln, 50937 Köln — [2]Department of Aeronautics and Astronautics, University of Tokyo, Japan — [3]Department of Cell Biology and Anatomy, University of Tokyo, Japan — [4]Department of Physics, Indian Institute of Technology, Kanpur, India

Motivated by recent experiments on KIF1A, a representative member of single-headed kinesin motor proteins family, we develop a theoretical model of intra-cellular transport by mutually interacting molecular motors. It explicitly accounts not only for the hydrolysis of ATP, but also for the ratchet mechanism which is believed to drive each individual KIF1A motor. We study the model by a combination of analytical and numerical techniques. A remarkable feature is that all parameters can be completely determined from experimental data. Our results in the dilute limit are in excellent quantitative agreement with the empirical data from single molecule experiments. In the high density regime the predictions of the model also agree qualitatively with the corresponding experimental observations. We derive a phase diagram that shows the influence of hydrolysis and Langmuir kinetics on the collective spatio-temporal organization of the motors. Finally, we provide experimental evidence for the existence of domain walls in our in-vitro experiment with fluorescently labeled KIF1A; these domain walls correspond to the shocks observed in the density profiles of our theoretical model.

AKB 21.2 Thu 11:00 ZEU 260

Multicriticality in a driven transport process on two coupled lanes — •Tobias Reichenbach, Thomas Franosch, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstrasse 37, D-80333 München, Germany

Intracellular transports constitute important examples of biological systems that exhibit interesting collective phenomena. Molecular motors, like myosin, kinesin, and dynein, move along cytoskeletal filaments. When considering a large assembly of such motors, their interaction gives rise to various phenomena.
One can study such transport processes on the basis of driven stochastic systems far from equilibrium. Boundary induced phase transitions and phase separation [1] are among the unexpected phenomena which arise. Here, we present a two-lane model that, incorporating these features, exhibits a rich variety of phases. Both first order and second order phase transitions arise. At their intersections, multicritical behaviour emerges. An analytical treatment is feasible via a mean field approach. We compare our results to Monte-Carlo simulations.
[1] A. Parmeggiani, T. Franosch, and E. Frey, Phys. Rev. Lett. 90, 086601 (2003)

AKB 21.3 Thu 11:15 ZEU 260

Traffic of molecular motors in the presence of obstacles — •Yan Chai, Stefan Klumpp, and Reinhard Lipowsky — Max Planck Institute for Colloids and Interfaces, Golm, Germany

The traffic of molecular motors along cytoskeletal filaments is studied theoretically using lattice gas models. These models describe the movements of a molecular motor along a filament as a biased random walk which is defined by a set of stepping probabilities for forward steps along the filament, binding to the filament and unbinding from the filament. We consider the case where obstacles such as lattice defects or additional proteins are present on the filament. We distinguish three basic types of defects, which differ from non-defect filament sites in only one of the motors' stepping parameters. We determine the motor current and density profiles using analytical calculations and Monte Carlo simulations.

AKB 21.4 Thu 11:30 ZEU 260

Traffic jams of molecular motors in tube-like compartments — •Melanie Müller, Stefan Klumpp, and Reinhard Lipowsky — Max-Planck-Institut für Kolloid- und Grenzflächenforschung, 14424 Potsdam

Processive molecular motors move along cytoskeletal filaments in a directed manner. However, even processive motors have only a finite walking distance after which they unbind from the filament and then undergo undirected diffusive motion in the surrounding aqueous solution. We consider theoretical models which map this interplay of directed and diffusive motion onto random walks on a lattice. Taking into account the mutual exclusion of the motors from the binding sites on the filament, this leads to variants of driven lattice gas models or exclusion processes, where the driving is localized to the filament.

Using analytical calculations and computer simulations, we obtain motor density and motor current profiles for several systems with different geometries. In particular, we study tube-like compartments which mimic the geometry of an axon. For high motor densities, the motors form traffic jams induced by their mutual exclusion, which leads to a reduction of the motor transport for high motor densities. The length of these traffic jams is determined as a function of the transport parameters of the motors.

AKB 21.5 Thu 11:45 ZEU 260

Driven diffusive gas of dimers: a model for molecular motors collective properties. — •Paolo Pierobon[1,2], Thomas Franosch[1,2], Mauro Mobilia[1], and Erwin Frey[1] — [1]Arnold Sommerfeld Center, Theresienstr.37, D-80333 Muenchen — [2]Hahn Meitner Institut, Glienicker str.100, D-14109 Berlin

One dimensional driven lattice gases have been extensively used to model traffic of molecular motors on microtubules. The standard model is the Totally Asymmetric Simple Exclusion Process (TASEP): a lattice gas model where particles move unidirectionally with a fixed rate and the flux depends on the entrance and exit rate. Inspired by recent models in intracellular transport, we discuss the properties of a TASEP of dimers (representing kinesins or dyneins) without particle conservation in the bulk (on/off kinetics). We investigate the phase diagram and the stationary average density profile by means of Monte Carlo simulations and rationalize the results through a refined mean field theory. We concentrate on experimentally measurable quantities and we investigate the effects of one defect in the lattice.

AKB 21.6 Thu 12:00 ZEU 260

Fluorescence Microscopy reveals the mechanistic details of nano-sized gene carrier transport in living cells — •Ralf Bausinger[1], Nadia Ruthardt[1], Karla de Bruin[1], Katharina von Gersdorff[2], Manfred Ogris[2], Ernst Wagner[2], Andreas Zumbusch[1], and Christoph Bräuchle[1] — [1]Department of Chemistry and Biochemistry, LMU München, Butenandtstr. 5-13, 81377 München — [2]Department of Pharmacy, LMU München, Butenandtstr. 5-13, 81377 München

Non-viral vectors consisting of the cationic polymer polyethyleneimine (PEI) and plasmid DNA are widely used for gene delivery into living cells. A detailed knowledge about the different stages which occur during the polyplex entry into the cell and its nucleus are prerequisite for further optimising the transfection process. We use highly sensitive fluorescence wide-field microscopy techniques to visualise the interaction of PEI/DNA polyplexes with the eGFP-labeled actin and tubulin cytoskeleton of living Huh-7 cells. Besides normal diffusion within the cell membrane we observe anomalous diffusion of the polyplexes due to their interaction with actin filaments as well as active directed transport along the microtubules [1]. In long-term experiments during mitosis we investigate the association of polyplexes to the spindle apparatus as a possible nuclear entry mechanism. We also compare the behaviour of these classical PEI/DNA polyplexes to more advanced non-viral vectors with polyethyleneglycol shielding and epidermal growth factor targeting.
[1] Bausinger et al., Angew. Chem., accepted

AKB 21.7 Thu 12:15 ZEU 260

Anomalous diffusion and viscoelasticity in living cells due to crowding — •Matthias Weiss and Gernot Guigas — Cellular Biophysics Group (BIOMS), Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 580, 69120 Heidelberg

Using fluorescence correlation spectroscopy (FCS) we show that (inert) macromolecules and gold beads exhibit anomalous diffusion in the cytoplasm and nucleoplasm of living cells. By accompanying these observations with model simulations and in vitro experiments it is demonstrated that this behavior is a generic consequence of 'molecular crowding' [1].

In other words, the anomality of the diffusion yields a quantifiable measure for the 'crowdedness' of a fluid on the molecular scale. Based on the observation of anomalous diffusion, we determine experimentally the 'nanorheology' of the cell's interior, i.e. we find that the cytoplasm and the nucleoplasm are strongly viscoelastic for frequencies above 1 kHZ with a typical elasticity of about 100 Pa.

[1] Weiss, Elsner, Kartberg, Nilsson, Biophys. J. **87**, 3518 (2004).

AKB 22 Sensory Biophysics and Signal Transduction

Time: Thursday 14:30–16:15 Room: ZEU 255

Invited Talk AKB 22.1 Thu 14:30 ZEU 255

Signal processing by clusters of membrane receptors — •T.A.J. Duke and I. Graham — Cavendish Laboratory, JJ Thompson Avenue, Cambridge CB3 0HE, UK

One of the main ways that cells receive information about their environment is through the equilibrium binding of ligand molecules to membrane receptors. Typically, ligand binding causes a change in receptor conformation that triggers a signal transduction cascade in the cell. We investigate the logical repertoire of clusters composed of homologous receptors that can bind more than one type of ligand and show that they are capable of quite sophisticated processing. All of the elementary logical functions can be implemented by appropriate tuning of the ligand binding energies and cooperative interactions between receptors can greatly enhance the sharpness of the response. Receptor clusters can therefore act as digital logical elements whose activity can be abruptly switched from fully inactive to fully active, as the concentrations of the regulators pass threshold values. We discuss a particular instance in which this type of protein logic appears to be used in signal transduction - the chemotaxis receptors of E. coli.

AKB 22.2 Thu 15:00 ZEU 255

Precision of Morphogen Gradients — •Tobias Bollenbach[1], Periklis Pantazis[2], Karsten Kruse[1], Marcos González-Gaitán[2], and Frank Jülicher[1] — [1]MPI for the Physics of Complex Systems, Nöthnitzerstr. 38, 01187 Dresden — [2]MPI for Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, 01307 Dresden

A fundamental problem in the field of animal development is to understand how well-defined cellular patterns can emerge in the presence of fluctuations. A well-established means of tissue patterning is given by morphogens. These are signaling molecules that spread from a restricted source into an adjacent target tissue forming a concentration gradient. The fate of cells in the target tissue is determined by the local concentration of such morphogens. In the presence of fluctuations, it is an important question how precise the positional information encoded in a morphogen gradient can be. Here, we investigate the precision of the gradient of the morphogen Dpp in the Drosophila wing disk both experimentally and theoretically. We measure the normalized fluctuations of the Dpp gradient as a function of the distance to the source. We find that these fluctuations grow monotonously for large distances to the source, while close to the source they can decrease. Our theoretical analysis reveals that cell-to-cell variability in the target tissue can generate the observed behavior of the fluctuations. This suggests that the concentration fluctuations in the gradient reflect the random components of intercellular signaling and transport.

AKB 22.3 Thu 15:15 ZEU 255

Polarized dynamics of individual G-protein coupled receptors in Dictyostelium chemotaxis. — •Thomas Schmidt[1], Sandra de Keijzer[1], Freek van Hemert[1], Herman Spaink[2], and Ewa Snaar-Jagalska[2] — [1]Physics of Life Processes, Leiden University — [2]Cell Biology, Leiden Univesity

Single molecule microscopy was used to unravel the role of the G-protein coupled cAMP receptor, cAR1, in establishing polarity during chemotaxis of living Dictyostelium discoideum cells. We analyzed the mobility of individual cAR1-eYFP under different physiological conditions. In all cells an immobile and a mobile receptor fraction was found. The latter increased from 38% to 54% at the anterior of chemotaxing cells. The mobile fraction was characterized by a diffusion constant D = 0.19 um2/s. The anterior/posterior mobility shift was neither caused by a difference in membrane viscosity nor by a conformational change of the receptor due to phosphorylation. Comparison with studies on Ga2-protein deficient cell lines allowed us to conclude that the mobility shift of the receptors at the leading edge resembles the uncoupling/activation of the Ga2-protein. Our data further suggest that the mobility shift is directly related to the primary amplification steps in chemotaxic signalling and leads to a straightforward molecular explanation of the parameters in current models.

AKB 22.4 Thu 15:30 ZEU 255

***Dictyostelium discoideum* Chemotaxis: Threshold for Directed Motion** — •Carsten Beta[1,2], Loling Song[1,3], Sharvari Nadkarni[1], Hendrik Boedeker[1,4], Albert Bae[1,2], Carl Franck[1], Wouter-Jan Rappel[5], William Loomis[6], and Eberhard Bodenschatz[1,2] — [1]LASSP, Department of Physics, Cornell University — [2]Max Planck Institute for Dynamics and Self-Organisation, Göttingen — [3]Harvard Medical School, Department of Cell Biology — [4]Institut für Angewandte Physik, WWU Münster — [5]Department of Physics, University of California at San Diego — [6]Division of Biological Sciences, University of California at San Diego

The chemotactic response of *Dictyostelium discoideum* cells to stationary, linear gradients of cyclic adenosine 3',5'-monophosphate (cAMP) was studied using microfluidic devices. In shallow gradients of less than $10^{-3}\,\mathrm{nM}/\mu\mathrm{m}$, the cells showed no directional response and exhibited a constant basal motility. In steeper gradients, cells moved up the gradient on average. The chemotactic speed and the motility increased with increasing steepness up to a plateau at around $10^{-1}\,\mathrm{nM}/\mu\mathrm{m}$. In very steep gradients, above $10\,\mathrm{nM}/\mu\mathrm{m}$, the cells lost directionality and the motility returned to the sub-threshold level. In the regime of optimal response the difference in receptor occupancy at the front and back of the cell is estimated to be only about 100 molecules.

AKB 22.5 Thu 15:45 ZEU 255

Chemotaxis in Microfluid Channels — •Danica Wyatt[1,2], Carsten Beta[1,2], Wouter-Jan Rappel[3], William Loomis[4], and Eberhard Bodenschatz[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Goettingen — [2]LASSP, Department of Physics, Cornell University — [3]Department of Physics, University of California at San Diego — [4]Division of Biological Sciences, University of California at San Diego

Directional sensing in eukaryotic cells has been subject of intensive research over the last decade. Much of this work has been done using the amoeba Dictyostelium discoideum as a model system. Dicty exhibits signaling pathways that appear to be well-conserved in mammalian chemotaxis. To investigate the dynamics of its signaling proteins, experiments must generate stimuli that can be controlled on the same time scale as the intracellular response. Also, it is essential to percisely characterize and manipulate the immediate chemical environment of a cell. Together, these requirements suggest an approach in which the chemoattractant is delivered directly to points of interest on the cell membrane. I will present microfluidic innovations for generating a variety of such stimuli and show how they led to observations of novel cell responses that could not be triggered by traditional experimental methods.

AKB 22.6 Thu 16:00 ZEU 255

PROCEEDINGS IN ODORANT RECEPTOR EXPRESSION: FROM CELLULAR SYSTEMS TOWARDS IN VITRO SYSTEMS — •Eva Sinner[1,2], Rudolf Robelek[1], Eva Lemker[2], Birgit Wiltschi[2], and Dieter Oesterhelt[2] — [1]MPI for Polymer Research , Ackermannweg 10, 55128 Mainz — [2]MPI for Biochemistry, Am Klopferspitz 18a, 82152 Martinsried

An in vitro strategy is now available to generate a platform for investigation of complex membrane proteins, such as odorant receptors. Coding for a complex membrane protein, an odorant receptor OR5 was used as challenging example to be inserted in an artificial planar lipid membrane system. We show the presence and orientation of resulting OR5 protein in the planar lipid membrane by tag-specific immuno- labelling in combination with surface plasmon enhanced fluorescence spectroscopy. Integration of the OR5 proteins are shown by radioactive labelling and a proof of function (specific ligand binding) is shown by surface enhanced infrared spectroscopy.

AKB 23 Photo-Biophysics

Time: Thursday 16:15–17:15 Room: ZEU 255

AKB 23.1 Thu 16:15 ZEU 255

Living Optical Fibers in the Vertebrate Retina — •Jochen Guck[1], Kristian Franze[1], Stefan Schinkinger[1], Jens Grosche[2], Ortrud Uckermann[2], Kort Travis[1], Detlev Schild[3], and Andreas Reichenbach[2] — [1]Insitute for Soft Matter Physics, Universität Leipzig — [2]Paul-Flechsig Institute for Brain Research, Universität Leipzig — [3]Department of Neurophysiology and Cellular Biophysics, Universität Göttingen

The retina of the vertebrate eye is inverted with respect to optical function. Light must pass through a significant thickness of scattering tissue before reaching the light-sensitive photoreceptor cells. We have investigated the retina as a phase object and could show that the retina contains optical fibers that guide light from the vitreous body through the scattering layers to the photoreceptor cells. These optical fibers are identified as Müller cells, which are radial glial cells spanning the entire thickness of the retina. For this we measured the transmission and scattering properties of Müller cells both in their natural matrix, applying confocal microscopy to eye-cup preparations and retinal whole-mounts, and as isolated cells, using a modified dual-beam laser trap. This finding ascribes a new function to glial cells and presents the inverted retina as an optical fiber phase-plate.

AKB 23.2 Thu 16:30 ZEU 255

Interactions of Biological Cells with Coherent Light — •Kort Travis and Jochen Guck — Universität Leipzig, Fakultät für Physik und Geowissenschaften, Abteilung Physik der weichen Materie; Linnéstrasse 5, 04103 Leipzig, Germany

Understanding near-field interactions of coherent infrared light with biological cells is critically important for modern optical manipulation and trapping applications, such as the optical stretcher or the optical tweezers. With respect to classical scattering theory, considerations of refractive index and size classify cells in the "anomalous diffraction" regime. Although there is significant published work applying numerical techniques such as the finite difference time domain (FDTD) technique to analyze these electrodynamic interactions, the use of higher order, more analytic techniques such as Mie theory, has been quite limited. In the present discussion, the system transfer operator (T-matrix) formalism is used to evaluate general features of optical fields in and around cells. Specifically, the discussion will cover: electrodynamic characteristics of all objects in this optical size range; effects of surface deviations from ideal shape; effects of the inclusion of large organelles such as the nucleus and mitochondria; and finally, effects associated with local inhomogeneities in the refractive index. Key points in the analytical discussion are illustrated with examples from numerical simulation and from experimental results.

AKB 23.3 Thu 16:45 ZEU 255

Single Molecule Spectroscopy of Light Harvesting Complexes — •Sebastian Mackowski, Stephan Wörmke, Christoph Jung, Andreas Zumbusch, Moritz Ehrl, and Christoph Bräuchle — Department Chemie, Ludwig-Maximilians Universität München, Butenandtstrasse 11, 81377 München, Germany

Light harvesting complexes are ideal candidates for studying the interactions between proteins and chromophores. One of the least known is peridinin-chlorophyll-protein (PCP) complex - a photosynthetic molecule composed of a barrel of hydrophobic protein, which shields two subunits each comprising of a single chlorophyll molecule dressed by four peridinin molecules, which are responsible for the light harvesting in the blue-green spectral range. Here we report on single molecule spectroscopy measurements of different types of light harvesting molecules. The experiments carried out at room temperature show that the wild type PCP complexes are quite unstable and they bleach out within several seconds. On the other hand, in order to observe ultranarrow zero-phonon-line emission of this complex at cryogenic temperatures we combined the recently developed vibronic excitation scheme with a solid immersion lens. In this way, the significant increase of the effective numerical aperture of collection optics enables us to monitor time- and energy scales of spectral jumps characteristic for single chromophore fluorescence. Detailed analysis of these spectral fluctuations should provide unique information about the interaction between the protein and the chlorophyll, and should shed light onto the energy landscape of this protein complex.

AKB 23.4 Thu 17:00 ZEU 255

Evaluation of a Possible Pathway for Ubiquinone Shutteling in the Photosynthetic Unit of the Purple Bacteria Rhodospirillum rubrum — •Andrew Aird[1], Carsten Tietz[1], Jörg Wrachtrup[1], and Klaus Schulten[2] — [1]3. Physikalisches Institut, Universität Stuttgart — [2]Theoretical and Computational Biophysics Group, University of Illinois at Urbana-Champaign

The core complex of the photosynthetic unit of the purple bacteria *Rhodospirillum rubrum* plays a cruical role in the conversion of light into chemical energy. In the reaction center a Quinone molecule functions as electron carrier to transport the electrons, created in the first step of photosynthesis, from the inside of the core complex to the Cytochrome bc_1-complex. The exact pathway of the Quinone molecule is still unknown. Molecular Dynamics Simulations of the shutteling of the Quinone molecule were performed to see if the molecule is able to diffuse through the closed LH1 ring.

AKB 24 Brownian Motion and Fluctuation Theorems

Time: Thursday 17:15–18:00 Room: ZEU 255

AKB 24.1 Thu 17:15 ZEU 255

Observation of nondiffusive Brownian motion of an isolated particle — •Sylvia Jeney[1], Branimir Lukic[1], Christian Tischer[2], Andrzej Kulik[1], Laszlo Forro[1], and Ernst-Ludwig Florin[3] — [1]Institut de Physique de la Matière Complexe, Ecole Polytechnique Fédérale de Lausanne, CH-1015 Lausanne, Switzerland — [2]European Molecular Biology Laboratory, Meyerhofstrasse 1, D-69117 Heidelberg, Germany — [3]Center for Nonlinear Dynamics, University of Texas, Austin, Texas 78712, USA

The thermal position fluctuations of a single micron-sized sphere immersed in a fluid were recorded by optical trapping interferometry with nanometer spatial and microsecond temporal resolution. We find, in accord with the theory of Brownian motion including hydrodynamic memory effects, that the transition from the ballistic to the diffusive motion is delayed to significantly longer times than predicted by the standard Langevin equation. This delay is a consequence of the inertia of the fluid. On the shortest time scales investigated, the sphere*s inertia has a small, but measurable, effect. Furthermore, our study gives insight on the particle's behavior, when confined in a harmonic potential. Surprisingly the hydrodynamic memory effects coming from the inertia of the fluid and the harmonic potential act at the same time scale for the studied system.

AKB 24.2 Thu 17:30 ZEU 255

Fluctuation-Dissipation Relations for Non-Equilibrium Steady States — •Thomas Speck and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57/III, 70550 Stuttgart

In non-equilibrium, the fluctuation-dissipation theorem (FDT) relating the response function of an observable with its auto-correlation is violated. This violation has been studied intensely, especially in the context of aging systems and glasses, where it allows to define an effective temperature. In the case of colloidal systems, the heat permanently dissipated in order to maintain the violation of detailed balance has been identified as "housekeeping" heat [1,2]. As the crucial ingredient, this heat involves two aspects of the velocity, namely the actual velocity and the *local* mean velocity. Studying a paradigmatic single colloidal particle moving in a periodic potential, we discuss the close connection between the violation of the velocity FDT and the violation of detailed balance. We derive an explicit expression for this violation and illustrate our results with numerical simulations.

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[2] T. Speck and U. Seifert, J. Phys. A: Math. Gen. **38**, L581 (2005)

AKB 24.3 Thu 17:45 ZEU 255

Short-time inertial response of viscoelastic fluids: observation of vortex propagation — •Maryam Atakhorrami[1], Gijsberta H. Koenderink[2], Daisuke Mizuno[1], Tanniemola Liverpool[3], Christoph F. Schmidt[1], and Frederick C. MacKintosh[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Division of Engineering and Applied Sciences, Harvard University, Cambridge, MA 02138, USA — [3]Department of Applied Mathematics, School of Mathematics, University of Leeds, Leeds, LS2 9JT, UK

We probe the response of viscous and viscoelastic fluids on micrometer and microsecond length and time scales using two optically trapped beads. In this way we resolve the flow field, which exhibits clear effects of fluid inertia. Specifically, we resolve the short time vortex flow and the corresponding motion of this vortex, which propagates diffusively for simple liquids. For viscoelastic fluids, this propagation is shown to be faster than diffusive and the displacement correlations reflect the frequency dependent shear modulus of the medium. The phenomenon is related to long-time tails in scattering experiments.

AKB 25 Cell Mechanics I

Time: Thursday 15:00–18:00 Room: ZEU 260

AKB 25.1 Thu 15:00 ZEU 260

F-actin bundle mechanical properties — •Mark Bathe[1], Mireille Claessens[2], Claus Heussinger[1], Andreas Bausch[2], and Erwin Frey[1] — [1]Ludwig-Maximilians-Universitaet Muenchen — [2]Technische Universitaet Muenchen

Animal cells express a myriad of actin-binding proteins (ABPs) that associate with Filamentous actin (F-actin) to form stiff bundles in vivo. The physiological function of F-actin bundles varies from passive mechanical structures such as microvilli present on the surface of epithelial cells in the intestinal lining to active structures such as filopodia formed at the leading edge of cells during migration.

A biomimetic emulsion technique, recently introduced by our lab, has been used to measure directly the bending stiffness of isolated F-actin bundles associated with biologically-relevant ABPs. Results demonstrate that bundle stiffness depends sensitively on the number of actin filaments constituting the bundle, bundle length, and ABP type and concentration. Here, we use a combination of molecular simulation and analytical theory to elucidate the origin of the observed bundle mechanical properties. We also determine for the first time the molecular stiffnesses of the various ABPs examined.

AKB 25.2 Thu 15:15 ZEU 260

Phase behaviour and micro-mechanical properties of crosslinked actin-networks — •Oliver Lieleg and Andreas R. Bausch — Lehrstuhl für Biophysik E22, Physik-Department, Technische Universität München, D-85747 Garching, Deutschland

Cell shape, mechanics and motility are mainly determined by crosslinked actin-networks. Despite their importance, the mechanical function of crosslinking molecules is not well understood. As in living cells many different actin crosslinking molecules are used simultaneously, it is necessary to study their effect in in vitro systems. Here two structural related crosslinking molecules are compared: α-actinin and I-plastin. Their effect on the structure and mechanics of in vitro actin networks is investigated. Actin networks crosslinked by α-actinin or I-plastin show pronounced differences in their elastic properties as a function of the crosslinker-to-actin-ratio. Interestingly, these differences are observed although both crosslinking molecules use the same calmodulin-homologous domain for actin binding. For both systems at least three distinct phases of actin-networks with different viscoelastic properties are observed. By rheological and optical methods these are related to the microscopic structure of the networks. The occurrence of mixed networks containing bundles embedded in an isotropic network indicates that a sharp distinction between crosslinking and bundling proteins might be artificial and multiple phases could also be possible for other actin-crosslinking proteins.

AKB 25.3 Thu 15:30 ZEU 260

Nonlinear mechanical properties of entangled and cross linked actin networks — •Christine Semmrich, Rainer Tharmann, Bernd Wagner, and Andreas R. Bausch — Lehrstuhl für Biophysik E22, Physik-Department, Technische Universität München,D-85747 Garching, Deutschland

The mechanical response of cells is predominantly determined by the actin cytoskeleton. The nonlinear behaviour of crosslinked network show a pronounced dependence on the applied stresses spanning orders of magnitude in their elastic response. This can be related to the nonlinear mechanical behaviour of single filaments of this semiflexible polymer. In contrast, for purely entangled networks a tube model describes the mechanical response and thus no strain hardening is expected. By means of different rheological approaches we are able to investigate the nonlinear response of purely entangled actin networks. Interestingly, under standard conditions a strain hardening at temperatures below 23°C is observed. Highering the temperature, a strain softening occurs. The temperature dependence of the nonlinear behaviour is also highly dependent on the buffer salt concentration. This suggests that the interaction potential between filaments plays an important role for the observed behaviour. We discuss these results within theoretical predictions of entangled and crosslinked networks.

AKB 25.4 Thu 15:45 ZEU 260

Non-Affine Deformations: "elementary excitations" for the elasticity of random fiber networks — •Claus Heussinger and Erwin Frey — LMU Munich, Arnold-Sommerfeld-Zentrum, Theresienstr. 37, 80333 München

We numerically study the elasticity of random fibrous networks in two dimensions. Highly non-affine deformations on the scale of the single fiber are found to lead to anomalous elastic properties even on the macroscopic scale. This has to be contrasted with classical elasticity theory where material elements deform in an affine way and microstructure is not accounted for.

We identify the characteristic features of the microscopic deformation field and provide a scaling argument that allows the calculation of macroscopic quantities like the shear modulus.

Our work highlights the importance of architecture to the elastic response of fibrous structures and applies to diverse physical systems ranging from paper sheets to biological networks of semiflexible polymers like the cytoskeleton.

AKB 25.5 Thu 16:00 ZEU 260

Active and passive one- and two-particle microrheology in cytosksletal networks — •Daisuke Mizuno, Frederick C. MacKintosh, and Christoph F. Schmidt — Dept. Physics, Vrije Universiteit, Amsterdam, NL

We have developed a microrheology (MR) technique that uses micron sized particles to probe the viscoelastic properties of soft samples on small length scales and with high bandwidth. This can be done passively, by observing the Brownian fluctuations of particles embedded in the medium to be tested, or actively by moving the particle with a known force. One can measure the frequency dependent response of one particle on a force on it, or the response of a second particle to a force on the first. The latter (2-particle MR) makes it possible to get around surface artefacts. One can also measure response by actively moving a particle (n our case with an aousto-optic modulator) and observing the corresponding response. Comparison of active and passive experiments provides a test of the fluctuation-disspation theorem. We demonstrate agreement between the techniques in various samples including actin gels as long as samples are in equilibrium.

AKB 25.6 Thu 16:15 ZEU 260

High-frequency stress relaxation in semiflexible polymer solutions and networks — •Gijsberta H. Koenderink[1], Maryam Atakhorrami[2], Frederick C. MacKintosh[2], and Christoph F. Schmidt[2] — [1]Division of Engineering and Applied Sciences, Harvard University, Cambridge, USA — [2]Dept. Physics, Vrije Universiteit, Amsterdam, NL

We measure the linear viscoelasticity of sterically entangled as well as chemically crosslinked networks of actin filaments over more than five decades of frequency. The high-frequency response reveals rich dynamics unique to semiflexible polymers, in particular a previously unobserved relaxation due to rapid axial tension propagation. For high molecular

weight, and for crosslinked gels, we obtain quantitative agreement with theoretical predictions of the shear modulus in both amplitude and frequency dependence.

AKB 25.7 Thu 16:30 ZEU 260

Cytoskeletal mechanics and dynamics in living cells — •Carina Raupach, Philip Kollmannsberger, Johannes Pauli, Claudia Mierke, and Ben Fabry — Zentrum für Medizinische Physik und Technik, Henkestr. 91, 91054 Erlangen

Cytoskeletal (CSK) mechanics and dynamics are important for essential processes in living cells including crawling, division, and mechanochemical signal transduction. Here we measured the creep-response (passive mechanics) of subconfluent human vascular endothelial cells (HUVEC) and different human cancer cell lines. Step forces of ∼1 nN were generated with magnetic tweezers acting on superparamagnetic, fibronectin-coated beads bound to the cytoskeleton via cell adhesion receptors (integrins). We also measured the spontaneous motion of these beads (dynamics) and computed their autocorrelation function (AC). The AC displayed diffusive behaviour at short time scales (< 1 s) and superdiffusive behaviour at longer time scales that was well described by a power law: $AC(t) = \alpha \cdot (\frac{t}{t_0})^{\beta}$. The creep response γ also followed a power law: $\gamma(t) = a \cdot (\frac{t}{t_0})^{b}$. We found a significant ($p < 0.01$) correlation between α and a, but not between the power-law exponents β and b. These data suggest that different mechanisms give rise to power-law rheology and power-law superdiffusivity.

AKB 25.8 Thu 16:45 ZEU 260

Osmotically Driven Shape Instability in Axons — •Pramod Pullarkat[1], Paul Dommersnes[2], Pablo Fernandez[1], Jean-François Joanny[2], and Albrecht Ott[1] — [1]Experimentalphysik I, University of Bayreuth,*D-95440, Bayreuth, Germany — [2]Institut Curie, UMR 168, 26 rue d'Ulm, F-75248, Paris Cedex 05, France

We report a cylindrical–peristaltic shape transformation occurring in axons exposed to a controlled osmotic perturbation. The peristaltic shape relaxes and the axon recovers its original geometry within minutes. Using a flow chamber technique, we show that the shape instability depends critically on swelling rate and that volume and membrane area regulation are responsible for the shape relaxation. We propose that volume regulation occurs via leakage of ions driven by elastic pressure, and present an analysis for the peristaltic shape dynamics taking into account the internal structure of the axon. The results obtained provide a framework for understanding peristaltic shape dynamics in nerve fibers occurring *in vivo*.

AKB 25.9 Thu 17:00 ZEU 260

Quantitative force measurements during cystogenesis — •Jens Ulmer[1], Aldo Ferrari[2], Ruth Kroschewski[2], and Joachim Spatz[1] — [1]Max-Planck-Institute for Metals Research, Heisenbergstr. 3, 70569 Stuttgart, Germany — [2]Institut f. Biochemie, Schafmattstr. 18, ETH-Hoenggerberg, CH-8093 Zuerich

Adhesion of cells to the extracellular matrix (ECM) is a crucial event in developing multi-cellular organism. It can modulate cellular processes such as cell growth, differentiation, apoptosis and is mediating epithelial morphogenesis through mechanical interactions between cells and the ECM network. We studied cyst formation of Madin-Darby Canine Kidney (MDCK) cells in a three-dimensional (3D) culture connected to a force sensitive surface. Microfabricated PDMS posts, which have a post height dependent spring constant between 0.2-0.04N/m were developed in order to obtained cell exerted forces during cystogenesis. Further on it was shown that anisotropic vicinity can alter cyst morphology from spherical to tubular like structures. With the biomimetic capabilities of the microfabricated arrays it should be possible to provide a more natural environment for epithelial cells, combined with the ability to measure quantitative forces from multicellular structures during development.

AKB 25.10 Thu 17:15 ZEU 260

Micromechanics of the pericellular matrix — •Jennifer Curtis[1,2], Heike Boehm[1,2], Christian Schmitz[1,2], Ralf Richter[1,2], and Joachim Spatz[1,2] — [1]University of Heidelberg, Department of Biophysical Chemistry, INF 253, D-69120 Heidelberg — [2]Max-Planck-Institute for Metals Research, Department New Materials & Biosystems, Heisenbergstr. 3, D-70569 Stuttgart

In recent years, much attention has been directed towards the properties and activities of the cell surface. In particular, the coupling of the membrane to the underlying protein polymer network called the actin cortex, plays an important role in many events. The other side of the cell surface is less studied, although it too often has a bound polymer network comprised of gigantic cross-linked polysaccharides (sugars). Called the pericellular matrix (PCM), it is associated with many cells including fibroblasts, chondrocytes, endothelial and smooth muscle cells. Its thickness can vary from 10's of nanometers to 10 microns and it is associated with adhesion dependent events like migration and mitosis. Biologists often hypothesize that its viscoelastic properties are responsible for modulating adhesion activities. To investigate this idea, we measure the PCM's viscoelasticity using microrheology and probe the sharpness of its edge and its mesh size. The elastic modulus of the PCM under different condition is determined, and we characterize the long, elastic cables that can be pulled from the PCM. These results are compared with an externally reconstituted model PCM on the cell surface.

AKB 25.11 Thu 17:30 ZEU 260

Force Generation during Tumor Cell Invasion in Three-Dimensional Collagen Gels — •Thorsten Koch, Johannes Pauli, Claudia Mierke, and Ben Fabry — Friedrich-Alexander-Universität Erlangen-Nürnberg - Zentrum für Medizinische Physik und Technik - Lehrstuhl für Physikalisch-Medizinische Technik - Henkestraße 91 - D-91052 Erlangen

Tumor cells exert forces on surrounding tissue during invasion, but the magnitudes of these forces are unknown. We measured forces during invasion by extending methods for 2-D traction microscopy to 3-D. We used collagen gels ($E = 300$ Pa) to provide an *in vitro* environment for tumor cell invasion. MDA-MB-231 breast cancer cells were plated on the gel surface and allowed to invade for two days. Cells assumed a spindle-shaped morphology and contracted the gel mainly along their primary axis. To quantify gel contraction, fluorescent beads serving as fiducial markers were embedded in the gels. The 3-D bead positions were determined with a center-of-mass algorithm applied to images taken at various focal depths. To obtain the undeformed state of the gels, we disrupted the actin cytoskeleton and hence force transmission by treatment with cytochalasin-D (4 μM). We then calculated the dipole moment of the cells from the bead displacements between the initial and cytochalasin-D treated states. The magnitudes of dipole moments were on the order of 10^{-12} Nm, comparable to those generated by maximally contracted smooth muscle cells in 2-D culture (Butler JP et al., Am J Physiol Cell Physiol 282:C595, 2002). Our results show that MDA-MB-231 tumor cells exert substantial forces on surrounding tissue during invasion.

AKB 25.12 Thu 17:45 ZEU 260

Cell Characterization by Optical Deformability — •Stefan Schinkinger, Falk Wottawah, Bryan Lincoln, Franziska Lautenschlaeger, and Jochen Guck — Universitaet Leipzig; Institut fuer Experimentelle Physik I, Abt. PWM; Linnestrasse 5, 04103 Leipzig

In an optical stretcher, infrared laser light is used to exert surface stress on biological cells, causing an elongation of the trapped cell body along the laser beam axis. These optically induced deformations allow rheological measurements of individual cells and characterization by their optical deformability. Analyzing the deformation behavior of various cancer cell lines and primary stem cells, significant differences in axial elongation to control populations, even for small sample sizes, are measurable. It is shown that differentiation of stem cells and functional de-differentiation in different states of cancer progression allows to be classified with the optical stretcher, as functional and mechanical properties are strongly connected. When integrated within a microfluidic chamber delivering cells into the trap high throughput rates are possible. That way this technique allows measurement of statistically significant numbers of cells within short time. This enables for diagnosis of diseases, on a cellular level, that are associated with cytoskeletal processes. Additionally, the characterization of differentiation states during cell maturation ultimately allows sorting of cells with high accuracy in a non-contact manner.

AKB 26 Cellular Computation and Gene Regulation

Time: Friday 11:00–12:00 Room: ZEU 255

Invited Talk AKB 26.1 Fri 11:00 ZEU 255

The physics of cellular computation — •Pieter Rein ten Wolde — FOM Institute for Atomic and Molecular Physics (AMOLF), Kruislaan 407, 1098 SJ, Amsterdam, The Netherlands

Gene regulatory networks are the central processing units of life. They orchestrate cell development, control the cell cycle and allow the cell to integrate different signals and thereby allow the cell to recognize patters in, for instance, the food supply of the organism. While gene regulatory networks can perform computations analogous to electronic circuits, their design principles are markedly different. We use database analyses, theory and computer simulations to unravel the design principles of gene regulatory networks. We show that the molecular character of the components makes gene regulatory networks intrinsically stochastic and thus prone to biochemical noise, yet also allow them to process information in a very sophisticated manner.

AKB 26.2 Fri 11:30 ZEU 255

Optimal target search on a fast folding DNA with volume exchange — •Ralf Metzler, Michael Lomholt, and Tobias Ambjoernsson — NORDITA, Blegdamsvej 17, DK-2100 Copenhagen

We study the search process of a target on a rapidly folding DNA by an ensemble of proteins, whose search combines 1D diffusion along the chain, Lévy type diffusion [1] mediated by chain looping, and volume exchange. A rich behavior of the search process is obtained with respect to the physical parameters, in particular, for the optimal search. Thus, it turns out that the Lévy search component leads to much more efficient target search and under certain conditions renders 3D volume diffusion obsolete [2]. The model includes the special cases of the 'standard' 3D/1D exchange [3] as well as pure 1D search [4]. The model is expected to pertain to typical in vivo studies of genetic regulation, and predicts significantly higher targeting rates than previous models. It is suggested that the Lévy contribution can be studied experimentally under low salt conditions disfavouring protein unbinding from the DNA.

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AKB 26.3 Fri 11:45 ZEU 255

Stepwise bending of DNA by a single TATA-box Binding Protein — •Simon F. Tolic-Norrelykke[1,2,3], Mette B. Rasmussen[2], Francesco S. Pavone[3], Kirstine Berg-Sorensen[2,4], and Lene B. Oddershede[2] — [1]Max-Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]The Niels Bohr Institute, DK-2100 Copenhagen O, Denmark — [3]European Laboratory for Non-linear Spectroscopy, 50019 Sesto Fiorentino (Fl), Italy — [4]Dept. of Physics, Technical University of Denmark, DK-2800, Kgs. Lyngby, Denmark

The TATA-box binding protein (TBP) is required by all three eukaryotic RNA polymerases for the initiation of transcription from most promoters. TBP recognizes, binds to, and bends promoter sequences called "TATA-boxes" in the DNA. We present results from the study of individual Saccharomyces cerevisiae TBPs interacting with single DNA molecules containing a TATA-box. Using video microscopy, we observed the Brownian motion of beads tethered by short surface-bound DNA. When TBP binds to and bends the DNA, the conformation of the DNA changes and the amplitude of Brownian motion of the tethered bead is reduced compared to that of unbent DNA. We detected individual binding and dissociation events and derived kinetic parameters for the process. Dissociation was induced by increasing the salt concentration or by directly pulling on the tethered bead using optical tweezers. In addition to the well defined free and bound classes of Brownian motion we observed another two classes of motion. These extra classes were identified with intermediate states on a three-step, linear, binding pathway. Biological implications of the intermediate states are discussed.

AKB 27 Cell Mechanics II

Time: Friday 11:30–13:00 Room: ZEU 260

AKB 27.1 Fri 11:30 ZEU 260

Investigating phagocytosis by optical tweezers-based microscopy — •Holger Kress[1], Ernst H.K. Stelzer[1], Gareth Griffiths[1], and Alexander Rohrbach[2] — [1]European Molecular Biology Laboratory (EMBL), Meyerhofstr. 1, 69117 Heidelberg, Germany — [2]Institute of Microsystem Technology (IMTEK), University of Freiburg, Georges-Köhler-Allee 102, 79110 Freiburg, Germany

Phagocytosis is a central cellular mechanism in the innate mammalian immune system. When an invading bacterium binds to the membrane of a macrophage cell, the cell membrane starts to wrap around the invader and internalizes the bacterium. Thereby, the bacterium is enclosed into an intracellular membrane-organelle, the phagosome.

Coated latex beads are used as bacterial model systems to investigate phagocytosis by optical tweezers-based photonic force microscopy. The motion of an optically trapped bead is tracked interferometrically in 3D with nanometer precision at a microsecond timescale. Measuring the thermal fluctuations of a trapped bead during the binding to the cell membrane provides information about the dynamics of the binding process. Once the bead is bound to the cell, the motion of the bound bead reveals the mechanical cellular response to the binding event. Here the optical trap serves as a mechanical force transducer and also as an indicator of the cellular forces. After the bead is taken up by the cell, the phagosome is tracked in 3D during its intracellular transport. We found stepwise intracellular transport with a step size of about 36 nm indicating single molecular motor activity.

AKB 27.2 Fri 11:45 ZEU 260

Viscoelastic Properties of Glial Cells and Neurons — •Yun Bi Lu[1,2], Kristian Franze[2], Josef Käs[2], and Andreas Reichenbach[1] — [1]Paul-Flechsig-Institut für Hirnforschung, Universität Leipzig, Jahnallee 59, 04109 Leipzig, Deutschland — [2]Abteilung Physik Weicher Materie, Universität Leipzig, Linnéstr.5, 04103 Leipzig, Deutschland

To achieve a better understanding of the physical support function of glia (meaning 'glue'), we investigate the mechanical properties of glial cells and neurons by using atomic force microscope. Müller cells, the principal glial cells of the retina, are the only cells spanning its entire thickness. We investigated the viscoelastic properties of different parts along Müller cells (endfoot, inner process, soma and outer process) and of bipolar cell (i.e., neuronal) somata. The results showed that Müller cell somata are more elastic (i.e., stiffer) than their processes and endfeet. If compared to bipolar cell somata, Müller cell somata were shown to be less elastic (i.e., softer). For both cell types, the ratio of elastic part to viscous part of the response was above 1, which means that their biomechanics are dominated by elastic rather than viscous properties. We performed similar measurements on astrocytes (glial cells) and pyramidal cells (neurons) isolated from brain hippocampus. The astrocytes were found to be less elastic than the pyramidal cells, and both cell types displayed dominant elastic properties. In conclusion, we suggest that glial cells are softer than neurons, and both cell types are elastic rather than viscous. This means that glial cells are neither 'glue' nor 'support cells'; most likely, they constitute very soft 'springs' generating an optimal substrate for neuronal cell process growth and plasticity.

AKB 27.3 Fri 12:00 ZEU 260

Investigating the Minimuscle — •Dan Strehle, Brian Gentry, Michael Gögler, David Smith, Katja Taute, and Josef Käs — Soft Matter Physics, Universität Leipzig, Linnéstraße 5, 04103 Leipzig

Skeletal muscle cells are made up of sarcomeres which align to form myofibrils. Myofibrils are the essential component of the muscular contraction mechanism. Its operation is determined by the interaction of actin filaments and myosin mini-filaments. Single myosin proteins have been extensively studied with optical tweezers. We are investigating the properties of the entire contraction structure. Thin actin bundles attached to polystyrene beads are exposed to myosin mini-filaments in ATP-depleted conditions. Upon addition of ATP myosin starts operating and the movement of the beads held in optical tweezers is observed.

AKB 27.4 Fri 12:15 ZEU 260

Cell spreading as a viability test for cells deformed in the Microfluidic Optical Stretcher — •Franziska Wetzel, Brian Lincoln, Jochen Guck, and Josef Käs — Universität Leipzig, Fakultät für Physik und Geowissenschaften, Abteilung Physik der weichen Materie, Linnestrasse 5, 04103 Leipzig

A Microfluidic Optical Stretcher (MOS) is a two-beam laser trap where individual suspended cells are deformed by optical forces on the cell surface. The MOS can be used to distinguish and sort cells. To enable subsequent analysis it is essential that the cells are not damaged during this process. Therefore we investigated the impact of optical stretching using cell spreading which, being an active actin- and myosin-dependent process accomplished only by vital cells, is an ideal indicator for viability. Powers and duration times in a range typical for stretch experiments were applied on NIH/3T3 cells (mouse embryonic fibroblast cell line). Ambient temperature was set to 37°C to keep cells as close to culture conditions as possible. In the talk we will show that cells can spread after the application of optomechanical stress. Conclusively, cells remain viable in the MOS and, in consequence, the MOS can be used to sort cells (e.g. stem cells) for further analysis or culture.

AKB 27.5 Fri 12:30 ZEU 260

Diagnosing oral epithelial carcinomas by elasticity-based flow cytometry — •Falk Wottawah, Julia Dietrich, Stefan Schinkinger, Bryan Lincoln, Franziska Lautenschlaeger, Susanne Ebert, and Jochen Guck — Fakultaet fuer Physik und Geowissenschaften, Universitaet Leipzig

Despite recent advances in identifying the genetic and proteomic patterns characteristically altered in cancers and related to different stages of cancer, it is difficult, if not impossible, to use this information as biomarker for distinguishing individual cells. Polymer physics offers a much more general and unifying approach based on known molecular changes in the cytoskeleton, and its importance for the mechanical properties of the cell, during the progression of cancer. By measuring cellular deformability as a characteristic, cumulative marker of the various molecular changes using a microfluidic optical stretcher, it is possible to monitor the progression of diseases that affect the cytoskeleton, such as cancer. We establish the applicability of this innovative approach by using small sample sizes for diagnosing oral epithelial carcinomas in a clinical setting.

AKB 27.6 Fri 12:45 ZEU 260

Viscoelasticity and motility of murine fibroblasts transfected with additional filamin and actin measured with AFM-based microrheology technique — •Karla Mueller, Claudia Brunner, Bernd Kohlstrunk, Jens Gerdelmann, and Josef A. Kaes — Institut für Experimentelle Physik I, Physik der weichen Materie, Universität Leipzig, Linnestr 5, 04103 Leipzig

Malignantly transformed SVT-2 fibroblasts exhibit enhanced motility of the lamellipodium and decreased viscoelastic strength compared to normal fibroblasts. These properties are the result of an altered cytoskeleton. SVT-2 serve as a model cell line for cancer cells with a high metastatic potential. We present our efforts to reduce malignant cell motility by the insertion of additional cytoskeletal components with the goal to find a way to stop cancer metastasis. We transfected SVT-2 with actin to increase the number of filaments and filamin to increase the crosslinker density and probed the cell lines for their viscoelastic behaviour using the AFM microrheology technique as well as for the speed of lamellipodial extension.

AKB 28 Single Molecule Probes

Time: Friday 12:00–13:00 Room: ZEU 255

AKB 28.1 Fri 12:00 ZEU 255

Optical trapping and tracking: novel approaches in cell biophysics — •Alexander Rohrbach[1,2] and Holger Kress[2] — [1]Institute of Microsystem Technology (IMTEK), University of Freiburg, Georges-Köhler-Allee 102, 79110 Freiburg — [2]European Molecular Biology Laboratory (EMBL), Meyerhofstrasse 1, 69117 Heidelberg

Optical micromanipulation has open new possibilities for investigating infrequent events. Especially optical traps allow increasing the interaction probability between interacting partners. Energy fluctuations and diffusion are maintained inside the optical trap, enabling a natural dynamic interaction, which is not given e.g. in AFM experiments. However, only a fast and precise three-dimensional detection system allows measuring the broad spectrum of interaction dynamics. Although holographic traps enable fascinating possibilities of optical manipulation, particle tracking and thus measurements are strongly limited in speed and precision. This drawback can be overcome with e.g. scanning optical traps. In this talk I demonstrate, how fluctuation dominated processes in cell biology can be controlled and measured with nanometer precision and at a rate of 1 kHz to 1 Mhz. On the one hand, the uptake, binding and intracellular transport of particles to/in macrophages are investigated. On the other hand, a complete helical bacterium (a 200 nm thin spiroplasm) is oriented and tracked interferometrically in a scanning optical trap. This allows new insights into the complex flexing and rotation dynamics of this simplest form of life.

AKB 28.2 Fri 12:15 ZEU 255

Theoretical analysis of single-molecule force spectroscopy experiments: heterogeneity of chemical bonds — •Peter Reimann and Martin Raible — Universitaet Bielefeld

We show that the standard theoretical framework in single-molecule force spectroscopy by Evans and Ritchie [Biophys. J. 72, 1541 (1997)] has to be extended in order to consistently describe the experimental findings. The basic new concept is to take into account heterogeneity of the chemical bonds, resulting in excellent agreement between theory and experiment.

AKB 28.3 Fri 12:30 ZEU 255

A Combined Setup for Single Molecule Manipulation and Optical Spectroscopy — •Volker Walhorn, Rainer Eckel, Christoph Pelargus, Joerg Martini, Dario Anselmetti, and Robert Ros — Experimental Biophysics, Physics Department, Bielefeld University, Germany

Atomic force microscopy (AFM) as well as fluorescence microscopy (FM) are both intensively used techniques to elucidate interactions, dynamics and structures of single biomolecules. Synchronous fluorescence- and atomic force microscopy allow diverse new approaches in single molecule techniques. We present our novel setup capable of simultaneously performing total internal reflection fluorescence microscopy (TIRFM) and atomic force microscopy/spectroscopy. For topographical or force readout a home-built AFM head is mounted on an inverted optical microscope equipped with a TIRFM objective, significantly reducing background noise. Spectral information is obtained by excitation with an Ar+ laser and fluorescence detection with a high speed CCD camera. Temporal and spatial correlation of topographical, force and fluorescence data can yield important information of the dynamics and molecular mechanisms of guest-host-interactions as well as protein folding pathways.

AKB 28.4 Fri 12:45 ZEU 255

Metal coated full body glass tips as high resolution probes for SNOM fluorescence imaging — •Heinrich Gotthard Frey[1], Carsten Bolwien[2], Robert Ros[1], and Dario Anselmetti[1] — [1]Experimentelle Biophysik und angewandte Nanowissenschaften, Fakultät für Physik, Universität Bielefeld, Universitätsstraße 25, 33615 Bielefeld — [2]Frauenhofer-Institut für Physikalische Messtechnik IPM, Heidenhofstraße 8, 79110 Freiburg

For biological applications, scanning near-field optical microscopy of single fluorescent dye molecules require probes which combine high near-field intensities with high optical and topographical resolution.

Such probes can be realised by full body glass tips completely covered by a thin metal layer. In order to achieve strong fields at the tip apex, it is important to illuminate the tip under an inclination angle with the polarisation parallel to the inclination plane. Optimised values for metal layer thickness and inclination angle have been investigated by multiple multipole simulation showing that the achievable optical resolution is roughly given by the tip radius.

These probes have been tested by imaging single fluorescent dye molecules. They show fluorescence patterns with one or two peaks, which can be explained by means of the electrical field distribution at the tip apex. For an aluminium coated tip with 25 nm tip radius, the fluorescence patterns have peaks with a full width half maximum of about 15 nm.

This optical probe is especially suited for cantilever probes, where the inclined illumination can easily be realised.

AKB 30 Poster Session I

Time: Monday 15:30–18:00 Room: P1

AKB 30.1 Mon 15:30 P1

Effects of Foraging Dynamics on Food-web Topology and Stability — •Satoshi Uchida and Barbara Drossel — Institut für Festkörperphysik, TU Darmstadt, Hochschulstr. 6, D-64289 Darmstadt, Germany

We investigate dynamic food web models including both population dynamics and foraging dynamics. The population dynamics determines the population density of each species, and the foraging dynamics describes the adaptation of individuals to the abundacies of their prey, given a limited total search time. We explain that the topology and stability of the resulting food webs are strongly influenced by the foraging dynamics, and are much less sensitive to the types of functional responses in the population dynamics (Lotka-Volterra, Holling or Beddington type). In particular, we see that the nature of the constraints on foraging behavior is crucial to the web structure and stability. It is known that with conventional linear constraints, the resulting food webs are more stable than simple model food webs including only population dynamics, in the sense that species are less likely to become extinct. However, at the same time adaptive dynamics introduces a strong constraint on the topology of webs, namely that the number of visible links must be smaller than twice the number of species. If we take into account in the model that a predator can feed on accidentally encountered species that are similar to the one it is searching for, which leads to nonlinear constraints, the resulting food webs are stable and have more links.

AKB 30.2 Mon 15:30 P1

Structural characterization of recombinant spider silk protein films immobilized to solid surface — •Ezzeldin Metwalli[1], Ute Slotta[2], Thomas Scheibel[2], and Christine Papadakis[1] — [1]Physikdepartment E13, Technische Universität München, James-Franck-Str. 1, 85747 Garching, Germany. — [2]Chemiedepartment, Lehrstuhl für Biotechnologie, Technische Universität München, Lichtenbergstr. 4, 85747 Garching, Germany.

Mapping the conformational alterations associated with protein adsorption to solid surfaces is important for some applications such as biosensors and chromatographic separations. Recombinant spider silk protein is chosen for our investigation because of excellent mechanical properties, biocompatibility and biodegradability of silk-based materials. A circular dichroism (CD) study [1] on biosynthesized spider silk protein film immobilized to solid surface indicates conformational changes from alfa-helix to beta-sheet structure upon chemical treatment with either methanol or phosphate buffer. Using grazing-incidence small-angle x-ray scattering (GISAXS), the structure of the protein layer before and after the chemical treatments was investigated. This technique provides structural information on a large range of length scales from a few nm up to few microns which helps to characterize the structure of the attached protein layer in relation to the conformational alterations. The 2D GISAXS images of treated versus untreated protein films shows drastic structural variations which is in agreement with the formation of a beta-sheet rich layer upon chemical treatment. [1] D. Huemmerich, U. Slotta, T. Scheibel, Applied Physics A, In press 2005.

AKB 30.3 Mon 15:30 P1

High resolution imaging of dsDNA by means of scanning tunneling microscopy — •Mihail Brezeanu, Frank Hubenthal, and Frank Träger — Institut für Physik and Center for Interdisciplinary Nanostructure Science and Technology - CINSaT, Universität Kassel, Germany

Scanning probe microscopies (SPM) are versatile tools to image the structure of biomolecules, but only scanning tunneling microscopy (STM) provides the possibility of achieving molecular resolution. In recent years, progress has been made to develop new preparation methods for visualizing DNA molecules with high resolution. However, successful imaging of the molecular structure of DNA has remained a challenge. In this contribution we present our latest results of high resolution imaging of DNA molecules by means of STM, the motivation being to visualize DNA damage induced by heavy ion bombardment for cancer treatment. For this purpose, linear double stranded DNA (dsDNA) with 280 base pairs (bp) has been deposited on highly oriented pyrolytic graphite (HOPG) and subsequently investigated with our CP-R Scanning Probe Microscope. The measurements were carried out under ambient conditions at a humidity of 50% to increase the conductivity. Our images show very clearly the helical turns of the DNA molecules, having a smaller height and larger width than usual. Nevertheless, the calculated circumference agrees well with the parameters normal DNA. Further analysis of DNA on different substrates, as well as further improvement of the resolution are in progress.

AKB 30.4 Mon 15:30 P1

Studying Slow Membrane Dynamics with Continuous Wave Scanning Fluorescence Correlation Spectroscopy — •Jonas Ries and Petra Schwille — TU Dresden, Biophysik, Tatzberg 47-51, 01307 Dresden

Two Photon Scanning Fluorescence Correlation Spectroscopy (SFCS) has been shown to be a useful technique to analyze the dynamics of model membranes (GUVs). Here we discuss the application of SFCS using continuous wave excitation. The improved countrate enables the study of very slow diffusion in model membranes and cells as well as parameter-free determination of diffusion constants using two foci fluorescence cross correlation spectroscopy. Two color fluorescence cross correlation spectroscopy with continuous or pulsed interleaved excitation (PIE) allows binding studies on membranes. Reduction of photobleaching, reproducibility and stability compared to traditional FCS on membranes and the simple implementation in a commercial microscopy setup make SFCS a valuable addition to the pool of fluorescence fluctuation techniques.

AKB 30.5 Mon 15:30 P1

Towards Nanotomography of Bovine Bones — •Stephanie Röper, Nicolaus Rehse, Heidemarie Teichmann, and Robert Magerle — Chemische Physik, TU Chemnitz, D-09107 Chemnitz

Natural materials such as bone and teeth are nanocomposites of proteins and minerals, which exhibit many levels of complex structure from macroscopic to microscopic length scale. Nanotomography is a novel approach to image such complex structures. We focus on bovine bone, which is first embedded in a methacrylate resin and then microtomed. For Nanotomography the specimen is ablated layer-by-layer by wet chemical etching and imaged with scanning force microscopy after each etching

step. From the resulting series of images the three-dimensional structure is reconstructed. Finding a proper etching method for both components, the mineral platelets and the collagen matrix is the first requirement for successful Nanotomography imaging. On our poster we will present our results on etching experiments with oxidizing solutions.

AKB 30.6 Mon 15:30 P1

Single molecule fluorescence imaging of the photoconverting fluorescent protein Kaede — •Stephan P. Schäfer[1], Eugene P. Petrov[1], Petra S. Dittrich[2], and Petra Schwille[1] — [1]Institute for Biophysics, Tatzberg 47, 01307 Dresden — [2]Department of Miniaturization, Institute for Analytical Sciences, 44013 Dortmund

We investigated the photoconversion and photobleaching behavior of the fluorescent protein Kaede immobilized in polyacrylamide gel matrix at room temperature using single molecule wide-field fluorescence microscopy. Based on a highly sensitive low-noise CCD, fluorescence emission of single molecules was detected in two color channels ("green/red") as function of time. In order to address the noise present in the low-intensity images (i.e. read out noise, photonic shot noise, fluorescence background noise), an interactive MATLAB-based analysis algorithm was developed (incl. spectral channel selection, background reduction, spot labeling, fitting and classification). Statistical analysis of intensity trajectories of single molecules revealed four major types of fluorescence dynamics behavior upon short illumination by a violet light pulse (405 nm): First, the green-to-red photoconversion and second, the photoactivation of green fluorescence without emission of red fluorescence. Two other major groups show neither photoconversion nor red emission and demonstrate photoinduced partial deactivation and partial revival of green fluorescence. The significantly lower green-to-red conversion ratio as compared to bulk measurements in aqueous solution might be induced by the immobilization of the protein molecules within a polyacrylamide gel.

AKB 30.7 Mon 15:30 P1

Energy landscapes of model proteins — •Frank Dressel[1,2], Sigismund Kobe[2], and Michael Schroeder[1] — [1]Biotechnologisches Zentrum, TU Dresden, D-01062 Dresden — [2]Institut fuer Theoretische Physik, TU Dresden, D-01062 Dresden

Proteins are molecular machines in living cells. Their functions are largely dependent on their spatial structure. Therefore, the knowledge of protein folding pathways and structural changes is important to understand possible malfunction as Alzheimer disease or mucoviscidosis. Despite of the huge complexity of the problem, a simple model for structure prediction can be applied [1] to investigate the exact low-lying energy landscape of proteins. The energy landscapes for some small proteins (e.g. Trp-cage (1L2Y) and Cecropin-Magainin hybrid (1D9J)) are presented. The ground state accessibility and the competition between ground state and metastable states are investigated and the relation to native states will be discussed.

[1]: F. Dressel, S. Kobe: "Global optimization of proteins using a dynamical lattice model", arXiv:q-bio.BM/0412031

AKB 30.8 Mon 15:30 P1

A genetic circuit that memorizes a signal on command — •Georg Fritz[1,2], Nicholas E. Buchler[3], Terence Hwa[4], and Ulrich Gerland[1] — [1]Department of Physics and CeNS, LMU München, Theresienstrasse 37, 80333 München, Germany — [2]Albert-Ludwigs University Freiburg, Hermann-Herder-Strasse 3, 79104 Freiburg, Germany — [3]Center for Studies in Physics and Biology, The Rockefeller University, New York, NY 10021 — [4]Physics Department and Center for Theoretical Biological Physics, University of California at San Diego, La Jolla, CA 92093-0374

While a detailed understanding of large genetic networks is still beyond reach, small genetic circuits consisting of only a few interacting genes are amenable to explicit characterization, both experimentally and theoretically. A paradigmatic example is the genetic toggle switch, which Gardner *et al.* constructed in *E. coli* [1]. It consists of two mutually repressing genes and displays the functional trademark 'bistability'. In principle, a bistable device can function as a memory. However, it would be useful for the cell only if it can store a signal on command, in order to memorize e.g. the state of its environment during its last cell division. To achieve this desirable property, we propose an extension of the genetic toggle switch, which could be realized experimentally through the addition of two well-characterized proteins. We characterize the resulting gene circuit theoretically, using both deterministic and stochastic models. We discuss its functional properties for typical experimental parameters of bacterial genes and proteins.

[1] T.S. Gardner *et al.*, Nature **403**, 339 (2000)

AKB 30.9 Mon 15:30 P1

Nonlinear Thermophoresis — •Stefan Duhr and Dieter Braun — Noether Group on Dissipative Microsystems, Applied Physics, Ludwig Maximilians Universität München, Amalienstr. 54, 80799 München, Germany

Thermophoresis is the drift of molecules in a temperature gradient. In the past, the effect was phenomenologically based on Onsager non-equilibrium thermodynamics: thermophoretic drift velocity rises linearly with the applied temperature gradient. We experimentally check this relation using fluorescence single particle tracking in microthermally heated microfluidics. For small particles and flat temperature gradients, the relation holds. Molecule concentration follows an exponential function of the applied temperature difference over two orders of magnitude, very similar to a Boltzmann-distribution. This confirms entropic, thermodynamic models of thermophoresis.

For large particles, we find a nonlinear drift relation for $aS_T\nabla T > 1$, violating the Onsager foundation of thermophoresis. In the limit relation, a is the molecule radius, S_T the Soret coefficient and ∇T the temperature gradient. Thermophoresis is linear if thermophoretic directed drift is slower than diffusive random drift. Or in the thermodynamic description of thermophoresis, the interfacial enthalpy is symmetric within kT. Compared with the zeta-potential limit of electrophoresis, the limit of thermophoresis can be avoided by the experimenter by simply reducing the temperature gradient.

AKB 30.10 Mon 15:30 P1

Electronic structure of surface-layer proteins probed by resonant photoemission — •Denis Vyalikh[1], Vlodimir Maslyuk[2], Andreas Kade[1], Steffen Danzenbächer[1], Alexandr Kirchner[3], Yuri Dedkov[1], Michael Mertig[3], Ingrid Mertig[2], and Serguei Molodtsov[1] — [1]Institut für Festkörperphysik, TU Dresden, D-01062 Dresden — [2]Martin-Luther-Universität Halle-Wittenberg, Fachbereich Physik, D-06099 Halle — [3]Max-Bergmann-Zentrum für Biomaterialien and Institut für Werkstoffwissenschaft, TU Dresden, D-01062 Dresden

The electronic structure of the regular, two-dimensional surface-layer proteins (S layer) of Bacillus sphaericus NCTC 9602 has been examined by conventional and resonant photoemission (PE), near-edge x-ray absorption fine structure (NEXAFS) spectroscopy. The results were compared with density-functional theory (DFT) calculations using a linear combination of atomic orbitals (LCAO) approach. It is demonstrated that a series of characteristic NEXAFS peaks can be assigned to particular molecular orbitals of the amino acids using a phenomenological building-block model. Applying this model, lineshape evaluation of the core-level PE spectra can successfully be used for quantitative chemical analysis of the protein structure. We have demonstrated that by tuning the photon energy in the vicinity of the C 1s absorption edge, strong changes in intensity of the resonant PE peaks corresponding to participator decay channels are observed. Thus, an interpretation of valence electronic states is achieved experimentally from resonant decay spectra that also is in a good agreement with our DFT-LCAO calculations.

AKB 30.11 Mon 15:30 P1

Cell vitality probed by noise analysis of thickness shear mode resonators: a new means to measure vertical cell motility — •A. Sapper[1], A. Janshoff[1], and J. Wegener[2] — [1]Institute of Physical Chemistry, University of Mainz, 55128 Mainz, Germany — [2]Institute for Biochemistry, University of Münster, 49151 Münster, Germany

A fundamental property of mammalian cells is their motility, which correlates with the metastatic behavior of cancer cells. Thus detection of cell motiliy is important for understanding the metastatic process and developing clinical measurements for diagnosis and treatment of cancer. We report a new approach to expose cell motility using the quartz crystal microbalance (QCM). The QCM is known as an excellent and sensitive tool to follow adsorption in liquid environment like the attachment and spreading of mammalian cells. The technique is based on a quartz resonator sandwiched between two metal electrodes that are used to excite mechanical shear displacements of the piezoelectric quartz disks electrically. Measuring cell motility is done by evaluating the noise of the cell-covered quartz crystal in the resonant frequency response produced by active formation and breakage of noncovalent bonds as well as vol-

ume changes that might be produced by periodic contraction of actin stress fibers. We show how the QCM could be used to monitor shape fluctuations of living cells with a prospective application as an assay for biological activity of cells as found in metastasis of tumor cells. The QCM provides a quantitative means to monitor mechanical vibration of cells with amplitudes in the nanometer regime at high time resolution and might be used to distinguish between malign and benign cells.

AKB 30.12 Mon 15:30 P1

Diffusive target-site search on a dynamic polymer — •Thomas Schötz and Ulrich Gerland — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for Nanoscience (CeNS), LMU München

During the biophysical search process of DNA-binding proteins for their specific functional target sites, the DNA conformation is typically neither frozen nor completely equilibrated. We study the interplay of the DNA polymer dynamics and the protein search dynamics within a simple toy model on a lattice. In this model, the DNA conformation evolves according to the generalized Verdier-Stockmayer kinetic Monte Carlo scheme, while the proteins search their target sites using a combination of three-dimensional diffusion through the solvent, inter-segment transfer at places where loops in the DNA conformation are spontaneously formed, and one-dimensional sliding along the DNA. We study explicitly the breakdown of correlations in the search dynamics as a function of the relative rate for DNA and protein movement. The observed behaviour can be understood with the help of a dynamic scaling argument.

AKB 30.13 Mon 15:30 P1

Intracellular CARS spectral imaging. — •Alexander Kovalev, Patincharath Nandakumar, and Andreas Volkmer — 3rd Institute of Physics, University of Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

For cellular components that either do not fluoresce or cannot tolerate the toxicity associated with staining and the photo bleaching of fluorophores, their intrinsic chemical properties can be used as contrast mechanisms through coherent anti-Stokes Raman scattering (CARS) microscopy. We report on the noninvasive vibrational imaging and microspectroscopic study of individual intracellular compartments within live eucaryotic cells. The spectroscopic information recorded by means of multiplex CARS microscopy allows differentiating between cellular organelles. The internal state and changes in composition of the organelles and cytoplasm could be monitored within range of the CH-stretching vibrations between 2800 cm-1 and 3000 cm-1. Examples of spectra from intracellular compartments in yeast cells and in differentiated 3T3 L1 cells will be presented.

AKB 30.14 Mon 15:30 P1

Spatially and spectrally resolved fluorescence correlation spectroscopy — •Markus Burkhardt and Petra Schwille — Biotec/ TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

Fluorescence Correlation Spectroscopy (FCS) is based on time dependent fluorescence intensity fluctuations of labeled biomolecules as they enter and leave a diffraction-limited optical detection volume. From simple autocorrelation analysis, concentrations, diffusion and binding coefficients are easily obtained. An accurate measure of inter- and intramolecular dynamics is attainable by evaluating the concomitant fluctuations of two or more spectrally distinct fluorophores.

In a standard FCS setup, all these information are collected from one specific focus position inside the sample. For the investigation of cellular mechanisms however, there is a great interest in large scale transport and flow properties which cannot directly be assessed.

The aim of the current project is the realization of a flexible multi-spot illumination and array detection platform. First proof of principle FCS measurements with spatially and spectrally resolved detection systems show the feasibility of such an approach.

AKB 30.15 Mon 15:30 P1

Offdiagonal Complexity: Characterizing graph complexity from nondiagonal link correlations - Application to biological networks — •Jens Christian Claussen — Institut für Theoretische Physik und Astrophysik, Christian-Albrecht-Universität Kiel, Germany

A vast variety of biological, social, and economical networks shows topologies drastically differing from random graphs; yet the quantitative characterization of their "complexity" remains unsatisfactory from a conceptual point of view. Motivated from the discussion of small scale-free networks, a biased link distribution entropy is defined, which takes an extremum for a power law distribution. This approach is extended to the node-node link cross-distribution, whose nondiagonal elements characterize the graph structure beyond link distribution, cluster coefficient and average path length. From here a simple (and computationally cheap) complexity measure can be defined [1]. This approach is applied to a protein interaction network in comparison to randomized surrogates, and to the spatial evolution of a cell aggregate adjacency matrix as a function of time [2].

[1] J.C. Claussen, arXiv.org e-print q-bio/0410024
[2] J.C. Claussen, Offdiagonal complexity: A computationally quick network complexity measure. Application to protein networks and cell division (submitted)

AKB 30.16 Mon 15:30 P1

Molecular modeling of transport through OmpF channels — •U. Kleinekathöfer[1] and M. Winterhalter[2] — [1]Institut für Physik, Technische Universität Chemnitz, 09107 Chemnitz — [2]International University Bremen, 28725 Bremen

The outer membrane protein F (OmpF) is a non-specific pore in the outer membrane of *Escherichia coli* and permits translocation of ions and small molecules such as antibiotics [1]. Since the structure of OmpF has been determined to high resolution, it is possible to study the transport through this protein in computer simulations [2,3]. The time-scale problem in simulating the passing of substrate molecules through channels can be overcome by using Steered Molecular Dynamics (SMD) which artificially speeds up the process. This allows to simulate processes on time scales which would not be accessible by an atomic level description otherwise especially diffusive processes. Trajectories obtained from SMD simulations allow to determine the ion current through the protein, its electrostatic map and the potential of mean force.

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

AKB 30.17 Mon 15:30 P1

Negative thermal expansion and confomation changes in the smallest chiral amino acid, Alanine — •Heloisa Nunes-Bordallo[1], Dimitri Argyriou[1], Jörg Strempfer[2], Mariette Barthès [3], and Françoise Dénoyere[4] — [1]Hahn-Meitner-Institut, Berlin. — [2]Max-Planck-Institut für Festkörperforschung, Stuttgart. — [3]Université Montpellier II, Montpellier, France — [4]Université Paris XI, Orsay, France

Amino acid construction consists of a carboxylic acid (-COOH) and an amino (-NH_2) functional group attached to the same tetrahedral carbon atom, the α-carbon. Every amino acid, with the exception of glycine, comes in two forms, a left-handed (L) and a right-handed (D) version, which are identical mirror images of each other. We report on high resolution X-ray and neutron diffraction as well as quasi-elastic neutron scattering (QENS) studies on crystalline L- and D-alanine over a wide temperature range. Our aim is to verify the possibility that a phase transition, related to a break of the as C α-H bond, occurs in alanine. While no change in the space group symmetry was observed, a negative thermal expansion, by discrete steps, along the c- axis is observed till the melting point. Additional anomalies are also noticed in the a and b lattice constants at 170K. Moreover, the evolution of the mean-square displacement, obtained from the QENS, data shows a steadily increase on heating, but near 150K and again near 200K a deviation from the expected behavior is observed. The results suggest the excitation of new degrees of freedom, possibly due to a progressive conformational change of the NH^{3+} group.

AKB 30.18 Mon 15:30 P1

Effect of genome sequence on the force induced unzipping of a DNA molecule — •Navin Singh[1,2] and Yashwant Singh[2] — [1]Max Planck Institute for Polymer Research, Mainz, Germany — [2]Department of Physics, Banaras Hindu University, Varanasi, India

We considered a dsDNA polymer in which distribution of bases are random at the base pair level but ordered at a length of 18 base pairs and calculated its force elongation behaviour in the constant extension ensemble. The unzipping force $F(y)$ vs. extension y is found to have a series of maxima and minima. By changing base pairs at selected places in the molecule we calculated the change in $F(y)$ curve and found that the change in the value of force is of the order of few pN and the range of the effect depending on the temperature, can spread over several base pairs.

AKB 30.19 Mon 15:30 P1

Two protein species binding cooperatively and specifically to DNA: physical and functional constraints — •Nico Geisel[1] and Ulrich Gerland[2] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC), Georg-August-Universität Göttingen, LMU München — [2]Arnold Sommerfeld Center for Theoretical Physics (ASC), Center for Nanoscience (CeNS), LMU München

Cooperative binding of proteins to specific sites on the genomic DNA is indispensable for many genetic mechanisms, in particular in the context of transcription regulation. The equilibrium and non-equilibrium properties of this binding process can be strongly affected by the presence of the genomic background, i.e. the overwhelming majority of the non-functional sites on the DNA. For a single protein species binding independently to the DNA, this background effect has been characterized in Ref.[1]. Here, we extend this analysis to the case of two protein species which bind DNA cooperatively. We consider an explicit theoretical model based on biochemical experiments. We study its equilibrium behavior analytically and its dynamics through kinetic Monte Carlo simulations. We determine the parameter range where physical constraints do not limit the biological functionality.

[1] U. Gerland, J.D. Moroz, and T. Hwa (2002) Proc. Natl. Acad. Sci. USA **99**, 12015

AKB 30.20 Mon 15:30 P1

Single-molecule enzyme kinetics in picoliter confined volumes — •Wolfgang Staroske, Fedor Malik, and Petra Schwille — BIOTEC/TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany

Studying the activity of few or single enzyme molecules under physiological conditions is an exciting task for quantitative biochemistry and biophysics. In particular, the role of confinement in small compartments needs to be determined to better understand these molecules in their cellular environment. We show that using microfluidic devices, homodisperse buffer droplets can be easily prepared in variable sizes, containing very low quantities of enzyme down to the limit of one enzyme molecule per droplet. By observing the fluorescence signal as a measure for substrate or product concentration in a temperature-controlled incubation chamber on an inverted microscope, enzyme activity can be precisely determined. Because of the exact and easy replication of the droplets, it is possible to observe many single enzyme kinetics at once. As a perspective, we aim to elucidate the kinetics of the 20S-Proteasome as a protein degradation machinery.

AKB 30.21 Mon 15:30 P1

Thermodynamics along a stochastic trajectory for chemical reaction networks — •Tim Schmiedl and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57/III, 70550 Stuttgart

We model chemical reaction networks by a master-equation approach. Defining the thermodynamic state variables energy and entropy along a stochastic trajectory, we develop a consistent theory of thermodynamics including the first and second law. Entropy fluctuations are constraint by a fluctuation theorem, which can be regarded as an extension of the second law of thermodynamics. This fluctuation theorem is valid for systems driven arbitrarily far out of equilibrium. The reaction system can be maintained in a nonequilibrium steady state (NESS) where detailed balance is violated. Furthermore, transitions between equilibrium steady states due to time dependent rates generate nonequilibrium distributions if they are not driven infinitesimal slowly (adiabaticly). We examplify these results for a three-species cyclic reaction network with time dependent rates and discuss NESS as well as rate-driven transitions between steady states. For large systems, a usual approach to solve master equations approximatively is the system-size expansion by van Kampen. We discuss how the fluctuation theorem transfers to this mesoscopic description for two paradigmatic reaction networks.

AKB 30.22 Mon 15:30 P1

Calibration of optical tweezers using a piezo-electric translation stage — •Simon F. Tolic-Norrelykke[1,2], Erik Schaeffer [3], Francesco S. Pavone [2], Jonathon Howard[3], Frank Julicher[1], and Henrik Flyvbjerg[4,5] — [1]Max Planck Institute for the Physics of Complex Systems, Nothnitzer Strasse 38, 01187 Dresden, Germany — [2]European Laboratory for Non-linear Spectroscopy, via Nello Carrara 1, 50019 Sesto Fiorentino (Fl), Italy — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 01307 Dresden, Germany — [4]Biosystems Department and Danish Polymer Centre, Riso National Laboratory, DK-4000 Roskilde, Denmark — [5]Isaac Newton Institute for Mathematical Sciences, Cambridge, U.K.

We use a piezo-electric stage that is commonly found in optical tweezers setups to calibrate the x-y-z position detection system of optical tweezers. By driving the piezo stage harmonically, a known motion is added to a trapped object's Brownian motion. This motion produces a sharp spike in the power spectrum, and this spike serves as a "scale-bar" and thus enables the calibration of the detection system. It is not necessary to know friction coefficients, hence neither the viscosity, or temperature of the surrounding fluid. Force calibration is possible if the local temperature is known. We test the method experimentally and find it to be accurate to within 0.5% and have a relative precision better that 1% for both the position and force calibration. The main advantages of this method are the low level of instrumentation required, that it can be applied in situ, and that it is both precise (small error-bars) and accurate (returns true value).

AKB 30.23 Mon 15:30 P1

AFM measurements of living cells — •Michael Holzwarth, Katrin Hübner, Alexander Gigler, and Othmar Marti — Department of Experimental Physics, Ulm University, D-89069 Ulm, Germany

Recently, the Atomic Force Microscope (AFM) has become a powerful tool for the investigation of biological samples. In the work presented here, the AFM is used for a variety of measurements on living cells. Several types of cells varying in size and especially height are analysed. For the measurements contact mode as well as Pulsed Force Mode (PFM) are used. Topography images of miscellaneous cells will be presented. Additionally, mechanical properties of the cells and their ability to adhere on different substrates will be discussed.

AKB 30.24 Mon 15:30 P1

Binding of TmHU to single ds-DNA observed by optical tweezers — •Mathias Salomo[1], Klaus Kroy[1], Kati Kegler[1], Christof Gutsche[1], Marc Struhalla[2], Jörg Reinmuth[1], Wiktor Skokov[1], Claudia Immisch[3], and Friedrich Kremer[1] — [1]University of Leipzig — [2]c-LEcta GmbH, Leipzig — [3]ACGT Progenomics AG, Halle

We employed optical tweezers to study the binding and disruption of the histone-like protein TmHU (from Thermotoga maritima) on DNA at a single molecule level. For the binding reaction, a force-independent reaction rate was observed, in contrast to earlier findings for histone/DNA complex formation. This suggests that there are no force dependent kinetic barriers involved. For the disruption process, pronounced sawtooth like patterns were observed in the measured force-extension relation. The data were brought in direct relation to a microscopic model, which evaluates the energetics of the reaction based on the bending of the DNA in the course of interaction. It suggests that the independent binding of individual proteins to the DNA is kinetically delayed and explains the abrupt halt of the binding reaction at stretching forces of about 20-25 pN. It moreover provides compelling evidence for a (yet unknown) cooperative reaction mechanism.

AKB 30.25 Mon 15:30 P1

Synchrotron x-ray diffraction from solid supported membranes: Cholesterol enriched mixtures — •Christian Reich, Joachim Rädler, and Bert Nickel — Department für Physik, Ludwig-Maximilians-Universität, München, Germany

Phase separation and lipid-protein interactions are important processes occurring in cell membranes. Useful model systems are single supported lipid bilayers, which retain to a high extent the properties of real cell membranes. We use a novel microfluidic setup that allows to employ complementary methods such as high resolution synchrotron reflectivity and fluorescence microscopy on the same sample [1]. These two dictinct but highly complementary methods allow for the first time to get a full

micro- and nanoscopic picture of membrane properties such as structure, packing density, homogeneity and fluidity.
Current research topics in our group focus on the molecular arrangement of complex lipid mixtures in supported membranes and their transport properties. Recent results are presented.
[1] C. Reich et al., Rev. Sci. Instr. 76, 095103 (2005)

AKB 30.26 Mon 15:30 P1

Targeted transfection and gene-silencing using femtosecond laser pulses — •Elke Haustein, Thomas Ohrt, and Petra Schwille — TU Dresden, Institute for Biophysics, Tatzberg 47-51, D-01307 Dresden

To manipulate cellular function and morphology, molecules that can specifically affect intracellular processes have to be transported through the plasma membrane. Small interfering RNAs are key intermediates of a post-transcriptional gene-silencing mechanism known as RNA interference (RNAi). This technique allows for a temporary, easy-to-use and specific protein knockdown and thus can be applied both to biological research and future therapeutic applications. To achieve optimal results, controlling both the kinetics of RNA delivery and the final amount of probe substance within the target cell is mandatory. So far, different techniques have been tested to deliver siRNAs in situ, most of which depend on cellular uptake mechanisms. But to avoid delivery-related artefacts, the siRNAs have to enter the cytoplasm directly. Therefore, we propose an alternative means to deliver RNA to cells. Using a confocal setup, the parallel infrared laser beam is directed into an inverted microscope and focussed onto the cell membrane. The cells are then exposed to femtosecond laser pulses for varying time intervals. The resulting perforation of the plasma membrane allows uptake of the RNA added to the surrounding medium. Using a fluorescence-based assay, the effectivity of this "photoporation" approach can be characterised by fluorescence-based techniques as well as with biochemical means.

AKB 30.27 Mon 15:30 P1

Microscopic fluctuations determine global behavior of cells — •Alexander Skupin and Martin Falcke — Hahn-Meitner-Institut, Glienicker Str. 100, 14109 Berlin

In the last years, the understanding of the influence and importance of noise in biological systems has substantially increased. Here we show how thermal fluctuations on a microscopic level, i.e. the stochastic manner of ion channels, effect the global behavior of cells. Therfore we present biological experiments which have been done and analyzed in a physical way to characterize the underlying stochastic process and to show the importance of noise. In this context astrocytes are ideal objects of interest. These cells represents the majority of cells in the brain and show spontaneous oscillations of the cytosolic Ca^{2+} concentration. They are caused by the stochastic opening of ion channels releasing Ca^{2+} from internal stores into the cytosol. This liberated Ca^{2+} can activate adjoining channels resulting in a global Ca^{2+} wave within the cell. We analyzed the periods of these oscillation and the influence of Ca^{2+} buffer to specify this stochastic mechanism, which seems to be a general one in cells. Due to their coupling to neurons and their role for the genesis of synapses astrocytes might influence the self evolution of the brain in a significant way. Thus, microscopic fluctuations can determine macroscopic biological objects like the brain.

AKB 30.28 Mon 15:30 P1

Nanoelectrode Arrays for On-Chip Manipulation of Organic Substances and Proteins in Aqueous Solutions — •Cheng-Ping Luo, Andreas Heeren, Wolfgang Henschel, and Dieter P. Kern — Institute of Applied Physics, University of Tübingen, Auf der Morgenstelle 10, 72076 Tübingen, Germany

Dielectrophoresis is a convenient method for manipulation of dielectric substances in liquid. Since organic and biological substances are mostly dielectric, they can be trapped in or released from a specific area by applying electrical signals of proper frequency and amplitude to an appropriate set of electrodes. In our previous experiments, AC signals were applied to microelectrodes. In the case of positive dielectrophoresis, dielectric substances congregated in the gaps between electrodes, especially at edges, in which the field intensities are strongest. However, for substances at the nanoscale, higher fields are required. Then turbulence due to electro-osmosis flow, which is caused by non-uniform electric field and electrical double layer and is proportional to the square of the applied voltage, will strongly disturb the movement and arrangement of the substances. In this work, devices based on dielectrophoresis using nanoelectrode arrays have been investigated to reduce the electro-osmosis flow. Nanoscale organic substances and biomolecules in aqueous solution, for example, polystyrene beads, bovine serum albumin and antibody molecules, were successfully trapped between the nanoelectrodes. Furthermore, the results demonstrate that the required applied voltage can be reduced by a factor of five in comparison with those using microelectrodes.

AKB 30.29 Mon 15:30 P1

Stress fluctuation and microrheology in endothelial cells — •Daniel Paranhos Zitterbart, Carina Raupach, and Ben Fabry — Zentrum für medizinische Physik und Technik, Henkestr. 91, 91052 Erlangen

Mechanical processes of living cells are controlled by cytoskeletal (CSK) dynamics, which can be measured from the motion of CSK-bound beads. Bead motion has been reported to follow a superdiffusive behavior that arise from ATP-driven intracellular stress fluctuations (e.g. polymerization processes and motor proteins) with a power spectrum $P_u(\omega) \propto 1/\omega^2$ (Lau et al, Phys Rev Lett 91:198101). Here we report direct measurements of force fluctuations that are transmitted to the extracellular matrix (ECM) by plating human vascular endothelial cells onto a collagen coated elastic polyacrylamide hydrogel. Force fluctuations were computed from gel deformations that we obtained from the displacements of gel-embedded fluorescent beads. In addition, we measured CSK dynamics using fibronectin coated fluorescent beads that were bound to the cell via integrin receptors. Bead motion of both CSK-bound and ECM-bound beads were expressed as mean square displacement (MSD) and showed a superdiffusive behavior that was well described by a power law: $MSD = a \cdot t^b$. Surprisingly, we found the same exponent b of 1.6 for both CSK-bound and ECM-bound beads. This finding suggests that the spontaneous motion of CSK-bound beads is driven by stress fluctuations with a $1/\omega^{b+1}$ power spectrum, and that CSK dynamics and CSK stress fluctuations are closely coupled.

AKB 30.30 Mon 15:30 P1

Nonlinear Viscoelasticity of Single Fibroblasts — •Pablo Fernandez, Pramod Pullarkat, and Albrecht Ott — Experimentalphysik 1, Universität Bayreuth, Universitätsstraße 30, D-95440 Bayreuth

We perform single-cell uniaxial stretching experiments on 3T3 fibroblasts. By superimposing small amplitude oscillations on a cell under stress, we find a relation between the viscoelastic moduli and the average force. Data from different cells over several stress decades can be uniquely scaled to obtain a transition from stress-independent moduli to power law stress hardening. Remarkably, this master-relation holds independently of deformation history, adhesion biochemistry, and intensity of active contraction. We propose that it reflects the statics of the force bearing actin cytoskeleton, and show that it can be explained as strain hardening arising from actin filament bending. We also show preliminary results from frequency and amplitude sweeps. At large amplitudes, a roughly linear relation between force and length is observed, in marked contrast with the stress hardening behavior given by the master-relation. This holds irrespective of frequency in the range 0.1 – 1 Hz.

AKB 30.31 Mon 15:30 P1

Hybridization and melting experiments on oligonucleotide microarrays — •Thomas Naiser and Albrecht Ott — Physikalisches Institut, Universität Bayreuth, 95440 Bayreuth

DNA microarrays are becoming an increasingly important tool for the quantitative determination of gene expression levels. We use a light-directed in situ synthesis process, employing a 'programmable mask' based photolithography technique, to produce short oligonucleotide microarrays, comprising a multitude of different features. Each feature contains a large number of surface bound probe molecules of the same, given sequence. We apply the fluorescently labeled target strands to the microarray surface in a buffer solution. Driven by diffusion, these strands can freely move over the microarray surface to make contact with a large number of different probe molecules. They form a relatively stable duplex with complementary sequence probe molecules. The fluorescence intensity of these hybridized targets provides an estimate for the abundance of a particular target nucleic acid. In hybridization and melting experiments we study how sequence mismatches between probe and target molecules affect hybridization efficiency. Secondary structure of the targets (caused by intramolecular base pairing) is supposed to affect the accessibility of the sequence ranges targeted by the probes.We investigate the effects of target secondary structure on probe sensitivity by probing long cRNA targets with sets of all 25mer probe sequences, which are complementary to the particular cRNA target.

AKB 30.32 Mon 15:30 P1

Hydrogen Forces in DNA — •Hauke Schollmeyer[1,2], Youli Li[2], and Cyrus Safinya[2] — [1]Institute for X-Ray Physics, Georg-August-University, Friedrich-Hund-Platz 1, 37077 Göttingen — [2]Materials Rasearch Laboratory, University of California at Santa Barbara, CA, USA

It has been found that DNA has two predominant conformations, both of which are a double helix, existing in nature: the B form, characterized by a pitch of 34 Å, a diameter of 20 Å, and a rise per base pair of 3.4 Å; and the A form, characterized by a pitch of 28 Å, a diameter of 23 Å, and a rise per base pair of 2.6 Å. It is well accepted that DNA undergoes the conformational change by 75% in relative humidity at room temperature; however, little is known about the exact position in relative humidity space of the transition, or even the nature of the transition itself. DNA is also known to undergo a transition from a 2-D hexagonal to a 3-D hexagonal, but the nature of this has not been carefully studied. It has been reported that DNA exists in vivo in concentrations relevant to these phase transitions, so the study performed in the presented work has direct biological relevance. This study has further implications in understanding self interactions among neighboring DNA molecules. We have performed experiments using x-ray fiber diffraction to further examine the phase behavior.

AKB 30.33 Mon 15:30 P1

Th1–Th2 Regulation and Allergy: Bifurcation Analysis of a Stroboscopic Map — •Reinhard Vogel and Ulrich Behn — Institut für Theoretische Physik, Universität Leipzig, POB 100 920, 04009 Leipzig

A previously proposed mathematical model [1] based on a simplified scheme of Th1–Th2 regulation mediated by the cytokine network which describes the population dynamics of allergen-specific naive T-cells, Th1 and Th2-cells, autocrine and cross-suppressive cytokines, and allergen is closer investigated. The model provides a theoretical explanation of the switch from a Th2 dominated response to a Th1 dominated response to allergen in allergic individuals as a result of a hyposensitization therapy.

We present a bifurcation analysis of the non-autonomous dynamical system driven by periodic allergen injections. The stability of the fixed points of a stroboscopic map is investigated. The set of unstable fixed points forms the dynamical separatrix between the regions of Th2 dominated response and Th1 dominated response which is crossed during a successful therapy. The maintenance phase of the therapy holds the system near the stable fixed point of the stroboscobic map. We further discuss the dependence of the fixed point manifolds on the dose of the allergen injections and on small variations of the cytokine background.

[1] J. Richter, G. Metzner, U. Behn, Venom immunotherapy: A mathematical model, J. Theor. Med. **4**, 119–132 (2002)

AKB 30.34 Mon 15:30 P1

Transport in Random Media with an Orientational Degree of Freedom — •Felix Höfling[1], Thomas Franosch[1,2], and Erwin Frey[2] — [1]Hahn-Meitner-Institut Berlin, Abteilung Theoretische Physik, Glienicker Str. 100, 14109 Berlin, Germany — [2]Arnold Sommerfeld Center and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München, Germany

Towards an understanding of the complex dynamics of a semiflexible polymer in a biological polymer network, we concentrate on a minimal model that is based on the two-dimensional Lorentz model: instead of a structureless tracer particle a needle moves through a random array of obstacles. Therewith, the original model is enriched by an orientational degree of freedom. The phase diagram of the system is now governed by two control parameters: the obstacle density and the ratio between needle length and obstacle diameter. Above a critical line, the tracer is expected to be always trapped by the obstacles. This line should coincide with the percolation threshold of the phase space.

An interesting case is given for point-like obstacles. Then, the medium lacks a percolation transition, and the strong influence of the percolation scenario is stripped off the dynamics. Thus, new insight into different mechanisms for slow dynamics can be gained.

We present first results from Molecular Dynamics simulations for the mean-squared displacements and orientational correlation functions. These data are supplemented by an Boltzmann-Enskog theory.

AKB 30.35 Mon 15:30 P1

Detection of single oxygen molecules by single-molecule fluorescence microscopy — •Wolfgang Erker, Sven Sdorra, and Thomas Basché — Department of Physical Chemistry, University of Mainz, Welderweg 11, 55099 Mainz, Germany

Hemocyanins, the respiratory proteins of arthropods, bind oxygen with high affinity and specifity. Bound oxygen produces two charge-transfer absorption bands in the UV and visible range. Covalent attachement of fluorophores converts the absorption signal into a fluorescence intensity [1]. This conversion is caused by FRET upon oxygen binding of the protein due to close proximity and spectral overlap. Consequently, fluorescence intensity of the attached labels tells whether the protein has oxygen bound or not. This signal can be detected at the single molecule level and enables the detection of single oxygen molecules [2]. The technique opens new perspectives for the development of small and sensitive oxygen sensors as well as for the investigation of cooperative oxygen binding in respiratory proteins.

[1] Erker W, Schoen A, Basché T, Decker H: Fluorescence labels as sensors for oxygen binding in arthropod hemocyanins. Biochem Biophys Res Com 2004, 324, 893-900

[2] Erker W, Sdorra S, Basché T: Detection of single oxygen molecules with fluorescence labelled hemocyanins. J. Am. Chem. Soc. 2005, 127, 14532-14533

AKB 30.36 Mon 15:30 P1

FORCE SPECTROSCOPY ON SINGLE INTEGRIN-INVASIN BONDS — •Agnieszka Ligezowska[1,2], Kristian Boye[1,3], Johannes Eble[4], Bernd Hoffmann[1], and Rudolf Merkel[1] — [1]Institute of Thin Films and Interfaces, Research Centre Juelich, 52425 Juelich, Germany — [2]Jagiellonian University Cracow, Institute of Physics, Reymonta 4, 30-059 Cracow, Poland — [3]University of Southern Denmark, Memphys Center for Biomembrane Physics, Campusvej 55, DK-5230 Odense M, Denmark — [4]Institute for Physiological Chemistry, Muenster University Hospital, 48149 Muenster, Germany

Force-induced dissociation of single specific bonds is a stochastic process which has attracted considerable interest during the last decade.

We have investigated the force-induced dissociation of bonds between two integrins, $\alpha 3\beta 1$ and $\alpha 7\beta 1$, and the ligand invasin 497. These proteins were immobilized in their active form on melamine microbeads and the single-bond regime was reached by receptor blocking with free invasin. Piconewton forces were applied by osmotically swollen red blood cell which acted as an ultrasoft spring. This system allowed us to measure yield forces at specified bond loading rates and different transducer stiffnesses.

AKB 30.37 Mon 15:30 P1

The role of lipids with positive curvature in the formation of membrane pores — •Jakob C. Schweizer and Petra Schwille — Biotec/TU Dresden, Tatzberg 47-51, 01307 Dresden

It is assumed that lipids with a positive curvature, e.g. large headgroup and small chain, play an essential role in the formation toroidal structures like membrane pores or edges of planar and supported membranes. Using single-chained lipid probes with an appropriate attachment of the fluorophore should reveal localization and orientation of such lipids within the membrane and therefore migth indicate the involvement in toroidal structures. In a first approach, this can be demonstrated in the case of membrane edges and large pores using simple epi-fluorescence microscopy.

AKB 30.38 Mon 15:30 P1

Dual-Color Single-Virus Tracing: Investigating the Entry Pathway of HIV — •Stefan Riegelsberger[1], John A. G. Briggs[1], Barbara Müller[2], Marko Lampe[2], Thomas Endress[1], Don C. Lamb[1], Hans-Georg Kräusslich[2], and Christoph Bräuchle[1] — [1]Physical Chemistry, Department of Chemistry and Biochemistry, Ludwig-Maximillians-Universität München, Butenandtstr. 11, Haus E, 81377 München, Germany — [2]Abteilung Virologie, Universitätsklinikum Heidelberg, Im Neuenheimer Feld 324, 69120 Heidelberg, Germany

Detailed information about the interactions between virus particles and living cells can be obtained by visualising and tracking individual virus particles in real time. For the investigation of HIV entry, we have developed a novel, dual-colour HIV derivative that allows us to distinguish between complete viruses and those that have undergone fusion. We are observing the infection pathway of these particles using a dual-colour

microscope. The microscope is based on wide-field microscopy with laser excitation and ultrasensitive fluorescence detection. The laser beams are guided through a vibrating, multimode optical fiber to remove interference fringes in the image plane, creating a very homogenous excitation profile. Improved depth resolution is achieved using a Köhler illumination scheme. The excitation sources are interleaved such that green and red fluorophores are excited on alternate images, and the emitted light is further spectrally separated onto two regions of the camera. This set up removes cross-talk between the two fluorescent labels, and allows us to distinguish broad-spectrum cellular autofluorescence from the viral signals and to correct for it.

AKB 30.39 Mon 15:30 P1

Investigation of the first steps of TNF-mediated apoptosis by FCS and FCCS in live cells — •Felix Neugart[1], Carsten Tietz[1], Magarita Gerken[1], Andrea Zappe[1], Anja Krippner-Heidenreich[2], Peter Scheurich[2], and Jörg Wrachtrup[1] — [1]3. Physikalisches Institut, Universit"at Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart — [2]Institut f"ur Zellbiologie und Immunoligie, Universit"at Stuttgart, Allmandring 31, 70569 Stuttgart

Due to its high sensitivity fluorescence correlation spectroscopy is suited to investigate processes in live cells where the endogenous concentration of the participating molecules are low, e.g., in many signaling cascades. Here, FCS is used to unravel dynamics of the membrane receptors TNFR1 and TNFR2 which play important roles in apoptotic signaling pathways. Although structurally similar in their transmembrane domains both receptors behave markedly different in the cell membrane. Upon binding of the ligand TNF the diffusion constant of TNFR2 is reduced from 3.3×10^{-9} to 0.8×10^{-9} cm^2/s. Experiments on receptors without its binding domain in the cytoplasm show that interaction of the receptor signaling complex with immobile parts of the cellular interior is not responsible for the reduction in diffusion rate. Rather it appears that the TNFR2 receptor attaches to slowly diffusing membrane microdomains after stimulation. Using a new set-up for cross-talk free FCCS with the fluorophore pair CFP and YFP it was shown that there is no pre-association behavior of TNFR2 before stimulation.

AKB 30.40 Mon 15:30 P1

Investigation of the mechanical properties of lipid bilayers with nanomechanical cantilever array sensors — •Ioana Pera and Jürgen Fritz — International University Bremen, School of Engineering and Science, 28759 Bremen, Germany

It has been observed in both model and natural systems that the shape and mechanical properties of lipid membranes are influenced by their composition. So far, such properties of bilayers have mainly been studied indirectly at the air-water interface, using lipid monolayers as models or by investigating the surface curvature of lipid vesicles. Here, we are interested in the influence of lipid - lipid and lipid - solid surface interactions on the mechanical properties of lipid bilayers. We report on direct measurements of the bending of microfabricated cantilever arrays upon the formation and modification of physi- and chemisorbed supported lipid bilayers on cantilever surfaces. Implications for the detection of membrane processes with cantilever sensors (such as protein binding, cholesterol incorporation and extraction, or phospholipase activity), along with our primary models will be discussed.

AKB 40 Poster Session II

Time: Wednesday 16:30–19:30 Room: P3

AKB 40.1 Wed 16:30 P3

Effects of Eye-phase in DNA unzipping — •Sanjay Kumar — Department of Physics, BHU, Varanasi, India — MPIPKS, Noethnitzer str. 38 01187, Dresden Germany

The onset of an "eye-phase" and its role during the DNA unzipping is studied when a force is applied to the interior of the chain. The directionality of the hydrogen bond introduced here leads to a saw-tooth like behaviour which was earlier seen in the protein unfolding experiments. The effects of intermediates (hairpins) and stacking energies on the melting profile can also be studied.

AKB 40.2 Wed 16:30 P3

Macroscopic crystallographic structure of *Strongylocentrotus purpuratus* and *spisula solidissima* by pole figure analysis — •Simone Herth[1], Jeremy K. Bigness[2], and Robert H. Doremus[1,2] — [1]Rensselaer Nanotechnology Center, Rensselaer Polytechnic Institute, Troy, NY, USA — [2]Department of Materials Science and Engineering, Rensselaer Polytechnic Institute, Troy, NY, USA

The shells of sea animals, such as the sea urchin *Strongylocentrotus purpuratus* and the clam *spisula solidissima*, provide strong protection against enemies while retaining low weight. In *Strongylocentrotus purpuratus* the high toughness of the skeleton is achieved by the combination of a strong, but 50 % porous backbone made of the mineral calcite and proteins, which distribute stress concentrations. In contrast, the shell of *spisula solidissima* consists of the mineral aragonite and has a very low porosity. However, little is known about the macroscopic texture of these surprisingly strong composites, which was studied by a pole figure analysis of an oral and an aboral piece of the sea urchin skeleton and a small part of the clam shell. The sea urchin exhibits a strong texture in only a few crystallographic directions indicating a preferred macroscopic orientation of the calcite planes. The orientation of the planes in the aboral part is slightly more symmetric with about the same degree of texture. In contrast, the texture of the clam shell is very weak.

AKB 40.3 Wed 16:30 P3

Simulation studies of lipid bilayer around a conical inclusion and mediated interactions between inclusions. — •Gregoria illya and Markus Deserno — MPI Polymer Research, Ackermannweg 10, 55128 Mainz, Germany

We present a mesoscopic model for lipid bilayers with embedded conical inclusions, which is investigated using a solvent free coarse-grained simulation technique [1].

Above the gel-fluid transition temperature, i.e., in the fluid phase, the lipids are not in a spontaneously tilted phase. Inserting a conical object into the membrane will impose a local tilt on the surrounding lipids and also bend the membrane. The tilt of the lipids will decay with some characteristic decay length [2]. We measure this lipid tilt decay length for an almost flat membrane where the inclusion only imposes a tilt on the lipids and for a membrane where the inclusion also bends it.

Since transmembrane inclusions can deform the membrane, these deformations will generate interactions between the inclusions. We are currently investigating the force between two inclusions mediated by the tilt field and the membrane deformation, and compare the results with the theoretical prediction [2].

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AKB 40.4 Wed 16:30 P3

Conformational properties of semiconductor-binding synthetic peptides — •Gökhan Gökoglu[1,2], Michael Bachmann[1], Tarik Çelik[2], and Wolfhard Janke[1] — [1]Institut für Theoretische Physik, Universität Leipzig, Germany — [2]Fizik Mühendisliği Bölümü, Hacettepe Üniversitesi Ankara, Turkey

We investigate thermodynamic properties of three 12-residue synthetic peptides with generalized-ensemble Monte Carlo simulations [1]. In recent experiments [2,3] it was found that these peptides, although similar in their amino acid content, adsorb with noticeably different strength to a GaAs (100) surface. In our study, we analyze the differences of the characteristic helix-coil transitions observed in our simulations employing an all-atom model based on the ECEPP/2 force field in vacuum and implicit solvent. Here we primarily focus on the folding channels as seen in the free-energy landscape, where the free energy is expressed as a function of a suitably defined overlap parameter [4].

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AKB 40.5 Wed 16:30 P3

Traction Force Microscopy on Elastic Layers of Finite Thickness — •Rudolf Merkel, Claudia Cesa, Bernd Hoffmann, and Norbert Kirchgessner — Institute of Thin Films and Interfaces 4, Research Centre Jülich, Germany

Most living cells adhere to solid substrates and apply sizeable mechanical forces to them. Such forces are applied predominantly at focal adhesion sites which are micron sized protein complexes in the adhesion zone. In recent years traction force microscopy was introduced as a technique to discern the force contributions of different focal adhesion sites of one cell [1,2]. Here cells are cultivated on very soft films that are deformed by cell forces. The resulting deformation fields are measured by tracking microstructures on the film surface. Data evaluation relies on the fact that forces and displacements are connected by the mechanical Greens' tensor. Here we present expressions for the Greens' tensor of an elastic film of finite thickness bonded to a rigid substrate. These results show distinct deviations from the Greens' tensor of an elastic half space that has been exclusively used in this technique up to now. Moreover, we validated these results experimentally.

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[2] Balaban et al., Nature Cell Biol. **3** (2001) 466.

AKB 40.6 Wed 16:30 P3

Competition of Diffusion and Driven Motion in Lattice Gases — •Hauke Hinsch[1], Paolo Pierobon[1,2], and Erwin Frey[1] — [1]Arnold Sommerfeld Center and CeNS, Department of Physics, LMU München, Germany — [2]Hahn-Meitner-Institut, Abteilung Theorie, Berlin, Germany

Driven and diffusive lattice gases have proved useful as model systems for a variety of biological transport processes like ribosomal mRNA transcription or the motion of molecular motors along microtubules. Furthermore, they have attracted interest as a paradigm of non-equilibrium systems in statistical physics which exhibit a surprisingly rich phase behavior. Recently, the total asymmetric exclusion process (TASEP) has been extended by equilibrium bulk ad- and desorption dynamics resulting in interesting competitive effects (Parmeggiani, PRL 90, 2003). We study the competition of driven and diffusive motion on two one-dimensional lattices. An investigation with mean-field theory and Monte Carlo techniques reveals novel behavior and limitations of mean-field theory.

AKB 40.7 Wed 16:30 P3

Two-Dimensional Dynamics of a Semiflexible Polymer in Flow — •Tobias Munk and Erwin Frey — Arnold-Sommerfeld-Center, LMU München

In this poster we address the question how a single stiff polymer moves in a viscous fluid environment. The model system we refer to is the bio-polymer F-actin. The polymer is represented by a continuous two-dimensional space curve with a fixed length and a curvature-dependent bending energy. Furthermore we account for the constraint of inextensibility by introducing a Lagrange multiplier into the hamiltonian. By invoking suitable eigenfunctions we obtain a system of coupled first order stochastic differential equations of Langevin type, which can be solved numerically.

We present results for the polymer's motion in two simple flow fields: In a shear flow, the semiflexible filament periodically tumbles. Each of these tumbling events induces a transient buckled conformation, induced by the interplay of elastic, viscous and stochastic forces. In a toggled elongational flow, we observe the dynamics of the force extension and tension propagation.

Our numerical results nicely complement recent experiments with DNA in flow. Furthermore, they predict some behaviour specific to F-actin, which is considerably stiffer than DNA, to be observed in future experiments.

AKB 40.8 Wed 16:30 P3

Vasculature remodeling in tumor-induced angiogenesis – a stochastic model — •Raja Paul[1], Katalin Bartha[2], and Heiko Rieger[3] — [1]BIOMS, IWR, Ruprecht-Karls-University Heidelberg, D-69120 Heidelberg, Germany — [2]Department of Medical Biochemistry, Semmelweis University, Budapest, Hungary — [3]Theoretische Physik, Universität des Saarlandes, D-66041 Saarbrücken

Based upon a recently introduced model[1] for vascular network remodeling via vessel cooption, regression and growth in tumors[2] we study a dynamically evolving two-dimensional biconnected network incorporating the effect of probabilistic neo-vascularization and vessel collapse. The morphology of a regular vasculature is drastically changed in the presence of an expanding tumor. Independent vessel collapse results in a percolation transition of the network, flow correlated collapse stabilizes the network in the tumor center at a non-vanishing microvascular density (MVD). MVD, blood flow and shear force has been computed for a wide range of parameters and found to be in good qualitative agreement with experimental data[3] for human melanoma.

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AKB 40.9 Wed 16:30 P3

Influence of lipid rafts on cell signalling — •Stefan Semrau and Thomas Schmidt — Biophysics, University Leiden

Heterogeneities such as lipid rafts are believed to play a major role in cell signalling by influencing the diffusion and localization of proteins in the plasma membrane. Colocalization of proteins seems to be crucial at the beginning of the signal transduction pathway. Lipid rafts, whose existence in living cells is suggested by many experiments, are cholesterol and sphingolipid enriched membrane domains in which the lipid phase is probably different from that of the environment. We study lipid rafts in controllable model systems that are much less complex than living cells but suitable to mimic lipid rafts: structured supported lipid bilayer membranes and giant unilamellar vesicles (GUVs) from lipid mixtures. The influence of e.g. the size, shape, boundary behaviour and composition of membrane domains on the diffusion of fluorescently labelled proteins or lipids is studied by single-molecule tracking and Monte-Carlo simulations.

AKB 40.10 Wed 16:30 P3

Topological correlations enhance pattern formation in reaction-diffusion processes on scale-free networks — •Sebastian Weber[1], Marc-Thorsten Hütt[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstr. 8, 64289 Darmstadt, Germany — [2]Theoretische Biologie und Bioinformatik, Technische Universität Darmstadt, Schnittspahnstr. 3, 64287 Darmstadt, Germany

We study the reaction-diffusion processes $A + A \to \emptyset$ and $A + B \to \emptyset$ on uncorrelated, disassortative, and assortative scale-free networks. A method to suitably compare the pattern formation on these different networks is developed. We apply this method to quantify the residual pattern formation occurring on uncorrelated networks. The analogous analysis of disassortative and assortative networks shows that degree correlations substantially alter the dynamical behavior and that such topological correlations yield an enhanced pattern formation.

[1] S. Weber, M.-Th. Hütt, and M. Porto (submitted)

AKB 40.11 Wed 16:30 P3

Prediction of site-specific amino acid distributions and limits of divergent evolutionary changes in protein sequences — •Markus Porto[1], Ugo Bastolla[2], H. Eduardo Roman[3], and Michele Vendruscolo[4] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstr. 8, 64289 Darmstadt, Germany — [2]Centro de Biología Molecular 'Severo Ochoa', Cantoblanco, 28049 Madrid, Spain — [3]Dipartimento di Fisica, Università di Milano Bicocca, Piazza della Scienza 3, 20126 Milano, Italy — [4]Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge CB2 1EW, UK

We derive an analytic expression for site-specific stationary distributions of amino acids. The stationary distributions that we obtain have a Boltzmann-like shape, and their effective temperature parameter, measuring the limit of divergent evolutionary changes at a given site, can be predicted from a site-specific topological property. These analytic results, obtained without free parameters, are in very good agreement with the site-specific amino acid distributions obtained from the Protein Data Bank.

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AKB 40.12 Wed 16:30 P3

Elastic properties of viral capsids — •Mathias Puhlmann and Peter Lenz — AG Komplexe Systeme,Philipps-Universität Marburg,Renthof 6, 35032 Marburg

Empty viral shells have astonishing elastic properties. Recent experiments on bacteriophage $\phi 29$ [1] have shown that these nano-containers

withstand nano-newton forces. Their elastic response to applied point forces is nonlinear and varies across the surface. To elucidate these phenomena we study numerically discrete elastic models. Our simulations reveal the connection between the geometry of viral capsids and their mechanical properties. The numerically determined distribution of elastic spring constants agrees well with the experimental findings. By measuring the stress distribution we are able to predict the rupture probabilities across the capsid surface.

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AKB 40.13 Wed 16:30 P3

Supramolecular organization of photosynthetic complexes in model membrane systems — •Tobias Pflock[1], Manuela Dezi[2], Giovanni Venturoli[2], Jürgen Köhler[1], and Silke Oellerich[1] — [1]Experimentalphysik IV, Universität Bayreuth, D-95445 Bayreuth — [2]Dept. of Biology, University of Bologna, Italy

A common feature of biological membranes is the supramolecular organization of proteins within the membrane to functional units. This process involves a close interaction between the membrane lipids and proteins. Therefore, it is of particular interest to understand the role of lipids for the spatial membrane organization of the proteins. In order to direct this question in a fundamental way, we chose to reconstitute proteins into model membrane systems. This approach allows to sensitively control the membrane lipid composition as well as the lipid-protein ratio. An interesting system for these studies is the photosynthetic unit of purple bacteria, consisting of the reaction centre (RC) and the light-harvesting complexes LH2 and LH1. These pigment-protein complexes organize very efficiently to highly functional units within the natural photosynthetic membrane. The spatial organization of these proteins in model membranes as a function of the membrane composition can be studied by using "Giant unilamellar vesicles" (GUV). These vesicles allow a direct observation of protein diffusion and clustering within the membrane by the use of fluorescence wide-field imaging, which can be employed with a sensitivity down to the single-molecule level. For these studies, we succeeded in establishing a protocol for the efficient preparation of GUVs over a wide range of lipid-protein ratios.

AKB 40.14 Wed 16:30 P3

Pumping Nanofluidics Optically along Freely Defined Patterns — •Franz Weinert and Braun Dieter — Noether Group on Dissipative Microsystems, Applied Physics, Ludwig Maximilians Universität München, Amalienstr. 54, 80799 München, Germany

Liquid is pumped in thin films by nonlinear thermal expansion. The flow geometry is not defined by channels, but by the focus movement of an infrared laser scanning microscope. The fluid follows the laser path in reverse direction. Pumping matches a theory based on temperature dependent viscosity. For decreasing chamber thickness, pump speed rises quadratically, reaching 20um/s for 2.5um. Highly viscous liquids are pumped equally well. The technique frees micro- and nanofluidics from the load of channel lithography, delicate interfacing and complex pump design.

AKB 40.15 Wed 16:30 P3

Conductivity of unordered denatured and hybridized DNA — •Thomas Kleine-Ostmann[1], Christian Jördens[1], Kai Baaske[1], Thomas Weimann[2], Martin Hrabe de Angelis[3], and Martin Koch[1] — [1]Inst. f. Hochfrequenztechnik, Schleinitzstr. 22, 38106 Braunschweig — [2]Physikalisch-Technische Bundesanstalt, Bundesallee 100, 38116 Braunschweig — [3]GSF National Research Center for Environment and Health, Ingolstädter Landstr. 1, 85764 Neuherberg

The electronic properties of DNA remain highly controversial. Depending on the technique and the experimental conditions, a variety of - sometimes contradictory - results have been obtained. They are of paramount importance for two visionary technologies: self-assembled nanoelectronics and marker-free gene tests. Here, we report on the conductivity of natural DNA under ambient conditions. We examined both single-stranded and double-stranded herring DNA in buffer solution that consists of 120-3000 nucleotides. It was spotted and dried on Au nanocontacts deposited on oxidized Si with a gap size of 100 nm. I-V curves are obtained in a sealed measurement chamber that allows for the adjustment of the ambient relative humidity in a wide range from 10 to 100 percent. We find an exponential humidity dependence of the conductivity that is identical for single- and double-stranded DNA within the measurement accuracy. While the small conductivity of dry DNA is comparable to that of a large band-gap semiconductor, we attribute the increased conductivity of DNA at high humidity levels to water molecules accumulated at the phosphate backbone. We observe s-shaped I-V curves that can be well explained by the dissociation of water attached to the DNA molecules.

AKB 40.16 Wed 16:30 P3

The Stress of Leaves in our Climatic Environment — •Agnieszka Krol-Otwinowska, Karl Hieble, and Margret Giesen — Institut für Schichten und Grenzflächen, ISG 4, Forschungszentrum Jülich, D 52425 Jülich

Climatic changes as well as industrial pollution may have a dramatic effect on the health condition of plants. Our goal is to gain a new understanding of the correlation between the functionality of plant leaves and environmental factors from a surface sciencist*s point of view. For that purpose we introduce for the first time measurements of the surface stress of cuticular wax layers under climatic realistic conditions. The origin of surface stress is the local polarization of the electron charge density due to the chemical bonding of adsorbates. Using the laser deflection method (1) surface stress changes of the order of 0.01 N/m are detectable. Changes in the surface stress are hence sensitive indicators for interaction-induced charge changes and structural surface relaxations. We present studies of the surface stress of wax layers from cherry laurel (Prunus Laurocerasus) and apple leaves (Golden Delicious) as a function of climatic relevant parameters (e.g. gas dose, air humidity, pH, temperature, UV-light). (1) Rev. Sci. Instrum. 66(9), (1995), 4734

AKB 40.17 Wed 16:30 P3

The effect of differentiation on the deformability of cells — •Franziska Lautenschläger, S. Schinkinger, M. Jungnitsch, J. Schwarz, and J Guck — Universität Leipzig, Abteilung Physik der weichen Materie, Linnéstr. 5, 04103 Leipzig, Germany

From molecular biology it is known that during differentiation there are characteristic changes in the three main constituents of the cytoskeleton-microtubules, actin, and intermediate filaments. Since the cytoskeleton is the main structural element in cells these changes should be reflected to varying degrees in their mechanical properties. To test this hypothesis, we investigated the impact of differentiation and specific toxins on cell elasticity with the Optical Stretcher. In our experiments we used human neural precursor cells (HPCM) which were differentiated into glia cells, GABAergic, and dopaminergic neurons as well as hematopoietic precursor cells (NB4 cells) treated with retinoic acid (ATRA) to differentiate them into mature blood cells. Our results show an increasing stiffness and a decreasing variance during differentiation. This suggests using deformability as a new cell marker for stem cell characterization and sorting.

AKB 40.18 Wed 16:30 P3

Probability for specific bond formation for a Brownian particle in linear shear flow above a wall — •Christian Korn[1,2] and Ulrich S. Schwarz[1,2] — [1]University of Heidelberg, Im Neuenheimer Feld 293, D-69120 Heidelberg, Germany — [2]Max Planck Institute of Colloids and Interfaces, D-14424, Potsdam, Germany

Cohesion in biological systems and biotechnological applications is usually provided by specific bonds between receptors and ligands. The formation of these bonds requires a physical transport process which brings receptors and ligands to sufficient proximity for binding.
As a non-trivial example here we study the motion of a rigid spherical Brownian particle in linear shear flow carrying receptors for ligands covering a planar boundary wall. This situation is relevant for the binding of white blood cells to blood vessel walls, which can be studied quantitatively in flow chambers. The appropriate mobility matrix follows from the Stokes equation and is position-dependent due to the presence of the wall. This leads to a non-trivial multiplicative noise term in the corresponding Langevin equation.
We determine the mean time for receptor-ligand encounter as a function of the Péclet numbers, which describe the transition from diffusive to deterministic transport. We also show in quantitative detail how the results are influenced by the values of receptor and ligand coverage.

AKB 40.19 Wed 16:30 P3

Towards surface-based model systems of the pericellular coat — •Ralf Richter[1,2] and Joachim Spatz[1,2] — [1]University of Heidelberg, Department of Biophysical Chemistry, INF 253, D-69120 Heidelberg — [2]Max-Planck-Institute for Metals Research, Department New Materials & Biosystems, Heisenbergstrasse 3, D-70569 Stuttgart

The pericellular coat of many cell types constitutes an intriguing self-organized system with multiple roles in cell division, migration, adhesion

and signaling. The polysaccharide hyaluronan is a vital structural component of this strongly hydrated matrix. The nature of hyaluronan and its interaction with hyaluronan binding proteins determine the mechanical properties of the coat which are intimately related to its biological function.

Due to the complexity of living cells, the understanding of self-organization and mechanical properties of the pericellular coat in vivo or in vitro constitutes a considerable challenge. Complementary to investigations on living cells, simplified model systems can help to address specific questions in a controlled manner.

In our work, we aim to create models of the pericellular coat on flat supports. Our approach allows for the application of a whole range of surface sensitive label-free characterization techniques. The immobilization of hyaluronan on a solid-supported lipid membrane is an example of the envisaged bottom-up approach that allows the creation of models of increasing complexity that mimic various aspects of the pericellular coat. With these models we expect to gain information about the relationship between composition, structure and mechanics of the pericellular coat.

AKB 40.20 Wed 16:30 P3

Statistics of local sequence alignments — •Stefan Wolfsheimer and Alexander K. Hartmann — Institut für theoretische Physik, Göttingen, Germany

Sequence alignment is a tool used for comparison in protein and DNA databases. Widely used algorithms are e.g. BLAST and FASTA. Knowledge about the distribution of gaped optimal subalignment scores of random sequences is essential in order distinguish relevant alignments from alignments that occurred by chance[1]. Analytical solutions are only available for the ungaped case, and yield the Gumbel distribution. Nevertheless, for database applications gaped alignments schemes are much more relevant.

Here we use a method to obtain regions of the distribution on a wide range, including the rare event tail down to $p \sim 10^{-40}$. This is similar to the problem of obtaining the density of states of a complex physical system, like spin glasses and therefore methods from statistical mechanics could be adopted [2]. The optimum alignment score corresponds to the ground state of the physical system. By simulated annealing techniques and using the sequences as dynamic variables, rather than the alignments, the distribution of scores is obtained. We study different BLOSUM and PAM scoring matrices and quantifiy in each case the deviations in the rare event tail from the Gumble distribution.

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[2] A.K. Hartmann, Phys. Rev. E **65**, 056102 (2002)

AKB 40.21 Wed 16:30 P3

Light scattering measurements on single cells in a dual beam laser trap — •Moritz Kreysing, Kort Travis, and Jochen Guck — Institute for Soft Matter Physics, Universität Leipzig, Linnéstr. 5, 04103 Leipzig

The principle aim of this work is the development of an easy to handle fast working method to measure light scattering properties of single cells in aqueous media. Therefore we made use of the high symmetry of cells lying directly on the axis of a dual beam laser trap. Additionally to the common setup of this trap laser light in the visible range is emitted by one of the fibers, scattered by the cell and is then partly coupled into the opposite fiber. Measuring this recoupled light while varying the position of the cell by modifying the trapping lasers power allows to calculate the scattered light's intensity as a function of the angle. Comparing this to standards measured with a confocal microscope and models based on Mie theory provides information about average refractive index, size, and deformation of the cell, for example caused by using the setup as optical stretcher. Further insights into the dielectric properties of cell organelles and surface morphology can be obtained. This could eventually be utilized in cell sorting applications.

AKB 40.22 Wed 16:30 P3

Phase behaviour of DMPC and farnesol mixtures — •Maria Hanulova and Sergio S Funari — Hasylab at Desy, Notkestr. 85, D-22603 Hamburg

Farnesol is a 15carbon polyisoprenol derived from the mevalonate pathway. It regulates the cell cycle, post-translationally attaches to proteins and so helps protein sorting in cell membranes, inhibits neural channels, enhances drug penetration and sensitizes bacteria to antibiotics.

We studied the phase behaviour of DMPC (dimyristoyl phosphatidylcholine) and farnesol mixtures in the temperature range 5-80°C using X-ray diffraction and polarized optical microscopy. The mixtures were prepared in water or in buffer (10mM HEPES, 100mM NaCl, 1mM EDTA, pH 7.4).

Farnesol itself does not form ordered structures and does not mix with water, but incorporates into lipid membranes. DMPC + farnesol mixtures form lamellar phases at low temperatures. The gel-fluid transition is broader than in DMPC and occurs at lower temperatures. The DMPC ripple phase is suppressed. In the fluid state, we usually observed two coexisting lamellar phases, probably farnesol-rich and farnesol-poor domains.

In mixtures with farnesol contents up to 50 mol%, the lamellar phase persists till 80°C. Interestingly, at higher farnesol content the lamellar phase vanishes at 40-45°C and new ordered structures assemble on further heating. At about 60°C a cubic phase occurs and an additional hexagonal phase is seen above 70°C. The thermal behaviour nearly does not change for mixtures with 60 to 95 mol% farnesol.

AKB 40.23 Wed 16:30 P3

Cell rheology at high stress — •Philip Kollmannsberger, Johannes Pauli, Claudia Mierke, Carina Raupach, and Ben Fabry — Zentrum für Medizinische Physik und Technik, Henkestr. 91, 91054 Erlangen

Rheology measurements in many cell types have established that cells exhibit a power-law creep modulus, or equivalently, a weak frequency dependence of the storage and loss moduli according to a power-law. These findings indicate that cell rheology is governed by multiple processes that play out on vastly different time scales. Previous measurements, however, where carried out in the linear regime, where stress and strain are related by a simple linear relationship, and the superposition principle holds. Here we measured the displacement of CSK-bound superparamagnetic beads in a feedback-controlled magnetic field gradient at high forces up to > 10 nN for which linearity, superposition and time scale free behavior of responses have not been established. At all forces, bead displacement d during during the on-phase (creep) and off-phase (relaxation) was well described by a power law: $d(t) = a \cdot (t/t_0)^b$. For forces less than 2 nN, power-law parameters during creep and recovery were identical. At higher forces, however, the recovery became progressively incomplete (a decreased) and faster (b increased). These results suggest that at higher forces, stable, long-lived stress-bearing structures within the cytoskeleton are disrupted. Subsequent structural rearrangements are then expected to contribute to a speed-up of relaxation processes.

AKB 40.24 Wed 16:30 P3

Controlling the Surface Density of DNA on Au by Electrically Induced Desorption — •Kenji Arinaga[1,2], Ulrich Rant[2], Jelena Knežević[2], Erika Pringsheim[2], Marc Tornow[2], Shozo Fujita[1], Naoki Yokoyama[1], and Gerhard Abstreiter[2] — [1]Fujitsu Laboratories Ltd., 10-1 Morinosato-Wakamiya, Atsugi 243-0197, Japan — [2]Walter Schottky Institut, Technische Universität München, 85748 Garching, Germany

Self-assembled DNA layers on solid surfaces have been of great interest and widely introduced to various techniques for bio-molecular investigations. Recently, we have investigated the active electrical manipulation of oligodeoxynucleotides on Au, employing optical means. We showed that the packing density within the DNA layer crucially determines the free mobility (rotatability) of individual molecules on the surface [1]. While this parameter bears a particular significance, very few investigations have been reported that address methods for controlling the surface density of DNA on Au. In this contribution, we discuss the adsorption mechanisms of thiolated DNA on gold as well as desorption properties under controlled substrate potentials. The adsorption strongly depends on the diffusion of DNA and the ionic strength of electrolyte. On the other hand, we show in situ and in real time that electrochemically induced desorption can efficiently be controlled by tuning the magnitude and application-time of the substrate voltage. As a result, it is demonstrated that this method of electrical desorption provides effective means to adjust the surface density of DNA on gold surfaces.

[1] U. Rant, K. Arinaga et al., Nano Letters 2004, 4, 2441.

AKB 40.25 Wed 16:30 P3

Modelling cell-population growth of in-vitro monolayers — •Michael Block[1], Dirk Drasdo[2], and Eckehard Schöll[1] — [1]Institut für Theoretische Physik, Technische Universität Berlin, Hardenbergstr. 36, 10623 Berlin — [2]IZBI University Leipzig, Härtelstrasse 16-18, 04107 Leipzig, Germany

Which mechanisms determine the growth kinetics and phenotypes of tumors is still largely unknown and - due to unknown influences - can even in cell cultures often not be clearly re-solved. We here present computer simulations of growing monolayers that permit a systematic analysis of the effect of migration, cell-cell adhesion, apoptosis, the cell cycle time distribution, biomechanical influences, mutations and medium properties on the bulk and surface growth dynamics. For this purpose we consider a kinetic Monte Carlo approach on a random lattice on which, as we explicitly show, lattice artifacts are eliminated. The model is calibrated according to off-lattice models that represent kinetic and bio-physical parameters explicitly ([1]). We compare our simulation results quantitatively with experimental findings by Bru et. al. ([2]), propose alternative mechanisms for their explanation and predict how it may be possible to distinguish between them by suitable experiments.

[1] Drasdo, D. and Höhme, St., Phys. Biol. 2, 133-147 (2005).
[2] Bru et al., Biophys J. 85, 2948-61 (2003).

AKB 40.26 Wed 16:30 P3

Counterion profile at a planar charged interface by anomalous x-ray reflectivity — •Klaus Giewekemeyer and Tim Salditt — Institut für Röntgenphysik, Universität Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen

The distribution of counterions in the vicinity of charged surfaces is a theoretically well-studied subject with high relevance for biological problems like protein adsorption to membranes, membrane fusion etc. Although theoretical research on the subject has produced very detailed results that go far beyond the mean field approach (e.g. ion-ion correlation effects, particle volumes), accurate experimental evidence even for the historic Poisson-Boltzmann (PB) mean field result is rare and not completely satisfying. Here an approach to the problem is made by studying the simplest, in the PB theory still analytically solvable case of a planar charged surface at the solid liquid interface. As an experimental realization of this system a DODAB (Di-Octadecyl-Dimethyl-Ammonium-Bromide) monolayer adsorbed to an OTS (Octadeyl-Trichloro-Silane) monolayer bound to a Silicon substrate is chosen. The distribution of the systems Bromide counterions in aequous solution has been probed with resonant small angle x-ray reflectivity. Furthermmore, the variation of the Gouy-Chapman length of the counterion cloud has been studied by changing the charge density of the amphiphilic layer on top of the OTS by mixing the cationic DODAB with zwitterionic DPPC (Di-Palmitoyl-Phosphatidyl-Choline). Selected results and their analysis from an experiment at ESRFs ID 1 beamline are presented.

AKB 40.27 Wed 16:30 P3

Control of Single Nanocrystal Fluorescence Emission in a combined TIRFM/AFM Setup — •Rainer Eckel[1], Volker Walhorn[1], Christoph Pelargus[1], Thomas Nann[2], Dario Anselmetti[1], and Robert Ros[1] — [1]Experimental Biophysics and Applied Nanosciences, Faculty of Physics, Bielefeld University, Universitaetsstr. 25, 33615 Bielefeld, Germany — [2]Freiburg Materials Research Center (FMF), Stefan-Meier-Str. 21, 79104 Freiburg, Germany

Optomechanical switching and local energy transfer between individual nanoobjects are concepts of growing importance for investigating and manipulating matter at the nanoscale. We report on a new possibility to switch the fluorescence emission of a single semiconductor nanocrystal (quantum dot) by external, optomechanical intervention of an AFM tip. The experimental setup combines atomic force microscopy (AFM) and total internal reflection fluorescence microscopy (TIRFM) in a way that enables laser induced fluorescence imaging of single fluorophores and their simultaneous mechanical addressing with an AFM probe. The fluorescence quenching of an individual semiconductor quantum dot could be controlled mechanically, using an AFM tip functionalized with gold nanoparticles as the quenching agent. It was possible to repeatedly switch the fluorescence emission from the bright (blinking) state to the dark (quenched) state. This opens fascinating possibilities for future simultaneous force spectroscopy and fluorescence resonant energy transfer measurements on single biomolecular complexes.

AKB 40.28 Wed 16:30 P3

Highly oriented liquid water within the cationic lipid DODAB — •Lydia Woiterski[1], Josef A. Käs[1], David W. Britt[2], and Carsten Selle[1] — [1]Institute of Experimental Physics I, University of Leipzig, Linnestraße 5, D-04103 Leipzig,Germany — [2]Department of Bioengineering, University of Utah, Salt L ake City, UT , 84112, USA

Cationic lipid membranes spontaneously form complexes with DNA. Therefore, cationic synthetic lipids are widely used for the preparation of gene transfection systems.

We performed a fundamental attenuated total reflection (ATR) Fourier-Transform infrared (FTIR) spectroscopic study on the phase behavior and hydration properties of the cationic lipid dioctadecyldimethylammonium bromide (DODAB).

A unique shape of the ν(OH)-absorption band was detected that arises from liquid water in the vicinity of the polar lipid headgroup. Six subbands of the OH-absorption can be assigned to different populations of highly oriented water molecules. Furthermore, the spectroscopic properties of the headgroup bound water were observed to be strongly sensitive to the halide counterion present.

Another newly found feature of DODAB is a drastic change in the ν(CNC)-absorption which is attributed to a strong conformational alteration in one of the alkyl chains when the water is completely removed.

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An Intestinal Drug Transport Model — •Niko Komin and Raúl Toral — IMEDEA, Palma de Mallorca, Spain

Drug absorption in the intestinal tract happens due to two different processes: passive diffusion proportional to the concentration difference and active transport via a molecular pump. The active transport is usually described as a Michaelis-Menten process.

Little is known about the number and location of the pumps (inside/outside the intestine) and its governing parameters. Experiments and nonlinear parameter regression try to know more about the process, but a deeper understanding of the underlying process would facilitate the experimentators work and help on the drug development, meaning less experiments, safer and maybe more specific drugs.

In this work differential equations describing the continuous concentration transport are analysed. Long term and short term solutions are desired. Besides we try to explain the variability in the measurements, introducing variablitiy or noise into the equations.

AKB 40.30 Wed 16:30 P3

Purification and characterisation of nacre proteins and their interaction of nacre proteins with $CaCO_3$ at the molecular scale — •Laura Treccani, Fabian Heinemann, and Monika Fritz — Institut of Biophysics, University of Bremen, Germany

Nacre (mother of pearl) of certain molluscs furnishes an elegant model to investigate biomineralizing processes. Nacre is a polymer-ceramic composite material consisting mainly of $CaCO_3$ and biomolecules (chitin and proteins). It shows a highly ordered hierarchical structure consisting of parallel layers of aragonite tablets (500 nm thickness) alternated with layers of organic material (10 nm thickness). Nacre has a high mechanical strength and resistance against corrosion in seawater that far exceeds the properties shown by the inorganic $CaCO_3$ mineral. Organic molecules are necessary for a controlled nucleation and growth of the material. The role of several water-soluble proteins purified from nacre of *H. laevigata* has been investigated. Crystallization experiments were performed with the AFM (Atomic Force Microscope) in aqueous solution on a calcite surface and with the ammonium carbonate method. It has been elucidated that each protein influences the crystal growth in a different way. Some proteins can act as nucleators, where others can act as inhibitors. Recently small proteins directly incorporated into the mineral phase have been detected. The characterisation of the single biomolecules and their roles in self-organizing mechanisms of nacre formation could lay the basis for a better understanding of biomineralization and the development of new synthetic biomaterials.

AKB 40.31 Wed 16:30 P3

Orientation of the Membrane-Active Peptide Gramicidin S within Model Membranes — •Stefan Surber — Universität Leipzig, Lehrstuhl für die Physik Weicher Materie, Fakultät für Physik und Geowissenschaften, Linnestr. 5, D-04103 Leipzig

S. Surber, J.A. Käs and C. Selle

The amphipathic peptide gramicidin S (GS) attacks the integrity of membranes but the detailed mode of action is still unclear. In order to unravel the orientation of GS within models for bacterial and mammalian membranes - which is considered crucial for fundamental interactions between GS and membrane lipids - we performed an attenuated total reflection (ATR) Fourier transformed infrared (FTIR) spectroscopic study. For this purpose, mixtures from GS and phospholipid from neutral and

anionic phospholipids representing bacterial and mammalian membrane components were used. The effect of varied hydration on the peptide-lipid interactions was also investigated. For the first time, the orientation of GS within model membranes was directly measured utilizing the related amide I IR spectroscopic absorptions. First results on the orientation of GS in Langmuir-Blodgett transferred lipid monolayers are also presented.

AKB 40.32 Wed 16:30 P3

Electrostatic Interactions modulated within Monolayers of charged Amphiphilic Peptide — •Ann Falk, Stefan Surber, Lydia Woiterski, Josef Käs, and Carsten Selle — Universität Leipzig, Fakultät Physik & Geowissenschaften, Exphysik I, PWM

We performed a fundamental investigation on the effect of the antimicrobial peptide gramicidin S (GS) on the properties of lipid monolayers as membrane mimics. As a first step, pure GS monolayers on subphases of physiologic ionic strength were characterized at room temperature (I ˜ 0.19 M). Pressure-area isotherms of GS monolayers were recorded indicating a phase transition from a liquid to a solid phase in two dimensions that was dependent on the subphase pH. This variation can be explained by pH-dependent basic amino acid side group charges of GS. Brewster-Angle-Microscopy was used to monitor the solid-phase domain growth during the 2 D phase transition. We observed that the shape of the solid domains is surprisingly sensitive to pH alterations over ten orders of magnitude. X-ray reflectivity and grazing incidence diffraction measurement were performed under analog conditions. First results of experiments on the interactions of GS with various phospholipids representing bacterial and mammalian membrane components are also presented.

AKB 40.33 Wed 16:30 P3

Dynamics of the denaturated protein Ribonuclease A — •Ralf Biehl[1], Bernd Hoffmann[2], Michael Monkenbusch[1], Aurel Radulescu[1], Bela Farago[3], Rudolf Merkel[2], and Dieter Richter[1] — [1]Institut fuer Festkoerperforschung, Forschungszentrum Juelich, Germany — [2]Institut fuer Schichten und Grenzflaechen, Forschungszentrum Juelich, Germany — [3]Institut Laue-Langevin, Grenoble, France

The protein folding and function is strongly coupled to the structure and the thermal equilibrium fluctuations. In view of the macromolecule energy landscape the protein folding follows a path from the unfolded state at high energy to the low energy state at the final configuration with intermediate states in between. Thereby the secondary and ternary structure is determined. Catalytic activities or transport mechanisms follow transitions between intermediate states in the energy landscape. All involve configurational changes on length scales from single amino acids to sizes of complete a helices or b sheets and the total size of the protein. Timescales reach from picoseconds to microseconds. A way to explore the energy landscape at equilibrium is to observe thermal fluctuations of the protein. By changing environmental parameters e.g. temperature the level of energy is changed. We present here measurements on bovine Ribonuclease A by means of SANS and Neutron Spinecho Spectroscopy together with DLS measurements. The protein dynamics was examined under conditions providing the possibility of refolding to the natural state. We compare our experimental results with simple and more complex protein models to reproduce the observed dynamics.

AKB 40.34 Wed 16:30 P3

Self-assembled phagosome crystal structures in fibroblasts — •Vamsi Kodali[1,2], Joachim Spatz[1,2], and Jennifer Curtis[1,2] — [1]Max-Planck-Institute for Metals Research, Department New Materials & Biosystems,Heisenbergstr. 3, D-70 569 Stuttgart. — [2]University of Heidelberg, Department of Biophysical Chemistry.

During phagocytosis, cells actively deform their plasma membranes to engulf foreign objects. The engulfed object(phagosome)is then actively transported towards the nucleus by dynein motors in a process called retrograde motion. In this study we present the surprising observation that fibroblast cells ingest large numbers of latex microspheres and arrange them in beautiful 2D crystals with hexagonal order in the perinuclear region. We study the process of the crystallization which occurs for bead sizes ranging from 750 nm up to at least 6 microns, where the upper limit has not been fully explored. We also consider the influence of the crystallization of the beads on normal cell processes such as cell proliferation and study the impact of this massive volumetric intrusion on the organelles and the cytoskeleton of the fibroblasts. It was also found that there is an area limitation for the crystal structures in the cell and this limited area depends on the cell size and is independent of the bead size. Finally, we present the counterintuitive observation that mixed sizes of microspheres tend to phase separate with the large spheres moving to the center even under biased initial conditions.

AKB 40.35 Wed 16:30 P3

Transport along freely suspended actin cortex models in a controlled microfluidic environment — •Simon Schulz[1,2], Tamas Haraszti[1,2], Wouter Roos[2], Christian Schmitz[1,2], Jens Ulmer[1,2], Stefan Graeter[1,2], and Joachim P. Spatz[1,2] — [1]Max-Planck-Institute for Metals Research, Department New Materials & Biosystems, Heisenbergstr.3, D-70569 Stuttgart — [2]University of Heidelberg, Department of Biophysical Chemistry, INF 253, D-69120 Heidelberg

Arrays of microfabricated pillars are constructed to serve as a template for mimicking the actin cortex of cells. The 3D template surface prevents interaction of the actin filaments hanging between pillars. A special flow-cell design enables applying flow around a network of actin freely suspended between polydimethylsiloxane pillars. This opens new possibilities to study the biomechanics of two-dimensional actin networks as a function of actin-crosslinkers, to observe the active diffusion of molecular motors operating on pending networks and to investigate the alternations in the transport of microscopic particles, coated by different proteins and molecular motors, along these actin cortex models under the drag of flow.

Additionally, actin filaments act as tracks for guiding passive and active transport of cargo such as organelles or microspheres by molecular motors like myosin-V. The stiffness of the F-actin can be tuned by bundling through various cross-linkers.

These transport problems are biomimetic studies of tracks and external driving force on a statistical process of two-dimensional networks isolated from the complicated and undetermined cellular environment.

AKB 40.36 Wed 16:30 P3

Effect of cholesterol on the collective dynamics ofphospholipid membranes — •Beate Brüning[1,2], Tim Salditt[2], Arno Hiess[1], and Maikel C. Rheinstädter[1] — [1]Institut Laue-Langevin,B.P. 156,6 rue JulesHorowitz,38042 Grenoble,France — [2]Institut für Röntgenphysik,Friedrich-Hund-Platz1,37077 Göttingen,Germany

Phospholipid membranes often serve as simple model systems to understand basic properties of their far more complex biological counterparts. Only recently, the collective short wavelength dynamics in a model membrane system (DMPC), i.e., the corresponding dispersion relation, were investigated by inelastic neutron scattering techniques [1]. The insertion of the membrane-active molecule cholesterol, which is known to regulate membrane fluidity, membrane permeability and the lateral mobility of proteins, is now a first step towards the understanding of coherent dynamics in physiologically relevant membrane systems.

While the structure of phospholipid/cholesterol systems is well studied, their short scale dynamics are so far largely unknown. We have studied the influence of cholesterol to the collective short wavelength fluctuations of the phospholipid acyl chains using inelastic neutron scattering. The measurements were carried out with thermal as well as cold neutrons on the three-axis spectrometers IN12 and IN8 at the high flux reactor of the ILL in Grenoble, France. We were able to determine the dispersion relations within the plane of the membranes in the fluid and the liquid ordered phases of samples with two different cholesterol contents, namely 3% and 35%.

[1] M.C. Rheinstädter *et al.*, Phys. Rev. Lett. 93, 108107 (2004).

AKB 40.37 Wed 16:30 P3

Approximation of localised calcium fluxes — •Kajetan Bentele and Martin Falcke — Hahn Meitner Institut Berlin, Glienickerstrasse 100, 14109 Berlin, Germany

To model spatially resolved intracellular calcium-dynamics, it is necessary to investigate the calcium current through a single channel. An open channel can be modelled as a pore connecting an intracellular calcium store, the endoplasmic reticulum (ER), with the cytosol. The radius of such a channel is about 6 nanometres in contrast to the diameter of the cell ranging from 10 to 100 micrometres. Opening of such a channel leads to a localised increase of the cytosolic calcium concentration nearby the channel. This process is the fundamental building block in the concentration dynamics of global events such as calcium waves and oscillations.

We present a quasi-steady state approximation of the single-channel current with a simplified dynamics. The approximation is based on the

observation that the channel current exhibits multiple time scales: infinitely many fast time scales and a long time-scale that can be up to 5 orders of magnitude larger. The former play a prominent role in building up the concentration-peak around the channel. The slow time scale is determined by the average concentration in the ER and therefore can be mimicked by a quasi steady state approximation. This approximation will be used in simulations to eliminate spatial dynamics in the ER.

AKB 40.38 Wed 16:30 P3

DNA elasticity and specific binding — •Nils Becker and Ralf Everaers — MPI Physik Komplexer Systeme, Dresden

In essential biological processes, DNA interacts with proteins in an indirect way. In some complexes the double helical structure of DNA remains intact, but is strongly deformed. Binding then depends on the deformability of the DNA. This indirect readout mechanism allows for binding to specific sequences based on their elasticity and structure.

An understanding of this kind of specific interaction requires detailed information about sequence-dependent DNA elasticity. Modeling DNA as a chain of rigid elements, the base pairs, this information can be encoded in elastic potentials between each step of two base pairs. Harmonic base pair step potentials have been determined in rather dissimilar ways from high-resolution structural data [1] and by molecular dynamics computer simulation of oligonucleotides [2].

We examine the relation of these two parametrizations. On this basis we give a measure for estimating how much the elastic deformation of a given base pair contributes to sequence specificity in a given complex. As a test case, we show results for the bacteriophage 434 repressor, a well-studied such complex [3], in which some base pairs are not contacted by the protein but still when mutated, greatly modify binding affinity.

[1] W. Olson et al., PNAS 95(19), 11163, 1998
[2] F. Lankas et al., Biophys J 85(5), 2872, 2003
[3] G.B. Koudelka et al., PNAS 85(13), 4633, 1988

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Molecular Dynamics Study of the Chromophore Binding pocket in Rhodopsin — •Minoru Sugihara[1,2], Markus Gruner[2], Peter Entel[2], and Volker Buss[1] — [1]Theoretical Low-Temperature Physics — [2]Theoretical Chemistry, University of Duisburg-Essen

The 11-cis retinal protonated Schiff base (pSb) is the chromophore in rhodopsin, the black/white photoreceptor in the vertebrate eye. The chromophore is covalently attached to Lys296 via a pSb and has a salt-bridge with the negatively charged counterion, Glu113. The first crystal structure of bovine rhodopsin[1] has revealed that the chromophore is fixed in the pocket by hydrophobic interaction at the β-ionone ring and polar interaction, in paticular by a salt-bridge. Upon illumination with light, the chromophore photoisomerizes from 11-cis to all-trans. The first intermediate, bathorhodopsin, stores 32-35 kcal/mol of the photon energy in the twisted all-trans form. The starting model of the chromophore binding pocket (534 atoms) was taken from the crystal structure[2]. In this study, the chromophore conformation inside the pocket, the origin of the twisted conformation, and the stability of the protonation state[3] will be discussed. For molecular dynamics study, the plane wave code, VASP[4] was used. The calculations were carried out on the IBM BlueGene/L at the Reseach Center Jülich. [1] Palczewski, K., Okada, T. et al. Science 289 (200 739.[2] Okada, T., Sugihara, M. et al. J. Mol. Biolog. 342 (2004) 571. [3] Buss, V. Chilarity 13 (2001) 13. Sugihara, M., Buss, V. et al. Biochemistry 41 (2002) 15259. Sugiahra, M., Buss, V. et al. J. Phys. Chem. B 108 (2004) 3673. Sugihara, M., Hufen, J. Biochemistry in press. [4] Kresse, G., Furhermüller J. Phys. Rev. B 54 (1996) 11169.

AKB 40.40 Wed 16:30 P3

DNA Melting in Aggregates: Impeded or Facilitated? — •Andrey Cherstvy[1] and Alexei A. Kornyshev[2] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Germany — [2]Department of Chemistry,Faculty of Physical Sciences, Imperial College London, SW7 2AZ, London, United Kingdom

How does DNA melt in columnar aggregate relative to its melting in diluted solution? Is the melting temperature increased or decreased with the aggregate density? Have DNA-DNA interactions, predominantly of electrostatic nature, an effect on the character of the melting transition? In attempt to answer these questions, we have incorporated the theory of electrostatic interactions between DNA duplexes [1,2] into the simplest model of DNA melting. The analysis shows that the effect of aggregate density is very different for aggregates built of homologous (or identical) DNA fragments relative to the case of DNA with random base pair sequences. The putative attraction between homologous DNA helices hampers their melting and increases the melting temperature and can even dramatically change the character of the transition [3]. In the aggregate of nonhomologous DNAs, the pattern of electrostatic interactions is more complicated, and their effect could be opposite; in some cases we may even expect electrostatically induced melting [3]. These findings define new directions for melting experiments in dense DNA assemblies.

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AKB 40.41 Wed 16:30 P3

Optical manipulation of neuronal cells in 3D scaffolds — •Andreas Christ and Jochen Guck — Institut für Physik weicher Materie, Universität Leipzig, Linnéstraße 5, 04103 Leipzig

Control of neuronal outgrowth is an important objective in neuroscience, cell biology and medicine. It already has been shown that this is possible in 2D by surface patterning or optically by gradient forces and in 3D environments by chemical gradients.

The aim of our research is to optically influence growth of neurites in a 3D scaffold. For this purpose we grow neuronal cells (NG-108) in fibrin gels and direct a non-focused low-power laserbeam into the region of cell growth. The gradient force exerted by the laser should pull the growth cone of neurites into the beam. The radiation pressure exerted by the laser on the growing neurite will then tend to direct the neurite into the direction of the beam propagation. This is confirmed by Confocal Laser Scanning Microscopy of the GFP-transfected cells.

AKB 40.42 Wed 16:30 P3

Study of DNA/RNA strand interactions using lattice models — •Christian Simm, Sanjay Kumar, and Ralf Everaers — Max-Planck-Institut für Physik komplexer Systeme, Dresden

Research in binding properties of DNA/RNA is key for the understanding of many biological processes - like hairpin formation in ssDNA and miRNA, RNA secondary structure, and bubble formation during DNA transcription. We study lattice models of DNA which account for base stacking and polarity of the DNA strands. We draw comparisons to simpler models without these features to get a better understanding of the effects of stacking and polarity. We use exact enumeration and Monte-Carlo simulation techniques to test assumptions of the nearest-neighbour model.

AKB 40.43 Wed 16:30 P3

Optimal Foraging Strategy: Angle Matters — •Udo Erdmann[1], Sebastian Göller[1], Lutz Schimansky-Geier[1], Igor M. Sokolov[1], and Frank Moss[2] — [1]Institut für Physik, Humboldt-Universität zu Berlin — [2]Center for Neurodynamics, University of Missouri at St. Louis

We report a theory to describe the motion of zooplankton. Into contrast to move just randomly like a classical Brownian particle, zooplankters like *Daphnia* or *Copepods* pick their turning angle from a distribution which is far from being Gaussian or equally distributed. This leads to different behavior in the motion compared to normal diffusion. The question which can be asked here is: Is there an evolutionary reason to forage for food in the aforementioned manner? The talk is planned to give an answer into that direction.

AKB 40.44 Wed 16:30 P3

Relating microstructure of biomaterials to mechanical properties — •Boris Breidenbach[1], Adrian Sheppard[2], Ulrike Wegst[3], and Klaus Mecke[1] — [1]Institut für theoretische Physik I, Universität Erlangen-Nürnberg, Staudtstr. 7, 91058 Erlangen — [2]Applied Mathematics, Australian National University, Canberra, Australia — [3]Max-Planck-Institut für Metallforschung, Heisenbergstr. 3, 70569 Stuttgart

Although biomaterials like wood or nutshells consist mainly of cellulose, they exhibit a broad range of mechanical properties. As woods mainly consist of cellulose, the explanation for this behaviour lies in the microscopic structure of the pore space. We have studied the structure of wood using phase contrast X-ray tomography at a resolution of $0.3\mu m$ to resolve the fibrous structure.

Using parallel implementations of anisotropic diffusion and a region growing algorithm, we can extract the pore space of the 2000^3 voxel large data sets. For these structures we calculate the Minkowski valuations, a

complete set of morphometric tensors which allow for a characterization of anisotropy in materials. The extracted wood structure can also be used to numerically measure the elasticity tensor. The aim is to relate the elastic properties of heterogeneous materials to Minkowski tensors.

AKB 40.45 Wed 16:30 P3

Investigation of ion channel function with a high frequency approach — •Michael Olapinski[1], Andrea Brüggemann[2], Michael George[2], Niels Fertig[2], Stephan Manus[1], and Friedrich C. Simmel[1] — [1]Department für Physik, Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 München, Germany — [2]Nanion Technologies GmbH, Pettenkoferstr. 12, 80336 München, Germany

Due to the limited bandwidth of the measurement setup, classical patch-clamp techniques cannot be used to study fast dynamical processes within ion channel proteins which may influence ionic transport. To overcome this limitation, chip-based methods are explored to study ion channel dynamics with the help of high-frequency (HF) techniques.

We present an approach, where a patch-clamp on-a-chip system is combined with an open-end coaxial probe that is positioned in close proximity to the cells under investigation. Ionic currents through the cell membrane are measured in whole-cell configuration while HF fields are applied at frequencies from MHz to 40 GHz. The ionic currents measured with rat basophil leukaemia (RBL) cells containing a potassium channel are sensitive to the applied HF field in specific frequency ranges and depend on the presence of potassium ions and the applied membrane potential. However, local heating of the buffer can be shown to play an important role in this case. Using a lock-in technique with a modulated HF excitation, it becomes possible to differentiate between thermal effects caused by the HF irradiation and intrinsic effects in which the field couples to membrane polarization and ion channel dynamics.

AKB 40.46 Wed 16:30 P3

Temperature dependent voltage-induced gating of OmpF — •Catalin Chimerel[1], Liviu Movileanu[2], and Mathias Winterhalter[1] — [1]International University Bremen, Germany — [2]Syracuse University, New York, USA

OmpF porin is a trimeric β-barrel channel from the outer cell wall of E.coli. A characteristic of the channel is its complete closure at transmembrane voltages (˜ 130 mV at room temperature), which depend on the experimental conditions. We employed single-channel and macroscopic current recordings in planar lipid bilayers to examine the gating fluctuations leading to transient or permanent closure as a function of applied voltage in a temperature range between 2 and 72 °C. The OmpF single-channel conductance, the amplitude of the gating blockades, and the lifetime of the closure sub-states were strongly temperature-dependent. Increasing the temperature increases the number of short-lived fluctuations, their lifetime, and the OmpF single-channel conductance in a non-linear manner, but decreases the threshold transmembrane voltage above which a complete closure occurs. These data reveal different mechanisms for channel closure that are discussed.

AKB 40.47 Wed 16:30 P3

Nanoindentation studies of full and empty viral capsids and the effects of capsid protein mutations on elasticity and strength — •Irena L. Ivanovska[1], Jean Philippe Michel[2], M. M. Gibbons[3], W. S. Klug[3], C. M. Knobler[2], Gijs. J.L. Wuite[1], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Department of Chemistry and Biochemistry, University of California Los Angeles, Los Angeles, CA 90095-1569, USA — [3]Department of Mechanical and Aerospace Engineering, University of California Los Angeles, Los Angeles, CA 90095-1597, USA

The elastic properties of capsids of the cowpea chlorotic mottle virus (CCMV) have been examined at pH 4.8 by nano-indentation measurements with an atomic force microscope. Studies have been carried out on wild-type capsids, both empty and containing the RNA genome, as well as on full capsids of a salt-stable mutant and empty capsids of the subE mutant. Full capsids resisted indentation more than empty capsids but all of the capsids were highly elastic. There was an initial reversible linear regime that persisted up to indentations varying between 20 and 30 % and applied forces of 0.6 to 1.0 nN; it was followed by a steep drop in force that was associated with irreversible deformation. A single point mutation in the capsid protein increased the capsid stiffness. The experiments are compared with calculations by finite element analysis of the deformation of a homogeneous elastic thick shell. These calculations capture the features of the reversible indentation region, and allow Young's moduli and relative strengths to be estimated for the empty capsids.

AKB 40.48 Wed 16:30 P3

Multifunctional liposomes: controlled permeability and micromanipulation — •Yannic Ramaye[1], Joana Gomes[1], Tristan Ruysschaert[2], Didier Fournier[2], Jürgen Fritz[1], and Mathias Winterhalter[1] — [1]International University Bremen, Germany — [2]Institut Pharmacologie et Biologie Structurale, UMR5089, Toulouse, France

Enzymes are able to accelerate biochemical reactions by many orders of magnitudes and it is tempting to use them for biotechnological synthesis. However, instability, their low recovery during biocatalytic processes and their high cost make them commercially less advantageous. A possible method to protect proteins from hostile environment is via encapsulation in vesicles. We control the permeability of water soluble substance by reconstitution of natural or bio-engineered channel forming proteins. For example, Acetylcholinesterase is highly sensitive to pesticides and was engineered to become a tool for pesticide detection. We have shown that encapsulation into liposomes stabilizes the enzyme against dilution effect and protects it against proteolytic agents. High encapsulation yield was achieved using affinity to bind the free enzyme to the capsule surface. Vesicles with covalently bonded complementary strands were bound to the surface of a DNA-chip. This allows to functionalize a large number of capsules on specific areas. Magnetic liposomes are synthetized by swelling dried lipids with magnetic fluid based on maghemite citrated nanoparticles. The incorporation of these nanoparticles allows liposome manipulation by applying a magnetic field. To increase stabilization, vesicles can easily be coated with polyelectrolytes.

AKB 40.49 Wed 16:30 P3

Temperature dependence of X-ray photoreduction and EXAFS Debye-Waller factors suggest role of protein-specific dynamics — •Paola Loja — FU-Berlin

In oxygenic photosynthesis, driven by lights the Mn4-complex of Photosystem II (PSII) cycles through four semi-stable intermediate states denoted as S-states. As revealed by X-ray absorption spectroscopy (XAS, EXAFS), the S-state transitions are coupled to significant rearrangements of the nuclei of the tetra-manganese complex (Dau et al., 2000; Haumann et al, 2002). Nonetheless the energetic efficiency is extraordinary high (small enthalpic losses) and the involved activation energies are surprisingly low. Are protein-specific dynamics of importance?

AKB 40.50 Wed 16:30 P3

Shear-dependency of von Willebrand factor measured in hydrodynamic flow and by micro-pipette aspiration technique — •J. Opfer, A. Wixforth, and M. F. Schneider — Universität Augsburg

Von Willebrand factor (vWf) is a biopolymer, which is known to play an important role in hemostasis. Dysfunction entails severe bleeding disorders. Recently it was shown that vWf reactivity is increased by shear stress, which is presumably caused by a coil-fiber transition. On the other hand, a shear-induced loss of efficiency has been found. Hence the correlation between shear forces and vWf effectivity is of great interest.

In order to study this correlation we mimic blood flow using novel designed bio-chips by means of surface acoustic waves (SAW), which are launched into the fluid containing vWf polymers and generate a laminar flow. The method allows sample volumes of only a few microliters, a wide spectrum of flow velocities and the imitation of any physiological relevant geometry.

Besides micro-pipette aspiration technique is applied for measuring homotypic interactions of vWf molecules, which have undergone different shearing forces. Mono-laminar phospholipid vesicles are coated with vWf and exposed to a vWf-covered wall. The vesicle's deformation reflects the magnitude of adhesive forces mediated by the polymer and permits observing its self-association kinetics.

AKB 40.51 Wed 16:30 P3

Interaction of the small G-protein Ms-Rac1 from Medicago sativa with GTP — •Daniel Wesner[1], Martina Brecht[2], Karsten Niehaus[2], Dario Anselmetti[1], and Robert Ros[1] — [1]Faculty of Physics, Experimental Biophysics & Applied Nanosciences, University of Bielefeld, 33615 Bielefeld, Germany — [2]Faculty of Biology, Genetics, University of Bielefeld, 33615 Bielefeld, Germany

Small GTP-binding proteins are important molecular regulators in the signal transduction chains of eukaryotic cells. The protein Ms-Rac1 from

Medicago sativa can switch from an active to an inactive state, controlled by the binding of the nucleotides GTP and GDP, respectively. We characterize the interaction of Ms-Rac1 with fluorescently labeled GTP by using fluorescence correlation spectroscopy (FCS). The labeled, protein-bound GTP can be competitively displaced by an excess of unlabeled GTP. The binding and dissociation of GTP and Ms-Rac1 are significantly accelerated by reducing the concentration of magnesium. The off-rates were determined to be 3.0 x 10-4 s-1 and 3.2 x 10-3 s-1 at a concentration of Mg2+ of 510 and 3.8 μM, respectively. Moreover, we found a reduced hydrodynamic radius of the protein-GTP-complex with increasing salt concentration, indicating the formation of oligomers of approx. 25 subunits at low ionic strength. At higher ionic strength the fraction of bound GTP shows a hyperbolic dependence on the concentration of Ms-Rac1, where the reaction displays a pseudo-first order kinetics. In addition, the influence of guanine nucleotide dissociation inhibitors (GDI) on these interactions was quantified. Incubation of Ms-Rac1 with RhoGDI reduces the observed binding rate of labeled GTP by a factor of 1.7.

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Motion by Stopping: Brownian motors without asymmetric potential — •Susan Sporer, Christian Goll, and Klaus Mecke — Institut für Theoretische Physik, Universität Erlangen-Nürnberg, Staudtstrasse 7, 91058 Erlangen, Germany

The Brownian motion of a particle in a liquid can be biased without thermal gradients or macroscopic force fields, if the shape of the particle is asymmetric and relaxation in equilibrium is prohibited by external force. In contrast to previous work the external potential does not need to be asymmetric, it is sufficient to arrest the particle at periodic intervals. We analysed by molecular dynamics simulations the dependence of the drift velocity on the particle shape and the fluid density. In the limit of a dilute gas an exact analytic calculation of the shape dependence is possible.

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Form follows function: how PufX–induced dimerization improves the efficiency of the light harvesting complexes of *Rb. sphaeroides* — •Tihamer Geyer — Zentrum für Bioinformatik, Universität des Saarlandes, D-66041 Saarbrücken

Lately there has been renewed interest in the "mystery"protein PufX, which occurs in the purple bacteria *Rb. sphaeroides* and *Rb. capsulatus*. It is responsible there for a dimerization of the light harvesting complexes of type I (LH1). It's key function seems to be to open the LH1 rings for eased diffusion of the quinones to the enclosed reaction centers (RC).

We show that the symmetry breaking induced by PufX also has an important effect on the main purpose of the LH1s, which is to help the RCs to absorb light. For this we extend a simple dipole model of the bacteriochlorophyll (Bchl) arrays of the LH1 and the RC [Hu etal, J. Phys. Chem 101 (1997) 3854] to calculate the absoprtion properties of the PufX induced LH1 dimers and their coupling to the special pair Bchls of the RCs. Comparison with the closed monomeric LH1/RC unit shows that the dimer has the same photosynthetically effective absorption cross section per monomer though it contains less Bchls. Additionally, the dimeric setup reduces the statistical fluctuations in the photon rate for the two RCs, thus further increasing the efficiency of photosynthesis.

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Normal heart beat, alternans and fibrillation in a model for the rabbit ventricles — •Steffen Bauer , Georg Röder , and Markus Bär — Physikalisch-Technische Bundesanstalt, Abbestr. 2-12, 10587 Berlin

Cardiac propagation is investigated by simulations of the modified Beeler-Reuter model using the geometry and muscle fibre orientation of the ventricles taken from the San Diego rabbit heart. Electrical excitation is introduced by a periodic pacing of the apex of the heart. Depending on the pacing frequency qualitatively different dynamics are observed namely normal heart beat, alternans and fibrillation at small, intermediate and large pacing frequencies, respectively. The simulated electric potential on the heart surface during normal heart beat agrees well with experimental data. The onset of alternans and fibrillation are in line with simulations of a one-dimensional model, where the corresponding instabilities are analyzed in more detail.

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SFM-Investigations on cell motility — •C. Brunner[1], M. Gögler[1], A. Ehrlicher[1], B. Kohlstrunk[1], D. Knebel[2], and J. Käs[1] — [1]Institute for Soft Matter Physics, University of Leipzig, Linnéstr. 5, 04103 Leipzig — [2]JPK Instruments AG, Bouchéstr. 12, 12435 Berlin

A cells ability to move is essential for various functions in nature, such as morphogenesis, immune response, and the invasiveness of cancer. On the molecular level, actin polymerization and molecular motors, such as myosin, are involved in cell motility, but the mechanism as a whole is not very well understood. We used a scanning force microscopy (SFM) technique to directly measure the forward forces actively generated at the leading edge, the cell body, and in lamellar fragments of fish keratocytes. We glued polystyrene beads with 2-3 um radii to cantilever tips to provide a well-defined probe geometry and avoid puncturing the cell. The bead was positioned in front of a moving cell which pushed the bead out of its path and therefore bent the cantilever. The forward force was calculated using the detected vertical deflection of the cantilever in an elastic wedge model, which considers cellular deformation. To reveal more about the force generation machinery used during protrusion, we treated keratocytes with the drug cytochalasin D, which interrupts actin polymerization by capping the actin filaments. The cells velocity decreases depending on the drug concentration. Comparison of the protrusion forces with and without cytochalasin D reveals the importance of actin polymerization in keratocyte motility.

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Two-photon scanning fluorescence correlation and cross-correlation spectroscopy — •Zdeněk Petrášek and Petra Schwille — Biotechnologisches Zentrum der TU Dresden; Institut für Biophysik; Tatzberg 47 - 51; 01307 Dresden; Germany

Fluorescence correlation and cross-correlation spectroscopy methods (FCS and FCCS) obtain information about molecular diffusion and inter- and intramolecular processes by analysing fluctuations of the fluorescence intensity reflecting the fluctuations of various physical parameters. The fluctuations are quantified by means of the autocorrelation function of the measured signal $F(t)$. In order for the autocorrelation to be representative of the investigated system the averaging in the autocorrelation calculation has to be performed over sufficiently high number of statistically independent events. This may be difficult to achieve when the diffusion of the fluorescent particles is slow, resulting in insufficient turnover of the particles in the measurement volume.

The scanning FCS (SFCS) combines the standard FCS with relative movement of the sample and the excitation beam. This improves the statistical accuracy by averaging over more independent locations within the sample. Furthermore, photobleaching effects can be reduced since the excitation dose is distributed over a larger part of the sample. We have employed a home-build two-photon laser scanning system to compare SFCS and SFCCS with their stationary counterparts, using several scanning patterns. The focus is on achieving a good signal-to-noise ratio and minimizing photobleaching effects while keeping the measurement time and the total light dose low.

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Transitions in a bistable model of the calcium/calmodulin-dependent protein kinase-phosphatase system in response to LTP and LTD protocols — •Michael Graupner and Nicolas Brunel — Laboatoire de Neurophysique et Physiologie, CNRS UMR 8119, Université René Descartes - Paris V, Paris, France

The calcium/calmodulin-dependent protein kinase II (CaMKII) plays a key role during induction of long-term post-synaptic modifications following calcium entry. The biochemical network involving CaMKII and its regulating protein signaling cascade has been hypothesized to be a bistable realization of such a switch. However, it is still unclear whether LTP/LTD protocols lead to transitions between these two states in realistic models of such a network. A detailed biochemical model of the CaMKII autophosphorylation and the protein signaling cascade governing the CaMKII dephosphorylation is presented. As reported by Zhabotinsky [Biophys J 2000; 79:2211], two stable states of such a system exist at resting intracellular Ca(2+) concentration: a weakly-(DOWN) and a highly-phosphorylated (UP) state of the CaMKII. A transition from the DOWN to the UP state can be achieved by high calcium elevations. Intermediate Ca(2+) concentrations enhance CaMKII dephosphorylation. This results in depotentiation - switching from the UP to the DOWN. Finally, it is shown that the CaMKII system can qualita-

tively reproduce results of plasticity outcomes in response to standard experimental induction paradigms of long-term modifications.

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DNA transport during bacterial transformation — •Madeleine Leisner[1], Martin Clausen[2], Irena Draskovic[3], Dave Dubnau[3], and Berenike Maier[2] — [1]LMU, Department für Physik, LS Rädler, Munic, Germany — [2]Institut üfr allgemeine Zoologie und Genetik, Westfälische Wilhelmsuniversität, Münster, Germany — [3]Department of Microbiology and Molecular Genetics, University of Medicine and Dentistry of New Jersey, Newark, USA

Bacteria employ a variety of molecular motors near the cell envelope to move and communicate with their environment. We are particularly interested in the molecular machines that transport DNA through the bacterial envelope during transformation. Bacteria can acquire genetic diversity by horizontal gene transfer. Many bacteria are naturally competent for uptake of naked DNA from the environment in a process called transformation. Recently, we used optical tweezers to demonstrate that the DNA transport machinery in Bacillus subtilis is a force generating motor, that processively transports macromolecular DNA through nanopores. Currently, we are investigating how the concentration of the single strand binding protein YwpH affects DNA transport properties and transformation efficieny.

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Fluorescence analysis of environmental stress response of single cells within a bacterial population — •Judith Leierseder[1], Kirsten Jung[2], and Joachim Rädler[1] — [1]Physik Department LMU — [2]Biologie Department LMU

Gene regulatory networks play a crucial role for the survival of bacteria as they allow them adaptation to varying environmental conditions. In our study we investigate the dynamics of gene expression in bacteria monitored by quantitative and time resolved image processing of GFP-hybrid proteins. This allows the acquirement of time traces of distinct proteins produced in response to environmental stress, which are used as input data for mathematical models. The analysis of many traces in an automated procedure measures the distribution of gene expression in a bacterial population. It allows conclusions on the regulatory mechanism and resolves cell-to-cell variations within a population. As a model system we studied the gene encoding GFP under the control of the arabinose promoter in E.coli. The change in GFP content following the exposure to different concentrations of arabinose was measured.

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Structure and Stability of Thiol Containing Collagen Peptides — •Christian Renner[1,2], Ulrike Kusebauch[1], Sergio Cadamuro[1], and Luis Moroder[1] — [1]Max-Planck-Institut für Biochemie, D-82152 Martinsried — [2]School of Biomedical and Natural Sciences, Nottingham Trent University, Nottingham NG11 8NS, UK

Collagen is the most abundant protein in mammals and as a natural biomaterial confers stability and strength to tissue. The dominant structural element is the right-handed triple helix that consists of three left-handed poly proline II-like helices formed by the single amino acid chains and coiled around each other. These trimeric super-helices build chemically cross-linked fibrils or networks that can associate to even larger structures. Cysteine residues are present in native collagens in non-triple helical portions where during maturation interchain disulfide knots are formed to crosslink the constituent three chains, but single cysteine residues of unknown structural and/or biological function are also found in triple-helical sequence portions. In the present study we have synthesized and analysed collagen peptides based on the regular structure (Gly-Pro-Hyp)n (Hyp is (4R)-hydroxyproline) where one or two amino acids were exchanged for cysteine. The reactivity of the thiol groups thus introduced allows to crosslink peptide chains within the triple helix or link different triple helices for forming a stable biomaterial. Moreover, selective 15N-labeling of individual glycine residues was expected to allow monitoring of thermal unfolding of the triple helix at defined sites and thus to analyze with spatial resolution the structural stability of the overall rod-like collagen triple helix.

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Characterisation of the affinity improvement of antibody mutants with dynamic force spectroscopy — •Julia Morfill and Kerstin Blank — Lehrstuhl für angewandte Physik, LMU München, Amalienstrasse 54, 80799 München

Many biotechnological and pharmaceutical applications require antibodies with high specificity and affinity. To optimise antibody-antigen interactions, a detailed knowledge of the structure of the binding pocket is useful. We investigated four different mutants of a recombinant antibody fragment with a known crystal structure specific for a peptide with single molecule force spectroscopy. The results of these measurements show a loading rate dependent unbinding force. For the clone with the highest affinity (KD = 5.2 pM) we achieved a spontaneous dissociation rate in the order of 10e-4 1/s and a potential width of 0.9 nm. The clone with the lowest affinity (KD = 2.6 nM) has a similar potential width and a dissociation rate in the order of 10e-3 1/s. Interestingly, the two clones only differ in a few amino acids, which do not directly interact with the antigen. In order to explain the affinity improvement, it is therefore necessary to have a more detailed look at the dynamics of the unbinding process.

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Close contact fluctuations: the seeding of signalling domains in the immunlogical synapse — •Amit Chattopadhyay — Universita' degli Studi di Padova, Facolta' di Ingegneria, Dipartimento di Fisica G. Galilei, Via Marzolo 8, 35131 Padova, Italy

We study the effects of thermal membrane fluctuations on the size and density of regions of close contact in cell:cell contact interfaces. Such regions are vital for the generation of early signals in T-cell contact interfaces and for the stabilisation of the contact and development of an immunological synapse. Our calculations indicate that these regions are on the nanometer scale, while the corresponding density rapidly decays with membrane-membrane separation. Our method is a generalisation of probability of first crossing techniques to a system without reflection symmetry.

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Proton-driven rotation within the F_0-motor of ATP synthase — •Nawid Zarrabi[1], Monika Düser[1], Dan J. Cipriano[2], S. Dunn[2], and Michael Börsch[1] — [1]3. Physikalisches Institut, Universität Stuttgart, Germany — [2]Department of Biochemistry, University of Western Ontario, London, Canada

ATP formation by F_0F_1-ATP synthase requires conformational changes that are induced by the stepwise rotation of the \gamma and \epsilon subunit. The opposite direction of rotation during ATP synthesis and hydrolysis was confirmed by single-molecule fluorescence resonance energy transfer (FRET) [1,2]. Rotation of \gamma and \epsilon is coupled to the rotation of the c subunits of the ion-driven F_0 motor. ATP hydrolysis resulted in a three-stepped rotation of the c-ring of F_0 from a thermophilic bacterium. However, ATP synthesis by the sodium-translocating enzyme from \textit{P. modestum} was associated with a multi-stepped rotation. To distinguish between the two mechanisms we have developed a single-molecule FRET assay to monitor the c-ring rotation in F_0. Our first data strongly support a stepwise movement of the c-ring during ATP synthesis and hydrolysis in contradiction to a quasi-continuous rotation. \Zitat{1}{Diez, M., B. Zimmermann, M. Börsch, M. König, E. Schweinberger, S. Steigmiller, R. Reuter, S. Felekyan, V. Kudryavtsev, C.A.M. Seidel, and P. Gräber: Nat. Struct. Mol. Biol. 11:135-142, 2004} \Zitat{2}{Zimmermann, B., M. Diez, N. Zarrabi, P. Gräber, and M. Börsch: EMBO J. 24:2053-2063, 2005} \Zitat{3}{Düser, M. G., Y. Bi, S. D. Dunn, and M. Börsch: Biochim. Biophys. Acta-Bioenergetics 1658:108 S Supplement, 2004}

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Surface-diffraction from proteins interacting with solid supported membranes — •Kirstin Seidel[1], Christian Daniel [2], Bert Nickel[1], and Joachim Rädler[1] — [1]Ludwig-Maximilians Universität, Department für Physik and Center for Nanosciences, München — [2]Technische Universität München

We study the interaction of Annexin 2 with anionic lipid membranes using neutron and x-ray synchrotron scattering techniques. Annexin 2 interacts with negatively charged phospholipids in a calcium dependant manner. Furthermore annexin is able to bind two adjacent membranes. The solid supported membranes were achieved by spreading large unilamelar vesicles (100nm) of lipid mixtures of neutral (POPC) and negatively charged (POPS) phospholipids on silicon substrates. The protein was provided by B. Windschiegl and C.Steinem, Universität Regensburg. The system was characterized by fluorescence microscopy the same samples were then measured with x-ray reflectivity at Hasylab (D4). With these methods we gained information about the homogeneity, fluidity

and thickness of the underlying membrane. In future experiments we will use neutron reflectometry at FRM2 (REFSANS) to visualize the protein layer. Here we want to benefit from the possibility of contrast variation due to the scattering length density difference between deuterium oxide and water.

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Capacitive Stimulation of Neurons by Opening Na^+ Channels with Silicon Chips — •Ingmar Schoen and Peter Fromherz — Max Planck Institut für Biochemie, Abteilung Membran- und Neurophysik, 82152 Martinsried bei München

We demonstrate that opening Na^+ channels by capacitive coupling with a silicon chip is a feasible, non-invasive method for neural stimulation in planar neuroelectronic devices.

Experiments were carried out with neurons from the pond snail *Lymnaea stagnalis* on silicon chips with HfO_2 as insulator. The cell was contacted with a patch pipette and ramps were applied to chip voltage. Capacitive coupling evoked an ionic current flow along the cleft in cell adhesion that led to an extracellular voltage drop therein. With a negative extracellular voltage, the adhesion membrane was depolarized. Voltage clamp experiments verified successful opening of ion channels and allowed for a detailed characterization of ionic currents and the optimization of Na^+ influx. This charge inflow was capable of triggering action potentials in current clamp in a limited parameter range. In the case of positive extracellular voltage, the upper membrane was directly depolarized and sodium channel opening reliably led to action potentials.

This method provides a thorough understanding and control of stimulated neural excitation without malignant electroporation of the cell membrane or electrochemical reactions at the substrate surface.

[1] I. Schoen and P. Fromherz, *Appl. Phys. Lett.* **87**, 193901 (2005).

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Mesoscopic simulations of membrane protein diffusion and membrane-protein interactions — •Gernot Guigas and Matthias Weiss — Cellular Biophysics Group (BIOMS), Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 580, 69120 Heidelberg

We use dissipative particle dynamics (DPD) to study the diffusion of membrane proteins and how active proteins alter the membrane's (elastic) properties. We find that the size-dependent diffusion coefficient $D(R)$ of integral membrane proteins with radius R is best described by the Saffman-Delbrück relation. To our knowledge, this is the first computational confirmation of the logarithmic dependence of D on R. We further show that active proteins can considerably alter the membrane's (elastic) properties, e.g. phospholipase A_2 softens the membrane while cleaving phospholipids into lysolipids and fatty acids [1].

[1] Jakobsen, Mouritsen, Weiss, J. Phys. Condens. Mat. **17**, S4015 (2005).

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Imaging of Electrical Dynamics in Cultured Brain Slices by Multi-Transistor-Array (MTA) Recording — •Armin Lambacher[1], Michael Hutzler[1], Martin Jenkner[2], Björn Eversmann[2], Roland Thewes[2], and Peter Fromherz[1] — [1]Max Planck Institute for Biochemistry, Department of Membrane and Neurophysics — [2]Infineon Technologies, Corporate Research, München, Germany

Direct electrical interfacing of semiconductor chips with neuronal tissue may lead to novel experimental approaches in brain research and also give rise to hybrid computational devices. Here we report on a time-resolved imaging of the electrical activity in organotypic brain slices from rat hippocampus by multi-transistor-array (MTA) recording on an area of 1 mm^2 at a resolution of 7.8 μm and 0.5 ms. Brain slices were cultured on the inert titanium dioxide surface of silicon chips fabricated by an extended CMOS process. Upon stimulation in the CA3 region we observed fast propagating waves of negative field potentials which we assign to orthodromic and antidromic action potentials in the mossy fibers and slower transient field potentials of postsynaptic activity in CA3 and CA1 with negative sign in stratum radiatum and positive sign in stratum pyramidale. The transistor signals matched local micropipette recordings of electrical field potentials in amplitude and shape. Direct interfacing of an MTA chip provides a complete observation of neuronal signaling in an extended area of brain tissue. This technique is suitable to elucidate the functionality of planar neuronal systems at a high resolution.

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Adaptive Resolution Scheme for Efficient Multiscale Molecular Dynamics Simulations — •Matej Praprotnik, Luigi Delle Site, and Kurt Kremer — Max-Planck-Institut für Polymerforschung, Ackermannweg 10, D-55128 Mainz, Germany

A novel adaptive resolution method for efficient hybrid atomistic/mesoscale molecular dynamics (MD) simulations is presented. The unique feature of the method is that it allows for a dynamical change of the number of molecular degrees of freedom during the course of MD simulation by an on-the-fly switching between the atomistic and mesoscopic levels of detail. The new approach is general and can be applied to any molecular system of biological relevance, e.g., water, but at present tested on a model system of a liquid of tetrahedral molecules. The simulation box is divided into two regions: one containing only atomistically resolved tetrahedral molecules, the other containing only one particle coarse-grained spherical molecules. The molecules can freely move between the two regions while changing their level of resolution accordingly. The simulation results show that the hybrid and the corresponding all-atom systems have the same statistical properties.

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Diffusion along Microfluidic Channels — •Andreas Heeren[1], Cheng-Ping Luo[1], Guenter Roth[2], Alexander Ganser[3], Roland Brock[3], Karl-Heinz Wiesmueller[2], Wolfgang Henschel[1], and Dieter Kern[1] — [1]Institute of Applied Physics, University of Tuebingen, 72076 Tuebingen, Germany — [2]EMC microcollections GmbH, 72070 Tuebingen, Germany — [3]Institute for Cell Biology, University of Tuebingen, 72076 Tuebingen, Germany

Living cells respond simultaneously to a variety of different stimuli. To achieve a specific cellular response a well defined mixture of stimuli or agents is required. However, in order to identify optimum mixtures of even few different compounds with respect to their relative and absolute concentrations, large numbers of biological tests are needed. Diffusion represents a highly efficient means for the generation of substance mixtures, namely continuously varying concentration profiles, with a minimum of pipetting steps. Here we present an array of microfluidic channels for the generation of binary substance mixtures with only two pipetting steps. For this purpose a microfluidic structure with a height of 500 μm was fabricated using the negative tone resist SU8. In a test diffusion of fluorescein dissolved in water was observed by fluorescence microscopy. The diffusion constant was determined by analyzing the fluorescence micrographs. Furthermore a procedure to detect unwanted flow in the channels was developed.