BIOLOGISCHE PHYSIK (AKB)

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ÜBERSICHT DER HAUPTVORTRÄGE UND FACHSITZUNGEN

(Hörsaal TU H2013)

Fachinternes Symposium:
"Polymer networks and beyond: From molecular structure to materials and biological functions"
Samstag, 08:30–18:45, TU C243

Organisation:
Jens-Uwe Sommer, CNRS Mulhouse
Erwin Frey, Hahn-Meitner-Institut Berlin
Annette Zippelius, Universität Göttingen
Eberhard Riedle, Universität München

Fachübergreifendes Symposium:
"Biological und Social Networks"
Montag, 10:00-12:30, TU HE101

Organisation:
Ulrich Gerland, Universität München
Stefan Bornholdt, Universität Bremen

Einstein Symposium:
"Brownian Motion, Diffusion and Beyond"
Dienstag, 10:00-12:30, TU HE101

Organisation:
Igor Sokolov, Humboldt Universität Berlin
Erwin Frey, Hahn-Meitner Institut Berlin
Erich Sackmann, TU München
Lutz Schimansky-Geier, Humboldt Universität Berlin

Hauptvorträge

AKB 10.1	Fr	09:45	(TU H2013)	**Interfacial Forces move DNA in Thermal Gradients**, Dieter Braun
AKB 10.2	Fr	10:15	(TU H2013)	**Driven Stiff Polymers**, Roland Netz
AKB 15.1	Fr	11:30	(TU H2013)	**Cellular mechanics investigations with holographic optical tweezers**, Jennifer Curtis, Christian Schmitz, Joachim Spatz
AKB 20.1	Fr	14:00	(TU H2013)	**Conflict and Cooperation in Biological Systems** , Peter Hammerstein
AKB 20.2	Fr	14:30	(TU H2013)	**Systems Biology of the JAK-STAT signalling pathway**, Jens Timmer, Ursula Klingmüller
AKB 40.1	Mo	14:00	(TU H2013)	**Around the World in 80 Days - Forecasting the Spreading of SARS in a Network Model**, T. Geisel, D. Brockmann, L. Hufnagel
AKB 45.1	Mo	14:30	(TU H2013)	**Coupled dynamics of DNA-breathing and binding of proteins that selectively bind to single-stranded DNA**, Ralf Metzler, Tobias Ambjörnsson
AKB 55.1	Di	14:00	(TU H2013)	**The Role of Diffusion in the Mechanism of Motor Proteins - Thermal Ratchets and all that**, Jonathon Howard
AKB 55.2	Di	14:30	(TU H2013)	**Bacterial motion: molecular motors and switches**, Berenike Maier
AKB 70.1	Mi	09:45	(TU H2013)	**Biophysics of Mechanosensory Localization: What, Where, and Why**, J. Leo van Hemmen
AKB 75.1	Mi	10:15	(TU H2013)	**The Physics of Chemoreception - an Encore**, U. Benjamin Kaupp

Fachsitzungen

AKB 10	**Biopolymers**	Fr	09:45–11:30	TU H2013	AKB 10.1–10.5
AKB 15	**Cell Mechanics and Rheology**	Fr	11:30–13:15	TU H2013	AKB 15.1–15.6
AKB 20	**Systems Biology and Bioinformatics**	Fr	14:00–15:30	TU H2013	AKB 20.1–20.4
AKB 25	**Active Networks and Cell Motility**	Fr	15:30–17:30	TU H2013	AKB 25.1–25.8
AKB 30	**Biomaterials**	Fr	17:30–19:00	TU H2013	AKB 30.1–30.6
AKB 40	**Biological Networks**	Mo	14:00–14:30	TU H2013	AKB 40.1–40.1
AKB 45	**Single Molecule Biophysics**	Mo	14:30–16:00	TU H2013	AKB 45.1–45.5
AKB 50	**Imaging and Microscopy**	Mo	16:00–18:15	TU H2013	AKB 50.1–50.9
AKB 55	**Molecular Motors**	Di	14:00–15:45	TU H2013	AKB 55.1–55.5
AKB 60	**Membranes and Vesicles**	Di	16:00–17:45	TU H2013	AKB 60.1–60.7
AKB 70	**Neurophysics**	Mi	09:45–10:15	TU H2013	AKB 70.1–70.1
AKB 75	**Nonlinear Phenomena and Pattern Formation**	Mi	10:15–11:45	TU H2013	AKB 75.1–75.5
AKB 80	**Microfluidics**	Mi	11:45–12:30	TU H2013	AKB 80.1–80.3
AKB 85	**Biosensors and Biohybrid Systems**	Mi	12:30–13:30	TU H2013	AKB 85.1–85.4
AKB 90	**Protein Folding and Molecular Dynamics**	Mi	14:00–15:30	TU H2013	AKB 90.1–90.6
AKB 100	**Poster Session I**	Sa	16:45–18:45	Poster TU D	AKB 100.1–100.82
AKB 200	**Poster Session II**	Di	17:00–19:00	Poster TU C	AKB 200.1–200.71

Mitgliederversammlung des Fachverbands Arbeitskreis Biologische Physik

Mo 18:30–19:30 TU H2013

In der Mitgliederversammlung sollen insbesondere folgende Themen besprochen werden:

- Gemeinsame Tagung mit EPS in 2006

- Themen für fachinterne und fachübergreifende Symposien

- Organisation von Parallelsitzungen

- Vorschläge fuer Plenarvortraege

- Vorschläge fuer Hauptvortraege

Fachsitzungen

– Haupt-, Kurzvorträge und Posterbeiträge –

AKB 10 Biopolymers

Zeit: Freitag 09:45–11:30 Raum: TU H2013

Hauptvortrag AKB 10.1 Fr 09:45 TU H2013

Interfacial Forces move DNA in Thermal Gradients — •Dieter Braun — Noether Group on Dissipative Biosystems, Applied Physics, LMU München, Amalienstr. 54, D-80799 München

Temperature gradients can induce large effects at microscopic dimensions. We discuss the first measurement of thermophoresis of DNA [1] and show how this effect can be used to accumulate and separate Microparticles or DNA [1-3]. Within microfluidic environments, the field gradients can be applied freely by IR optics. Finite element methods allow the in-depth simulation of thermophoresis, thermal conduction and fluid flow to compare with experiments even in complicated settings. We discuss measurement approaches and applications of thermophoresis, show how thermophoresis can complement our new approach of convective PCR [4] and speculate whether the effect might have played a role in molecular evolution [5].

[1] Trapping of DNA by Thermophoretic Depletion and Convection, Physical Review Letters 89: 188103 (2002)

[2] Thermophoresis of DNA determined by Microfluidic Fluorescence, European Physical Journal E, in press

[3] 2D Colloidal Crystals formed by Thermophoresis and Convection, in preparation

[4] Exponential DNA Replication by Laminar Convection, Physical Review Letters 91: 158103 (2003)

[5] Thermal force approach to molecular evolution, Physical Biology 1: P1-P8 (2004)

Hauptvortrag AKB 10.2 Fr 10:15 TU H2013

Driven Stiff Polymers — •Roland Netz — Physik Department, TU Muenchen, 85748 Garching

We consider stiff polymers in various non-equilibrium situations. Polymers that are anchored to surfaces, so-called brushes, are subject to shear flow and as a result deform and screen the hydrodynamic flow to various degrees, as relevant for glycocalix layers at endothelial cells in the blood stream. Conversely, stiff polymers at surfaces that are beating back and forth can be used to pump liquids over surfaces, which is a concept realized by ciliae but also attractive for synthetic designs. Elasticity is important here because for rigid rods the pumping efficiency is zero.

AKB 10.3 Fr 10:45 TU H2013

Discontinuous unbinding transitions of filament bundles — •J. Kierfeld, T. Kühne, and R. Lipowsky — MPI für Kolloid- und Grenzflächenforschung, 14424 Potsdam

The unbinding transition of bundles of semiflexible filaments, e.g., cytoskeletal F-actin filaments, is studied theoretically. We consider bundles formed due to attractive filament interactions mediated by crosslinking sticker molecules. Using a combination of analytical arguments and Monte-Carlo simulations, it is shown that the formation of bundles of parallel filaments requires a threshold concentration of linkers which becomes independent of the filament number for large bundles. Unbinding of bundles happens in a single, discontinuous transition. We discuss the behaviour of the bundle thickness at and below the transition. In the bound phase, large bundles tend to segregate into sub-bundles due to slow kinetics. Our results are in agreement with experiments on F-actin in the presence of the crosslinking α-actinin protein.

AKB 10.4 Fr 11:00 TU H2013

Towards a theory of the equilibrium phase behaviour of stiff polymer solutions — •Sven van Teeffelen, Erwin Frey, and Klaus Kroy — Hahn-Meitner-Institut Berlin

We study the equilibrium collective properties – packing structure and phase behaviour – of solutions of entangled stiff polymers that are isotropically dissolved in an aqueous salty solution in the presence of small flexible polymers mediating an additional depletion attraction. In order to make contact with well established liquid-state theories we calculate a microscopic effective pair potential between the filaments. We find that the bare interactions (hard core, depletion, electrostatic, van der Waals) are drastically renormalized by thermal fluctuations. In order to account for non-trivial cooperative effects at finite filament densities we make use of a scaling argument extending the tube model of semiflexible polymers. In particular, we find the spinodal in agreement with recent experiments on in vitro solutions of F-actin and Polyethylenglycol.

AKB 10.5 Fr 11:15 TU H2013

Relaxation of highly stretched DNA — •Oskar Hallatschek[1], Erwin Frey[1,2], and Klaus Kroy[1] — [1]Abteilung Theorie, Hahn-Meitner Institut, Glienicker Str. 100, 14109 Berlin, Germany — [2]Fachbereich Physik, Freie Universität,14195 Berlin, Germany

We have investigated theoretically the effect of local properties such as bending stiffness and inextensibility on the large scale dynamics of semiflexible polymers. In this talk we will focus on the contraction dynamics of highly stretched DNA after a sudden tension release. The polymer passes through various dynamical regimes during the relaxation from a completely stretched to a coiled conformation. Before entering the universal Rouse relaxation described by the "stem–flower"model, the relaxation dynamics exhibits features unique to a worm–like chain. In particular, we predict a novel relaxation mode which is fast compared to the diffusive contraction predicted by the stem–flower model. On a logarithmic time scale this regime actually supersedes the latter, and consequently our predictions should be accessible to experiments if pushed to larger force and higher time resolution.

AKB 15 Cell Mechanics and Rheology

Zeit: Freitag 11:30–13:15 Raum: TU H2013

Hauptvortrag AKB 15.1 Fr 11:30 TU H2013

Cellular mechanics investigations with holographic optical tweezers — •Jennifer Curtis, Christian Schmitz, and Joachim Spatz — Biophysical Chemistry Group, Institute for Physical Chemistry, University of Heidelberg, Im Neuenheimer Feld 253, 69120 Heidelberg, Germany

Cells utilize exquisite control mechanisms for the production and organization of various molecules to maintain their own mechanical viability. How cells manifest this control and how these materials enable the mechanical outcome are key questions. One example is the biochemical control of the actin cortex and actin stress fibers for cell motility. Another is the expression of the gel-like pericellular matrix for gross modulation of surface adhesion. Another is the spontaneous fusion of vesicles to finely adjust and maintain plasma membrane tension. This talk will present the development and use of holographic optical tweezers (HOTs) for several cell biophysical applications including studies of the actin cortex, the pericellular matrix, and the membrane reservoir in the context of both their physical and biological questions. In particular, HOTs ability to selectively position measurement probes at the cell surface, the measurement of local tension and/or viscoelasticity at several points simultaneously, and the non-invasive detection of cell components will be described.

AKB 15.2 Fr 12:00 TU H2013

A Characteristic Relaxation Time of Suspended Cells Revealed by Optical Rheology — •Falk Wottawah, Stefan Schinkinger, Bryan Lincoln, Maren Romeyke, Josef Käs und Jochen Guck — Institute for Soft Matter Physics, University of Leipzig, Linnéstrasse 5, 04103 Leipzig

The measurement of the mechanical properties of individual cells has received much attention in recent years. Whole cell rheology of individual suspended fibroblasts in an optical stretcher displays a single passive relaxation, arising from transiently crosslinked polymers. This result is in stark contrast to recent rheological measurements on adherent cells. The measured frequency-dependent complex shear modulus reveals characteristic viscoelastic signatures of the underlying cytoskeleton and its dynamic microscopic properties. These are consistent with an isotropic actin cortex underlying the cellular plasma membrane. The elastic to fluid transition occurs at a relaxation time of 2.8±0.5 s, coinciding with unbinding times of actin crosslinking proteins. Elastic contributions from slowly relaxing entangled actin filaments are negligible. The symmetrical geometry of suspended cells, in contrast to adherent cells, ensures a minute statistical variability. Yet, distinctive viscoelastic features between different cell types are seen. Mechanical stimuli on longer time scales of minutes trigger active structural responses with internal forces on the order of 1 nN.

AKB 15.3 Fr 12:15 TU H2013

Spektroskopie aktiver Zellkräfte mittels SFM — •Claudia Brunner[1], Allen Ehrlicher[1], Michael Gögler[1], Bernd Kohlstrunk[1], Detlef Knebel[2] und Josef Käs[1] — [1]Universität Leipzig, Experimentelle Physik I, Physik weicher Materie, Linnéstr 5, 04103 Leipzig — [2]JPK Intruments, Bouchéstr 12, 12435 Berlin

SFM Messungen an biologischen Proben beschränken sich bisher auf die Bildgebung durch Abscannen und auf die Bestimmung elastischer und viskoelastischer Eigenschaften durch Kraft-Abstandskurven. Diese Verfahren ermitteln nur passive Materialeigenschaften und werden so dem lebendigen Charakter dieser Objekte nicht gerecht. Zellen sind in der Lage, aktiv Kräfte aufzubauen, um sich z.B. durch Gewebeverbände bewegen zu können. Das SFM hat die geeignete Sensitivität im nN-Bereich um diese Kräfte zu bestimmen. Eine auf eine Cantileverspitze geklebte Polystyrolkugel wird im Weg einer sich bewegenden Zelle positioniert. Die Zellen, hier Keratozyten bewegen sich unter deutlicher Verformung unter der Kugel hindurch. Der so ausgelenkte Cantilever detektiert die vertikal wirkende Kraft, die es erlaubt, die Vorwärtkräfte der Zellen zu berechnen. Im gemessenen Signal sind Lamellopodium und Zellkörper gut zu unterscheiden. Erst wenn die Kraft, mit der die Kugel auf den Boden drückt, zu groß ist, wird die Zelle gebremst. Diese Methode der Kraftmessung wird ausführlich beschrieben.

AKB 15.4 Fr 12:30 TU H2013

Stiff Polymers, Foams and Fibre Networks — •Claus Heussinger and Erwin Frey — Hahn-Meitner Institut, Berlin

The linear elastic properties of cellular materials like open cell foams are readily understood when considering stretching or bending compliance of a single cell. On the contrary, fibrous materials, for example the paper you most likely read this abstract from, are considerably more complicated because of the relevance of the additional scale of the fibre length l_f. While stretching dominated systems remain foam-like, bending dominated networks show collective effects with a highly non-affine strain field that cannot be explained by single cell properties.

In this work we will be concerned with two-dimensional networks of stiff polymers, that differ from the purely *mechanical* fibres ($T = 0$) in having an *entropic* stretching compliance. We show that upon addition of these thermal effects, it is the foam-like stretching dominated regime that is unstable, giving way for an intermediate asymptotic region with a non-trivial mixing of the bending and the stretching mode.

The numerical results can be explained by taking into account the whole distribution of stretching compliances of the polymer strands. In contrast to the importance of the *average cell* in purely enthalpic models, the polymer networks are dominated by the (fat) *tails* of the distribution which are of Levy-index $\mu = 5/4$.

AKB 15.5 Fr 12:45 TU H2013

One-Bead Microrheology with Rotating Particles — •Holger Stark and Michael Schmiedeberg — Universität Konstanz, Fachbereich Physik, D-78457 Konstanz

We lay the theoretical basis for one-bead microrheology with rotating particles, i.e, a method where colloids are used to probe the mechanical properties of viscoelastic media. Based on a two-fluid model, we calculate the compliance and discuss it for two cases. We first assume that the elastic and fluid component exhibit both stick boundary conditions at the particle surface. Then, the compliance fulfills a generalized Stokes law with a complex shear modulus whose validity is only limited by inertial effects, in contrast to translational motion. Secondly, we find that the validity of the Stokes regime is reduced when the elastic network is not coupled to the particle.

AKB 15.6 Fr 13:00 TU H2013

Mapping Vortex Diffusion in Viscous and Visoelastic Fluids — •Maryam Atakhorrami[1], Gijsberta H. Koenderink[2], Daisuke Mizuno[1], Frederick C. MacKintosh[1], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Dept. Physics, Harvard University, Cambridge, MA, USA

One of the fundamental questions in hydrodynamics is the response of liquids to the displacement of a small immersed object. At low Reynolds numbers the velocity response of a simple liquid at a distance r from a point force is long-ranged, varying as 1/r. This "Stokes" flow accurately describes the motion of micron-size objects in water on time scales longer than a few microseconds. Over short times, however, the inertia of the liquid prevents the long-range stress propagation implicit in Stokes flow, and the disturbance of the fluid remains confined to a small region. In incompressible liquids this must involve back flow, i.e. a ring vortex is set up, which diffuses away from the point disturbance leaving in its wake the usual Stokes flow. Simulations and theoretical studies have demonstrated this phenomenon, while experiments have only observed indirect consequences, e.g. the "long-time tail" in scattering experiments. We have directly resolved the spatio-temporal structure of such vortices by measuring correlated thermal fluctuations and driven motions of micron sized particles in viscous and viscoelastic media at high frequency (100kHz). We find good agreement between experimental flow patterns and theoretical calculations for simple viscous fluids. Furthermore, we show how the vortex-like propagation is modified in viscoelastic media.

AKB 20 Systems Biology and Bioinformatics

Zeit: Freitag 14:00–15:30 Raum: TU H2013

Hauptvortrag

AKB 20.1 Fr 14:00 TU H2013

Conflict and Cooperation in Biological Systems — •Peter Hammerstein — Humboldt Universitaet

In biology, the components of a living organism are often compared with parts of a well designed machine, assuming that the evolutionary process acts somewhat like a human engineer. This picture has been used many times as a powerful heuristic tool but it can be misleading. The wheels of a machine have no "incentive"to act improperly, but parts of an organism can be under selection to actively undermine the performance of that organism. Mitochondria, usually regarded as the cell's "power plant", are subject to selective forces under which they would in principle benefit by suppressing male function. The same is true for intracellular symbiotic bacteria found in many insect species. These bacteria kill males or turn them into females or effectively sterilize them. Medicine needs to recognize that there are enemies within.

Hauptvortrag

AKB 20.2 Fr 14:30 TU H2013

Systems Biology of the JAK-STAT signalling pathway — •Jens Timmer[1] and Ursula Klingmüller[2] — [1]Centre for Data Analysis and Modelling, University of Freiburg, Eckerstr. 1, 79104 Freiburg — [2]German Cancer Research Center, Im Neuenheimer Feld 280, 69120 Heidelberg

Considerable progress has been made in identifying the molecular composition of cellular signalling networks. However, to reveal the systems' properties, quantitative models based on experimental data have to be developed. To demonstrate this Systems Biology approach, we investigate

the core module of the JAK-STAT pathway of the Epo-receptor. Based on time resolved quantitative measurement of the involved proteins, we estimate the parameters in differential equations describing the pathway. The results show that the so far believed assumption of a feed-forward cascade to describe the pathway does not hold. A generalization of the model that includes nucleocytoplasmatic cycling is suggested and validated by successfully predicting the outcome of a new experiment. From this model, we infer the time courses of the unobserved STAT populations and show that, on a systems level, fast nucleocytoplasmatic cycling of STAT serves as a remote sensor to closely couple gene activation to receptor activity.

AKB 20.3 Fr 15:00 TU H2013

A Solvable Sequence Evolution Model and Genomic Correlations — •Philipp W. Messer[1,2], Peter F. Arndt[2], and Michael Lassig[1] — [1]Institute for Theoretical Physics, University of Cologne, Zuelpicher Str. 77, 50937 Koeln, Germany — [2]Max Planck Institute for Molecular Genetics, Ihnestr. 73, 14195 Berlin, Germany

We study stochastic sequence evolution processes whose elementary steps are duplication, mutation, insertion, and deletion of single letters. Such processes are found to generate long-range correlations in the frequencies of letters as long as the sequence length is growing, i.e., the combined rates of duplications and insertions are higher than the deletion rate. For constant sequence length, on the other hand, all initial correlations decay exponentially. These results are obtained analytically and are supported by simulations. Their implications for explaining the long-range correlations in genomic DNA are discussed.

AKB 20.4 Fr 15:15 TU H2013

Dynamics of Multi-Allele Evolution on a Fitness Landscape — •Julia Schwartz and Ulrich Gerland — Department für Physik, LMU München

The evolution of a populations genotype can be represented by the motion of a cluster through sequence space. The Wright-Fisher model is a widely accepted way to describe its dynamics. It includes mutation, selection, and random genetic drift due to the finite population size. However, simulations based on this model are not feasable for large populations or high mutation rate due to the enormous number of mutations, most of which are quickly lost from the population. We have developed a method to approximate the dynamics of the Wright-Fisher model, so that simulations in these regimes become possible. The method is based on a combination of the continuum approximation with a heuristic truncation scheme for the cluster dynamics. The latter incorporates an adjustable parameter which controls the tradeoff between accuracy and computational effort.

AKB 25 Active Networks and Cell Motility

Zeit: Freitag 15:30–17:30 Raum: TU H2013

AKB 25.1 Fr 15:30 TU H2013

Molecular motors in cells: A rapid switch of biopolymer organization — •David Smith[1], Falko Ziebert[2], Walter Zimmermann[2], and Josef Käs[1] — [1]Institute for Soft Matter Physics, University of Leipzig, Linné Str. 5, D-04103 Leipzig, Germany — [2]Theoretical Physics, University of the Saarland, D-66041 Saarbrücken, Germany

All eukaryotic cells rely on the self-assembly of protein filaments to form a cytoskeleton. Motility and reaction to stimuli require pathways to reversibly change cytoskeletal organization. We report a mechanism whereby the molecular motor myosin II induces order-disorder transitions in actin-myosin networks. Bulk activity of the motors, which causes sliding on an individual filament level, maintains a dynamically disordered network. During depletion of ATP, an increasing fraction of molecular motors becomes inactive, crosslinking actin filaments to small clusters. The remaining active motors combined with continually increasing crosslinking foster further growth of these clusters, resulting in a variety of ordered macro-molecular structures such as asters, networks resembling neuronal architectures, and condensed super-precipitates. Experiments with photo-activated motors demonstrate the quick reversible restoration of the disordered state. This nonequilibrium pathway to switch between order and disorder is much faster than any structural changes driven by Brownian motion in thermodynamic equilibrium. This ability for rapid, isothermal motor-induced transitions between different degrees of self-organization indicates that molecular motors, in general, may substantially contribute to dynamic cellular organization.

AKB 25.2 Fr 15:45 TU H2013

Polymerization-Forces in Cell-Motility — •Cosima Koch, Claudia Brunner, Allen Ehrlicher, and Josef Käs — Universität Leipzig, Physik der weichen Materie

Over the last decade cell motility has been a subject of major research in cell biology, bio-medicine and biophysics. However, even up to date the detailed mechanisms of cell translocation are not completely understood. To tackle this problem we explore the effects of the actin-polymerization-disrupting drug cytochalasin D on the locomotion of fish epidermal keratocytes. The actin polymerization is essential for the protrusion of the cell's leading edge, the lammelipodium, which is elongated by the new polymerization of actin filaments. Nevertheless it is known that there are other mechanisms involved, like the rotation of the cell body and the generation of substrate traction forces. To gain insight into the interplay of the different processes we use substoichiometric concentrations of cytochalasin D which disrupts the lammelipodial protrusion by inhibiting the actin polymerization. The time dependence of the velocity and the area of fish keratocytes for different concentrations of cytochalasin D will be evaluated and discussed.

AKB 25.3 Fr 16:00 TU H2013

Simulation of collective filament dynamics in motility assays for motor proteins — •P. Kraikivski, R. Lipowsky, and J. Kierfeld — MPI für Kolloid- und Grenzflächenforschung, 14424 Potsdam

We present a model for the simulation of filament dynamics in two-dimensional motility assays of motor proteins and cytoskeletal filaments. The model contains deformable filaments that move under the influence of forces from molecular motors and thermal noise. Motor tails are attached to the substrate and modeled as elastic springs, motor heads perform a directed walk with a given force-velocity relation. Filament interactions are repulsive and characterized by a crossing probability. We study the collective filament dynamics and pattern formation as function of the motor and filament density, the force-velocity characteristics and detachment rate of motor proteins and the filament interaction. In particular, we investigate the formation and statistics of filament clusters due to blocking effects if filament crossing is inhibited.

AKB 25.4 Fr 16:15 TU H2013

Self-organization of cytoskeletal systems: formation of contractile rings and mitotic spindles — •Alexander Zumdieck, Karsten Kruse, and Frank Jülicher — Max-Planck-Institut für Physik komplexer Systeme, 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 discuss the self-organization of filament motor systems in the presence of filament polymerization and depolymerization. Starting from a microscopic picture, we develop a coarse grained theory for the dynamics of the system [1]. We apply these theories to systems of filaments representing stress fibers or contractile rings in linear and cylindrical geometry and find that contractile rings could form on a cell membrane by self-organization phenomena. We furthermore discuss the contraction dynamics of the contractile ring. Application of these theories to mitotic spindles reveals conditions for spindle formation and stability.

[1] K. Kruse, A. Zumdieck and F. Jülicher, Europhys. Lett. 64, 716 (2003)

AKB 25.5 Fr 16:30 TU H2013

The Bipolar Mitotic Kinesin Eg5 Moves on Two Microtubules — •Lukas C. Kapitein[1], Erwin J.G. Peterman[1], Benjamin H. Kwok[2], Jeffrey H. Kim[2], Tarun M. Kapoor[2], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Lab. Chem. Cell Biol., The Rockefeller University, New York, NY, USA

During cell division mitotic spindles dynamically self-assemble with the help of microtubule-based motor proteins. The bipolar organization of spindles is essential for proper segregation of DNA and in eukaryotes requires BimC motor proteins, a family of homotetrameric kinesins. Hypotheses for bipolar spindle formation include the "push-pull mitotic muscle" model in which BimC and opposing motor proteins act between overlapping microtubules. The mitotic spindle is, however, very different from skeletal muscle in that it is a very dynamic structure which turns over its components within minutes while maintaining its shape and exerting forces. We have shown using in vitro assays with single-molecule fluorescence microscopy and optical tweezers that the BimC kinesin Eg5 drives sliding of microtubules dependent on their relative orientation at speeds comparable to spindle pole separation rates. Additionally, we found that Eg5 can tether microtubule plus-ends, suggesting an additional microtubule-binding mode for Eg5. Based on these data we suggest a physical model in which BimC kinesins contribute to mitotic spindle assembly by aligning and pushing apart microtubules.

AKB 25.6 Fr 16:45 TU H2013

Optical Deformability as an Intrinsic Differentiation Marker for Stem Cells — •Stefan Schinkinger, Falk Wottawah, Bryan Lincoln, Frank Sauer, and Jochen Guck — Universität Leipzig, Abteilung Physik der Weichen Materie, Linnéstr. 5, 04103 Leipzig

Despite major efforts in stem cell research, there is no unequivocal molecular marker available for characterization and sorting of stem cells or their state of differentiation. We use a microfluidic Optical Stretcher to determine the material properties of individual cells as a non-invasive cell marker. The mechanical properties measured are mainly influenced by the cytoskeleton, a polymeric protein network in the cell. Because the cytoskeleton also plays a major role in the function of cells, with this technique we are able to follow cell progression through the various stages of differentiation. Experiments were performed with a promyelocytic leukemia cell line called HL-60. Comparison with mature neutrophils and experiments with different precursor cells support our hypothesis. As no labeling is required, preparation time of samples is reduced and the risk of activation or differentiation due to stress can be kept minimal. Especially for therapeutic applications of stem cells where labeling of any kind is prohibitive, characterization by optical deformability as an intrinsic marker provides a reasonable alternative.

AKB 25.7 Fr 17:00 TU H2013

Resolving the Cell Cycle by Measuring Optical Deformability with a Microfluidic Optical Stretcher — •Bryan Lincoln, Maren Romeyke, Frank Sauer, Stefan Schinkinger, Falk Wottawah, and Jochen Guck — Universität Leipzig, Abteilung Physik der Weichen Materie, Linnéstr. 5, 04103 Leipzig

The Optical Stretcher is a dual-beam optical trap capable of measuring the deformability of suspended biological cells. Previous measurements with this system have shown relevant differences between various cell types and have supported the idea that there is a strong correlation between a cell's cytoskeletal structure and its deformability. A microfluidic delivery system has been developed in order to measure cells at a high enough rate to acquire the necessary statistics to resolve elasticity changes within a single cell type. The cytoskeleton reorganizes as a cell grows and divides, so we find changes in deformability during various phases of the cell cycle as well. These various stages are identified by quantitative single-cell fluorescent DNA analysis. Results are presented using a three-element viscoelastic model and implications for deformability as a cell marker are discussed. Additional experiments using Laser Scanning Cytometry are presented that correlate position in the cell cycle with amount of F-actin in both the adhered and suspended state.

AKB 25.8 Fr 17:15 TU H2013

Dynamics of Cilia and Flagella — •Andreas Hilfinger[1], Ingmar Riedel[2], Amit Chattopadhyay[1], Karsten Kruse[1], Jonathon Howard[2], and Frank Jülicher[1] — [1]Max-Planck-Institute for Physics of Complex Systems, D-01187 Dresden, Germany — [2]Max-Planck-Institute of Molecular Cell Biology and Genetics, D-01307 Dresden, Germany

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 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 describe the axoneme as an elastic filament, driven by internally generated stresses. 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. Focusing on beats confined to a surface we compare our results to recent data from bull sperm flagella. Our approach can be generalised to three dimensions enabling us to discuss helical and rotary wave patterns.

AKB 30 Biomaterials

Zeit: Freitag 17:30–19:00 Raum: TU H2013

AKB 30.1 Fr 17:30 TU H2013

Proteoglycan conformation and mechanical properties: A molecular modeling investigation — •Mark Bathe[1], Gregory C. Rutledge[2], Alan J. Grodzinsky[2], and Bruce Tidor[2] — [1]HMI Berlin, Germany — [2]MIT Cambridge MA, USA

Proteoglycans (PGs) play a central role in determining the structural and biomechanical properties of tissues ranging from articular cartilage to the central nervous system. They are high molecular weight comb biopolymers consisting of anywhere from one to one hundred glycosaminoglycans (GAGs) (anionic polysaccharides) grafted to a linear protein backbone. PG chemical composition varies considerably with the disease state of tissues, making it of fundamental importance to biology to understand their composition-function relationship.

Towards this aim, we simulate PG conformation and osmotic pressure using a coarse-grained molecular model. GAG molecular weight, degree of sulfation, and grafting density affect significantly the apparent persistence length of PGs, whereas GAG sulfation type (4 vs. 6) and pattern do not. Similarly, GAG osmotic pressure is influenced primarily by its sulfation density. Our results reaffirm that variations in PG composition may be used to alter significantly the structural and biomechanical properties of a variety of tissues, and provide quantitative new insight into the structure-function relationship of this important class of biomolecules.

AKB 30.2 Fr 17:45 TU H2013

The Influence of the Thermal Treatment of Hydroxylapatite Scaffolds on the Physical Properties and the Bone Cell Ingrowth Behaviour — •Alexander Woesz[1], Monika Rumpler[1], Inderchand Manjubala[1], Christine Pilz[1], Franz Varga[2], Nadja Fratz-Zelman[2], Paul Roschger[2], Klaus Klaushofer[2], Juergen Stampfl[3], and Peter Fratzl[1] — [1]Max Planck Institute of Colloids and Interfaces, Dept. of Biomaterials, Potsdam , Germany — [2]Ludwig Boltzmann Institute of Osteology, 4th Medical Department, Vienna, Austria — [3]Institute of Materials Science and Technology, University of Technology, Vienna, Austria

The usage of rapid prototyping (RP) methods and ceramic gelcasting enables the production of 3D scaffolds as future bone replacement materials with almost arbitrary architecture from bioceramics like hydroxylapatite. A suspension of synthetic hydroxylapatite powder in water was cast into a mould produced by RP-methods. After demoulding the ceramic particles were sintered. Sintering temperature and atmosphere affected the physical properties like phase composition and surface roughness as well as the cell ingrowth behaviour, which was assessed in cell culture experiments using a pre-osteoblastic cell line. With increase in sintering temperature decomposition of the synthetic hydroxylapatite into tricalciumphosphate increased, the sintering atmosphere seemed to influence the surface roughness, but had no impact on the phase composition. Cell ingrowth was observed to be highest at a sintering temperature of 1300°C in nitrogen atmosphere followed by a post-treatment at 1200°C in air.

AKB 30.3 Fr 18:00 TU H2013

Bone Remodelling is regulated by a Mechanical Feedback Loop — •M. A. Hartmann[1], R. Weinkamer[1], Y. Brechet[2], and P. Fratzl[1,3] — [1]MPI-KGF, Dept. Biomaterials, 14476 Potsdam-Golm, Germany — [2]ENSEEG, LTPCM, 38402 Domaine Universitaire de St. Martin d'Heres, Cedex, France — [3]LBIO, Hanusch Hospital and UKH-Meidling, Vienna, Austria

Biological processes can be regulated by a mechanical feedback loop, i.e. the mechanical loading is sensed by cells and this information is fed back to control the action of other cells. A prominent example is the (re)modelling of bone. Despite many years of intensive research many of the properties of this feedback still remain unclear: What exactly is the mechanical stimulus the cells are sensing? How do the cells respond to this stimulus (i.e. the remodel law)? How is the stimulus sensed by the cells? In [1] we proposed a model to study trabecular bone remodelling and ageing governed by mechanical feedback. Our approach is to study the effect of different remodel laws (like a continuous, linear vs. a discontinuous, step-like response) and its influences on bone histomorphometric parameters. Depending on the remodel law we found differences in bone volume fraction and the geometry of the bone structure. Comparing the simulation results to data from real bone, we try to draw indirect conclusions on the underlying feedback loop.

[1] Weinkamer et al., PRL, 2004

AKB 30.4 Fr 18:15 TU H2013

Nitric Oxide Production in Mechanosensitive Osteocytes — •Daisuke Mizuno[1], Aviral Vatsa[2], Theo H. Smit[3], Jenneke Klein-Nulend[2], Frederick C. MacKintosh[1], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Dept. Oral Cell Biol., ACTA, Vrije Universiteit, Amsterdam, NL — [3]Dept. Clin. Phys.&Informatics, Univ. Hospital, Vrije Universiteit, Amsterdam, NL

Osteocytes are a type of bone cells that are embedded in the bone matrix, and whose main function is believed to be mechanosensing. If bone is mechanically loaded, activated osteocytes produce nitric oxide (NO) which controls in a sophisticated control network the activity of other types of bone cells which deposit or resorb bone matrix. This single-cell level mechanosensing and chemical signaling is essential for bone repair and adaptation. In this study we 1) apply well characterized mechanical stimuli to single osteocytes and 2) quantify the resultant chemical signaling with NO at the single cell level. Results were: i) Intracellular NO increased up to about 10 μM after stimulation with forces on the order of 10 pN generating about 1% strain. ii) The cell membrane is not a significant diffusion barrier for NO. iii) Surrounding cells occasionally more than 100 microns away from a stimulated one were seen to react rapidly (within 10s) to the stimulation.

AKB 30.5 Fr 18:30 TU H2013

Influence of Water on the mechanical Properties of wood investigated by X-ray diffraction — •Ingo Grotkopp[1], Henrik Lemke[1], Klaas Kölln[1], Sergio S. Funari[2], Martin Domach[2], and Martin Müller[1] — [1]Institut für Experimentelle und Angewandte Physik, Christian-Albrechts-Universität zu Kiel — [2]HASYLAB, DESY, Hamburg

The influence of water on the mechanical behaviour of wood is tremendous. Softwood was investigated by means of X-ray diffraction during tensile tests with different moisture contents. In this way, the influence of the water molecules on the changes in the orientation of the cellulose crystals could be observed. A second mechanism found in these experiments is the deformation of cellulose crystals. Here a comparison between single cells, small wood samples and large timber at different humidity is carried out and first conclusions are developed.

AKB 30.6 Fr 18:45 TU H2013

Plant Cell Walls for Hygrosensitive Switches — •Helfried Mollay[1], Ingo Burgert[1], Peter Fratzl[1] und Josef Eberhardsteiner[2] — [1]Max-Planck-Institute of Colloids and Interfaces, Department of Biomaterials, 14476 Potsdam, Germany — [2]Vienna University of Technology, Institute for Mechanics of Materials and Structures, A-1040 Vienna, Austria

Wood is an anisotropic and hygroscopic biomaterial which can absorb water and swells or shrinks due to changes of humidity. On the one hand, the resulting deformations can lead to severe complications with respect to the utilisation of wood. On the other hand, from a biomaterials point of view, the coherence between water absorption and structural modification is a matter of particular interest. The objective of our study was to make use of the hygroscopic behaviour of wood at the microscale by constructing wood-based switches. Thin wood tissue sheets of different ability to swell and shrink were combined as such as a bimetal. Thus, the wooden bi-layer bent during humidity changes and could be used in terms of a hygrosensitive switch.

AKB 40 Biological Networks

Zeit: Montag 14:00–14:30 Raum: TU H2013

Hauptvortrag AKB 40.1 Mo 14:00 TU H2013

Around the World in 80 Days - Forecasting the Spreading of SARS in a Network Model — •T. Geisel[1], D. Brockmann[1], and L. Hufnagel[2,1] — [1]MPI für Strömungsforschung und Fakultät Physik, Univ. Göttingen — [2]KITP, UCSB, Santa Barbara, CA, USA

The rapid worldwide spread of the severe acute respiratory syndrome (SARS) demonstrated the potential thread an infectious disease poses in a closely interconnected and interdependent world. Here we introduce a probabilistic model which describes the worldwide spreading of infectious diseases and demonstrate that a forecast of the geographical spread of epidemics is indeed possible. It combines a stochastic local infection dynamics between individuals with stochastic transport in a worldwide network which takes into account the national and international civil aviation traffic. Our simulations of the SARS outbreak are in surprisingly good agreement with published case reports. We show that the high degree of predictability is caused by the strong heterogeneity of the network. Our model can be used to predict the worldwide spreading of future infectious diseases and to identify endangered regions in advance. The performance of different control strategies is analyzed and our simulations show that a quick and focused reaction is essential to inhibit the global spreading of epidemics.

AKB 45 Single Molecule Biophysics

Zeit: Montag 14:30–16:00 Raum: TU H2013

Hauptvortrag AKB 45.1 Mo 14:30 TU H2013

Coupled dynamics of DNA-breathing and binding of proteins that selectively bind to single-stranded DNA — •Ralf Metzler and Tobias Ambjörnsson — NORDITA, Blegdamsvej 17, DK-2100 Copenhagen OE

Under physiological conditions, the double-helix is the thermodynamically stable configuration of DNA. A long-standing puzzle had been why the presence of selectively single-stranded DNA binding proteins (SSBs) does not lead to full DNA-denaturation, as SSB binding is thermodynamically favorable. By detailed single-molecule studies, it was corroborated quantitatively that for the gp32-SSB there exists a kinetic block for SSB-binding: below the melting temperature of DNA, that is, the lifetime of a bubble is shorter than the typical binding time of an SSB, counteracting the expected helix-destabilization through the SSBs. We derived a dynamical model to quantify the coupled dynamics between a fluctuating DNA-bubble and SSBs that attempt to bind to it. Depending on the system parameters (temperature, external force, SSB binding rate and strength, SSB size), the presence of SSBs leads to enhanced bubble lifetime. Effectively, the bubble free energy is lowered, or even full denaturation caused by SSBs.

AKB 45.2 Mo 15:00 TU H2013

Kinetics of driven RNA translocation through nanopores — •Ulrich Gerland[1] and Ralf Bundschuh[2] — [1]Department Physik and CENS, LMU München, Germany — [2]Department of Physics, The Ohio State University, Columbus, Ohio

Motivated by recent experiments, we study the translocation of structured RNA molecules through narrow pores that allow single but not double strands to pass. The translocation dynamics is coupled to the base pairing dynamics of the RNA molecules, which we incorporate explicitly in kinetic Monte Carlo simulations. For a number of exemplary molecules as well as for random sequences, we characterize the translocation dynamics as a function of the driving force. For strongly driven translocation, we find a narrow distribution of translocation times with a mean that scales linearly with the RNA length. In contrast, for weakly driven translocation we observe a pronounced sequence-dependence in the distribution of translocation times. Simple physical arguments can explain these two limiting regimes. Furthermore, we identify the sequence-specific properties of RNA molecules that are reflected in the translocation times.

AKB 45.3 Mo 15:15 TU H2013

Dynamcis of Force-Induced DNA Slippage — •Richard Neher and Ulrich Gerland — Department für Physik, LMU München

In double-stranded DNA with repetitive sequences, one strand may locally slip with respect to the other, leading to the creation, annihilation, or diffusion of bulge loops. We study the physics of periodic DNA theoretically, focusing on the dynamics under a shear force, which can be probed experimentally with single molecule devices [1]. Using an explicit model, we find a rich dynamical behavior with clear signatures in experimental observables. In particular, at a lower critical force f_c the system displays reptation-like dynamics with a mean rupture time that scales with the sequence length as $\langle\tau\rangle \sim N^3$. In an intermediate regime $f_c < f < f^*$, the distribution of rupture times is well described by drift-diffusion theory, up to an upper critical force f^*, where a *dynamical* transition to an unraveling mode of strand separation occurs [2]. We predict that periodic DNA sequences display a viscoelastic behavior with time and force scales that can be *programmed* into the sequence.

[1] T. Strunz *et al.*, PNAS **96**, 11277 (1999).
[2] R. A. Neher and U. Gerland, PRL **93**, 198102 (2004)

AKB 45.4 Mo 15:30 TU H2013

Molecular Details of Specific Protein-DNA Interaction — •Frank Wilco Bartels[1], Birgit Baumgarth[2], Christelle Bahlawane[2], Christoph Metzendorf[2], Anke Becker[2], Dario Anselmetti[1], and Robert Ros[1] — [1]Experimental Biophysics, Faculty of Physics, Bielefeld University — [2]Genetics, Faculty of Biology, Bielefeld University

Specific protein-DNA interaction is fundamental for all aspects of gene expression. A regulatory model system is the biosynthesis of exopolysaccharides (EPS) in the nitrogen-fixating bacterium *Sinorhizobium meliloti* 2011. These sugar polymers promote the bacterium's symbiosis with alfalfa plants, a process of agricultural importance.

The EPS biosynthesis is controlled by a complex interplay of several proteins, most prominently the transcriptional activator ExpG. In a combination of standard biochemical and single molecule experiments, we demonstrated that the protein ExpG binds to three different DNA target sequences in a sequence specific manner, albeit with distinct differences in the energy landscape.[1] Dynamic force spectroscopy based on the atomic force microscope (AFM) proved to be sensitive even to small variations of the binding motif. Experiments with DNA mutants lead to a deeper understanding of the binding mechanism.[2]

The method is now applied to other proteins from the same regulatory system.

[1] F.W. Bartels et al., J Struct Biol 143 (2003) 145-152
[2] B. Baumgarth et al., Microbiol (2004), in press

AKB 45.5 Mo 15:45 TU H2013

Tail Induced Interactions of Nucleosome Core Particles — •Christian Holm, Frank Mülbacher, and Helmut Schiessel — Max-Planck-Institut für Polymerforschung, Ackermannweg 10, 55128 Mainz

We present a MD simulation study of the interactions between nucleosome core particles (NCPs). Each NCP consists of a core of eight histone proteins and a strand of DNA, which is wrapped around about two times. Special emphasis was placed on the role of the histone tails. We model the histone core and the wrapped DNA by a charged sphere, while the histone tails are represented by oppositely charged polyelectrolyte chains grafted onto the sphere's surface, interacting via a Debye-Hückel potential. We find that the effect of tail bridging between the spheres does indeed account for the observed attraction, thus reproducing the qualitative features of the experimental results. We further modify our model to use either only one interacting tail, or charge patches instead of the tails in order to isolate the quantitative features of the tail interactions. The reduction of the charge fraction of the tails, that corresponds to the process of acetylation, leads to a reduction or even the disappearance of the attraction, which subsequently can lead to the unfolding of the chromatin fiber, thereby activating genes.

AKB 50 Imaging and Microscopy

Zeit: Montag 16:00–18:15 Raum: TU H2013

AKB 50.1 Mo 16:00 TU H2013

FRET Studies of the Mobility of TBP-DNA Complexes upon Binding of NC2 — •Don C. Lamb[1,2,3], Peter Schlüsche[1,3], Christoph Bräuchle[1,3], Gertrard Stelzer[4], and Michael Meisterernst[4] — [1]Physical Chemistry, LMU Munich, Munich, Germany — [2]Department of Physics, University of Illinois at Urbana-Champaign, Urbana, IL, USA — [3]Center for Nanoscience, LMU, Munich, Germany — [4]National Research Center for Environment and Health, Munich, Germany

Transcription of DNA into RNA is an essential process in life and the initiation of the transcription processes is a popular target for gene regulation. Transcription is initiated with binding of the TATA box binding protein (TBP) to the promoter site on the DNA and recruiting other elements of the transcription complex. When negative cofactor 2 (NC2) is present, transcription is down regulated. NC2 binds to TBP with high affinity. Biochemical evidence suggests that upon binding, the TBP-NC2 complex diffuses along the DNA. Hence, transcription is down regulated because the TBP is not longer located at the promoter site. To verify this hypothesis and to investigate the mobility of the TBP-NC2 complex upon NC2 binding, we have performed fluorescence resonance energy transfer (FRET) experiments on single molecules. TBP was labeled specifically with a donor molecule while a short piece of double-stranded DNA containing a TATA box in the center was labeled with an acceptor. The FRET efficiency was measured before NC2 and after addition of NC2 to solution to investigate the dynamics of individual TBP-NC2 complexes.

AKB 50.2 Mo 16:15 TU H2013

Multi Focal 2-Photon Laser Scanning Microscopy of Cells and Biological Tissue — •Jörg Martini, Katja Tönsing, and Dario Anselmetti — University of Bielefeld, Experimental Biophysics, 33615 Bielefeld, Germany

Near infrared 100fs laser pulses focussed through a high numerical aperture objective lens provide an energy density, that is high enough to induce 2-photon excitation of native fluorophors and fluorescent dyes in the focal volume. By scanning the back aperture of the objective lens with the laser beam, confocal like collection of the fluorescence signal from a single optical plane up to hundreds of μm inside the sample is possible. Varying the distance between the lens and sample, i.e. measuring a depth dependent stack of optical planes, produces a 3D fluorescence scan of the sample with sub μm resolution. The output of today's Ti:Sa-lasers in the focal volume is much higher than the destruction threshold of almost all biological samples. By splitting up the laser power and directing several beams into the objective lens, we create up to 64 foci in the sample.

This setup allows for short acquisition times while minimizing the photo damage to the sample. We will present our results on the 3D-distribution of fluorescence and second harmonic generation signal in single cells and biological tissue and their spectral properties.

AKB 50.3 Mo 16:30 TU H2013

Single fluorescent molecules imaged by the near-field of a metal tip — •Heinrich Gotthard Frey[1] and Reinhard Guckenberger[2] — [1]Universität Bielefeld, Fakultät für Physik, Universitätsstr. 25, 33615 Bielefeld, Germany — [2]Max-Planck-Institut für Biochemie, Abt. Molekulare Strukturbiologie, Am Klopferspitz 18, 82152 Martinsried, Germany

We show experimentally that a sharp metal tip, illuminated by a close-by aperture, can be used as high resolution optical near-field probe with an unique combination of good qualities [1]:

Single Cy3 molecules covalently bound to DNA were imaged as test sample. The fluorescence images of such single molecules show patterns with one or two peaks. The width of these peaks can be as small as 10 nm. A simple model allows to explain these patterns. By fitting model calculations to the data, the positions of the dye molecules can be determined with an accuracy better than 1 nm. The 3D orientation of the dyes is also provided by the fit. The positions of two single molecules with only 12 nm distance and overlapping fluorescence patterns could still be determined. The metal tip also provides a topographical signal simultaneously to the optical one. The topographical and optical images have nearly the same resolution and the lateral shift between these images is smaller than the resolution. So, optical and topographical information can be measured simultaneously at the same point, what is of high importance for time dependent measurements.

[1] H.G. Frey, S. Witt, K. Felderer, and R. Guckenberger, Phys. Rev. Lett., in press

AKB 50.4 Mo 16:45 TU H2013

Infrared-spectroscopic mapping of a single virus by near-field microscopy — •Markus Brehm, Thomas Taubner, and Fritz Keilmann — MPI für Biochemie, 82152 Martinsried (München)

Infrared fingerprint spectroscopy has traditionally been a powerful tool for chemical and structural analysis, but because of diffraction could not solve problems requiring $< 5\mu m$ microscopic resolution.
Scattering scanning near-field optical microscopy (s-SNOM) overcomes this limit by exploiting the near-field coupling between a sharp tip and the sample, allowing resolutions of 20 nm even at mid-infrared wavelengths [1,2].
Here we show infrared-spectroscopic mapping of a single virus within the spectral range of the protein amide-I band ($\approx 1600 - 1700\,\mathrm{cm}^{-1}$) demonstrating a resolution of ≈ 100 times better compared to conventional infrared microscopy. We therefore believe that this method can be of significant use to some problems in biology.

1. T. Taubner, R. Hillenbrand, and F. Keilmann, "Performance of visible and mid-infrared scattering-type near-field optical microscopes,"Journal of Microscopy, vol. 210, pp. 311-314, 2003.
2. T. Taubner, R. Hillenbrand, and F. Keilmann, "Nanoscale polymer recognition by spectral signature in scattering infrared near-field microscopy", Applied Physics Letters, vol. 85 (22), 2004.

AKB 50.5 Mo 17:00 TU H2013

Imaging of molecular interactions with Photonic Force Microscopy — •Alexander Rohrbach[1], Ernst Stelzer[1], Holger Kress[1], and Nils Becker[2] — [1]European Molecular Biology Laboratory (EMBL), Meyerhofstr. 1, 69117 Heidelberg — [2]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden

Molecular interactions are controlled by the thermal environment of the binding partners. The resulting energy fluctuations offer a broad spectrum of orientations, distances and kinetics to the molecules enabling an optimal interaction. This concept is exploited in photonic force microscopy: An optically trapped probe fluctuates in its position as a function of the trapping parameters and the probes local environment. The probe position can be tracked interferometrically in the MHz range with a precision of 1 - 5 nm in three dimensions. The fluctuations are altered by external enthalpic or entropic forces acting on the probe. These interactions can be visualized by recording the particles three-dimensional trajectories, resulting in an interaction profile with nm resolution. Two applications illustrate the potential of this technique: single molecule experiments with the protein Myosin II to determine its nano-mechanics; and experiments resolving the temporal and spatial binding of particles to macrophage membranes.

AKB 50.6 Mo 17:15 TU H2013

Subdiffraction Fluorescence Imaging with photoswitchable fluorescent proteins — •M. Hofmann, C. Eggeling, S. Jakobs, and S.W. Hell — MPI für biophysikalische Chemie, Dep. NanoBiophotonics

The resolution of optical imaging in conventional far-field microscopy is limited by the diffraction of light. We present fluorescence imaging beyond this barrier by controlling the light driven transition between the dark and fluorescent state of a photoschwitchable protein. Fluorescence emission in the outer region of a diffraction-limited excitation spot is deactivated in a saturated manner, thereby reducing the effective fluorescence volume. Scanning images of protein stained structures exhibit an increased resolution. This can be described on the basis of a photophysical model and its underlying rate constants, which were determined from spectroscopic experiments of the fluorescence emission. The data shows that a reversible saturable optical fluorescence transition of a protein can be utilized to achieve optical imaging beyond the diffraction limit.

Hell, S. W., Nature Biotechnol. 21(11): 1347-1355 (2003)
M. Hofmann, C. Eggeling, S. Jakobs, S. W. Hell "Subdiffraction Imaging with the photoswitchable fluorescent protein asCP"(in preparation)

AKB 50.7 Mo 17:30 TU H2013

Applications of Pulsed Interleaved Excitation — •Barbara K. Müller, Christoph Bräuchle, and Don C. Lamb — Department Chemie und Biochemie, LMU München, Butenandtstr. 5-13, 81377 München

Pulsed interleaved excitation (PIE) is used in multi-color experiments, whereby the excitation source of a detected photon is known. In our approach, we use a two channel confocal setup, pulsed lasers as excitation sources and a single photon counting card for data storage. The excitation pulses are delayed with respect to each other such that the fluorescence photons from one excitation source arrive before the other excitation pulse and vice versa. Hence, this technique enables one to eliminate crosstalk or to enhance the sensitivity of fluorescence resonance energy transfer (FRET) experiments. We show that this technique increases the sensitivity of fluorescence cross-correlation spectroscopy (FCCS) by removing the spectral cross talk as well as provides the possibility of accurate FCCS in presence of FRET. Moreover, PIE can be used in wide field spectroscopy or laser scanning microscopy, where multi-color detection with one detector is possible. In addition to the economic benefits, this allows higher precision in distance measurements between different fluorophores because both colors are imaged with the same optics. This technique also promises new possibilities in single-pair FRET measurements. With sub-nanosecond pulses, not only stoichiometric information are available, but also the fluorescence lifetime from the same measurements. Thus, the FRET-efficiency can be calculated from either the intensities of donor and acceptor dyes or from their lifetimes.

AKB 50.8 Mo 17:45 TU H2013

Single particle fluorescence microscopy enlights active and diffusive transport processes of nanoparticles in living cells — •Ralf Bausinger[1], Katharina von Gersdorff[2], Manfred Ogris[2], Christoph Bräuchle[1], Ernst Wagner[2], and Andreas Zumbusch[1] — [1]LMU München, Department of Chemistry, Butenandtstr. 5-13, Building E, D-81377 München — [2]LMU München, Department of Pharmacy, Butenandtstr. 5-13, Building D, D-81377 München

Biochemical experiments demonstrated the general applicability of cationic polyethyleneimine-DNA complexes for the delivery of genetic material into the cell nucleus. However only few mechanistic details about this transfection process are known so far. We use single-molecule sensitive fluorescence video microscopy for the tracking of individual nanoparticles inside the cell in combination with structured wide-field illumination for the imaging and three-dimensional reconstruction of labelled cellular structures. Our observations include the interaction of the polyplexes with parts of the cytoskeletton, namely the actin stress fibers and the microtubules. We further analyse the role of mitosis for the delivery of gene carriers into the cell nucleus.

AKB 50.9 Mo 18:00 TU H2013

Single Virus Tracing: Real-time visualization of the membrane attachment and cellular uptake of individual HIV particles — •Thomas Endress[1], Stefan Riegelsberger[1], Marko Lampe[2], Barbara Müller[2], Hans-Georg Käusslich[2], Don Lamb[1], and Christoph Bräuchle[1] — [1]Physikalische Chemie, Universität München, Butenandtstr. 11, 81377 München — [2]Virologie, Unversität Heidelberg, Im Neuenheimer Feld 324, 69120 Heidelberg

Viruses play a major role in biology and medicine. A detailed analysis of the different steps of a viral infection is not only necessary for understanding viral biology, but also for the development of efficient antiviral drugs. Single Virus Tracing (SVT) allows visualization of the infection pathway of an individual virus labelled with fluorescent dye molecules. The fluorescence of the marker molecule is imaged and used to follow the pathway of the virus with high spatial (40 nm) and temporal (10 ms) resolution (*Science, 294 (2001)1929*).
HIV was labeled in the shell with its matrix protein (MA) using eGFP and in the core via its viral protein (Vpr) with mRFP. This allows simultaneous observation of the outer shell and subviral core of the individual HIV in real time. Analysis of virus-cell interactions by SVT revealed a detailed picture of the membrane interactions and cellular surface factors like HSPG involved in typical membrane attachment of HIVs. We were able to distinguish between the very rapid entry ($\leq$ 1 min) of subviral particles by membrane fusion and a slower endosomal uptake of HIV ($\geq$ 12 min). Furthermore, two types of intracellular trafficking were observed.

AKB 55 Molecular Motors

Zeit: Dienstag 14:00–15:45 Raum: TU H2013

Hauptvortrag AKB 55.1 Di 14:00 TU H2013

The Role of Diffusion in the Mechanism of Motor Proteins - Thermal Ratchets and all that — •Jonathon Howard — Max Planck Institute for Molecular Cell Biology and Genetics

Motor proteins such as myosin, dynein and kinesin are enzymes that convert chemical energy, derived from the hydrolysis of ATP, into mechanical work used to power cellular motility. These proteins are unusual engines because the conversion into mechanical energy is direct rather than via an intermediate such as heat or electrical energy, as in everyday engines. A key concept for understanding the mechanism of energy transduction by motor proteins is the lever. Small, atom-sized conformational changes in the ATP-binding pocket of the protein (a few Angstroms) are amplified ten- to one hundred-fold into large conformational changes of the whole protein (several nanometers). The amplification is achieved via rigid-body rotations and translations of comparatively rigid protein domains. The transition between different chemical states is activated by thermal energy. In the case of motor proteins the transition is associated with large displacements corresponding to the protein conformational changes; for this reason, diffusion is expected to play an important role in the motor reaction. I discuss recent experimental and theoretical work on this question.

Hauptvortrag AKB 55.2 Di 14:30 TU H2013

Bacterial motion: molecular motors and switches — •Berenike Maier — CeNS, LMU München

Bacteria are the smallest free-living organisms. Having a diameter of only one micrometer, bacteria undergo random walks in aqueous solution. Bacteria have developed various molecular machines to overcome Brownian motion and to generate directed movement. In this talk we will explore kinetics, force generation and switching of the molecular machine responsible for 'twitching motility' at surfaces.

AKB 55.3 Di 15:00 TU H2013

Molecular dynamics simulations of spontaneous and forced motions of isolated subunits of F_1-ATPase — •U. Kleinekathöfer[1], B. Isralewitz[2], M. Dittrich[2], and K. Schulten[2] — [1]Institut für Physik, Technische Universität Chemnitz, 09107 Chemnitz — [2]Beckman Institute, University of Illinois, Urbana, USA.

The F_1 unit of ATP synthase converts a torque applied to its central stalk into chemical synthesis of ATP at binding sites nearly 100 Å away. F_1 has three-fold pseudo-symmetry, consisting of three non-catalytic α-subunits and three catalytic β-subunits. During synthesis, the torque-driven central stalk rotation causes the β-subunit to assume several different conformations at different points in the synthesis cycle. The reverse happens during hydrolysis: conformation changes in the β-subunits drive rotation of the central stalk. We examine the tendency towards spontaneous conformation change of isolated open, half-closed, and closed β-subunits of bovine mitochondrial F1-ATP synthase. In 10-ns molecular dynamics equilibrations, the subunit structural changes can be decomposed into two motions: one parallel to the pseudo-symmetry axis of F1 and one perpendicular to this axis. We also examine the behavior of the central stalk when a β-subunit is forced to close, simulating F1 functioning in hydrolysis mode. In a model system consisting of the central stalk and a single β- subunit, steered molecular dynamics transforms an isolated β-subunit from an half-closed state to a closed state, while the central stalk is constrained to rotate on the pseudo-symmetry axis. We describe how central stalk rotation proceeds as closing is enforced, and how several β-subunit structures effect the force transfer.

AKB 55.4 Di 15:15 TU H2013

Random walks and traffic of molecular motors — •Stefan Klumpp and Reinhard Lipowsky — Max-Planck-Institut für Kolloid- und Grenzflächenforschung, 14424 Potsdam-Golm

Molecular motors exhibit movements on various length scales. Movements on large scales are characterized by the binding to and unbinding from the filaments along which the motors move, and can be described by a class of lattice models [1]. In addition to providing a description of the random walks which arise from many diffusive encounters of motors with filaments, these models allow us to study motor-motor interactions.

The simplest and most obvious such interaction is the hard core repulsion or mutual exclusion of motors, in particular the mutual exclusion from the filament sites, which leads to a variety of cooperative phenomena such as traffic jams, the formation of density patterns and boundary-induced phase transitions [1,2].

In addition, we studied the case where two species of motors moving into opposite directions compete for the filament sites. For sufficiently strong motor–motor interactions, spontaneous symmetry breaking is observed [3]: One motor species occupies the filament while the other one is largely excluded from it. This symmetry breaking provides a mechanism for the formation of traffic lanes.

[1] R. Lipowsky, S. Klumpp, and Th. M. Nieuwenhuizen, Phys. Rev. Lett. **87**, 108101 (2001).
[2] S. Klumpp and R. Lipowsky, J. Stat. Phys. **133**, 233 (2003).
[3] S. Klumpp and R. Lipowsky, Europhys. Lett. **66**, 90 (2004).

AKB 55.5 Di 15:30 TU H2013

Filament depolymerisation by motor proteins — •Gernot Klein, Karsten Kruse, and Frank Jülicher — MPIPKS, Noethnitzerstr. 38, 01187 Dresden

Many active processes in cells are driven by highly specialized motor proteins, which interact with filaments of the cytoskeleton. Members of the Kin-13 kinesin subfamily are able to interact specifically with filament ends and induce depolymerisation of the filaments ends. Recent in vitro assays and single molecule studies have shown, that MCAK accumulates at both ends of stabilized microtubules and induces depolymerisation while at the same time MCAK molecules do not generate directed motion along the microtubules [1].

We analyse both, a stochastic model and a generic mean-field description of this process. We discuss conditions under which motors dynamically accumulate at the filament end. Such a dynamic accumulation occurs for processive cutting, which implies, that the motor can remain attached to the shrinking edge after subunit removal. For processive cutting, the depolymerisation speed as a function of the bulk motor concentration can exhibit several different types of behaviour, including the possibility of a dynamic instability. We discuss our results in relation to recent experiments.

[1]A.W. Hunter, et al., Mol. Cell 11, 445 (2003)

AKB 60 Membranes and Vesicles

Zeit: Dienstag 16:00–17:45 Raum: TU H2013

AKB 60.1 Di 16:00 TU H2013

Efficient tunable generic model for self-assembling fluid bilayer membranes — •Markus Deserno, Ira R. Cooke, and Kurt Kremer — Max-Planck-Institut für Polymerforschung, Ackermannweg 10, 55128 Mainz

We present a new model for the simulation of generic lipid bilayers in the mesoscopic regime (between a few nanometers and many tens of nanometers), which is very robust, versatile, and extremely efficient, since it avoids the need for an embedding solvent. Based entirely on simple pair potentials, it features a wide region of unassisted self assembly into fluid bilayers without the need for careful parameter tuning. The resulting membranes display the correct continuum elastic behavior with bending constants in the experimentally relevant range. It can be readily used to study events like bilayer fusion, bilayer melting, lipid mixtures, rafts, and protein-bilayer interactions.

AKB 60.2 Di 16:15 TU H2013

Shapes of crystalline domains on spherical vesicles — •Stefanie Schneider and Gerhard Gompper — Institut für Festkörperforschung, Forschungszentrum Jülich, D-52425 Jülich, Germany, Email: st.schneider@fz-juelich.de

The background to this work is the experimental observation of a variety of shapes of the crystalline domains on giant unilamellar vesicles, consisting of two different lipids as well as cholesterol [1]. Understanding these systems is important, because they serve as model systems for the far more complex biological lipid bilayers. Important biological functions, such as endocytosis, cell adhesion, signaling and protein organisation, are attributed to the formation of domains in lipid bilayers.

To further understand the domain formation in these systems, we have investigated crystalline domains of different shapes embedded in spherical fluid vesicles using the elasticity theory and Monte Carlo simulations. The stretching energy, which is necessary to deform an ideal crystalline patch onto the surface of a sphere has been calculated for different shapes of the patch (disc, stripe, and a disc including one disclination). A phase diagram has been constructed in which the equilibrium shapes and number of the patches are related to the Young modulus, the line tension between the fluid and the crystalline phase, and the relative area of the vesicle covered by the crystalline phase.

[1] J.Korlach, P. Schwille, W. Webb, G. Feigenson, Proc. Natl. Acad. Sci. USA, **96**, 8461(1999)

AKB 60.3 Di 16:30 TU H2013

Single- and multicomponent vesicles at finite temperature — •Thomas Gruhn, Gunnar Linke, and Reinhard Lipowsky — MPIKG Golm, D-14424 Potsdam

Vesicles at finite temperature are studied with the help of Monte Carlo simulations. At finite temperature, a vesicle with no volume constraint is preferentially aspherical. The free energy has two minima for prolate and oblate configurations. With increasing pressure difference between in- and outside of the vesicle, it becomes more and more spherical.

For vesicles adhered to a substrate the adhesion area decreases linearly with increasing temperature. This is found in simulation studies of adhered vesicles with and without volume constraints. The results allow to obtain experimentally the bending stiffness and the adhesion strength of an adhered vesicle by measuring the temperature dependence of the adhesion area.

In multicomponent vesicles the formation of domains occur for large enough line tensions. The domains may differ in their mechanical and chemical properties, an effect which allows to mimick specific interactions between cells or between a cell and a substrate. Various examples are presented.

AKB 60.4 Di 16:45 TU H2013

Collective Dynamics of Lipid Membranes studied by Inelastic Neutron Scattering — •Maikel Rheinstädter[1], Tilo Seydel[1], Wolfgang Häussler[2], and Tim Salditt[3] — [1]Institut Laue-Langevin, 6 rue Jules Horowitz, B.P. 156, 38042 Grenoble, France — [2]FRM II, Lichtenbergstrasse 1, 85747 München, Germany — [3]Institut für Röntgenphysik, Geiststrasse 11, 37037 Göttingen, Germany

While most spectroscopic techniques, as e.g. nuclear magnetic resonance or dielectric spectroscopy, are limited to the center of the Brillouin zone and probe the macroscopic response, inelastic neutron and X-ray scattering experiments give the unique access to microscopic dynamics at length scales down to intermolecular distances. Only recently, it has become possible to study collective dynamics of planar lipid bilayers using neutron spectroscopy techniques [1]. We determined the dispersion relations in the gel and in the fluid phases of a DMPC model membrane and could shed light on the evolution of structure and dynamics and the relation between them in the range of the gel-fluid main phase transition. Here, the scattering volume restriction for inelastic neutron experiments was overcome by stacking several thousand highly aligned membrane bilayers. By combining neutron triple-axis, backscattering and spin-echo spectroscopy, we present measurements of short and long wavelength collective fluctuations in biomimetic and biological membranes in a large length and energy range. A recent backscattering study for the first time gave access to the dynamics of the "membrane-water", i.e. the water layer in between the stacked membranes.

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

AKB 60.5 Di 17:00 TU H2013

Chemical Switching of Diblock Copolymer Monolayers at the Interface: Controlling Interactions between Solid Substrates and Biological Matter — •Florian Rehfeldt[1], Kirstin Seidel[1], Roland Steitz[2], Regine v. Klitzing[3], Steven P. Armes[4], Alice P. Gast[5], and Motomu Tanaka[1] — [1]Physik Dept. E22, TU München, James-Franck-Str., 85748 Garching, Germany — [2]HMI Berlin GmbH, BENSC SF1, Glienicker Str. 100, 14109 Berlin, Germany — [3]MPI f. Kolloid u. Grenzflächen, Golm, Germany — [4]Dept. of Chemistry, Univ. of Sheffield, South Yorkshire S3 7HF, UK — [5]Dept. of Chemical Engineering, M. I. T. Cambridge, MA 02139, USA

This study aims at the switching of interfacial interactions between soft, biological matter and planar solid substrates. As a switchable interlayer, a monolayer of (DMAEMA-*b*-MMA)is used. Specular neutron reflectivity experiments at solid/liquid interface demonstrated that the polymer chain conformation (thickness, hydration and surface roughness) can reversibly be switched in physiological environments due to charging and de-charging of the hydrophilic DMAEMA block. As next step, we carried out neutron reflectivity measurements of the polymer film with a supported lipid membrane. Upon pH titration between 5.5 and 8.5, we observe a clear switching in the membrane-substrate distance induced by the change in polymer chain conformation. The obtained results demonstrate that the diblock copolymer coating enables us to fine-tune the surface properties. The system established here suggests a great potential towards mimicking the extracellular matrix (ECM) to regulate the interfacial potential at substrate-membrane interface.

AKB 60.6 Di 17:15 TU H2013

Synchrotrondiffraction studies on solid-supported membranes in a microfluidicenvironment — •Bert Nickel[1], Christian Reich[1], Marion Hochrein[1], Bärbel Krause[2] und Joachim Rädler[1] — [1]Ludwig Maximilians Universität, München — [2]ESRF, Grenoble

We have developed a microfluidic flow chamber allowing for synchrotron diffraction studies of solid supported membranes at the solid liquid interface using x-ray energies of 20 keV. We demonstrate the potential of the method by comparing three standart preparation methods of lipid bilayers: (a) vesicle fusion, (b) solvent exchange, and (c) spin-coating. A complementary characterization of the solid supported lipid bilayer using fluorescence microscopy is possible.

AKB 60.7 Di 17:30 TU H2013

In situ Formation of Polyelectrolyte Multilayer Architectures with Embedded Lipids Studied by Neutron Reflectometry — •Thomas Gutberlet[1], Christophe Delajon[2,3], Rumen Krastev[2,4], and Helmut Möhwald[2] — [1]Paul-Scherrer-Institut, Villigen, Switzerland — [2]Max-Planck-Institut of Colloids and Interfaces, Golm, Germany — [3]ISIS Universite Louis Pasteur, Strasbourg, France — [4]Hahn-Meitner-Institut, Berlin, Germany

Biomimetic surfaces with tailored properties are major object of application oriented biophysical studies. Of particular interest are surface-grafted films of hydrophilic polymers which provide a biomimetic environment for membranes-spanning proteins and lipid-protein membranes.

We have studied the coupling of phospholipids to fully hydrated polymer cushions as potential planar biomimetic model membrane. A DMPC lipid bilayer was supported by polyelectrolyte multilayers (PEM). Positively and negatively charged polymer sample terminations were considered. Using neutron reflectometry it was shown that, whereas positively charged terminated samples did not favour deposition of a lipid layer, negatively charged terminated samples allowed deposition of a lipid bilayer. In the latter case, formation of a PEM on the phospholipid layer was possible and the formation of a polymer/lipid/polymer complex sandwich like structure has been proven. the results will be presented and potential applications discussed.

AKB 70 Neurophysics

Zeit: Mittwoch 09:45–10:15 Raum: TU H2013

Hauptvortrag AKB 70.1 Mi 09:45 TU H2013

Biophysics of Mechanosensory Localization: What, Where, and Why — •J. Leo van Hemmen — Physik Department, TU München, 85747 Garching bei München

Auditory localization means locating a sound source, an auditory object, through sound waves emanating from a source and exciting hair cells. There is a huge family of sensory detectors that all work through the same mechanism, the mechanosensory one. Audition is best known: Sound waves excite hair cells that then send their action potentials or spikes to the auditory system. Defining a 'map' to be a neuronal representation of the outside sensory world, we implicitly ask: What is a map and how does it arise? In addition to sound waves there are other mechanical means to generate a neuronal response at the detectors. A surface wave allows a sand scorpion to locate prey near to it in a desert. Water waves stimulate hair cells in superficial neuromasts (i.e., detectors at the skin) of, e.g., the clawed frog *Xenopus* and in both superficial and canal neuromasts of fish. It is fair to call the ensuing process mechanosensory localization and ask whether the underlying neuronal mechanisms exhibit any *universality*. In so doing we will present a theory as to 'what, where, and why'.

AKB 75 Nonlinear Phenomena and Pattern Formation

Zeit: Mittwoch 10:15–11:45 Raum: TU H2013

Hauptvortrag AKB 75.1 Mi 10:15 TU H2013

The Physics of Chemoreception - an Encore — •U. Benjamin Kaupp — Forschungszentrum Jülich, Institut für Biologische Informationsverarbeitung 1, 52425 Jülich

Sperm can navigate in a chemical gradient of attractants released by the egg. The attractant molecules bind to specific receptors on the surface of the sperm flagellum. Activation of receptors initiates a cellular signaling pathway. Within milliseconds, the intracellular messenger cyclic GMP is synthesized. This messenger opens ion channels in the envelope membrane, and Ca ions are flowing into the cell. A sperm cell is exquisitely sensitive: it can respond to the binding of a single attractant molecule. At the same time, sperm respond over a broad range of attractant concentrations (ca. 5 orders of magnitude). This remarkable dynamic range is achieved by two mechanisms. First, the receptor rapidly inactivates; second, the receptor lowers its binding affinity at higher states of occupancy. Both mechanisms enable sperm to escape saturation at high attractant concentrations near the egg. The increase in [Ca] changes the beat pattern of the flagellum. In the unstimulated state, sperm swim in circles. Upon activation by the attractant, sperm undergo a sequence of turns and straight swimming ('turn-and-run'). In a chemical gradient, the behavioural pattern produces epicycloid movements towards the source. The sequence of alternating 'turns' and 'runs' is produced by Ca oscillations in the flagellum that are evoked by the attractant. The Ca oscillations change the properties of motor proteins by unknown mechanisms.

AKB 75.2 Mi 10:45 TU H2013

Role of fluctuations in active hair-bundle mechanics — •Björn Nadrowski[1], Pascal Martin[2], and Frank Jülicher[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Stra"se 38, 01309 Dresden — [2]Laboratoire Physico-Chimie Curie, Unité Mixte de Recherche 168, Institut Curie, 26 rue d'Ulm, F-75248 Paris Cedex 05, France

Hearing relies on active filtering to achieve exquisite sensitivity and sharp frequency selectivity. In a quiet environment, the ears of many vertebrates emit one to several tones. These spontaneous otoacoustic emissions, the most striking manifestation of the inner ear's active process, result from self-sustained mechanical oscillations of aural constituents.

It has been shown that the mechanosensitive hair bundles of vestibular cells from the frog ear have the ability to oscillate spontaneously. This spontaneous oscillation leads to frequency-selective amplification and nonlinearity in the bundles mechanical response.

We discuss the physical principles underlying detection based on critical oscillation as well as specific mechanisms that can lead to oscillations and active behaviors by hair bundles. A simple description of active hair-bundle mechanics is presented. We present the state diagram and show that fluctuations influence the mechanical response functions. We discuss different sources of fluctuations and estimate their influence on the hair-bundle's mechanical properties. Furthermore, the linear and nonlinear response functions calculated numerically can quantitatively account for the observed properties of active hair-bundles.

Nadrowski, Martin, Julicher, PNAS 101, 12195 (2004)

AKB 75.3 Mi 11:00 TU H2013

Symmetry-breaking and axis establishment in Hydra — •Jordi Soriano[1], Sten Rüdiger[2], Pramod Pullarkat[1], Michael Kücken[2], Ernesto Nicola[2], Timo Mai[1] und Albrecht Ott[1] — [1]Experimentalphysik I, Universität Bayreuth. Universitätstraße 30, D-95448 Bayreuth, Deutschland — [2]Theoretische Physik II. Universität Bayreuth. Universitätstraße 30, D-95448 Bayreuth, Deutschland

Hydra may regenerate from a small piece of tissue or from an aggregate of dissociated cells. During the regeneration process the cells first form a hollow sphere made of a cell bi-layer that experiences a series of changes during which the isotropy is broken and a new axis is constituted. We have studied in detail the symmetry-breaking process from an experimental point of view, and focused on the morphogenic and genetic changes that the Hydra-ball experiences during regeneration. We have found that morphogenic oscillations are essential for symmetry-breaking, and that they may trigger the key genetic mechanisms responsible for the constitution and maintenance of the axis and the subsequent development. We also propose a new reaction-diffusion model to describe the symmetry-breaking process.

AKB 75.4 Mi 11:15 TU H2013

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

Morphogens are signaling molecules that play a key role in animal development. They 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. Morphogen transport through the tissue has been studied in experiments which lead to the suggestion of several transport mechanisms. While diffusion in the extracellular space contributes to transport, recent experiments on the morphogen Dpp in the fruit fly Drosophila provide evidence for the importance of a cellular transport mechanism that was termed "planar transcytosis". In this mechanism, morphogens are transported through cells by repeated rounds of internalization and externalization. Starting from a microscopic description of these processes, we derive nonlinear transport equations which describe the interplay of transcytosis and passive diffusion. We find that transcytosis leads to an increased robustness of the created gradients with respect to morphogen over-expression. This robustness has been observed in experiments. We finally relate our description to recent experiments.

AKB 75.5 Mi 11:30 TU H2013

Mechanical Properties of self-assembling biomolecular tubes — •Iwan A.T. Schaap[1], Pedro J. de Pablo[1], Catherine Tardin[1], Andrew Turberfield[2], Richard Berry[2], Cees G. de Kruif[3], Joanke Graveland[3], Bernd Hoffmann[4], Frederick C. MacKintosh[1], and Christoph F. Schmidt[1] — [1]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [2]Dept. Physics, Oxford University, Oxford, UK — [3]NIZO Food Research, Ede, NL — [4]Forschungsztr. Julich, Julich, D

Biomacromolecules often have the capability to self-assemble into either functional and well regulated or pathogenic unregulated structures. Examples for the former are cytoskeletal filaments such as microtubules, 25 nm hollow tubes made of tubulin protein. The latter occurs in many neurodegenerative diseases (amyloid formation). Molecular self-assembly can also be put to technical use, for example by engineering self-assembling DNA building blocks. We have employed an atomic force microscope (AFM) operated at well-controlled low forces to image under physiological conditions various tube-like structures at nm resolution, including microtubules with and without accessory proteins, protein amyloid tubes and DNA tubes. To measure mechanical properties, we have indented individual tubes locally with the AFM tip. The deformation is elastic for the few nm of indentation. By indenting with higher forces, we can exceeded elastic limits and produce local defects.

AKB 80 Microfluidics

Zeit: Mittwoch 11:45–12:30 Raum: TU H2013

AKB 80.1 Mi 11:45 TU H2013

Experimental Proof of Absolute Negative Mobility of Single Brownian Particles — •Jan Regtmeier[1], Ralf Eichhorn[2], Peter Reimann[2], Dario Anselmetti[1], and Alexandra Ros[1] — [1]Experimentelle Biophysik und Angewandte Nanowissenschaften,Universität Bielefeld, Universitätsstr. 25,33615 Bielefeld — [2]Condensed Matter Theory,Universität Bielefeld,Universitätsstraße 25,33615 Bielefeld

Recently, it has been predicted theoretically [1] that the average motion of a single Brownian particle can be opposite to a small applied force. This behaviour, which seems to contradict Newtonian laws, is called Negative Mobility and can only occur far from thermodynamic equilibrium.

We experimentally demonstrate that negative mobility of non-interacting Brownian particles can be observed in periodic and symmetric potentials, forming a landscape of gaps and traps. Carboxylated polystyrene particles of 2 μm diameter in fact show an average motion against a static electric force in a poly(dimethylsiloxane) microfluidic device with micrometer sized periodically alternating structures using electrokinetic driving forces in physiological buffer solution. This setup enables high parallelisation and opens the way to use the system for biological applications such as separation of biomolecules or sorting of cells.

[1] R. Eichhorn, P. Reimann, P. Hänggi, Phys. Rev. Lett. 88, 190601 (2002)

AKB 80.2 Mi 12:00 TU H2013

Surface coating strategies for poly(dimethylsiloxane) microchannels — •Wibke Hellmich[1], Jan Regtmeier[1], Stephan Altmann[2], Dario Anselmetti[1], and Alexandra Ros[1] — [1]Experimental Biophysics and Applied Nanosciences, Physics Faculty, Bielefeld University — [2]BASF AG, Polymer Physics, Ludwigshafen

Control of the surface properties in microfluidic systems plays an important role for successful bioanalytical applications. Especially the unspecific interaction of apolar biomolecules with hydrophobic microchannel surfaces highly affects the analysis efficiency in poly(dimethylsiloxane) (PDMS) devices. Therefore, detailed knowledge and derivatisation strategies of the surface properties of PDMS microchannels are of great importance. In this work, coating strategies for poly(ethyleneoxide) (PEO) molecules of different chain lengths are presented for the control of the surface properties of PDMS.
Contact angle measurements as well as atomic force microscopy revealed homogenous immobilisation of covalently attached PEO silanes and adsorbed triblock-copolymer (F108) to the PDMS surface. For F108, two different adsorption mechanisms to PDMS for hydrophobic (untreated) and hydrophilic (oxygen plasma treated) surfaces were observed. PEO coated microchannels revealed significant reduction of the electroosmotic mobility depending on the PEO chain length. The application of these coatings for protein separations in PDMS microfluidic devices is currently under investigation.

AKB 80.3 Mi 12:15 TU H2013

Neue Anwendungen von magnetischen sphärischen Sub-Mikropartikel in Mikrofluidik-Chips — •Claus Fütterer[1], Nicolas Minc[1], Kevin Dorfman[1], Marcella Slovakova[1], Zuzana Bilkova[2] und Jean-Louis Viovy[1] — [1]Institut Curie, Paris — [2]Univ. Pardubice, Tschechische Republik

Wir benutzen magnetische spherische Mikro- und Nanopartikel, welche sich im homogenen B-Feld in einem Gitter anordnen, in Verbindung mit einem neuartigen Mikrofluidikkontrollsystem um die Separation langer DNA Moleküle semiquantitativ durchzuführen. Dadurch wird der Vergleich mit Monte-Carlo Modellen ermöglicht. Im gleichen System können auch Einzelmolekülexperimente durchgeführt werden, welche die Untersuchung des Separationsmechanismus ermöglichen.

Desweiteren wird ein wiederverwendbares Chip-System zur Proteinanalyse vorgestellt. Dort wird Verdauung und Konzentration von Proteinen und Proteinfragmenten auf einem Chip vereinigt. Die dazu benötigten Enzyme sind auf magnetische Nano-Partikel immobilisiert. Letztere werden durch ein inhomogenes Magnetfeld zurückgehalten und verdichtet. Die Formierung dieses Pfropfens zeigt ausserdem interessante physikalische Phänomene.

AKB 85 Biosensors and Biohybrid Systems

Zeit: Mittwoch 12:30–13:30 Raum: TU H2013

AKB 85.1 Mi 12:30 TU H2013

Characterization of cell adhesion and cell properties on suspended nanoporous membranes — •Bernhard Wolfrum, Youlia Mourzina, Matthias Höller, and Andreas Offenhäusser — ISG2:Bioelectronic Signal Processing, Research Centre Jülich, 52425 Jülich, Germany

Suspended membranes of nanoporous materials like porous alumina and porous silicon facilitate the development of interesting biohybrid systems, particularly with regard to their good biocompatibility. For example, these materials can be used as carriers for artificial or natural cell membranes to study cell signalling in a bioelectronic hybrid system.

A close contact between porous structure and cell membrane is a precondition for the functionality of such a device. We therefore investigated the adhesion and morphology of cortical rat neurons and cells from cell lines on porous silicon and porous alumina membranes using scanning electron microscopy. The results were compared with the adhesion of cells to other substrates like silicon nitride and silicon oxide. Further, we characterized electrophysiological properties of adherent cells on porous structures using patch-clamp techniques. The adherent cells can thereby be chemically stimulated through the nanopores in the substrate.

AKB 85.2 Mi 12:45 TU H2013

Adsorption of Self-Assembled Polyelectrolyte Multilayers on a Silicon-on-Insulator based Sensor Device — •Petra A. Neff, Michael G. Nikolaides, Simon Q. Lud, and Andreas R. Bausch — Lehrstuhl für Biophysik - E22, Technische Universität München, 85747 Garching

Recently, a new Silicon-on-Insulator (SOI) based thin film resistor device for chemical and biological sensor applications was introduced. Its response against pH changes and variations of the salt concentration of an electrolyte on the native oxide surface was measured and compared to the theoretical predictions. It has been shown that the charge of different small peptides or proteins can be determined.

We study the adsorption of polyelectrolyte multilayers onto the SOI sensor devices. During the layer-by-layer deposition of the polycation poly(allylamine hydrochloride) (PAH) and the polyanion poly(styrene sulfonate) (PSS) by alternating buffer exchange, the response of a SOI sensor with a native oxide surface was observed as a change in its sheet resistance. The change in surface potential can be calculated from the sheet resistance applying calibration measurements. It corresponds to the surface charge density expected as a result of the multilayer build-up. The sensor signal amplitude was observed to be decreasing linearly with an increasing number of monolayers enabling the detection of more than 20 monolayers. To understand the sensor signal a theoretical model of the properties of the polyelectrolyte layers was compared to the measured data.

AKB 85.3 Mi 13:00 TU H2013

Time Resolved Dynamics of Electrically Switched Oligonucleotides on Au Surfaces — •Ulrich Rant[1], Kenji Arinaga[1,2], Yong Woon Kim[1], Shozo Fujita[2], Naoki Yokoyama[2], Roland Netz[1], Gerhard Abstreiter[1], and Marc Tornow[1] — [1]Technische Universitaet Muenchen, 85748 Garching, Germany — [2]Fujitsu Laboratories Ltd., 10-1 Morinosato-Wakamiya, Atsugi 243-0197, Japan

Macromolecules grafted to surfaces have been receiving considerable attention lately due to their interesting and complex behaviour at interfaces, but also in terms of applications (e.g., DNA sensors). In particular, the use of electrically addressable substrates permits many possibilities for manipulating charged molecules, which is accompanied by novel insights into interactions between the surface and the tethered polyelectrolytes. Recently, we reported on the dynamic manipulation of DNA on Au surfaces by electrically switching the strands while observing their orientations by optical means. Here we present time resolved experiments in which we study surface-tethered oligonucleotides of different lengths (24 and 48mer) in their single as well as double stranded conformation. We elucidate the dynamics of the molecules as they are repelled from, or attracted to the biased surface when reversing the charge on the metal substrate. By comparing the experimental data to hydrodynamic simulations, we are able to identify a distinctly different behaviour for single and double stranded DNA, respectively. Possibly, the identified mechanisms are of fundamental nature for the electrical manipulation of charged polymers with markedly dissimilar mechanical flexibilities.

AKB 85.4 Mi 13:15 TU H2013

Characterization of a chemically passivated GaAs based sensor device in electrolytes — •Sebastian M. Luber[1], Daniel Gassull[2], Dieter Schuh[1], Motomu Tanaka[2], Marc Tornow[1], and Gerhard Abstreiter[1] — [1]Walter Schottky Institut, TU München, 85748 Garching, Germany — [2]Lehrstuhl für Biophysik, E22, TU München, 85748 Garching, Germany

Functionalized field effect devices are promising candidates to act as smart substrates for sensor applications. For a use in biological systems an intermediate layer has to provide stabilization against electrochemical decomposition, and allow effective electrostatic coupling of the surface potential to the conductive channel.

We present a resistor device passivated with a 4'-substituted 4-mercaptobiphenyl self-assembled monolayer (SAM) for sensing applications. Starting material was a GaAs-AlGaAs heterostructure containing a quasi 2D electron gas 60nm beneath the surface. In the first part of our study we tested the stability of the device against aqueous solutions. Whereas a bare GaAs device degraded rapidly the coated samples showed a remarkable increase in stability. In the second part samples coated with monolayers with CH_3 (MBP-CH_3) and OH (MBP-OH) substituents in various buffered electrolyte solutions were characterized. For the MBP-OH coated sample, a change in pH induced a change in the resistance of the device. This behaviour can be expected due to non-specific adsorption at the hydrophilic surface of the $-$OH terminated SAM. However unexpectedly, the sample grafted with a MBP-CH_3 SAM with a hydrophobic surface also showed a clear response on pH.

AKB 90 Protein Folding and Molecular Dynamics

Zeit: Mittwoch 14:00–15:30 Raum: TU H2013

AKB 90.1 Mi 14:00 TU H2013

Helical Alanine Polypeptides: DFT versus Force-Field Results — •Marcus John, Joel Ireta und Matthias Scheffler — Fritz-Haber-Institut der Max-Planck-Gesellschaft

Recently it became possible to calculate different conformations of the secondary structure of proteins fully including the hydrogen bond (hb) cooperativity by means of density functional theory (DFT). Although the computational effort restricts this approach to the treatment of only a few conformations it nevertheless provides important insight into the stabilizing function of hbs. DFT in the PBE approximation to the exchange-correlation functional revealed the existence of three different minima on the potential-energy surface of a helix, corresponding to the π-, α-, and 3_{10} conformations [1]. A comparison with some existing force fields (CHARMM27 or AMOEBA) shows that they are not able to reproduce these different basins. We conjecture that this is due to the inability of current force fields to model the effect of cooperative hbs properly. In this contribution we provide an analysis of this phenomenon which may help to develop improved force fields.

[1] J. Ireta, M. Scheffler, J. Neugebauer, A. Rojo, M. Galvan submitted to PRL

AKB 90.2 Mi 14:15 TU H2013

A DFT-GGA based thermodynamic analysis of the secondary structure of proteins — •Lars Ismer[1], Joel Ireta[1], Matthias Scheffler[1], and Jörg Neugebauer[2] — [1]Fritz-Haber-Institut der MPG, Faradayweg 4-6, 14195 Berlin — [2]Theoretische Physik, Universität Paderborn, Warburger Str. 100, 33098 Paderborn

Studies of the thermodynamic stability of the secondary structure of proteins are important for understanding the protein folding process. We have therefore estimated the free energy change to fold a fully extended structure (FES) into the α-helical conformation for isolated infinite polyglycine (Gly) and -alanine (Ala) chains. The calculations have been performed employing DFT-GGA, a plane-wave pseudo-potential approach and the harmonic approximation. Our results reveal [1], that this approach leads to a significantly improved description of thermodynamic data with respect to previous studies based on empirical force fields. Further we find, that the enthalpy to transform an α-helix into an FES strongly reduces with increasing temperature: at room temperature the free energy difference for Gly is close to zero within the numerical error bar (0.5 kcal/mol), whereas for Ala the α-helix is by 1.0 kcal/mol more stable. We conclude, without recoursing to any empirical input parameters, that an isolated Ala-FES will even at room temperature spontaneously fold into an α-helix.

[1] L.Ismer, J. Ireta, S. Boeck and J. Neugebauer, submitted to Phys. Rev. E

AKB 90.3 Mi 14:30 TU H2013

Molecular mechanism of urea-induced protein unfolding — •Martin Stumpe and Helmut Grubmüller — MPI für biophysikalische Chemie, Theoretische und computergestützte Biophysik, Am Fassberg 11, 37077 Göttingen

Chemical denaturation is widely used to analyse protein stability and unfolding. Despite the common use of urea as denaturant, little is known about the molecular mechanism of urea-induced protein unfolding. Both, a direct interaction between urea and the protein as well as an indirect interaction via alteration of the water structure are possible and have been discussed. To shed light on this mechnism, we have carried out molecular dynamics simulations. Our studies of urea-water solutions revealed only minor perturbations of the water structure by the presence of urea. This finding provides new support for the direct interaction of urea with proteins during unfolding. We also achieved a detailled understanding of urea self-aggregation. Unfolding-simulations were performed with the Cold-Shock protein Bc-Csp and the human Prion protein fragment at elevated temperatures in physiological environment and in 8M urea solution. For these proteins, temperature-induced unfolding starts with a loss of secondary structure while the tertiary structure is conserved at the beginning and starts to decay only after the proteins have lost a substantial amount of secondary structure, in line with the hydrophobic-collapse models. Unexpectedly, and in contrast to room temperature results, at high temperatures urea does not seem to accelerate unfolding, which might point towards an entropy-dominated unfolding mechnism.

AKB 90.4 Mi 14:45 TU H2013

How parallel is protein (un)folding? — •Lothar Reich and Thomas R. Weikl — Max Planck Institute of Colloids and Interfaces, Theory Division, 14424 Potsdam

According to the 'old view', proteins fold along well-defined *sequential* pathways, whereas the 'new view' sees protein folding as a highly *parallel* stochastic process on funnel-shaped energy landscapes. We have analyzed parallel and sequential processes on a large number of Molecular Dynamics unfolding trajectories for the protein CI2 at high temperatures. Using rigorous statistical measures, we find that the degree of sequentiality depends on the structural level under consideration. On a coarse substructural level of whole β-sheets and helices, unfolding is predominantly sequential. In contrast, the unfolding process is more parallel on the level of individual contacts between the residues of the protein chain. On an intermediate structural level, the characteristic parallel and sequential events can be understood from simple loop-closure dependencies between the substructural elements.

AKB 90.5 Mi 15:00 TU H2013

All Atom Protein Structure Prediction with Stochastic Optimization Methods — •Wolfgang Wenzel, Thomas Herges, Alexander Schug, and Abhinav Verma — Forschungszentrum Karlsruhe, Institut für Nanotechnologie, Postfach 3640, 76021 Karlsruhe

The prediction of protein tertiary structure remains one of the outstanding problems in biophysical chemistry. According to the thermodynamic hypothesis, the native conformation of a protein can be predicted as the global optimum of its free energy surface with stochastic optimization methods[1] orders of magnitude faster than by direct simulation of the folding process.

We have recently developed an all-atom free energy forcefield (PFF01)[2] which implements a minimal thermodynamic model based on physical interactions. With this forcefield we were able to predictively fold the 20 amino acid trp-cage protein[3], the 40 amino-acid HIV accessory protein[4], the 36 amino-acid villin headpiece and the 60 amino acid bacterial ribosomal protein[5] using various stochastic optimization methods. We will disccuss advantages and limitations of these methods with respect to further improvements of this approach to in-silico all-atom protein strcuture prediction.

[1] W. Wenzel, K. Hamacher, PRL 59, 3003 (1999) [2] T. Herges, W. Wenzel, Biophys. J. 87, 3100 (2004) [3] A. Schug, W. Wenzel, PRL 91, 158102, 2003, EPL 67, 307 (2004) [4] T. Herges, W. Wenzel, PRL (in press) [5] A. Schug, W. Wenzel, JACS (in press)

AKB 90.6 Mi 15:15 TU H2013

Identification of Oxygen Channels in Proteins by Molecular Dynamics — •Jan Saam, Christopher Ozdoba und Hermann-Georg Holzhütter — Institut für Biochemie, Charité, Monbijoustr 2. 10117 Berlin

Cells contain a variety of enzymes that use molecular oxygen in the reactions they catalyze. In most cases the influence of oxygen-protein interaction on the reaction is unknown. We employed molecular dynamics simulations to determine the oxygen pathway from the solvent phase to the active site and to study the oxygen adsorption at the inner surface of two different oxygenases.

Our results show that in each enzyme there exists an oxygen channel different from the substrate entrance leading through the protein matrix to the catalytic site. The channels cannot be seen in the crystal structure but open their different segments temporarily yet allowing oxygen molecules to diffuse to the active center. With its high probability density for oxygen the interior end of the tunnel represents the ideal point for the stereo- and position specific insertion of dioxygen into the substrate. Subsequently these results could be confirmed by mutation experiments.

AKB 100 Poster Session I

Zeit: Samstag 16:45–18:45 Raum: Poster TU D

AKB 100.1 Sa 16:45 Poster TU D

Activation and characterization of a photoswitchabel GFP variant using two-photon absorption — •Marc Schneider[1], Sara Barozzi[2], Ilaria Testa[1], Mario Faretta[2], and Alberto Diaspro[1] — [1]INFM Genua, Via Dodecaneso 33, I-16146 Genoa, Italy — [2]European Institute of Oncology, Dept of Exp. Oncology, Via Ripamonti 435, I-20141 Milan, Italy

We report about a photoactivatable variant of the Aequorea Victoria green fluorescent protein (PA-GFP). As reported by Patterson and $Lippincott-Schwartz$[1] this special form of the molecule increases its fluorescence intensity when excited by 488 nm after irradiation with high intensity light with $\lambda = 413nm$. We will present data on the two-photon induced photoactivation of the PA-GFP molecule as well as two-photon excitation. Therefore experiments were performed using partially purified protein immobilised on microspheres. The molecular switches were irradiated with laser light in a range of wavelength of a Ti:Sapphire laser system coupled to an inverted microscope. The optimum frequency for activation was chosen to investigate fixed cells. A comparison between the conventional activation with a single photon at $\lambda = 405nm$ and two-photons demonstrates the much smaller activation volumes in the cell.
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(1) Patterson, G. H.; Lippincott-Schwarz, J. Science 2002, 297, 1873.

AKB 100.2 Sa 16:45 Poster TU D

Thermal Fluctuations of Individual Semiflexible Polymers in Confined Geometry — •Sarah F. Köster[1,2], Stephan Herminghaus[1,2], Myung C. Choi[3], Cyrus R. Safinya[3] und Thomas Pfohl[1,2] — [1]Department of Applied Physics, University of Ulm, Albert-Einstein-Allee 11, 89081 Ulm, Germany — [2]Max Planck Institute for Flow Research, Bunsenstraße 10, 37073 Göttingen, Germany — [3]Materials Research Laboratory, University of California, Santa Barbara, CA 93106, USA

Thermal fluctuations of individual actin filaments in confining microchannels fabricated by soft photolithography are studied by means of fluorescence microscopy. The channel dimensions are in the same order of magnitude as the mesh size of the actin cytoskeleton within the eukaryotic cell and thus mimic the native environment of the individual filament. We observe a strong dependence of the tangent correlation upon both the channel geometry and the filament length. Compared to freely fluctuating filaments, long filaments confined in narrow channels exhibit an enhanced tangent correlation revealing a local minimum and an oscillatory behavior. We also observe a clear deviation from existing theoretical models on small length scales, assumedly due to an intrinsic stiffness of the semiflexible chain. These unique characteristics may be qualitatively described by an analytical expression considering the bending energy as well as the confining energy assumed as a parabolic potential. We find the scaling law for the deflection length which has been reported before experimentally confirmed.

AKB 100.3 Sa 16:45 Poster TU D

Interactions of the Extracellular Matrix Protein Collagen I and the Actin Cytoskeleton — •Sarah F. Köster[1,2], Jennie B. Leach[2], Joyce W. Wong[2] und Thomas Pfohl[1] — [1]Max Planck Institute for Flow Research, Bunsenstraße 10, 37073 Göttingen, Germany — [2]Department of Biomedical Engineering, Boston University, 44 Cummington Street, Boston, MA 02215, USA

Both the extracellular matrix (ECM) where collagen is the most important building block and the actin cytoskeleton impact the mechanical properties of mammalian tissue. The study of these fibrous proteins and all the more their interaction is thus a very interesting field whenever looking at living beings. We use a microfluidic diffusive mixing device to create a defined pH gradient in a microchannel which in turn initiates the polymerization and concurrent alignment of soluble collagen into fibrils under hydrodynamic flow. We are thus able to investigate collagen fibrillogeneisis by means of polarization microscopy and x-ray diffraction. Furthermore, substrates prepared by using this technique are used as scaffolds for cell growth. Since the collagen structure has precise alignment in native blood vessels, study of the impact of highly anisotropic (aligned) collagen on vascular smooth muscle cells (VSMC) provides much-needed insights towards structure-property-function relationships between the ECM and the cytoskeleton. Anisotropic collagen induces alignment of the cytoskeleton and may facilitate the study of the cytoskeleton by means fluorescence microscopy and in addition by x-ray diffraction.

AKB 100.4 Sa 16:45 Poster TU D

Single Molecule FRET Experiments with the RNA Helicase YxiN — •Bettina Theissen and Dagmar Klostermeier — Experimentalphysik IV, Universität Bayreuth

RNA helicases unwind double helical RNA structures in an ATP-dependant manner. Their function is essential for all cellular processes that require structural reorganisation of RNA, for example transcription, translation or ribosome biogenesis. While little is known about the mechanism of unwinding, an opening and closing movement of a cleft between two domains during the catalytic cycle has been proposed. Such a movement leads to changes of intramolecular distances. Since fluorescence resonance energy transfer (FRET) can be used to measure distances between two fluorophores, it is a suitable tool for studying these conformational changes.

YxiN is a RNA-helicase from *Bacillus subtilis* that is involved in ribosome biogenesis. For FRET experiments the donor fluorophore alexa 488 and the acceptor fluorophore tetramethylrhodamine have been coupled site-specifically to genetically engineered cysteines on both sides of the cleft. With this doubly labelled protein we perform single molecule FRET experiments to directly observe conformational changes during unwinding of the RNA. These will lead to a detailed understanding of the catalytic mechanism of RNA-helicases.

AKB 100.5 Sa 16:45 Poster TU D

Analyse des Einflusses schwacher, statischer oder niederfrequent wechselnder Magnetfelder auf Fibroblasten — •Juliane Issle und Uwe Hartmann — Fachrichtung Experimentalphysik, Universität des Saarlandes, Im Stadtwald, 66123 Saarbrücken

Wie sich Magnetfelder auf biologische Materie auswirken ist noch nicht vollständig geklärt. Um speziell Effekte auf Menschen zu untersuchen, wurden Experimente an humanen Fibroblasten durchgeführt. Die verwendeten Magnetfeldstärken lagen im Bereich 800 μT bei 50 Hz-Wechselfeldern und 0,8 T bei statischen Feldern. Ebenso wurden Zellen in einer Abschirmkammer kultiviert, in der die maximale Magnetfeldstärke 180 nT betrug. Die Versuchszeiten variierten zwischen 48 h und 5 Tagen, während ein Teil der jeweiligen Zellen den verschiedenen Magnetfeldbedingungen unterzogen wurde und ein anderer parallel dazu als Kontrolle diente. Als Untersuchungsmethoden fanden die Lichtmikroskopie, die Elektronenmikroskopie, die Rasterkraftmikroskopie, Immunfärbungen und Western-Blot-Analysen der Proteine Aktin und Connexin Verwendung.

AKB 100.6 Sa 16:45 Poster TU D

Induktion der Zelldifferenzierung durch die Verwendung nanostrukturierter und funktionalisierter Oberflächen — •Susanne Kirsch, Juliane Issle und Uwe Hartmann — Fachrichtung Experimentalphysik, Universität des Saarlandes, Im Stadtwald, 66123 Saarbrücken

Adam S.G. Curtis hat 1964 die These aufgestellt, dass Zellen auf die Topographie ihrer Umgebung reagieren können. In den letzten vierzig Jahren konnten mehrere Zelltypen dokumentiert werden, die stark auf eine Umgebungsstruktur im Mikrometerbereich antworten. Kürzlich konnte jedoch gezeigt werden, dass Zellen in vitro auch im Nanometerbereich beeinflusst werden können. Hierbei haben Strukturen mit Unterschieden in Höhe oder Abstand unterschiedliche Auswirkungen auf die einzelne Zelle. Das Spektrum reicht hier von verbesserter Adhäsion der Zelle an das Substrat, was meist der erste Schritt der Differenzierung ist, bis zur Apoptose der Zelle, dem programmierten Zelltod. Aber nicht nur die Topographie der Oberflächen selbst hat Auswirkungen auf die Zelle, die Nanostrukturen können auch mit biologisch wirksamen Molekülen, wie z.B. Wachstums- oder Differenzierungsfaktoren, funktionalisiert werden.

AKB 100.7 Sa 16:45 Poster TU D

Self-assembled peptide fibrils as novel biomaterials — •Patrick Mesquida[1], Rachel McKendry[1], and Cait MacPhee[2] — [1]Department of Medicine, University College London, UK — [2]Department of Physics, University of Cambridge, UK

Amyloid fibrils are self-assembled, beta-sheet-rich superstructures of peptides or proteins. Although these aggregates have first been found in connection with protein-misfolding diseases there is evidence that the ability to form fibrils is a thermodynamic property of any polypeptide chain rather than a result of specific, disease-related amino-acid sequences. Fibrils can easily be formed in-vitro from non-disease-related proteins and even from artificially "bottom-up"-synthesized peptide chains which have no biological function at all. Furthermore, functional groups can be incorporated without significantly disturbing the fibril superstructure. This is why amyloid fibrils have recently attracted considerable interest as potentially useful, novel biomaterial. Here, we present investigations of the physical properties of a specific fibrillar system, which forms well-defined nanorods of ca 10nm diameter, and of its interaction with surfaces.

AKB 100.8 Sa 16:45 Poster TU D

Measuring Mechanical Forces of Adherent and Locomoting Cells — •Claudia M. Cesa[1], Bernd Hoffmann[1], Norbert Kirchgessner[1], Ulrich Schwarz[2], and Rudolf Merkel[1] — [1]Institute of Thin Films and Interfaces, ISG-4, Research Centre Jülich — [2]Max Planck Institute of Colloids and Interfaces, Golm

During adhesion and locomotion most cell types apply mechanical forces to their substrates. These forces are generated and transmitted by an intricate protein machinery composed of the cytoskeleton, adhesion complexes, and the extracellular matrix.

We will describe a new technique for measuring mechanical forces developed by cells on substrates. In this method cells are plated on elastomeric layers exhibiting a microstructured surface. Using light microscopy cells and micropattern can be observed simultaneously under physiological conditions. The elastomeric layer is deformed by cellular forces. This deformation can be determined by tracking the displacement of the surface microstructures. Exploiting elasticity theory we are able to calculate cell forces and cellular force fields from the deformation of the substrate.

We will present the fabrication of microstructured, elastomeric substrates, a detailed characterization of their mechanical properties, as well as the resolution of the technique.

AKB 100.9 Sa 16:45 Poster TU D

Mechanical Properties and Shape Instabilities of Axons — •Pramod Pullarkat — Experimentalphysik-I, Universität Bayreuth, D95440-Bayreuth, Gramany

We present studies on the mechanical properties of axons using a newly developed flow-chamber technique. The role of various cytoskeletal components and their visco-elastic contributions to the mechanical properties of the axon will be presented. The cytoskeleton also plays an important role in certain shape instabilities observed in axons under abnormal conditions, both in-vivo as well as in-vitro. We have studied one such instability which is induced by osmotic-shocks. The remarkable dynamics of this instability will be discussed.

AKB 100.10 Sa 16:45 Poster TU D

Pyrolysis of wood - in-situ synchrotron scattering and nanoindentation experiments — •Gerald A. Zickler[1], Sérgio S. Funari[2], Thomas Schöberl[3], and Oskar Paris[1] — [1]Max Planck Institute of Colloids and Interfaces, Dept. Biomaterials, Am Mühlenberg 1, D-14476 Potsdam, Germany — [2]Hamburger Synchrotronstrahlungslabor, HASYLAB, DESY, Notkestr. 85, D-22603 Hamburg, Germany — [3]Erich Schmid Institute of Materials Science, Austrian Academy of Sciences, University of Leoben, Jahnstr. 12, A-8700 Leoben, Austria

The present study is focusing on structural and mechanical aspects of non-oxidising pyrolysis of native spruce wood, with the aim to transform the hierarchical structure of wood into nano-structured oriented carbon. Synchrotron radiation was used in combination with a custom made furnace to study wood pyrolysis in situ. Detailed time resolved small-angle and wide-angle scattering data from single wood slices provided deeper insight into the kinetics of cellulose degradation for temperatures up to 400°C. Furthermore nanoindentation was applied to characterise changes of cell wall hardness, Young's modulus, elastic and plastic parameters of the carbonaceous residue up to 2400°C.

AKB 100.11 Sa 16:45 Poster TU D

Helium vs. Nitrogen cooling of biological samples for Cryo Electron Tomography — •Gabriele Schweikert[1], Guenter Pfeifer[1], Uwe Luecken[2], Stephan Nickell[1], Wolfgang Baumeister [1], and Juergen Plitzko[1] — [1]Max-Planck-Institute of Biochemistry, Struktural Biology, 82152 Martinsried, Germany — [2]FEI Company, 5600 KA Eindhoven, The Netherlands

In the life sciences, cryo electron microscopy is used increasingly due to its power to reveal the structure of single protein complexes within their cellular context. The radiation-sensitivity of biological specimens, however, sets a limit to the possible examination using highly energetic electrons. We will present our findings concerning radiation damage and

cryo-protection at L-He temperature in comparison to L-N2, especially with regard to the application of cryo electron tomography. We have obtained dose series of vitrified specimens of a crystalline surface layer (HPI-layer) at L-N2 and L-He temperature and analysed them by means of Fourier shell correlation. Additionally, we determined the relative mass loss during exposure using the log-ratio-technique. To assess the differences in ice density, we have measured the inelastic mean free path (MFP) of the electrons in low-density amorphous ice at L-N2 and high-density amorphous ice at L-He temperature at 300 kV accelerating voltage with an FEI Tecnai F30 instrument equipped with a Gatan imaging filter.

AKB 100.12 Sa 16:45 Poster TU D

Anomalous Flow in Microfluidic Poly(dimethylsiloxane) Channels — •Thanh Tu Duong, Alexandra Ros und Dario Anselmetti — Experimental Biophysics and Applied Nanosciences, Physics Faculty, Bielefeld University

The application of microfluidic devices in various bioanalytical fields requires a detailed knowledge of material properties. Today's microfluidic devices are fabricated using a variety of materials. Especially Poly(dimethylsiloxane) (PDMS) is the material of choice due to its low fabrication costs based on rapid prototyping. However, for microfluidic PDMS channels where one dimension is smaller than $20\mu m$, an anomalous flow behaviour is observed.
In a simple linear microfluidic channel sample from both reservoirs flows into the centre of the channel with a linear decreasing flow velocity. At first glance this behaviour is in contradiction to the equation of continuity, but on closer examination this phenomena is caused by the water permeability and evaporation of water through PDMS. Due to this effect the ionic strength of the buffer and hence the zeta potential changes in time. Therefore, control of the evaporation rate is crucial for future microfluidic applications based on PDMS. In this work we present a method to control and eliminate the evaporation of water through PDMS.

AKB 100.13 Sa 16:45 Poster TU D

DNA binding ligands investigated with optical tweezers. — •Andy Sischka[1], Katja Tönsing[1], Robert Ros[1], Heiko Ihmels[2], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanosciences, Faculty of Physics, Bielefeld University — [2]Organic Chemistry, University of Siegen

We used a compact, single beam optical tweezer system to investigate mechanical properties of double stranded DNA in the presence of different binding ligands. Individual binding modes could be distinguished by analyzing the mechanical response of a lambda-DNA molecule to an applied external force. We compared the effects of the minor groove binder distamycin-A, a major groove binding alpha-helical peptide, the intercalators ethidium bromide, YO-1 and daunomycin as well as the bisintercalator YOYO-1 on lambda-DNA. Significant force hysteresis effects occurring during stretching/relaxation cycles with different velocities were found for daunomycin and YOYO-1. These time dependent mechanical properties directly reflect the kinetics of the binding and unbinding behaviour. Furthermore, mechanical properties of organic dyes particularly intercalating with dsDNA were investigated. These dyes change their absorption and fluorescence properties upon binding, and induce DNA damage during irradiation with visible light. Both binding interactions and photochemical modifications of the DNA result in the change of DNA structure may be usefull in applications of photochemotherapy of cancer.

AKB 100.14 Sa 16:45 Poster TU D

Protein diffusion in living cells: anomalous is normal — •Matthias Weiss — MEMPHYS–Center for Biomembrane Physics,University of Southern Denmark, Odense, Denmark& BIOMS–Center for Modelling and Simulation in the Biosciences, Heidelberg, Germany

Using fluorescence correlation spectroscopy (FCS) it is shown that (inert) macromolecules in the cytoplasm exhibit a size- and conformation-dependent anomalous sub-diffusion, i.e. the particles' mean square displacement $v(t)$ grows less than linear in time ($v(t) \sim t^\alpha$, $\alpha < 1$). 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 α of the diffusion yields a quantifiable measure for the 'crowdedness' of a fluid on the molecular scale.

It is further highlighted that integral membrane proteins also move subdiffusively on organellar membranes, e.g. in the endoplasmic reticulum and the Golgi apparatus [2]. Using a simulation approach, this observation is shown to be consistent with the postulated transient formation of oligomers during the process of protein sorting.
[1] Weiss et al., Biophys. J. **87**, 3518 (2004).
[2] Weiss et al., Biophys. J. **84**, 4043 (2003).

AKB 100.15 Sa 16:45 Poster TU D

A combined Langevin and adhesive dynamics approach to rolling adhesion of leukocytes — •Christian Korn and Ulrich Schwarz — Max-Planck-Institut für Kolloide und Grenzflächen, 14424 Potsdam

Extravasation of white blood cells (leukocytes) from the blood flow is preceeded by rolling adhesion on the vessel walls, which can be studied under controlled conditions in flow chamber experiments. Due to low Reynolds numbers the hydrodynamics is described by the Stokes equation. For the initial stages of rolling adhesion, elastic effects can be disregarded. Therefore we model the leukocytes as hard spheres in shear flow above a wall. Combing Stokes equation and Brownian motion leads to a Langevin equation which is known as the Stokesian dynamics equation. The presence of the wall leads to mobility functions which dependent on position and thus result in non-trivial noise terms in the Langevin equation. Specific binding through receptors on the cell and ligands on the wall is included in the Langevin equation as spring-like external forces (adhesive dynamics). Within this conceptual framework, we study adhesion to patterned ligands, the effect of loading rate, bond cooperativity and competition between different receptor-ligand systems.

AKB 100.16 Sa 16:45 Poster TU D

Measurement of viscoelastic properties of lipid membranes on a chip — •Daniel Steppich, Achim Wixforth und Matthias F. Schneider — Lehrstuhl für Experimentalphysik I, Biophysik, Universität Augsburg, Universitätsstr. 1, 86135 Augsburg

Lipid membranes can strongly affect the properties of the biological cells by an enormous change of their physical behaviour induced by small changes in specific external conditions. A premise for the understanding of many biological processes is therefore the knowledge of the viscoelastic properties, e.g. the compressibility and the elasticity. The viscoelastic properties of lipid bilayers are investigated with surface acoustic waves (SAW) using a novel designed biochip. Since SAWs have a higher accuracy in determine the mass loading or the absorption on surfaces, because of the operating frequencies over 100 MHz. We can also adjust our chips to specific questions, such as mass loading, viscosity or fluidics by the chip design, which results in different types of SAWs. In addition we study the effects of different parameters, e.g. changing in temperature or pH, and the elastic properties of soft films in an aqueous environment.

AKB 100.17 Sa 16:45 Poster TU D

Helical polymer fluctuations: From rigid bodies to floppy lines — •Nils Becker and Ralf Everaers — MPI-PKS Dresden, Nöthnitzer Str. 38, 01187 Dresden

Continuous models for semiflexible polymers have been successful in explaining the elastic properties of, e.g. DNA, actin, or microtubules, as measured in many recent single-molecule experiments. Their common starting point is an interaction energy depending on the curvature of the molecule centerline. The helical symmetry of the molecule then entails a coupling between translational and rotational fluctuations.

However, the centerline is a not completely straightforward abstraction. E. g., it need not lie within the molecule material. The basic *physical* objects that constitute a helical molecule or filament are its monomers. They see only local interactions, which are constant along the molecule in the respective monomer body frames. It is the local energies that are important for biological interactions with filament-binding proteins and tight winding.

Both the monomer and the filament length scale are biologically relevant. To bridge their gap, we investigate possible definitions of the centerline and the corresponding elastic energy, starting from monomer-step coordinates and interactions. We also present a way for local averaging of the helix turns, and offer a description of the monomer fluctuations in terms of "screw modes".

AKB 100.18 Sa 16:45 Poster TU D

Protrusion forces driving rapidly translocating cells — •Michael Gögler[1], Claudia Brunner[1], Allen Ehrlicher[1], Bernd Kohlstrunk[1], Detlev Knebel[2], and Josef Käs[1] — [1]Institute for Soft Matter Physics, University of Leipzig, Linnéstrasse 5, 04103 Leipzig — [2]JPK Instruments AG, Bouchéstrasse 12, 12435 Berlin

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. To elucidate the sub-cellular force generation machinery, we additionally determined the forward force of locomoting lamellar fragments, which lack their nuclei but remain motile. We positioned an elastic spring, the cantilever of a scanning force microscope (SFM), in front of a moving cell, which pushes this spring out of the way. The forward force was calculated using the detected vertical deflection of the cantilever in an elastic wedge model, which considers cellular deformation. Our measurements of the propulsive forces, which are in the lower nN range and agree with expectations, will provide quantitative insight into how a polymeric network of active and passive molecular components act in concert as an active locomoting machine.

AKB 100.19 Sa 16:45 Poster TU D

Dynamcis of Protein Binding to Nucleosomal DNA — •Wolfram Möbius and Ulrich Gerland — Department für Physik, LMU München

Binding of proteins to DNA target sites which are buried inside nucleosomes is sterically hindered and enabled only through thermal fluctuations. Such fluctuations temporarily unwrap the DNA from the histone, exposing a target site during a small fraction of the time [1]. We study this site exposure mechanism using a simple physical model, and examine its equilibrium properties as well as the dynamics. In particular, we characterize the effective interaction between two DNA-binding proteins, which is generated by the presence of the histones. This interaction is relevant for the molecular processes involved in transcription regulation.

[1] J. Widom, Quarterly Reviews of Biophysics **34**, 269 (2001)

AKB 100.20 Sa 16:45 Poster TU D

Nanoquakes meet Soft Materials — •Matthias F. Schneider and Achim Wixforth — a

Surface acoustic waves (SAW) are applied to mimic protein tissue and cell-tissue interactions. In contrast to flow chamber experiments the experiments are done on an open, plane surface allowing to manipulate and optically monitor the experiment simultaneously. For the first time the unfolding of proteins under shear flow conditions could be shown, underlining the potential of this technique for mimicking blood flow scenarios. Furthermore shear waves are used as biosensors in the sense of viscoelasticity experiments under dynamic conditions. Here we study the kinetics of adsorption/adhesion of membranes and cells on functionalized surfaces and follow the time course of protein membrane interactions.

AKB 100.21 Sa 16:45 Poster TU D

Morphometry of nutshells and foams — •Boris Breidenbach[1,2], Ulrike Wegst[2], and Klaus Mecke[1,2] — [1]Institut für theoretische Physik, Universität Erlangen — [2]MPI für Metallforschung, Stuttgart

In the development and design of new materials and structures, researchers more and more turn to nature for inspiration and assistance. An understanding of real-world hierarchical structures across a range of length scales is considered to be the key to optimise physical properties. High resolution 3D micro-computed tomography data of nutshells, bones, wood, and foams open the possibility to characterise and model biological structures and to relate macroscopic physical properties to the microstructure. Fast imaging at ESRF makes it even possible to study dynamic behaviour, e.g., the coarsening of foams. Huge datasets (2000^3) require the development of massively parallel algorithms for fast image reconstruction, filtering (edge preserving anisotropic diffusion), and segmentation (region growing). Morphometry charts of Minkowski functionals such as volume V, surface area S, mean curvature H, and Euler characteristic χ provide robust structural indices of pore spaces to identify, for instance, scaling behaviour of pores. For isotropic and homogeneous sandstones the measurement of Minkowski functionals allows an accurate prediction of permeabilities and elastic properties directly from the segmented tomographic datasets of the pore space (PRL91,215506). Extending the integral geometric technique towards tensorial morphometric functionals, an application on biomaterials seems promising, because their generic anisotropic nature can be taken into account.

AKB 100.22 Sa 16:45 Poster TU D

Intramolecular dynamics of semiflexible macromolecules by Fluorescence Correlation Spectroscopy — •Roland G. Winkler[1], Simon Keller[2], and Joachim O. Rädler[2] — [1]IFF, Forschungszentrum Jülich, D-52425 Jülich — [2]Ludwig-Maximilians-Universität, Geschwister-Scholl-Platz 1, D-80539 München

A theoretical description of the dynamics of DNA molecules and actin filaments in solution as measured experimentally by fluorescence correlation spectroscopy is provided and compared to recent experimental results. Particular attention is payed to the contribution of the intramolecular dynamics to the fluorescence correlation function. Using a semiflexible chain model, a theoretical expression is presented for the fluorescence correlation spectroscopy correlation function. The dependence of this function on various model parameters like chain length, persistence length, and fluorescence label density is discussed. Our investigations show that the intramolecular dynamics provides a significant contribution or even dominates the correlation function as soon as the longest intramolecular relaxation time significantly exceeds the shortest experimentally accessible time.

AKB 100.23 Sa 16:45 Poster TU D

Overcharging of a sphere by a rodlike polyelectrolyte — •Andrey Cherstvy and Roland G. Winkler — IFF, Forschungszentrum Jülich, D-52425 Jülich

We investigate the complexation of a polyelectrolyte bendable rod with an oppositely charged spherical macroion. We take into account the electrostatic bending of the rod and its asymmetric charge neutralization by sphere charges. The spontaneous curvature of the rod towards the sphere results in a substantial overcharging of such a polyelectrolyte complex. Assuming a discrete helical charge distribution on the rod surface, we calculate its electrostatic energy and the electrostatic contribution to its bending and twisting elasticity modules. We show that the helix is easier bend than the corresponding linear array of charges and also that its electrostatic twist rigidity modulus may change sign when the helical pitch is changed. We compare our results with results of existing theories and discuss their possible applications for the description of the structure of nucleosome core particles and twisting/bending of DNA duplexes.

AKB 100.24 Sa 16:45 Poster TU D

Nonlinear Elasticity in Fibroblasts — •Pablo Fernandez, Pramod Pullarkat, and Albrecht Ott — Experimental Physik 1, Universität Bayreuth

Pulling 3T3 fibroblasts between two parallel surfaces and imposing small amplitude sinusoidal oscillations shows a crossover from a stress-independent elastic modulii regime to a stiffening one, where the elastic modulus E is approximately proportional to the average stress σ. Scaling the crossover stress σ_c by the zero stress elastic modulus E_0 leads to a universal "crossover strain"$\sigma_c/E_0 \simeq 8\%$. Experiments were done by sticking the cells either in a highly unspecific way (glutaraldehyde-aminosilane coating), or by means of fibronectin coating. In the first case, active responses are almost absent. The fibronectin coatings instead lead to rich active behaviour, and the stiffness and force scales are about one order of magnitude higher than with glutaraldehyde coatings. However, the stiffness-force relationship is qualitatively similar. Perturbing the cytoskeleton with specific drugs such as Latrunculin-A, ML-7 and Nocodazol strongly points towards the actomyosin system as responsible for the observed mechanical behaviour.

AKB 100.25 Sa 16:45 Poster TU D

On the behaviour of short Kratky-Porod chain — •Semjon Stepanow — Martin-Luther-Universität Halle, Fachbereich Physik, D-06099

Using the exact computation of a large number of moments of the end-to-end distribution function G(r,N) of the worm-like chain, we have established the analytical form of the coefficients in Taylor expansions of the moments for short chain lengths N. The knowledge of these coefficients enabled us to resummate the moment expansion of G(r,N) by taking into account consecutively the deviations of the moments from their stiff rod limit. Using this procedure we have derived the short chain expansion of the distribution function of the end-to-end distance, the structure factor, and the extension-force relation, which take into account the deviations of the moments from their stiff rod limit to the seventh order in N.

AKB 100.26 Sa 16:45 Poster TU D

ROTATION AND CONFORMATIONAL CHANGES OF THE EPSILON SUBUNIT OF F0F1-ATP SYNTHASE — •Marc Karle[1], Boris Zimmermann[2], Nawid Zarrabi[1], Monika Düser[1], Jörg Wrachtrup[1], and Michael Börsch[1] — [1]3. Physikalisches Institut, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart — [2]Institut für Physikalische Chemie, Universität Freiburg, Albertstr. 23a, 79104 Freibrug

Cellular ATP production is catalysed by membrane-bound F0F1-ATP synthase. An internal rotation of subunits couples the chemical reaction at three binding sites in the F1 part to proton translocation through the membrane-integrated F0 part. We apply single-molecule fluorescence resonance energy transfer (FRET) to examine the rotary subunit movements. Rotation is divided into three major steps with constant FRET level corresponding to three relative orientations (M. Diez et al. 2004 Nat Struct Mol Biol 11, 135). For epsilon-subunit rotation we have found distinct dwell times for the three different orientations, indicating heterogeneous catalytic rates at the three binding sites (M. Börsch et al. 2004 Biophys J 86, 181A, Part 2 Suppl). To support our single-molecule FRET analysis and to evaluate the statistical significance of the data set we also develop computer simulations of the signals, that help to unravel critical parameters. These simulations strongly support the non-equal catalytic rates.

AKB 100.27 Sa 16:45 Poster TU D

Proteins under shear stress on planar surfaces — •Stefan Nuschele[1], Stefan W. Schneider[2], Matthias F. Schneider[1], and Achim Wixforth[1] — [1]Universität Augsburg, Experimentalphysik1, Biophysik, Universitätsstr. 1, 86135 Augsburg — [2]Universität Münster, Abteilung Dermatologie, Von-Esmarch-Str. 56, 48149 Münster

Von-Willebrand-Factor (vWF) forms large fibers and mediates binding of blood platelets to the vascular endothelium at wounded and inflamed tissue. The released and activated protein undergoes a coil to fiber transition. In vivo among other things this procedure presumably is induced by blood shear flow. A dysfunction causes blood clotting diseases. By means of surface acoustic waves (SAW) we mimic the blood flow using a novel designed bio-chip. The blood vessels are imitated in two dimensions by hydrophilic channels in hydrophobic surface surrounding. The SAWs, adjustable in power, cause laminar flow. Using fluorescence microscopy we could proof the proposed model of activating the vWF. The combination of surface acoustic waves with flat fluidics and adapted surface structures enables new approaches to hemodynamic phenomena in vitro with reduction in sample volume to only a few μl.

Schneider at al. (2004) submitted APL

AKB 100.28 Sa 16:45 Poster TU D

Dynamics of Driven Polymers — •Xaver Schlagberger[1,2] and Roland Netz[1,2] — [1]Physics Dept., LMU München, Theresienstrasse 37, D-80333 München — [2]Physics Dept., TU München, James Franck Str., D-85748 Garching

Using hydrodynamic simulation methods and scaling arguments we consider an elastic rod which is moving in a gravitational or electric field through a quiescent fluid in the low-Reynolds-number limit. Hydrodynamic effects lead to rod bending and orientation perpendicular to the direction of motion, similar to what is seen in anomalous electric birefringence experiments on TM and FD viruses or polyelectrolytes. Static and dynamic scaling relations for the mean orientation as a function of rod length and elasticity are established. We also investigate the experimentally observed unfolding of polyelectrolyte coils in electric fields.

AKB 100.29 Sa 16:45 Poster TU D

An Analytical Approach to the Free-End Fluctuations of a Grafted Semiflexible Polymer — •Panayotis Benetatos[1] and Erwin Frey[1,2] — [1]Hahn-Meitner-Institut, Abteilung Theoretische Physik, Glienicker Straße 100, D-14109 Berlin, Germany — [2]Fachbereich Physik, Freie Universität Berlin, Arnimallee 14, D-14195 Berlin, Germany

Monte Carlo simulations have revealed a pronounced double-peak structure in the reduced probability distribution of the transverse fluctuations of the free end of a grafted semiflexible polymer with intermediate stiffness in two dimensions (Lattanzi et al., Phys. Rev E 69, 021801 (2004)). We show that this departure from unimodality is related to a similar behavior observed when a random walker is driven by a certain type of shear flow in the transverse dimension (ben-Avraham et al., Phys. Rev. A 45, 2315 (1992)). We explain it by adapting an effective-medium argument first used in the context of the diffusion-convection system. We also use this approach to obtain an approximate analytical expression for the complete probability distribution of the free-end fluctuations.

AKB 100.30 Sa 16:45 Poster TU D

Dynamics of Complex Crystal Growth in Diblock-Copolymer Solutions — •Antje Reinecke[1], Miles Page[1], Helmut Cölfen[1], and Hans-Günther Döbereiner[1,2] — [1]Max-Planck-Institute of Colloids and Interfaces, D-14424 Potsdam — [2]Departments of Biology and Physics, Columbia University, New York, NY 10027

We characterize $CaCO_3$ crystals grown from Na_2CO_3 and $CaCl_2$ solutions in a double jet reactor in the presence of Poly(ethyleneoxide)-block-Poly(methacrylic acid). We observe growth via rod, dumbbell and final sphere morphologies using electron and phase-contrast microscopy. It is well known that diblock-copolymer additives influence strongly crystal shapes and structure. However, so far, detailed structural and morphological sequences during crystal growth have not been reported. Extensive phase-contrast microscopy studies are statistically analyzed to provide the dynamics of shape distributions over time. Electron microscopy gives high-resolution images of faceted crystal shapes. X-ray scattering reveals lattice modifications and domain structure. Finally, we correlate crystal morphology to dynamic free ion concentration measurements using Ca^{++} sensitive electrodes.

AKB 100.31 Sa 16:45 Poster TU D

Dynamics of individual actin filaments in extensional flow — •Dagmar Steinhauser[1], Sarah Köster[1], Wolfgang Schnitzler[2], and Thomas Pfohl[1,2] — [1]Max-Planck-Institut für Strömungsforschung, Bunsenstraße 10, 37073 Göttingen — [2]Angewandte Physik, Universität Ulm, Albert-Einstein-Allee 11, 89081 Ulm

We are interested in the dynamics of biopolymers under extensional flow and the formation of condensed structures, bundles and networks induced by inter-chain and intra-chain linker molecules. Therefore, individual F-actin filaments were investigated in hydrodynamic focusing devices by means of fluorescence microscopy. The microfluidic devices were fabricated by using soft lithography and a stroboscopic laser light illumination was applied for imaging the biopolymers in a continuous flow. Adding actin binding proteins such as α-actinin or filamin, the dynamic of the association, bundling, and network formation of a few individual molecules can be observed.

AKB 100.32 Sa 16:45 Poster TU D

Conformations of worm-like chains in nanotubes — •Frederik Wagner[1], Gianluca Lattanzi[2], and Erwin Frey[1] — [1]Abteilung Theorie, Hahn-Meitner-Institut Berlin — [2]Physics Department, University of Bari

The conformations of polymers in a confining medium is not only a challenging problem in soft matter physics but also of great practical relevance. One ambitious goal is to localize transcription factors to a specific binding site on DNA which would require to confine DNA to structures smaller or at least comparable to its persistence length, $\ell_p \approx 50\,\mathrm{nm}$. In recent experimental setups [1] DNA was successfully confined to channels down to $35\,\mathrm{nm} \times 35\,\mathrm{nm}$ size.

These recent developments ask for a theoretical investigation of the statistical conformations of stiff polymers (e.g. DNA or F-Actin) in confining environments like tubes and channels. We have developed an off-lattice Monte-Carlo simulation as well as analytical approximations in the weakly-bending rod limit to arrive at a scaling relation for the (apparent) mean-square end-to-end distance $\langle R^2 \rangle$. All Monte-Carlo data are found to collapse on an universal scaling curve as a function of the ratio between persistence length ℓ_p and Odijk's deflection length ℓ_d. For fixed geometry this scaling plot can serve as a gauge in translating the experimental measured values into the real contour length L.

Three different scaling regimes are identified: the free polymer regime, an intermediate regime following de Gennes' 'blob' picture and — for strongly confined or stiff polymers — an Odijk scaling regime.

[1] Tegenfeldt, J. O. et al. Proc. Natl. Acad. Sci. 101, 10979 (2004)

AKB 100.33 Sa 16:45 Poster TU D

Beyond Replica-Exchange: An Efficient Method for Biomolecular Simulation — •Marcus Kubitzki and Bert de Groot — Max Planck Institute for Biophysical Chemistry, Computational Biomolecular Dynamics Group, Am Fassberg 11, 37077 Göttingen

Understanding protein function requires an extensive sampling of the systems' conformational space. In this respect, conventional molecular

dynamics (MD) simulations are rather inefficient because of the currently accessible timescales of typically nanoseconds. Put differently, this sampling problem arises from the system being trapped in local-energy minima from which it can only infrequently escape at physiological temperatures.

Generalized ensemble algorithms greatly alleviate this trapping-problem. Among these methods, replica-exchange MD (REMD) has in recent years successfully been applied to a number of conformational studies of proteins. However, for simulations with full atomic resolution including explicit solvent even REMD is computationally prohibitive for many systems.

The efficiency of the REMD method is basically determined by the temperature differences between the simulated replicas. In explicit solvent simulations, these temperature steps are limited by the large number of degrees of freedom in the simulated system. Here, we systematically study ways to circumvent this problem and to achieve a highly efficient method for the conformational sampling in molecular simulations.

AKB 100.34 Sa 16:45 Poster TU D

Form follows function in living cells — •Jens Gerdelmann[1,2], Stefan Hammerschmidt[3], Hubert Wirtz[3], and Josef Käs[1] — [1]Universität Leipzig, Institut für Experimentelle Physik I, Physik der weichen Materie, Linnéstrasse 5, 04103 Leipzig — [2]Universität Leipzig, Paul-Flechsig-Institut für Hirnforschung, Abt. Neuroanatomie, Jahnallee 59, 04109 Leipzig — [3]Universität Leipzig, Abt. Pneumologie, Johannisallee 32, 04103 Leipzig

Probing living cells with an atomic force microscope to determine their mechanical properties is an established method. It has already been used to characterize the role of different cytoskeletal elements in the cells elasticity. In these former studies actin microfilaments have been identifies as a key player. We applied substances onto lung cells that are thought to lower these cells resistance to stretching (to lower the risk of respiratory stress syndrome) and measured their elasticity. Having found no direct elastic change, we are now focusing on initial results that indicate a morphological change, i.e. a flattening, in treated versus untreated cells. We propose that the treated cells have undergone a structural alteration, i.e. a loss of cell volume through flattening, to compensate their minor cytoskeletal depolymerisation. This reduction of the cells volumes would increase the actin concentration within the cell and thus assure the mechanical stability of the cells. Further results will show to what extent there is a delicate balance between elasticity and cell morphology.

AKB 100.35 Sa 16:45 Poster TU D

Optical tweezers for force measurements during voltage-driven DNA-translocation through a nanopore — •U. F. Keyser, B. Koeleman, D. Krapf, R. Smeets, N. H. Dekker, and C. Dekker — Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands

We aim to measure in situ the forces acting on a DNA molecule that is traversing through a nanopore. We recently developed a technique for the controlled fabrication of nanometer sizes holes in silicon oxide or nitride membranes. We have shown that DNA molecules are pulled through such a nanopore by applying a voltage.

We have built optical tweezers with reflected light position detection that allow us to directly measure the forces and ionic current during the translocation process. The reflected light from the bead is used to monitor its position in three dimensions. A custom-made flow cell with optical access allows mounting nanopores in the optical tweezers and measure ionic currents.

We show simultaneous current and force measurements where polystyrene and silica beads in the optical trap are used to block pores with various sizes. We will report on currently on-going experiments where we probe the force on a bead that is attached to a long DNA molecule inserted in the nanopore.

AKB 100.36 Sa 16:45 Poster TU D

Length and Temperature Dependence of Voltage-Driven Single Stranded DNA translocation — •U. F. Keyser, N. M. Wennersbusch, N. H. Dekker, and C. Dekker — Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands

We study the translocation of single stranded DNA (ssDNA) molecules through alpha-hemolysin, a biological nanopore inserted into an artificial lipid bilayer. The stem of the pore has a diameter of only 1.5 nm which only can be passed by ssDNA. With a voltage we drive ssDNA through the pore which leads to a brief blockade of the ionic current. Our experiments show that the translcoation time increases linearly when adding poly(dA) ssDNA with a length ranging from of 20 to 100 bases. We studied also the influence of temperature on the translocation time between 8 and 20 degrees Celsius and find a non linear decrease with increasing temperature. It is possible to unzip double stranded DNA with the local electrical field in the pore. We present first measurements with several different molecules to investigate this effect.

AKB 100.37 Sa 16:45 Poster TU D

Morphology and mechanical characteristics of cellulose fibres. *In situ* investigations with X-ray scattering — •Klaas Kölln[1], Ingo Grotkopp[1], Manfred Burghammer[2], Stephan V. Roth[2,3], Christian Riekel[2], Sergio S. Funari[3,4], Martin Dommach[3,4], and Martin Müller[1] — [1]Institut für Experimentelle und Angewandte Physik, Christian-Albrechts-Universität zu Kiel — [2]ESRF, Grenoble, Frankreich — [3]HASYLAB, DESY, Hamburg — [4]MPI für Kolloid- und Grenzflächenforschung, Potsdam

Tensile tests on high-oriented natural fibres of flax and ramie combined with X-ray (micro) diffraction measurements were carried out at ESRF and HASYLAB. An improvement of the orientation function of the cellulose crystals with respect to the fibre axis upon increasing strain could be observed for the high-oriented fibres (cellulose I) as well as for fibres of regenerated cellulose (cellulose II). Scanning measurements with X-ray micro diffraction showed that regions which are already highly oriented suffer only minor effects while less well oriented regions undergo a marked increase of the orientation function at the beginning of the stretching procedure. The strain of the microfibrils during a constant strain rate experiment could be measured with a time resolution of a few seconds. On the basis of a simple mechanical model, Young's modulus of elasticity could be determined for the cellulose crystals. It is lower than values found in literature. The lateral contraction of the crystals could be observed both for cellulose I and cellulose II and Poisson ratios for these two materials were determined for the first time experimentally.

AKB 100.38 Sa 16:45 Poster TU D

Mechanical properties of microtubules measured with SPT: the effect of molecular motors — •Francesco Pampaloni[1], Gianluca Lattanzi[2], Thomas Surrey[1], Erwin Frey[3], Ernst H. K. Stelzer[1], and Ernst-Ludwig Florin[4] — [1]EMBL Heidelberg - Cell Biology and Biophysics Programme - Heidelberg (Germany) — [2]Physics Department - University of Bari (Italy) — [3]Department of Theoretical Physics - Hahn-Meitner Institute - Berlin (Germany) — [4]Center for Nonlinear Dynamics - University of Texas at Austin (USA)

Microtubules (MTs) play a fundamental role in imparting polarity to the cell, determining the plane of symmetry in cell division, and regulating cell movements and shape. With new powerful imaging and micromanipulation techniques and the application of theoretical models, the mechanical properties of single MTs and other cytoskeletal filaments can be analyzed in details. By using an assay based on single-particle tracking (SPT) and optical tweezers we recently discovered that the stiffness of MTs increases with their contour length; in other words, shorter MTs are more flexible than longer ones. This counter-intuitive property of MTs seems to have a fundamental role in the mechanics of the cell. There is also evidence that microtubules associated proteins (MAPs) can modulate the mechanical properties of MTs. In this talk, the effect of the kinesin-like protein Xklp1 on microtubules structure and mechanics is discussed. We also introduce a novel experimental approach aimed to elucidate the dynamic instability of MTs in three-dimension.

AKB 100.39 Sa 16:45 Poster TU D

Biomimetic adhesion studies on chemically biofunctionalized nanostructures — •Christine Selhuber[1], Irina Slizskaja[1], Nadine Walter[1], Fabian Czerwinski[1], Jaques Blümmel[1], and Joachim Spatz[1,2] — [1]Universität Heidelberg, Biophysikalische Chemie, INF 253, 69120 Heidelberg — [2]Max-Planck-Institut für Metallforschung, Stuttgart

Exploring the physics of cell adhesion is essential for a detailed understanding of highly complex biological processes involved in cell-cell or cell-tissue interactions.

We focus on experimental studies of adhesion as a function of ligand density and pattern architecture. Functionalized nanostructures from self-assembled diblock copolymers represent an ideal platform to vary these parameters. The nanostructures are described by hexagonal patterns of nanometer sized gold dots where location and separation of single dots can be precisely controlled over a wide length scale. Functionaliza-

tion of gold nanopatterns with streptavidin provides an adhesive model interface for biotinylated probes.

To extract the different physical contributions to adhesion on nanostructures we make use of two biomimetic model systems: On the one hand we are using biotin-covered elastic beads for measuring their adhesion induced deformation. This deformation can be related to surface energy and is a first parameter of adhesive strength. On the other hand, biotin-containing vesicles are a well-established tool to investigate adhesion kinetics. This is especially the case since it enables to study adhesion cluster stability by application of external forces.

AKB 100.40 Sa 16:45 Poster TU D

Dynamics of DNA Condensation Investigated by Small Angle X-Ray Microdiffraction — •Rolf Dootz[1], Alexander Otten[2], Bernd Struth[3], and Thomas Pfohl[1,2] — [1]Max-Planck-Institut für Strömungsforschung, Bunsenstrasse 10, D-37073 Göttingen — [2]Angewandte Physik, Universität Ulm, Albert-Einstien-Allee 10, D-89069 Ulm — [3]European Synchrotron Radiation Facility, 6 rue Horovitz, B.P. 220, F-38043 Grenoble Cedex

The combination of x-ray microdiffraction and microfluidics is used to investigate the dynamic behavior of soft materials. A microfocused x-ray beam enables the observation of the association of biomaterials inside microfluidic channels. Using a hydrodynamic focussing device, the evolution of the DNA condensation induced by polyimine dendrimers as well as by histone proteins can be studied. Due to an extensional flow at the center of this device alignment of the material is induced which allows for an improved structural characterization. Furthermore, the influence of strain applied to these materials can be tested.

AKB 100.41 Sa 16:45 Poster TU D

Mechanosensitivität von Keratinozyten — •Mireille Martin[1], Dieter Reissig[2], Jürgen Salvetter[3], Stefan Schinkinger[1], Jochen Guck[1] und Josef Käs[4] — [1]Universität Leipzig, Physik weicher Materie — [2]Universität Leipzig, Institut für Anatomie — [3]Biotechnologisch-Biomedizinisches Zentrum Leipzig, Angewandte Stammzellbiologie — [4]Universität Leipzig, Physik weicher Materie

Vor allem für die Regeneration nach Verletzungen spielen die Keratinozyten der menschlichen Haut eine entscheidende Rolle. In der normalen Haut existieren verschiedene Differentierungsgrade dieser Zellen, von den basalen Stammzellen über transiente Zellen bis hin zu den oberflächlichen postmitotischen Zellen. Es wurde die Elastizität menschlicher Hautzellen mit Hilfe des Optical Stretchers gemessen. Dabei zeigte sich, dass sich diese Zellen im Gegensatz zu anderen menschlichen Zellen wie z.B. Fibroblasten durch eine ausgeprägte Mechanosensitivität auszeichnen. Bereits geringe mechanische Aktivierungen genügen, um die Keratinozyten zu einer aktiven mechanischen Antwort zu veranlassen. Dieses Verhalten könnte die Fähigkeit der Hautzellen zum schnellen Wundverschluß und zur Reepithelialisierung nach Verletzungen erklären. Weiterhin zeigte sich ein strain-hardening-Effekt der Zellen, d.h. die Keratinozyten versteifen sich unter zunehmendem mechanischen Zug. Auch das lässt sich gut im Zusammenhang mit den Eigenschaften und Funktionen der menschlichen Haut (Abschluß nach außen, Schutzfunktion) verstehen.

AKB 100.42 Sa 16:45 Poster TU D

Noninvasive measurement of retrograde flow and actin polymerization in neuronal growth cones — •Timo Betz, Daniel Koch, Daryl Lim, Michael Gögler, Allen Ehrlicher, Björn Stuhrmann, and Josef Käs — Univeristät Leipzig, Fakultät für Physik und Geowissenschaften, Abt. PWM, Linnestrasse 5, 04103 Leipzig

Cell motility in most eukaryotic cells is maintained by a complex interplay of actin polymerization at the leading edge of a cell and a steady flow of the actin network away from the leading edge in a process called retrograde flow. Over a decade ago, the inverse relationship between retrograde flow and the protrusion of the leading edge was discovered, but up to now the exact mechanism which drives this process has not been unraveled. To gain further insight into the mechanisms driving retrograde flow, we developed a new method that applies a cross-correlation algorithm to time series images of GFP-actin transfected neuronal cells (NG108-15) to calculate the retrograde flow field in growth cones. Furthermore, an estimation of actin polymerization rates is possible by comparing measured retrograde flow with the protrusion of the leading edge. Thus, we provide a noninvasive tool to explore how the interplay of the two counterbalancing processes of actin-polymerization and retrograde flow results in locomotion of neuronal growth cones.

AKB 100.43 Sa 16:45 Poster TU D

Entropic forces act as crosslinkers in entangled actin networks — •Rainer Tharmann[1], Sven van Teeffelen[2], A.R Bausch[1], and K. Kroy[2] — [1]Technische Universität München, Lehrstuhl für Biophysik, James-Franck-Strasse 1, 85747 Garching, Germany — [2]Hahn-Meitner-Institut, Abteilung Theorie, Glienicker Strasse 100, 14109 Berlin, Germany

Here we analyze in a rheological study that entropic forces act as effective "pseudo cross linkers" (PCL) to in vitro actin networks. The addition of low concentrations of poly ethylene glycol (PEG) in entangled actin networks results in a significant increase of the moduli. Two regimes can be distinguished: at low volume fractions of PEG the increase of the moduli is small, while for concentrations of PEG higher than a critical concentration $c^\star$ an drastic linear increase of the moduli can be observed. This increase of the moduli is similar to the scaling with $\sim R^2 (R = c_{crosslinker}/c_{actin})$ as it is observed with biochemical crosslinkers. In sharp contrast to specific crosslinkers the entropically pseudo crosslinked networks show a not so pronounced shear hardening behavior. This can be explained by the possibility for the filaments to slip along the contour length.

AKB 100.44 Sa 16:45 Poster TU D

Texture analysis and 3D nanostructure of bone using synchrotron SAXS and WAXD — •Wolfgang Wagermaier[1], Himadri S. Gupta[1], Paul Roschger[2], Oskar Paris[1], Manfred Burghammer[3], Klaus Klaushofer[2], and Peter Fratzl[1] — [1]MPI-KGF, Biomaterials, Potsdam, Germany — [2]LBIO, 4th Med. Dept., Hanusch Hospital and UKH Meidling, Vienna, Austria — [3]ESRF, Grenoble, France

Bone is a biological composite material, consisting of a mineral particle reinforced collagen matrix, whose structure is adapted to physiological requirements. However, the design of the bone material at the sub-μm level is still poorly understood. Specifically, little is known about the material-level structure of the fundamental unit of compact bone - the lamellar osteon. We have combined microbeam (1 μm) synchrotron scanning diffraction and scattering with sample rotation to reconstruct the full 3D mineral particle distribution within single osteonal lamellae. Several osteons around blood vessels in compact bone were scanned. On the basis of the SAXS data a physical model was used to reconstruct the 3D orientation of the mineral particles. The wide angle x-ray diffraction (WAXD) data were analyzed by means of pole figures to find the mean orientation and texture of the mineral crystallite c-axis. Our results show mineral crystallite orientation has a fiber texture within single lamellae, but shows a smooth spatial variation around the cylindrical core of the osteon.

AKB 100.45 Sa 16:45 Poster TU D

Optical rheology of fibroblasts overexpressing different constituents of the actin cytoskeleton — •Karla Müller, Frank Sauer, Stefan Schinkinger, Jens Gerdelmann, and Josef Käs — Universität Leipzig, Fakultät für Physik und Geowissenschaften, Abteilung Physik der weichen Materie, Linnéstr. 5, 04103 Leipzig

The Optical Stretcher is a laser trap formed by two counter propagating divergent IR laser beams with tunable output power designed to determine the optical deformability of soft biological objects such as eukaryotic cells. Our initial results lead to the hypothesis that overexpression of actin filaments only in conjunction with the overexpression of an actin cross linking protein lead to significant cell stiffening. The rheological properties of cells can be determined by directly imposing a time, i.e. frequency, dependent stress on cells and monitoring the corresponding deformation, i.e. strain. From the measured data the complex shear modulus can be directly determined. The cell's elasticity and viscosity can be traced back to its molecular roots being a highly dynamic network of cytoskeletal polymers. In the talk, the rheological data presented will be compared to stress relaxation experiments performed with the optical stretcher and to other methods such as bead rheology or SFM techniques.

AKB 100.46 Sa 16:45 Poster TU D

Elasticity of Stiff Polymer Networks — •Claus Heussinger and Erwin Frey — Hahn-Meitner Institut, Berlin

We study the elasticity of two-dimensional networks of semiflexible polymers ("Mikado model"). The essential features incorporated into the model are the random geometry of the network and the anisotropic elasticity of its constituents.

In a first study, the elements are modeled as purely mechanical Euler beams (Wilhelm, Frey, PRL 2003). We show that there are three distinct scaling regimes, characterized by two characteristic length scales. In addition to a critical rigidity percolation region and a homogeneous elastic regime (dominated by beam compression) we find a novel intermediate scaling regime, where the elasticity of the network is dominated by bending deformations. The observations for the shear modulus can be rationalized by a crossover scaling ansatz that permits to collapse the data over eight orders of magnitude in the scaling variable.

In a second step, effective elastic properties of semiflexible polymers are implemented to study the entropic contributions to the polymer compliance and its effects on the scaling behaviour.

To get further insight into the nature of the force propagation, more complicated modes of deformation can be explored. As an example, we visualize force chains induced by the action of a microrheological probe.

AKB 100.47 Sa 16:45 Poster TU D

Structure formation in systems of mesoscopic rods — •Andreas Richter and Thomas Gruhn — MPI-KG, Am Mühlenberg 1, 14476 Golm

We perform Monte Carlo simulations of a system of spherocylindrical rods. The interaction of the rods is described by a square-well-rod potential (SWR potential) which, basically, is a spherical square-well potential integrated over the midaxes of the interacting rods. It resembles the interaction of hard spherocylinders with locally attractive forces such as van-der-Waals and/or depletion forces. We investigate a 1:1 bidisperse mixture of rods with rod lengths lx =(6+1)d and ly =(3+1)d where d is the diameter of the rods. We observe the formation of smectic monolayers that exclusively consist of the longer rods. The monolayers coexist with an isotropic mixture of short and long rods.

We also investigated a system of spherocylindrical rods with a length l = (8+1)d and an SWR model potential in the presence of planar substrates. Monte Carlo simulations for a monodisperse system of rods with a length l = (8+1)d were performed. High nematic order is found parallel with the walls in the first fluid layer that contacts the wall. In a slit pore between two coplanar substrates we observe nematic capillary condensation that depends on the pressure and the pore width.

AKB 100.48 Sa 16:45 Poster TU D

Protein adsorption on structured substrates — •Hubert Mantz, Anthony Quinn, Armin Nagel, and Karin Jacobs — FR 7.2 Experimental Physics - Soft Matter, Saarland University, D-66123 Saarbrücken

The ability of proteins to adsorb to almost all surfaces, plays a crucial role in both natural and synthetic processes, and can have unwanted but also desirable medical effects. In the oral cavity, for example, a protein film called pellicle, protects the integrity of oral hard tissues. Some of the adsorbed proteins subsequently facilitate bacterial adsorption and plaque growth as well.

The adsorption behaviour of proteins to surfaces depends on many factors, including the surface physicochemical properties. Self-assembled monolayers (SAMs) of thiols on gold are ideal for probing such interactions, because they are highly-ordered and their surface characteristics can be modified over a wide range (e.g. surface free energy). By patterning the surfaces, critical spatial dimensions for protein adsorption can be found.

This project aims to study the adsorption kinetics of different proteins in situ by using a SPR (surface plasmon resonance) measurement technique combined with ellipsometry, which has some advantages over the traditional approach. By that, more insight in the mechanisms of biofilm adsorption at solid/liquid interfaces shall be gained to control the adsorption of specific proteins, e.g. in the oral cavity. Offering the pellicle a substrate that allows adsorption only to certain proteins would be useful to prevent oral diseases.

AKB 100.49 Sa 16:45 Poster TU D

Protein conformation probed by fluorescence — •thomas gensch, thomas dertinger, thomas sorkalla, andreas helten, karl-wilhelm koch, ingo gregor, and joerg enderlein — IBI1, Research Centre Juelich

We study the protein-protein interaction of membrane proteins (ion channels, enzymes) with regulating proteins and activating cofactors by fluorescence spectroscopy methods (time-resolved fluorescence spectroscopy, single molecule spectroscopy, Förster resonance energy transfer). The proteins are made fluorescent in the visible spectral region by two methods: 1. production of fusion proteins of the protein of interest with an autofluorescent protein (like the green fluorescent protein). 2. Specific labelling of single Cysteins with organic fluorophores functionalised with a maleimide group. The properties of two regulating, Ca2+-binding proteins (Calmodulin, GCAP) labelled with different fluorophores have been investigated in detail. Different protein conformations have been identified by different fluorescence properties of the fluorophores. Their Ca2+ dependence is investigated as well as the influence of binding events. First results from model FRET experiments will be presented.

AKB 100.50 Sa 16:45 Poster TU D

Dynamics of Semiflexible Polymers in Simple Flow — •Tobias Munk[1], Chris H. Wiggins[2], and Erwin Frey[1] — [1]Ludwig-Maximilians-Universität, München — [2]Columbia University, New York

In this poster we address the question how a single stiff polymer moves in a two-dimensional viscous fluid environment. The model system we refer to is the biopolymer 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 function into the hamiltonian. By invoking suitable eigenfunctions we obtain a system of coupled first order stochastic differential equations of the Langevin type, which can be solved numerically. In addition to the behaviour in shear flow and its relatives we study the polymer's behaviour in external electric fields. Thus we are able to study e.g. single trajectories and autocorrelation functions.

AKB 100.51 Sa 16:45 Poster TU D

Kinetic and nanostructural analysis of protein adsorption on tailored substrates — •Anthony Quinn, Hubert Mantz, and Karin Jacobs — FR 7.2 Experimental Physics - Soft Matter, Saarland University, D-66123 Saarbrücken

The principal aim of this research is to identify the surface physicochemical properties that affect protein adsorption in the oral cavity, and ultimately to govern the structure and composition of the acquired salivary pellicle (the proteinaceous film that rapidly coats all intraoral surfaces). By controlling the composition of the pellicle on dental replacement materials via tailoring of their surface properties, it is anticipated that the rate and type of bacterial attachment can be reduced due to the highly specific nature of the bacteria/protein interaction. Hence the growth of dental plaque can be inhibited and the incidence of periodontal disease reduced.

A specific focus of this research will be on the effect of long-range forces emanating from the bulk material beneath any surface coating. For extremely thin surface coatings, such forces contribute to the total interfacial force, and hence alter protein adsorption. A combination of in-situ ellipsometry adsorption measurements, scanning probe microscopy, and wettability analysis are being undertaken to investigate these effects.

AKB 100.52 Sa 16:45 Poster TU D

Automated optical neuron guidance — •Björn Stuhrmann, Timo Betz, Allen Ehrlicher, Michael Gögler, Daniel Koch, and Josef Käs — Institute for Soft Matter Physics, Universität Leipzig, Linnéstr. 5, 04103 Leipzig

We have used a tightly focused near-infrared laser beam positioned at specific locations of actively advancing neuronal growth cones to influence important elements of neuronal growth such as the direction taken by a growth cone [Ehrlicher et al. "Guiding neuronal growth with light" PNAS (2002)] and the contact between growth cones and cell bodies of other nerve cells. Automation of our technique for a careful systematic investigation of the phenomenon is achieved with self-written image processing software. This software is able to react to cell morphological changes with automated, well defined adjustment of laser radiation with high time resolution. The aforementioned optically controlled elements of neuronal growth are essential for the *in vitro* creation of topologically defined neuronal networks. We are combining optical neuron guidance with established surface patterning techniques. While biochemical patterning reliably restricts neuronal growth to defined tracks, optical guidance will determine growth directions at track crossing points and precisely lead a growth cone to its target. Optical neuron guidance is a promising tool for the creation of defined neuronal networks as assays for the elucidation of interneuronal communication.

AKB 100.53 Sa 16:45 Poster TU D

Near-field Electrodynamics of Biological Cells — •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. For this regime, the near-fields are best analyzed using exact approaches such as Mie theory, or the system transfer operator (T-matrix) formalism. In the present discussion, 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 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 100.54 Sa 16:45 Poster TU D

Investigation of the TNF Mediated Apaptotic Pathway by Means of Fluorescence Correlation Spectroscopy — •Carsten Tietz[1], Margarita Gerken[1], Elmar Thews[1], Anja Krippner-Heidenreich[2], Peter Scheurich[2], and Jörg Wrachtrup[1] — [1]Institute of Physics, University of Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart — [2]Institute of Cell Biology and Immunology, University of Stuttgart, Allmandring 31, 70569 Stuttgart

We investigate the behavior of apoptosis mediating cell receptors (TNF-R1/2) before and after stimulation by means of FCS. Studies on TNF-R show that the response of the cell on stimulation with TNF is a slowing down of the diffusion by approximately one order of magnitude but only a very slight increase of the intensity per diffusing particle. Several experiments were carried out to reveal the origin of this slowing down. We can exclude aggregation of receptors, interaction of the cytoplasmic domain of the receptor with the cytoskeleton, and change of the viscosity of the whole plasma membrane. On the other hand, cholesterol depletion of the membrane with MβCD show no effect on the diffusion coefficient of activated TNF-R2 but TNF-R1 shows an increases of the diffusion coefficient after MβCD treatment. From this results we conclude that TNF-receptors can be associated with membrane micro domains. Whereas TNF-R1 can be associated with cholesterol rich domains, the TNF-R2 must be associated to a so far unknown type of domain.

AKB 100.55 Sa 16:45 Poster TU D

Self-organized vortical array of hydrodynamically entrained sperm cells — •Ingmar Riedel[1], Karsten Kruse[2], and Jonathon Howard[1] — [1]Max Planck Institute for Molecular Cell Biology and Genetics, Pfotenhauerstr. 108, D-01307 Dresden — [2]Max Planck Institute for Physics of Complex Systems, Noethnitzer Str. 38, D-01187 Dresden

The emergence of spatiotemporal patterns is of great interest in many scientific disciplines. Examples range from physical self-assembly, oscillating chemical reactions, complex cellular processes and even social interactions. The maintenance of order within and among biological cells usually requires a permanent flux of energy in which case it is said to be dynamically self-organized. Here we report on a new dynamically self-organized pattern that is ordered at two different levels. First, hydro-dynamically entrained sperm cells form vortices. And second, these vortices form a hexagonal array. The dynamics of a vortex resembles a quantized rotating wave. The vortical array emerges above a critical sperm density associated with a dynamic instability. Supported by numerical simulation we suggest a mechanism for the appearance of the array. This array represents an active gel with a chiral component.

AKB 100.56 Sa 16:45 Poster TU D

Structural studies and hydration kinetics of starch granules by synchrotron radiation microdiffraction — •Henrik Lemke[1,2], Jean-Luc Putaux[3], Manfred Burghammer[2], Martin Müller[1], and Christian Riekel[2] — [1]Institut für Experimentelle und Angewandte Physik, Christian-Albrechts-Universität zu Kiel — [2]European Synchrotron Radiation Facility, Grenoble, Frankreich — [3]CERMAV-CNRS, Grenoble, France

The structure and hydration kinetics of single starch granules from several biological sources were investigated by scanning X-ray microdiffraction. Combined small- and wide-angle scattering experiments at the 1 micron level allowed examining the variation of the amylopectin microstructure and the lamellar superstructure at multiple length scales in fully hydrated granules of 10-50 microns diameter. Differences in variation of azimuthal width of the equatorial 100-reflection and the meridional 9-nm peak agree to the model of a radial organization of amylopectin fibrils. Starch particles from different genetic origins appear to differ in small-angle scattering due to variations in lamellar ordering. A fast hydration kinetics of dried starch granules with about 7 sec half-time could be observed by synchronizing a drop-on-demand system with the data collection system. The timescale of hydration at the unit cell level and of the hydration-induced lamellar superstructure formation seem to be comparable.

AKB 100.57 Sa 16:45 Poster TU D

Φ-values and Transition States in Protein Folding — •Claudia Merlo and Thomas R. Weikl — Max Planck Institute of Colloids and Interfaces, Theory Division, 14424 Potsdam

Small single-domain proteins typically are two-state folders, i.e. they fold from the denatured to the native state without populating experimentally detectable intermediate states. The folding kinetics of two-state folders usually is explored through mutational Φ-value analysis. Φ-values are experimental measures of how the kinetics of protein folding is changed by single-site mutations. Φ-values measure *energetic* quantities, but are often interpreted in terms of the *structures* of the transition state ensemble. Here we present a simple analytical model of folding kinetics in terms of the formation of protein substructures. The model shows that Φ-values have both structural and energetic components. It thus provides a natural and general interpretation of Φ-values, including so-called "nonclassical"Φ-values less than zero or larger than one.

AKB 100.58 Sa 16:45 Poster TU D

Cross-talk Free Fluorescence Cross Correlation Spectroscopy in Living Cells — •Andrew Aird[1], Elmar Thews[1], Carsten Tietz[1], Reiner Eckert[2], and Jörg Wrachtrup[1] — [1]Institute of Physics, University of Stuttgart, Pfaffenwaldring 57, D?70550 Stuttgart — [2]Department of Biophysics, Institute of Biology, University of Stuttgart, Pfaffenwaldring 57, D?70550 Stuttgart

Fluorescence correlation spectroscopy (FCS) is now a widely used technique to measure small ensembles of labeled biomolecules even in living cells. Fluorescence cross correlation spectroscopy (FCCS) is more suited to detect synchronous movement of two biomolecules with different labels and so grants access to a wide variability of unsolved questions in cell biology. Autofluorescent proteins are labels being less cell perturbing in its appliance and highly specific in binding to the proteins in question. The method presented here fuses the advantages of these three techniques to analyze binding behavior of proteins in living cells. To achieve this, a common pair of autofluorescent proteins CFP and YFP is discriminated rather in excitation than in fluorescence to eliminate cross-talk in the detector channels and obtain an undisturbed cross correlation function. The setup is tested to work in living HeLa cells coexpressing the two fusion proteins Cx46/CFP and Cx46/YFP, which form hetero-labeled hexamers (connexones) and diffuse freely in the plasma membrane.

AKB 100.59 Sa 16:45 Poster TU D

Anisotropy of water adsorbed to cellulose fibres — •Ingo Grotkopp[1], Klaas Kölln[1], Stefan Janssen[2], and martin Müller[1] — [1]Institut für Experimentelle und Angewandte Physik, Christian-Albrechts-Universität zu Kiel — [2]SINQ, Paul-Scherrer-Institut, Villigen, Switzerland

Many unique features of water in plant cell walls have been reported over the last decades. Water adsorbed to the disordered regions of cellulose, the main constituent of plant cell walls, exhibits liquid dynamics below 0 °C and is therefore termed "non-freezing". The water molecules are thought to be inserted between individual hydrogen bonded cellulose chains, and they do not form crystalline ice networks. Upon cooling, an increasing part of the water molecules freezes in a gradual, heterogeneous glass transition to a new type of amorphous ice. The remainder is supercooled and is liquid down to 200 K with its dynamics being strongly retarded. Inelastic neutron scattering studies on water in oriented cellulose fibres show that the structural and dynamical properties of the water/ice network are anisotropic. This anisotropy allows us to conclude on the arrangement of water molecules in the semi-crystalline cellulose material.

AKB 100.60 Sa 16:45 Poster TU D

Coupling of driven and diffusive motion on one-dimensional lattices — •Hauke Hinsch, Paolo Pierobon, and Erwin Frey — Hahn-Meitner-Institut

The total asymetric exclusion process (TASEP) describes the driven motion of a single species of particles on a one-dimensional lattice with hard-core exclusion. Depending on the boundary conditions various non-equilibrium steady states of the density distribution are possible. For more realistic modelling of biological systems like motor molecules, TASEP has been extended recently (A. Parmeggiani et al, PRL 90, 086601) by coupling each lattice site to an infinite reservoir, resulting in the existence of multi-phase coexistence.

We present a study where the reservoir has a finite capacity. Specifically the reservoir is treated as lattice gas model with hard core particles governed not by driven but by diffusive motion. In this case it becomes important to take into account the time scales of the different processes. Upon studying the system by Monte-Carlo simulations and mean-field theory we have found that the density distribution depends crucially on the time scale ratio of the motion on the TASEP and the reservoir lane. Our results show that in some limiting cases the new model can be mapped on the original TASEP model with and without Langmuir kinetics.

AKB 100.61 Sa 16:45 Poster TU D

Toroids versus racquets: the collapse of semiflexible polymers of finite thickness — •Eugene Starostin and Ralf Everaers — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, D-01187 Dresden, Deutschland

We calculate the minimal energy shapes of a semiflexible polymer in a poor solvent. Following Schnurr, MacKintosh et al., our conformational energy includes the bending elastic component and the surface energy. We take into account the finite thickness of the molecule and reconsider the relative stability of rod-like, toroidal and "racquet" conformations. The main result is presented as a phase diagram computed for relatively short effective length. In agreement with earlier results in the zero-thickness approximation, thin filaments collapse into toroidal shapes. However, beyond a critical thickness, the kinetically preferred racquet state also turns out to be the ground state.

AKB 100.62 Sa 16:45 Poster TU D

Information theory reveals large-scale synchronisation of statistical correlations in Eukaryote genomes — •Manuel Dehnert[1], Werner E. Helm[2], and Marc-Thorsten Hütt[1] — [1]Bioinformatics Group, Department of Biology, Darmstadt University, Schnittspahnstr. 3-5, D-64287 Darmstadt — [2]Mathematics and Science Faculty, University of Applied Sciences, D-64295 Darmstadt

We study short-range correlations in DNA sequences with methods from information theory and statistics. We find a persisting degree of identity between the correlation patterns of different chromosomes of a species. Except for the case of human and chimpanzee inter-species differences in this correlation pattern allow robust species distinction: In a clustering tree based upon the correlation curves on the level of individual chromosomes distinct clusters for the individual species are found. This capacity of distinguishing species persists, even when the length of the underlying sequences is drastically reduced. In comparison to the standard tool for studying symbol correlations in DNA sequences, namely the mutual information function, we find that an autoregressive model for higher-order Markov processes significantly improves species distinction due to an implicit subtraction of random background.

AKB 100.63 Sa 16:45 Poster TU D

Domain Size Influences the Diffusive Behavior of Nano-Particles in Langmuir Monolayers — •Florian Rückerl[1], Douglas Martin[2], Martin Forstner[3], and Carsten Selle[1] — [1]Universität Leipzig, Inst. Exp. Physik I, PWM, Linnéstr. 5, 04103 Leipzig — [2]Brandeis University — [3]UC Berkeley

We modelled protein diffusion in inhomogeneous cell membranes utilizing lipid monolayers at the air/water interface where liquid-condensed (LC) domains coexist in a liquid-expanded (LE) phase. The motion of negatively charged fluorescent latex beads as model proteins within LE phase was monitored by Single-Particle-Tracking. The diffusion of those particles was apparently affected by dipole-dipole interactions leading to observation of domain-associated movement. We calculated the shape of the electric field of the condensed domains dependent on the distance r to the domain ($r_{bead} < r < 20\mu m$). On altering the domain sizes, the resulting potential changes from $U \propto 1/|r|^3$ for a single dipole to $U \propto 1/|r|$ for large domain radii ($R > 10\mu m$). This is a significant change from a short to a long ranged potential.

Monte Carlo simulations support the influence of the interactions on model protein diffusion. Furthermore, the diffusion is affected by the potential depth and shape, leading to anomalous diffusion on different time scales, corresponding to the time needed for the model protein to cover the area of the size of the domain.

AKB 100.64 Sa 16:45 Poster TU D

Solid domains in fluid vesicles — •Erwin Gutlederer, Thomas Gruhn, and Reinhard Lipowsky — Max-Planck-Institute of Colloids and Interfaces, 14424 Potsdam, Germany

Recent experiments reveal the existence of solid domains in fluid vesicles when they are cooled below a certain temperature. In our theoretical approach we analyse thermodynamic properties of this domain formation and investigate how the internal ordering of the solid membrane affects the morphology of the vesicle. Monte Carlo simulations allow us to estimate free energy differences between vesicles with different solid domain shapes.

AKB 100.65 Sa 16:45 Poster TU D

Refractive Index Measurements of Single Cells — •Susanne Ebert, Kort Travis, and Jochen Guck — Universität Leipzig, Abteilung Physik weicher Materie, Linnéstr. 5, 04103 Leipzig, Germany

Techniques using light for the manipulation of cells and for the measurement of cell properties, such as the optical stretcher and the optical tweezers, require exact knowledge of the cells' refractive index. For the most effective use of these single cell techniques, a method to measure the refractive index of single cells is also necessary. Such a method has value in its own right for application as an inherent cell marker. In the present work, two such refractive index measurement methods are demonstrated. The first method involves the imaging of forward scattering patterns of cells in a collimated laser beam, and the second method, the measurement of the velocities of cells accelerated by Gaussian laser beams. From this data, the index of refraction is extracted by comparison with exact T-matrix calculations, and a self-consistent model of the dielectric properties of the cell is developed.

AKB 100.66 Sa 16:45 Poster TU D

Towards Scanning Near-Field Optical Microscopy on Free-standing Biological Membrane — •Simone K. J. Johnas[1], Christiane Hoeppener[2], Andreas Naber[2], and Michael Herrmann[3] — [1]HASYLAB@DESY, Notkestr. 85, 22607 Hamburg — [2]Universtaet Karlsruhe, Institut fuer Angewandte Physik, Wolfgang-Gaede-Str.1, 76131 Karlsruhe — [3]Zoologisches Institut II, Universitaet Karlsruhe

The nuclear pore complex (NPC) is a large macromolecular protein assembly embedded in the nuclear envelope (NE) of an eukaryotic cell. It controls tightly the exchange of all kinds of molecules between the cytoplasm and the nucleus. Thus NPCs play an important role for e.g. the metabolism of the nucleus and the effects of medicaments. Since the NPCs are densely packed in the membrane, conventional optical microscopy is not able to distinguish between two neighboured NPCs. By means of scanning near-field optical microscopy (SNOM) we have attained an optically resolved fluorescence image of dye-labeled NPCs in a functionally intact NE for the first time. Thus the aim of this project is a time-resolved oberservation of single transport events. A major obstacle towards this goal is the need of two compartments below and above the NE which mimic its natural environment. Possible preparation techniques and ways to image a freestanding membrane in a buffer solution with SNOM will be discussed. A new approach of the SNOM set-up guarantees the integrity of the soft biological membrane.

AKB 100.67 Sa 16:45 Poster TU D

Cell adhesion studies with quantum dot labeled cells on structured surfaces — •Tim Liedl, Stefan Kudera, Wolfgang J. Parak, and Friedrich C. Simmel — Department Physik, LMU München, Geschwister-Scholl-Platz 1, 80539 München

The adhesion properties of various cell lines are investigated using microcontact printing techniques. Complex patterns composed of hydrophobic and hydrophilic regions are stamped onto a glass substrate to probe cell mobility and the minimal area required for cell adhesion. Several cell lines are investigated in co-culture after labeling the individual cell lines with fluorescent colloidal nanocrystals with different colors. Due

to their reduced tendency to photobleach, nanocrystals are particularly suitable as long term markers. Microcontact printing is performed with polydimethyl siloxane (PDMS) stamps with octadecyltrichlorosilane as an ink. Master stamps with feature sizes on the order of 1 μm are defined in the negative photoresist SU-8 using standard optical and electron beam lithography.

AKB 100.68 Sa 16:45 Poster TU D

High resolution CARS microscopy with chirped excitation — •Ondrej Burkacky and Andreas Zumbusch — Department Chemie, LMU München, Butenandtstraße 11, 81377 München

Coherent anti-Stokes Raman scattering (CARS) microscopy puts us in a position to obtain molecular information at high spatial resolution without the use of labels. Both chemical composition and structural features are visualized by their vibrational spectra.

For efficient signal generation in the nonlinear processes involved, ultrashort laser pulses with high peak intensities are needed. However, the corresponding broad bandwidths limit the spectral resolution achieved. Therefore we introduced the method of chirping the pulses in a well-controlled manner. This leads to a narrower instantaneous bandwidth of the chirped pulses and consequently to a higher spectral resolution. In addition, the narrow spectral region probed can be shifted within the range of the much broader laser bandwidth of the ultrashort laser pulses by simply varying the temporal delay between the two pulses. We demonstrate how this approach can be used to obtain spectral and spatial high resolution images with large contrast in a variety of specimens.

Th. Hellerer, A.M.K. Enejder, A. Zumbusch, Appl. Phys. Lett. 85 (2004) 25

AKB 100.69 Sa 16:45 Poster TU D

Merging Microfluidics and Optical Tweezers: a versatile Microtechnology Platform — •Christian Schmitz[1,2], Kai Uhrig[1,2], Jennifer Curtis[1,2], and Joachim Spatz[1,2] — [1]Max-Planck-Institut für Metallforschung, Stuttgart — [2]Universität Heidelberg, Biophysikalische Chemie, Heidelberg

Microfluidic devices offer unique advantages in handling of small sample volumes. This is particularly important in bioanalysis and biotechnology. Furthermore, the miniaturization of flow systems leads to remarkably improved performance in separation and detection of reagents. As a step towards a more flexible and versatile system design we created a new technology platform by merging the techniques of holographic optical tweezers (HOTs) and microfluidics. HOTs can produce and independently steer one to hundreds of optical traps. It provides the possibility to non-invasive assembly and manipulation of micrometer size objects as well as to measure forces. The scale at which the microtechnology platform operates allows complete spatial and chemical control of the microenvironment und thus for the study of biological and biomimetic systems at a cellular level. We apply the system for probing complex biopolymer networks: F-Actin networks are engineered and their physical properties are studied as actin cortex model systems.

AKB 100.70 Sa 16:45 Poster TU D

Stacking interactions in a lattice model of DNA/RNA — •Christian Simm[1], Sanjay Kumar[2], and Ralf Everaers[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden — [2]Department of Physics, Banaras Hindu University, Varanasi 221 005, India

The binding strength of DNA/RNA strands is of crucial importance for many biological processes. Examples are the formation of DNA bubbles during transcription, RNA secondary stucture or hairpin formation in ssDNA and miRNA. Current lattice models of DNA only include of the effects of hydrogen bonding between complementary bases. We introduce an extension which accounts for base stacking interaction and the polarity of the DNA strand. We use Monte-Carlo simulations of the model to present results which show the effects of this extension and compare it to the simpler model.

AKB 100.71 Sa 16:45 Poster TU D

Retinal Glial Cells as Living Optical Fibers — •K. Franze[1,2], S. Schinkinger[1], K. Travis[1], A. Reichenbach[2], and J. Guck[1] — [1]Abteilung Physik Weicher Materie, Universität Leipzig — [2]PFI für Hirnforschung, Universität Leipzig

Vision is one of our most important senses. The cells responsible for converting light into electrical impulses are the photoreceptor cells (PRs). However, due to the sequence of evolution, the vertebrate retina is the "wrong way round": in order for light to reach the PRs, it must first pass through several retinal layers of different types of cells. Especially under low-light conditions additional structures are required which guarantee optimal utilization of the light. These structures ideally span the entire thickness of the retina and guide the light through all of the cell layers to the PRs. Only the so-called Müller cells, the principal retinal glial cells, have this ability. Furthermore, these cells contact every single PR.

In the present work, the light guiding properties of individual Müller cells were studied. Cells were aligned in a two-beam IR laser trap, additional visible light was sent through the cells, and the light guiding efficiency of the cells for visible light was measured. These measurements unambiguously demonstrate the light guidance function of Müller cells. The observed intensity dependent transmittance might serve as a protective mechanism of the inverted retina against photo damage of the PRs.

AKB 100.72 Sa 16:45 Poster TU D

Dimers in a 1-d lattice gas: a model for molecular motors collective dynamics — •Paolo Pierobon[1,2], Thomas Franosch[1], and Erwin Frey[1,2] — [1]Hahn-Meitner Institut, Abteilung Theorie, Glienicker Str.100, D-14109 Berlin, Germany — [2]Fachbereich Physik, Freie Universität Berlin, Arnimallee 14, D-14195 Berlin, Germany

The transport of molecular motors along microtubules closely resembles the dynamics of a driven lattice gas of dimers without conservation of particles. The motion of the dimers is unidirectional, asymmetric and stochastic: its properties are encoded in the well studied totally asymmetric simple exclusion process (TASEP). We extend this model by including the possibility of attachment/detachment kinetics and the fact that as dimers they occupy two lattice sites. We study the stationary phase diagram by means of Monte Carlo simulations combined with a continuum description (based on an extended mean field theory). Novel unexpected regimes are identified, where the system is "frustrated".

AKB 100.73 Sa 16:45 Poster TU D

Cytoskeletal assembly in optical neuronal guidance. — •Allen Ehrlicher, Timo Betz, Bjoern Stuhrmann, Michael Goegler, Daniel Koch, and Josef Kaes — Universität Leipzig, Fakultät für Physik und Geowissenschaften, Linnestr. 5, D-04103 Leipzig

The ability to control neuronal growth is a fundamental goal of neuroscience. Although various techniques have been used previously, it has been shown recently that optical gradients can also be used to guide the advancing edge of the growth cone in neuronal cell lines [Ehrlicher et al. PNAS 2002]. While this effect has been observed for different neuronal cell types, the underlying interactions behind the effect are unclear. In this study we examine the contribution of microtubules to the effect. Using disrupting and stabilizing drugs such as nocodazole and taxol, we selectively modified the microtubule structure during and without optical guidance, and visualized their dynamic distribution using fluorescent markers. A better understanding of the cytoskeletal dynamics in optical guidance will not only help to improve the effect, but contribute valuable insight into neuronal growth as well as cellular motility in general.

AKB 100.74 Sa 16:45 Poster TU D

Adhesion-induced domain formation of membranes with long and short stickers — •Mesfin Asfaw, Reinhard Lipowsky, and Thomas R. Weikl — Max Planck Institute of Colloids and Interfaces, Theory Division, 14424 Potsdam

Biological membranes contain domains which serve important functions, e.g. in signaling, budding, or adhesion. The formation of these domains can be driven by a phase separation of the lipid bilayer, or by the aggregation of membrane-embedded macromolecules. We consider the adhesion of membranes with various types of adhesion molecules, or 'stickers'. The stickers differ in their characteristic lengths and binding energies. During membrane adhesion, the length mismatch of the stickers causes a separation into distinct domains, provided the sticker concentrations exceed a critical threshold. This mechanism of adhesion-induced phase separation into domains with long and short stickers has been recently observed during T cell recognition. We characterize the rich equilibrium phase behavior of these membranes using scaling estimates and Monte Carlo simulations.

AKB 100.75 Sa 16:45 Poster TU D

Loop-closure principles in protein folding kinetics — •Thomas R. Weikl — Max Planck Institute of Colloids and Interfaces, Theory Division, 14424 Potsdam

How fast and on which routes does a protein fold into its native structure? The answer to this central question of protein folding kinetics ap-

pears to depend, to some degree, on generic aspects of the protein structure. One of these aspects is the average localness of structural contacts, which correlates with the folding rates of small single-domain proteins. Another aspect is presented here: The folding routes of many small proteins seem to be dominated by simple loop-closure dependencies between the structural elements. These loop-closure dependencies help to rationalize why mutations in some structural elements strongly affect the kinetics, while mutations in other structural elements don't. They also explain characteristic changes in the kinetic impact of structural elements when the chain connectivity is altered by circularization or circular permutation.

AKB 100.76 Sa 16:45 Poster TU D

On the growth control of epithelial cell populations in-vitro — •Dirk Drasdo[1], Jörg Galle[1], and Markus Löffler[2] — [1]Interdisciplinary Center for Bioinformatics, Kreutzstr. 7a, 04103 Leipzig — [2]Institute for Medical Informatics, Statistics and Epidemiology, 04103 Leipzig

We present a 3d individual cell based biophysical model to study the effect of normal and malfunctioning growth regulation and control on the spatial-temporal organization of growing cell populations in vitro, ranging from monolayer growth to growing tumor spheroids. The model includes explicit representations of typical epithelial cell growth regulation and control mechanisms, namely (i) a cell-cell contact mediated form of growth inhibition, (ii) cell-substrate contact dependent cell-cycle arrest, and (iii) cell-substrate contact dependent programmed cell death. The model cells are characterized by experimentally accessible biomechanical and cell-biological parameters. We study by variation of these cell-specific parameters and apply selective knock-outs of growth regulation and control mechanisms to investigate how the different mechanisms collectively act together. We show that our simulation studies cover the growth behaviour of epithelial cell populations ranging from stem cell populations up to tumor cell lines in vitro.

AKB 100.77 Sa 16:45 Poster TU D

Active vs. Passive Microrheology — •Daisuke Mizuno, Frederick C. MacKintosh, and Christoph F. Schmidt — Dept. Physics, Vrije Universiteit, Amsterdam, NL

We have performed passive and active 2-particle microrheology (MR) in actin solutions by using the same micron-sized colloidal particles as a probes. In passive MR, viscoelasticity is measured from the correlated thermal fluctuations of the probe particles. In active MR, one probe particle is sinusoidally driven by an oscillating optical trap while the correlated motion of the other one is detected by laser interferometry. In equilibrium, both methods give the same results. In non-equilibrium, however, such as in living cells, random, nonthermal stress fluctuations prevent the use of the fluctuation-dissipation theorem. Probe motions are influenced by e.g. the activity of motor proteins or directional polymerization/depolymerization of actin and microtubules. Active components also modify the viscoelastic response of the cytoplasm. The main aim of our research is to gain a better understanding of microscopic dynamics in such non-equilibrium systems by combining active and passive microrheology.

AKB 100.78 Sa 16:45 Poster TU D

Dynamics of DNA looping under tension — •Ulrich Gerland — Department Physik and CENS, LMU München, Germany

The interaction of proteins bound to DNA is often dependent on the formation of DNA loops. The dynamics of this process can be probed in detail by applying a force to the ends of the DNA with single-molecule techniques. Motivated by ongoing experiments, I study both the equilibrium statistics and the dynamics of DNA looping under tension, using a combination of numerical and analytical techniques. In particular, I characterize the force-dependence of the peak in the looping probability and looping rate as a function of the separation between the DNA sites. I will discuss how the looping kinetics under tension can be used to indirectly obtain information on enzymes whose action depends on DNA looping.

AKB 100.79 Sa 16:45 Poster TU D

High-Frequency Microrheology of Wormlike Micelles — •Mark Buchanan[1], Maryam Atakhorrami[2], Jean-François Palierne[3], Frederick C. MacKintosh[2], and Christoph F. Schmidt[2] — [1]Dept. Physics, University of Oslo, Norway — [2]Dept. Physics, Vrije Universiteit, Amsterdam, NL — [3]Lab. Physique, Ecole Normale Sup. Lyon, FR

We have measured the frequency-dependent shear modulus of entangled solutions of wormlike micelles by high-frequency microrheology and have compared the results with those from macrorheology experiments done on the same samples. Using optical microrheology based on laser interferometry we have measured loss and storage moduli over six decades in frequency up to about 100 kHz. We present data over a decade in concentration in the entangled regime and find good agreement between micro- and macrorheology, thus validating recently developed microrheology techniques. By collapsing data for different concentrations, we furthermore determine both the concentration scaling of the plateau modulus and a power-law exponent of the complex shear modulus at high frequencies.

AKB 100.80 Sa 16:45 Poster TU D

Monte Carlo Simulation of Lipid Bilayers with Rigid Inclusions — •Olaf Lenz und Friederike Schmid — Universität Bielefeld, Fakultät für Physik

We have investigated the effects of inclusions (for example proteins) on a lipid bilayer close to it's fluid–gel (main) transition on a mesoscopic scale of a few tens of nanometers by means of a coarse-grained Monte-Carlo simulation.

We use a very efficient and simple bead-spring model of one hydrophilic head bead connected to six hydrophobic tail beads for the lipids and a model of "phantom" solvent beads that do not interact with each other for the solvent environment. In this model, the lipids self-assemble to form a lipid bilayer and the bilayer exhibits the fluid–gel transition. We observe a tilted gel state and an "interlocked" gel state which possibly is related to the well-known "ripple phase" of bilayers. The inclusions are represented by rigid, hydrophobic cylinders that roughly correspond to α-helices.

In the liquid phase, an ordering of the lipid tails is induced in the vicinity of the rigid inclusion. Close to the phase transition, the range of this effect grows. In the tilted gel phase, a long-ranged, directed point defect of the lipid tail ordering was observed. This defect leads to the destruction of the gel phase and therefore shifts the critical temperature of the phase transition to lower temperatures. Furthermore, the defect is expected to strongly influence the interaction between inclusions on a scale of a few times the size of the inclusion.

AKB 100.81 Sa 16:45 Poster TU D

Analysis of the Protein-Protein Association Free Energy Studied by Brownian Dynamics Simulations — •Alexander Spaar — Center for Bioinformatics, Saarland University, Im Stadtwald, D-66041 Saarbrücken, Germany

We carefully analyzed the trajectories from Brownian Dynamics (BD) simulations in order to study protein-protein encounter on the example of barnase and barstar, a well characterized model system of electrostatically steered diffusional association. The individual positions and orientations of the proteins during all trajectories are stored in occupancy maps. By interpreting the occupancy maps as probability distributions and by defining a local entropy function we are able to compute the 6-dimensional entropy landscape for the encounter of the two proteins. Together with the configuration dependent electrostatic and desolvation energies, the association free energy is obtained as the sum of these terms. In the free energy profile along the reaction path, which is defined as the path along the minima in the free energy landscape a characteristic minimum at small distances shows up, suggesting this to be used as the definition of the encounter state. The association free energy profiles are compared for different ionic strength and temperature of the solvent.

AKB 100.82 Sa 16:45 Poster TU D

In-plane and out-of-plane fluctuation of synthetic glycolipid lamellae under controlled osmotic pressure and temperature — •Emanuel Schneck[1], Florian Rehfeldt[1], Bruno Demé[2], and Motomu Tanaka[1] — [1]Technische Universität München — [2]Institut Laue-Langevin

The in-plane and out of plane cooperativity in artificial models of cell glycocalix was studied using the D16 membrane diffractometer coupled with a climate chamber. Rocking curves of oriented multilamellar stacks using the 2D detector (reciprocal space maps, $q_\parallel$ vs. q_x) allow for the analysis of the scattering along different orientations referring to in-plane and out-of-plane contributions independently. In-plane membrane fluctuations produce diffuse scattering along $q_\parallel$, while fluctuations of the periodicity affects the sharpness of the Bragg peaks along q_z (specular reflectivity). The analysis of the measured lamellar periodicities yields quantitative force-distance relationships, which clearly reveal the com-

petitive interplays of repulsive hydration forces and attractive "zipper" forces depending on the conformation of carbohydrate head groups.

AKB 200 Poster Session II

Zeit: Dienstag 17:00–19:00 Raum: Poster TU C

AKB 200.1 Di 17:00 Poster TU C

Probing of the proteasom-protein interaction with force-spectroscopy — •Mirjam Beuttler, Jens Schiener, and Reinhard Guckenberger — Max-Planck-Institut für Biochemie, 82152 Martinsried

Atomic force microscopy (AFM) is an established method to investigate biological samples in their physiological environment. In our group we are investigating the 20S proteasome from Thermoplasma acidophilum. Besides imaging we will focus on force-measuring.

The proteasome is a barrel-shaped enzyme of 15 nm height and 11 nm width with a small opening at both ends. Through these two entrances unfolded proteins can access the inner part of the proteasome with the catalytic centers in order to be degraded there. Our goal is to characterize the translocation mechanism, as the forces involved are currently unknown. First step is to immobilize the proteasomes in an upright position which is achieved in our case directly on mica. Imaging the samples ensures the right orientation and the density of the surface covering. Second step will be the investigation of the forces involved in the translocation mechanism. Therefore suitable proteins which are known to be degraded by the proteasome will be bound to the AFM-tip. The forces exerted on the proteins by the proteasomes are transmitted to the tip. While retracting the lever with the tip from the surface the deflection of the lever changes due to the forces. Similarly, when the lever is kept stationary it will be bent towards the sample when the protein is sucked into the proteasome. Such force-distance-curves are offering a promising route to a better understanding of the translocation mechanism.

AKB 200.2 Di 17:00 Poster TU C

Geometry of interface mediated interactions — •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

Soft interfaces can mediate interactions between particles bound to them. One example is the interaction of protein inclusions in a lipid membrane. Traditionally, this phenomenon is treated by calculating the total energy of the particle-interface-system as a function of particle positions. The forces between the bound particles can then be obtained via appropriate derivatives. Unfortunately, the intrinsic nonlinearity of the problem generally forces one to restrict to linear approximations of the energetics.

It is, however, possible to choose a different, covariant approach and gain some nonlinear results: The forces between the particles are mediated through the interface and are thus encoded in its geometry. In analogy to classical elasticity theory one can write them as integrals over the surface stress tensor, which itself depends in a transparent way on the interfacial energy density. For standard symmetric two-particle situations this approach yields exact formulas for the force in terms of the mid-plane geometry, the sign of which is sometimes evident.

AKB 200.3 Di 17:00 Poster TU C

Small angle scattering study of intermolecular interactions in protein solutions — •Marc Niebuhr und Michel H.J. Koch — European Molecular Biology Laboratory, Hamburg Outstation, EMBL c/o DESY, Notkestrasse 85, D-22603 Hamburg, Germany

The results a study of intermolecular interactions in protein solutions measured with small angle X-ray scattering are presented. According to the DLVO theory the main interactions between spherical particles are the hard-sphere interactions, a short range attraction, due to surface-surface forces, and a long range repulsion caused by the fact that the particles are charged. The most interesting finding is that structure factors of salt concentration series and their change upon addition of urea and TMAO are better described if the strength of the attractive potential decreases with increasing salt concentration. Previous work in the literature had relied on a constant attractive potential within a given series of measurements.

AKB 200.4 Di 17:00 Poster TU C

Hydrogen bonding vs. stacking interactions in DNA base pairs - a Diffusion Monte Carlo study — •M. Fuchs[1], C. Filippi[2], J. Ireta[1], L. Ismer[1], and M. Scheffler[1] — [1]Fritz-Haber-Institut der MPG, Berlin — [2]Instituut Lorentz, Univ. Leiden (NL)

Diffusion Monte Carlo (DMC) calculations can provide accurate total energies of molecular systems. DMC is thus useful for benchmarking (computationally cheaper) calculations based on density functional theory where one is relying on approximations for the exchange-correlation functional. On the other hand DMC remains computationally feasible even for larger systems where conventional correlated approaches such as Configuration Interaction or Coupled Cluster are at present too demanding. Here we explore DMC to study hydrogen bonded and stacked conformations of adenine-thymine and methylated adenine-thymine. Our results for the intermolecular interaction energies show that DMC predicts both hydrogen bond strengths and stacking interactions in agreement with results from the Coupled Cluster [CCSD(T)] approach, confirming these where they differ from MP2 data. We further show that gradient corrected density functionals (GGA-DFT) can yield reasonable bond strengths of the hydrogen bonded complexes but fail to bind the stacked conformations. Adding empirical corrections for the missing dispersion (van der Waals) attraction in GGA-DFT [1] we find that the stacked conformations do bind, yet markedly too strongly when compared to our DMC results. [1] Q. Wu and W. Yang, J. Chem. Phys. 116, 515 (2002).

AKB 200.5 Di 17:00 Poster TU C

Spectroscopic characterization of individual light-harvesting 2 complexes reconstituted into model membranes — •Martin Richter, Clemens Hofmann, Jürgen Baier, Silke Oellerich, and Jürgen Köhler — Experimental Physics IV, University of Bayreuth

Membrane-embedded pigment-protein complexes are the major players in photosynthesis. For a detailed study of these complexes, they are usually extracted from their native membrane, isolated and purified. The native membrane environment of these proteins is mimicked by detergent molecules in order to stabilize the complexes. However, this artificial protein environment can strongly affect the structural and spectroscopic properties of the pigment-protein complexes. Therefore, we reconstituted light-harvesting 2 (LH2) complexes, a photosynthetic pigment-protein complex from purple bacteria, into model membranes of phospholipids to study the influence of the protein environment on the structure and function of these complexes.

AKB 200.6 Di 17:00 Poster TU C

Biofilms of phototrophic systems in the evanescent field of light guides — •Davor Kosanic, Sven Schlicher, Sven Verpoort, Diana Fragel, and Hilmar Franke — Physics department, university of Duisburg-Essen, Lotharstr. 1, 47057 Duisburg, Germany

The interaction of biological systems with light has to be investigated for optical biosensors and for bioreactors. Especially when working with optical light guides the interaction takes place via the evanescent field. Therefore the particular field distributions have to be known.

The growth of algae on optical fiber tips or optical sensors has been investigated by video microscopy and by plasmon-leaky mode spectroscopy. For the latter method suspension of green algae in water has been regarded as an optical medium with high absorption coefficients. Model experiments have been performed using rhodamine/ethanol solutions.

The conventional plasmon-leaky mode set-up has been modified towards a compact method for monitoring solutions and suspensions with high absorption coefficients in the range of 50000 1/m , realistic values in algae suspensions.

AKB 200.7 Di 17:00 Poster TU C

Supramolecular Interaction at the Single Molecule Level — •Rainer Eckel[1], Robert Ros[1], Björn Decker[2], Jochen Mattay[2], and Dario Anselmetti[1] — [1]Experimentelle Biophysik und Angewandte Nanowissenschaften, Universität Bielefeld, Universitätsstrasse 25, 33615 Bielefeld — [2]Organische Chemie, Universität Bielefeld, Universitätsstrasse 25, 33615 Bielefeld

In supramolecular systems, the tailored non-covalent interaction between designed organic host and guest molecules opens fascinating concepts for the development of new materials for artificial molecular recognition, self-assembly and biosensor applications. We applied mechanical single molecule force spectroscopy to investigate the specific binding of individual resorc[4]arene-ligand host-guest complexes. The molecular binding forces, their dependence to external loading rates, the rate of dissociation, and its corresponding cavity length directly relate to the molecular properties of the supramolecular species and are consistent with an activated decay of a metastable bound state(1). This allows new insights into the mechanisms, kinetics and thermodynamics of intermolecular association in chemical and biological receptor systems.

(1) R. Eckel, R. Ros, B. Decker, J. Mattay, and D. Anselmetti, Angew. Chem. (in press).

AKB 200.8 Di 17:00 Poster TU C

Excitation beyond the monochromatic laser limit: Simultaneous 3-D confocal and multiphoton microscopy with a single white-light laser source. — •Daniel Koch[1], Timo Betz[1], Jörn Teipel[2], Wolfgang Härtig[3], Jochen Guck[1], Josef Käs[1], and Harald Giessen[2] — [1]Universität Leipzig, Fakultät f Physik und Geowiss., Linnéstr 5, 04103 Leipzig — [2]Universität Bonn, Institut f Angewandte Physik, Wegelerstr 8, 53115 Bonn — [3]Universität Leipzig, Paul Flechsig Institut f Hirnforschung, Jahnallee 59, 04109 Leipzig

Confocal and multiphoton microscopy are essential tools in modern life sciences. They allow fast and highly resolved imaging of a steadily growing number of fluorescence markers ranging from labeled antibodies and fluorescence proteins to quantum dots, used for the localization and quantitative detection of molecules within living cells and organisms. Up to now, only one physical limitation seemed to be unavoidable. Both confocal and multiphoton microscopy rely on lasers as excitation sources, and their monochromatic radiation allows only a limited number of simultaneously usable dyes. We have overcome this limitation by successfully replacing all excitation lasers in a standard confocal microscope with the pulsed 430 to 1300 nm white-light which is generated in a tapered silica fiber. With this easily reproducible method, simultaneous confocal and multiphoton microscopy was demonstrated. By developing a coherent and intense laser source with spectral properties comparable to a mercury lamp, we provide the flexibilty to excite any desired fluorophore combination.

AKB 200.9 Di 17:00 Poster TU C

Force Spectroscopy with a Novel Small Focus AFM — •Volker Walhorn[1], Joerg Martini[1], Rainer Eckel[1], Jeroen Steen[2], Tobias Kramer[2], Bjoern Decker[3], Robert Ros[1], Dario Anselmetti[1], Juergen Brugger[2], and Juergen Mattay[3] — [1]Department of Biophysics and Applied Nanosciences, University of Bielefeld, Germany — [2]Inst. de Microsystèmes, EPFL, Lausanne, Switzerland — [3]Department of Organic Chemistry, University of Bielefeld, Germany

Atomic force microscopy has become potent tool for investigating inter- and intramolecular interactions. Single molecule force spectroscopy on supramolecular guest-host-complexes reveal information about the depth of the binding pocket and thermal off-rates.

Sensitivity and resolution are immanently conntected to the cantilever's mechanical properties. The cantilever's thermal noise induced by Brownian Motion of the surrounding medium is a fundamental limit of resolution. As the Nyquist Theorem is valid for the thermal white noise of a cantilever, reduction of the viscous damping by downsizing the cantilever's dimensions is compulsory. Furthermore, the resonant frequency is increased which extends experimental bandwidth and thus enables high speed measurements. Unfortunately small cantilevers cannot be used with commercially available AFM, since the laserfocus is too large.

We present results of single molecule force spectroscopy measurements on Calixarene-Ammonium-Complexes acquired with our homebuilt small focus AFM. As predicted, small cantilevers show favourable properties as increased resonant frequency and lower viscous damping.

AKB 200.10 Di 17:00 Poster TU C

Peptide antibiotics: insights in membrane selectivity and interaction — •Regine Willumeit[1], Mont Kumpugdee[1], Sebastian Linser[1], Sergio Funari[2], Jörg Andrä[3], Thomas Hauss[4], and Raz Jelinek[5] — [1]GKSS-Forschungszentrum, Max-Planck-Str. 1, 21502 Geesthacht — [2]c/o HASYLAB, Notkestrasse 85, 22603 Hamburg — [3]Research Center Borstel, Parkallee 10, 23845 Borstel — [4]Hahn-Meitner-Institute, Glienicker Str. 100, 14109 Berlin — [5]Ben Gurion University, Beersheva 84105, Israel

The past decade has brought a worldwide resurgence of infectious diseases due to the evolution of antibiotic-resistant strains. As a potential class of novel antimicrobial agents antimicrobial peptides have recently emerged. These peptides are small molecules that are fast and lethal towards a broad spectrum of pathogens but quite inactive on eukaryotic cells. However, the interaction of antibacterial peptides with their target membrane is not well understood. One promising antibacterial peptide is NK-2. It corresponds to residues 39-65 of NK-lysin, exhibits low haemolytic activity and is devoid of cytotoxic activity against human cell lines. In this paper several approaches to investigate the interaction of antibacterial peptides with membranes are presented. These include especially scattering techniques (X-ray and neutron scattering) and colorimetric biosensors.

AKB 200.11 Di 17:00 Poster TU C

Vibrational imaging of cholesterol enriched micro-domains in the Stratum corneum model system by CARS microscopy — •A. Kovalev[1], N. Patincharath[1], M. Köhler [2], and A. Volkmer[1] — [1]3rd Institute of Physics, University of Stuttgart, 70550 Stuttgart — [2]Roswell Park Cancer Institute, Buffalo, NY 14263, USA

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. The CARS signal is resonantly enhanced when the difference in photon energies of the pump and the Stokes pulses coincides with the frequency of a Raman resonance. CARS microscopy has been demonstrated to exhibit high sensitivity, spatial and temporal resolution, noninvasiveness, and three-dimensional sectioning capability with sub-micron resolution. In this work, the application of CARS microspectroscopy to the study of a model system of Stratum corneum, the topmost barrier on the epidermis that prevents the penetration of external reagents through the skin is reported. Electroporation combined with application of vesicles formed by positively charged lipids makes the stratum corneum transparent for chemicals. This effect, which is important in transdermal drug delivery research, is not yet well understood. Investigations are carried out on model lipid mixtures consisting of ceramides, stearic acid and cholesterol, the three main lipid species of stratum corneum. A multiplex CARS scheme was employed for imaging and fast acquisition of CARS spectra revealing cholesterol-rich regions.

AKB 200.12 Di 17:00 Poster TU C

Imaging the interactions of functionalized, structured surfaces — •Peter Seitz, Ernst Stelzer, and Alexander Rohrbach — European Molecular Biology Laboratory (EMBL), Meyerhofstr. 1, 69117 Heidelberg

Functionalized surfaces can affect (bio-) chemical reactions and control spatially the affinity for various binding partners (receptor-ligand, antibody-antigene, etc.). These usually short-range interactions are initiated by long range electrostatic, electrodynamic and entropic interactions. We investigate the influence of long-range interactions on structured surfaces with Photonic Force Microscopy, where an optically trapped bead (probe) is scanned across the surface. The change of the bead's fluctuations encodes the interaction with the surface. The fluctuation traces are recorded interferometrically in three dimensions with nm-resolution and at scan-rates of several hundred kilohertz with a quadrant photodiode. Interactions can be imaged in the sub-piconewton range. The optical phase changes induced by the surface structure (e.g. an adhering cell) on the probing laser beam can be extracted from the signal of the trapped probe. In this way the extracellular matrix of biological cells not in contact with the coverslip can also be investigated.

AKB 200.13 Di 17:00 Poster TU C

NAD(P)H autofluorescence - an approach to cellular metabolism — •Bülent Peker, Raluca Niesner, and Karl-Heinz Gericke — IPC @ TU-Braunschweig, Hans-Sommer-Str. 10, D-38106 Braunschweig

The 2-Photon-excitation based Fluorescence Lifetime Imaging (FLIM) proved to be an excellent method for subcellular research in biological samples in the last few years. It is now a seminal method for "ex vivo"and "in vivo"non invasive visualisation research in extensive united cell structure and tissue with high resolution. The options given by these method like monitoring a reply to a stimulus were unfortunately deadlocked by too long data interpretation. Our technique of FLIM-Analysis allows an on-line monitoring by implementing a non-iterativ method. In addition to multiexponential NAD(P)H- Analysis successful applications in pH-, η- and τ-imaging in artificial skin constructs show the capability of our method.

AKB 200.14 Di 17:00 Poster TU C

Subcellular parameter probing using TPM based FLIM — •Stefan Quentmeier, Raluca Niesner, Bülent Peker, and Karl-Heinz Gericke — IPC @ TU-Braunschweig, Hans-Sommer-Str. 10, 38106 Braunschweig

Two-photon scanning microscopy (TPM) combined with fluorescence lifetime imaging (FLIM) provides an excellent method for probing cellular parameters on subcellular level. Depending on the dye used different parameters like pH, ionic strength, CO_2 and O_2 concentration and viscosity can be monitored in high resolution. FLIM gives us a non-invasive technique at hand possessing high intrinsic 3D resolution, large penetration depth, low photodamage and simple experimental setup as sample preparation is limited to simple staining. As fluorescence lifetime is not affected by experimental parameters the instrumental stability of standard intensity based TPM experiments is easily outperformed by FLIM. We performed FLIM for pH, n and viscosity mapping in artificial skin constructions (ASC) and genuine human skin.

AKB 200.15 Di 17:00 Poster TU C

Single cell manipulation in microfluidic networks by optical tweezers — •Kai Leffhalm, Andy Sischka, Wibke Hellmich, Thanh Tu Duong, Katja Tönsing, Robert Ros, Alexandra Ros, and Dario Anselmetti — Experimental Biophysics, Physics Department, Bielefeld University, Germany

Control and manipulation of single cells gain importance as a tool to better understand the migration behaviour of living cells in vivo and for single cell analysis. Microfluidic networks provide dimensions small enough to navigate and steer single cells with optical tweezers to different areas of an artificial network where the flow properties can be controlled by electrophoresis and electroosmosis.

Potential applications include microproteomics and monitoring of the expression level of individual cells, which can be stimulated or suppressed by changing the velocity of the flow or the concentration of substances, e.g. cytokines or (cytostatic) drugs, in the culture medium.

We will present our experimental setup and our first test experiments where a cell is captured between two electrodes where it can be destroyed by an electric field, i.e. an electric pulse. This is an initial point for future single cell analysis.

AKB 200.16 Di 17:00 Poster TU C

Model of intracellular Ca^{2+} oscillations due to negative feedback — •Peter Borowski[1], Jürgen Reidl[2], Anke Sensse[3], Martin Zapotocky[1], Jens Starke[2], and Markus Eiswirth[3] — [1]Max Planck Institute for Physics of Complex Systems, Dresden — [2]Institute of Applied Mathematics, University of Heidelberg & WIN-Research Group of Olfactory Dynamics, Heidelberg Academy of Science and Humanities — [3]Fritz-Haber-Institute of the Max Planck Society, Berlin

We present a mathematical model for calcium oscillations and fast adaptation in the cilia of olfactory sensory neurons. Stoichiometric network analysis is used for analysing the kinetic equations and finding the oscillatory regime. The underlying mechanism is based on direct negative feedback and does not require any autocatalysis such as calcium-induced calcium release. Results of the model using physiological parameter values agree quantitatively with experiment, both with respect to oscillations and to fast adaptation. The bifurcation diagram of the model is calculated to make predictions regarding the occurence of oscillations.

AKB 200.17 Di 17:00 Poster TU C

Study of Energy-Transfer Processes in Metallo-Porphyrin Artificial Light-Harvesting Molecules — •Joachim Zeller[1,2], Robert Hauschild[1], Gernot Riedel[1], Teodor S. Balaban[2,3], Heinz Kalt[1,2], N. Berova[4], and K. Nakanishi[4] — [1]Institut fuer Angewandte Physik, Universitaet Karlsruhe (TH), 76131 Karlsruhe — [2]Centrum fuer Funktionelle Nanostrukturen, Universitaet Karlsruhe (TH), 76131 Karlsruhe — [3]Institut für Nanotechnologie, Forschungszentrum Karlsruhe, 76021 Karlsruhe — [4]Columbia University, New York, USA

Artificial light harvesting molecules mimic photosynthesis in which light is transformed into chemical energy. They consist of an antenna, which absorbs light and acts as an energy donor, and an energy trap, to which the excitation is transferred. We investigated energy transfer in 3 conformationally different metallo-porphyrins using time-resolved fluorescence spectroscopy. They consist of a Zn-TPP moiety (antenna/energy donor) and a free-base-TPP moiety (energy trap) which are linked with a covalent steroidal bridge. An analysis of the time-resolved fluorescence spectra using the method of decay-associated spectra (DAS) reveals energy transfer between the Zn-TPP energy donor and the free-base-TPP energy trap with transfer times 0.91 ns, 0.99 ns and 1.1 ns for the 3 different molecule conformations. A comparison of the measured transfer times to the values expected from Foerster theory shows only limited agreement. These results will be compared to the energy transfer dynamics in H-bonded supramolecular porphyrin complexes.

AKB 200.18 Di 17:00 Poster TU C

Density Functional Theory Study on the Stability of left-handed alpha-Helix Polyalanine — •Franziska Grzegorzewski, Lars Ismer, Joel Ireta, and Matthias Scheffler — Fritz Haber-Institut der Max Planck-Gesellschaft, Faradayweg 4-6, 14193 Berlin

The left-handed α-helix, α_L, is an unusual conformation in proteins and, if observed, mainly built with glycine, a non-chiral amino acid. The discrimination of α_L-helix has been attributed to unfavorable repulsive interactions between the side chain and the backbone atoms (steric effect). In order to provide a deeper insight on the factors influencing the relative stability of α_L-helix we performed systematic ab-initio calculations for polyalanine in different left-handed helical conformations using density functional theory (DFT) in the PBE approximation to the exchange-correlation functional. The potential energy surface of the left-handed polyalanine was explored for numerous configurations using different helix twists and varying the increment along the helix axis per residue. We find three minima corresponding to π_L-, α_L-, and 3_{10L}-helix. Based on an harmonic vibrational analysis, we find that only considering the loss of vibrational entropy in addition to the steric effect, DFT-PBE predicts that a fully extended structure will not fold spontaneously into α_L-helix in vacuum at room temperature

AKB 200.19 Di 17:00 Poster TU C

Anomalous Dynamics of Action Potential Initiation in Cortical Neurons — •Björn Naundorf[1], Maxim Volgushev[2], Theo Geisel[1] und Fred Wolf[1] — [1]Max-Planck Institut für Strömungsforschung and Fakultät für Physik, Universität Göttingen, 37073 Göttingen — [2]Abteilung Neurophysiologie, Ruhr-Universität Bochum

Action potential (AP) initiation in neurons is fundamental to information processing in the brain. In most neurons, AP initiation is mediated by the activation of fast, voltage-dependent sodium channels, canonically described by Hodgkin-Huxley (HH) type equations. Here we describe features of the dynamics of AP initiation which differ qualitatively from the predictions of the HH theory. We show that APs from neocortical neurons recorded *in vivo* and *in vitro* initiate much more rapidly than predicted by the steady state sodium activation curve, while at the same time APs are emitted in a very large voltage range. We then show that the two effects are mutually exclusive in HH type models and can not be resolved within the framework of the HH theory.
Using a phenomenological model, we further demonstrate that the observed AP onset dynamics has important consequences for the information processing capabilities of neocortical neurons. Rather than, as commonly believed, acting as a low pass filter, the model suggests that cortical neurons are specifically tailored to support highly transient signals, while suppressing slowly varying inputs.

AKB 200.20 Di 17:00 Poster TU C

Calculation of solvent entropies from MD simulations — •Friedemann Reinhard and Helmut Grubmüller — MPI für biophysikalische Chemie, Abteilung 070 – Theoretische und computergestützte Biophysik, Am Fassberg 11, 37077 Göttingen

Solvent entropy is the main contribution to the hydrophobic effect. Its computation from molecular dynamics simulations however proves difficult. First, due to the diffusive motion of the solvent molecules, the configuration space is much too large to be sampled sufficiently. Second, the typically very shallow energy landscapes generate phase space densities with quite complex topology.

We address both problems by exploiting the permutation symmetry of the solvent molecules. For every ensemble element generated by the simulation, the water molecules are relabeled such that the permutated configurations fall into a compact volume in phase space. Thereby we greatly enhance sampling without affecting any thermodynamic quantities. Thus the established entropy estimation methods for proteins should become applicable to the relabeled solvent molecules too.

This expectation is confirmed by test calculations on simple model systems. Furthermore, the compactified phase space densities show comparatively simple topology, such that also the second problem is alleviated significantly. What remains to be done is to develop more elaborated density estimates, which is the subject of our current work.

AKB 200.21 Di 17:00 Poster TU C

Effect of receptor-ligand distance on adhesion cluster stability — •Thorsten Erdmann and Ulrich S. Schwarz — Max Planck Institute of Colloids and Interfaces, Theory Division, 14424 Potsdam

Cells in multicellular organisms adhere to the extracellular matrix through two-dimensional clusters of adhesion bonds. Single adhesion bonds have finite lifetimes and open and close stochastically. For many common receptor-ligand systems, the ligands are tethered to the substrate via polymeric spacers so that adhesion cluster stability crucially depends on receptor-ligand distance. Experimentally, the distance-dependent interplay of rupture and rebinding in adhesion clusters can be studied *in vitro*, e. g. by atomic force microscopy, the biomembrane force probe, or the surface force apparatus. In order to study this effect theoretically, we introduce a one-step master equation for the stochastic dynamics of parallel bonds. Binding requires stretching of the polymeric tether, which leads to a distance-dependent binding rate. Closed bonds correspond to stretched tethers and exert force on the receptors, which is counteracted by the elastic stiffness of the force transducer. This force accelerates unbinding, but it is also shared equally by all closed bonds. The formation of new bonds reduces receptor-ligand distance and increases the probability for further binding. These effects make receptor-ligand binding in adhesion clusters a cooperative and self-reinforcing process. A bifurcation analysis of a deterministic differential equation for the average number of closed bonds reveals the existence of a bistable region in which a bound and an unbound state coexist. In the stochastic treatment, the system continuously jumps between these two macrostates.

AKB 200.22 Di 17:00 Poster TU C

Tension-induced titin kinase activation studied by force-probe molecular dynamics simulations — •Frauke Gräter[1], Jianhua Shen[2], Hualiang Jiang[2], and Helmut Grubmüller[1] — [1]MPI fuer Biophysikalische Chemie, Am Fassberg 11, 37077 Goettingen — [2]Shanghai Insitute of Materia Medica, Zuchongzhi Lu 555, Zhangjiang Hi-Tech Park, 201203 Shanghai, China

The conversion of mechanical stress into a biochemical signal in a muscle cell requires a force sensor. Titin kinase, the catalytic domain of the muscle protein titin, has been suggested as a candidate. Its activation requires major conformational changes resulting in the exposure of its active site.

Force probe molecular dynamics simulations were used to obtain insight into the tension-induced activation mechanism. Our results suggest the rupture of two terminal beta-sheets as the primary unfolding steps. The low force resistance of the C-terminal relative to the N-terminal beta-sheet is found to be due to their different topology. A subsequent movement of the auto-inhibitory tail is seen to lead to the exposure of the active site, as is required for titin kinase activity. Thus, our reults support the hypothesis of titin kinase as a force sensor.

AKB 200.23 Di 17:00 Poster TU C

Use of carboxylic acids for the monitoring of anaerobic fermentation processes — •Dieter F. Ihrig[1], H. Michael Heise[2], Ulrich Brunert[1,2], Alexander Moor[2], Ruediger Kuckuk[2], and Martin Poschmann[1] — [1]University of Applied Sciences Suedwestfalen, Iserlohn, Germany — [2]ISAS - Institute for Analytical Sciences, Dortmund, Germany

We are studying anaerobic fermentation processes that involve a thermophilic first bioreactor stage and a mesophilic second stage. The developed anaerobic process is very efficient, but also rather unstable. For achieving a better process management, it is necessary to understand the interdependencies between process engineering parameters (for example, the hydraulic turn-over time or the organic biomass burden as characterized by the Chemical Oxygen Demand (COD) parameter) and biochemical variables such as the concentration of carboxylic acids. Results from the determination of carboxylic acids using steam extraction and Reversed-Phase-HPLC are discussed. Furthermore, activities were started using infrared spectroscopy for quasi-continuous process monitoring. Goal of the project is the development of an on-line sensor system based on infrared attenuated total reflection (ATR) measurements. For gathering practical experience, we constructed a micro-flow system for on-site spectroscopic measurements. The analytical results were compared to concentration values obtained by HPLC and to pH-readings of the bioreactor broth media. The project was funded by the German Federal Ministry for Education and Research (BMBF).

AKB 200.24 Di 17:00 Poster TU C

Molecular recognition of chemically structured substrates in a lattice model — •Thorsten Bogner, Andreas Degenhard, and Friederike Schmid — Condensed Matter Theory, Fakultät für Physik, University of Bielefeld, Universitätsstraße 25, E5 [5th floor]

We investigate the adsorption of polypeptides on a planar substrate by means of a coarse grained model on a lattice. The chemical composition of both, the peptide and the substrate, is modeled explicitly.

In particular we are interested in the emergence of specificity within the adsorption process. Despite its simplicity, we expect our model to exhibit the basic properties that lead to molecular recognition in 'real world' experiments. By analyzing the results of the simulations using methods from statistical data analysis, we find the small-scale structures of the peptide sequence to be a particular important factor regarding specificity. This is in qualitative agreement with existing binding experiments.

AKB 200.25 Di 17:00 Poster TU C

Membrane dynamics and membrane binding events investigated by photonic force microscopy — •Holger Kress, Ernst H. K. Stelzer, Gareth Griffiths, and Alexander Rohrbach — European Molecular Biology Laboratory (EMBL), Meyerhofstrasse 1, D-69117 Heidelberg, Germany

Optical tweezer based photonic force microscopy is used to study the binding of particles to the plasma membrane of macrophage cells. Macrophages are specialized cells that ingest particles such as bacteria or synthetic objects (e.g. latex beads) and enclose them into intracellular organelles. Optically trapped latex beads are moved to the plasma membrane of cells. The fluctuations of the trapped particle during the binding to the cell membrane and the following mechanical response of the membrane are tracked interferometrically. The tracked position fluctuations are measured in three dimensions with a precision of a few nanometers and a temporal resolution of 100 μs. The tracked position fluctuations encode information about the dynamics of the binding process itself and the following mechanical response of the cell to this stimulus.

AKB 200.26 Di 17:00 Poster TU C

Neuronal signal transmission in reconstructed neuronal networks on microfluidic Si-based devices: Towards an artificial chemical synapse chip — •Yulia Mourzina[1], Petra Schulte[1], Dmitri Kaliaguine[2], Simone Böcker-Meffert[1], and Andreas Offenhäusser[1] — [1]Institute of Thin Films and Interfaces, Research Center Jülich, Germany — [2]Faculty of Chemistry, St. Petersburg State University, Russia

Chemical synaptic transmission, the elementary interaction event between neuronal cells, is fundamental to understanding learning and memory. In order to perform long term studies about neuronal interactions in reconstructed neuronal networks, we intend to form an 'artificial chemical synapse' with spatially and temporally resolved non-invasive chemical

stimulation and detection methods.

We reconstruct the defined synaptical connections of cortical neuronal cells on microfluidic Si-based chips and align the reconstructed neuronal networks with microapertures connecting the microfluidic compartments. Natural conditions of chemical synapses are simulated by means of providing localized chemical stimuli to the cells with neurotransmitters via microfluidics. Cell response is characterized by means of electrophysiological recordings. Further on, we intend to develop a non-invasive recording of the synaptic events in neuronal networks by means of electrochemical methods.

AKB 200.27 Di 17:00 Poster TU C

In situ Synthesis of DNA Chips — •Thomas Naiser, Timo Mai, Wolfgang Michel, and Albrecht Ott — Physikalisches Institut, Universität Bayreuth, 95440 Bayreuth

DNA-Chips are biosensors for measuring gene activity on a genome wide scale. They have become an important tool in Biological Sciences. The underlying principle is the duplex formation of nucleic acids (hybridization), which is highly sequence-specific and can therefore be used to determine the composition of nucleic acid mixtures extracted from biological specimens. We have built a photolithographic micro-projection setup to manufacture high density DNA-Chips in a photochemically controlled synthesis process. Virtual lithography masks, generated with a Digital Micromirror Device (a spatial light modulator commonly used in video projectors), allow local control of the synthesis, so that we can produce an array of closely spaced spots (10-15 micron in size), each one containing a different sequence of single stranded DNA. The whole chip comprises up to 10^5 freely programmable sequences (15-25mers) on an area of $10mm^2$. We present results from hybridization assays performed to investigate the physics underlying DNA-Chip technology.

AKB 200.28 Di 17:00 Poster TU C

Local Distribution of Silica in Equisetum hyemale — •lanny sapei[1], sandra lehmann[2], robert nöske[3], peter strauch[3], and oskar paris[1] — [1]Max Planck Institute of Colloids and Interfaces, Biomaterial Department, Research Campus Golm, 14424 Potsdam — [2]UP TRANSFER GmbH, Gesellschaft für Wissens- und Technologietransfer an der Universität Potsdam, Am Neuen Palais 10, 14469 Potsdam — [3]Potsdam University, Chemistry Department, K-Liebknecht-Str. 24-25, 14476 Potsdam

Horsetail (Equisetum) is known as one of the strongest accumulators of silicon among higher terrestrial plants (up to 25% dry weight), mostly in the form of amorphous silica. This makes this plant an interesting candidate as a renewable resource of silica for the synthesis of biomorphous ceramics. We have examined the 3D Si-distribution in Equisetum hyemale using X-ray microtomography, supported by quantitative analysis with EDX mapping and Raman microscopy. The silica distribution within the plant tissue is quite heterogeneous, showing strong Si-accumulations in particular knobs at the epidermis. Scanning small-angle X-ray scattering (SAXS) with 0.1 mm spatial resolution reveals a strong scattering signal in these regions, quite different from the well known SAXS signal from cellulose in plant cell walls. This suggests that the silica is present in the form of nanoparticles.

AKB 200.29 Di 17:00 Poster TU C

Potential-Energy Surface of Infinite Helical Polypeptides — •Joel Ireta and Matthias Scheffler — Fritz-Haber-Institut der Max-Planck-Gesellschaft

The potential-energy surfaces of infinite polyalanine and polyglycine chains in helical conformation are studied using density-functional theory in the Perdew, Burke and Ernzerhof approximation to the exchange-correlation functional (DFT-PBE). Minima associated to a π-helix, α-helix and 3_{10}-helix conformations are identified for both polypeptides. For polyalanine the α-helix minimum is the lowest in energy. However for polyglycine π-helix and α-helix minima are degenerated within the DFT accuracy. The α-helix is found to undergo structural transitions to a π- or 3_{10}-helix when the length of the helix is strainend by more than 10%. The barriers for the structural transitions mainly associated to the breaking of the hydrogen bonds are considerably affected by the side group in polyalanine. We find this effect can not be solely attributed to repulsive interactions between the side group and the helix backbone but to sizeable changes in covalent bonds in the peptide unit of polyalanine with respect to polyglycine.

AKB 200.30 Di 17:00 Poster TU C

Synthesis and Characterization of De Novo Designed Peptides Modeling the Binding Sites of [4Fe-4S] Clusters in Photosystem I — •Mikhail Antonkine[1,2], Christoph Breitenstein[2], Boris Epel[2], Eckhard Bill[2], Wolfgang Gärtner[2], John Golbeck[3], and Wolfgang Lubitz[2] — [1]Institut für Experimentalphysik, Freie Universität Berlin, Arnimallee 14, D-14195 Berlin, Germany. Tel.: 49 30 838 53047, Fax: 49 30 838 56081. — [2]Max-Planck-Institut für Bioanorganische Chemie, Stiftstrasse 34-36, Mülheim an der Ruhr, D-45470, Germany. — [3]Department of Biochemistry and Molecular Biology, The Pennsylvania State University, University Park, PA 16802,USA.

Photosystem I (PS I) is a membrane-bound pigment-protein complex found in photosynthetic organisms. It converts the energy of light into chemical energy. The terminal electron transfer cofactors in PS I are three [4Fe-4S] clusters named Fx, Fa, Fb. The PsaC subunit of PS I harbors binding sites of Fa and Fb clusters. We modeled the binding sites of the [4Fe-4S] clusters Fa and Fb of PsaC by preparing sixteen amino acid peptides. Model peptides incorporate the consensus iron-sulfur binding motif and amino acids from the environment of the respective iron-sulfur cluster. The [4Fe-4S] clusters were successfully incorporated into these model peptides, as shown by their optical absorbance, EPR and Mössbauer spectra. We compare continuous wave and pulsed EPR, Electron Spin Echo Envelope Modulation (ESEEM) and Mössbauer spectra of the model [4Fe-4S] clusters with the respective spectra of Fa and Fb in unbound PsaC and in the fully assembled PS I.

AKB 200.31 Di 17:00 Poster TU C

Electron Transfer Rates at Low Temperatures Using Wilsons Renormalization Group — •Sabine Tornow, Ning-Hua Tong, and Ralf Bulla — Theoretische Physik III, Institut für Physik, Universität Augsburg, 86135 Augsburg, Germany

Electron transfer in biomolecules is the key process in photosynthesis, oxidative phosphorilation or DNA damage repair. In the biomolecule complexes electrons are tunneling between donor and acceptor sites which leads to their particular function. The latter is affected by the structure of the protein through the coupling between protein motion and electron transfer. To calculate the transfer rate taking into account this coupling the spin boson model provides a well established description. While limiting cases are well understood in certain parameter regimes non-perturbative methods are needed, e.g., in the crossover from the nonadiabatic to the adiabatic regime. We present a theoretical non-perturbative study of the electron transfer using Wilsons Numerical Renormalization Group method and calculate the thermal rate constant at low temperatures.

AKB 200.32 Di 17:00 Poster TU C

Towards a Combined Approach of Single Molecule Tracking and Fluorescence Correlation Spectroscopy — •Stephan Schäfer — Biotechnological Centre, TU Dresden

Wide-Field Microscopy based on CCD detection and tracking of single fluorescently labelled molecules (SMT) in lipid bilayer membranes has proved to be a promising tool for a deeper understanding of biologically active lipid- and protein molecules. However, tracking of single molecules with a high mobility remains difficult due to limitations in the camera read-out rate and signal collection time. Using giant unilamellar vesicles (GUVs) which have been proven to be a suitable and reliable model for biological lipid membranes restricting diffusive motion to their 2D membrane surface. Besides SMT we employes Fluorescence correlation spectroscopy (FCS) as a time-averaging fluctuation analysis of small molecular ensembles. Comprising maximum sensitivity and high statistical confidence, FCS is especially well suited for investigations within cellular membranes. We present first results of a comparative study on SMT and FCS performed on the lipid bilayer membrane of GUVs. There is strong indication of a purely Brownian diffusion for the investigated composition (50

AKB 200.33 Di 17:00 Poster TU C

Organophosphonate monolayers as functionalisation for silicon based biosensing devices — •Karin Buchholz[1], Michael D. Carolus[2], Jeffrey Schwartz[2], Marc Tornow[1] und Gerhard Abstreiter[1] — [1]Walter Schottky Institut, TU München, 85748 Garching, Germany — [2]Department of Chemistry, Princeton University, Princeton, New Jersey 08544-1009

Planar semiconductor sensing devices based on silicon-on-insulator (SOI) substrates have immense potential for applications such as label-

free, fast, and time resolved detection of biomolecule binding events due to their great sensitivity to surface potential changes via the field effect [1].

Phosphonate films are easy to apply and provide for stable silicon surface derivatization because they give dense, self-assembled monolayers that bond strongly to the native silicon oxide and that can be modified with tailored, substituted end groups [2].

We investigated the stability and current blocking properties of different alkylphosphonate layers over time by cyclic voltammetry and impedance spectroscopy. A maximum current blocking of 97 per cent at the reductive peak voltage of a reference sample was observed for samples coated with layers of hydroxyundecylphosphonic acids.

Concepts for biofunctionalisation of SOI sensors via Phosphonate acid monolayers will be discussed.

[1] M. G. Nikolaides et al., ChemPhysChem, vol. 4, 1104-1106 (2003)
[2] K. S. Midwood et al., Langmuir, vol. 20, 5501-5505 (2004)

AKB 200.34 Di 17:00 Poster TU C

Diamond-based biosensors — •Andreas Härtl[1], Jorge Hernando[1], Philipp Achatz[1], Tahmineh Pourrostami[1], Stefan Walter[2], Jose Garrido[1] und Martin Stutzmann[1] — [1]Walter Schottky Institut, Technische Universität München, Germany — [2]Institut für Organische Chemie und Biochemie, Technische Universität München, Germany

Diamond is known to be a per se biocompatible material, consisting just of carbon atoms. Other interesting properties are a large electrochemical potential window, low thermal background currents, fouling resistance, and chemical inertness. Together with the existance of a quasi-two-dimensional conductive layer at the surface of hydrogen terminated diamond, this suggests the use of diamond as an active substrate which can interact with biomolecules immobilized on it.

In this contribution we report on the functionalization of diamond surfaces with various biomolecules and on diamond based ion sensitive field effect transistors (ISFET). We have studied the immobilization of different proteins on the surface of single crystal and nanocrystalline diamond substrates, showing that covalent bonding can be achieved. Moreover, we have confirmed that the immobilized proteins retain their biological activity. First amperometric sensor applications have been realized and will be presented.

We also have fabricated ISFETs on single crystalline and polycrystalline H-terminated diamond substrates and have investigated their pH sensitivity.

AKB 200.35 Di 17:00 Poster TU C

Optical conductivity of wet DNA — •Arnd Hübsch[1], Robert G. Endres[2], Daniel L. Cox[1], and Rajiv R. P. Singh[1] — [1]Department of Physics, University of California, Davis, CA 95616 — [2]NEC Laboratories, Princeton, NJ 08540

DNA has attracted much attention in view of its possible application to nano-devices. Despite extensive efforts, however, the experimental results of the conductivity of DNA are still rather controversial. Motivated by recent optical experiments [1] we have studied the optical conductivity of DNA in its natural environment containing water molecules and counter ions. Our DFT calculations using the SIESTA code suggest a thermal activated doping of the DNA which leads to an electronic low-frequency absorption. The main contributions to the doping result from the DNA ends, breaks, or nicks.

[1] E. Helgren, A. Omerzu, G. Gruner, D. Mihailovic, R. Podgornik, and H. Grimm, cond-mat/0111299.

AKB 200.36 Di 17:00 Poster TU C

Covalent immobilisation of recombinant fusion proteins with hAGT for single molecule force spectroscopy — •Stefan Kufer and Hermann E. Gaub — Amalienstr.54(I); 80799 München

A genetically modified form of the human DNA repair protein O6-alkylguanine-DNA-alkyltransferase (hAGT) was used to immobilize different recombinant hAGT fusion proteins covalent and selective on gold and glass surfaces. Fusion proteins of hAGT with Glutathione S-Transferase (GST) and with tandem repeats of Titin Ig domains, were produced and anchored via amino-polyethylene glycol (PEG)-benzylguanine (BG). Anchoring was characterized and quantified with surface plasmon resonance (SPR), atomic force microscope (AFM) and fluorescence measurements. Individual fusion proteins were unfolded by single molecule force spectroscopy corroborating the selectivity of the covalent attachment.

AKB 200.37 Di 17:00 Poster TU C

Simulation of Fluorescence Anisotropy Experiments: Probing Protein Flexibility — •Gunnar Schröder[1], Ulrike Alexiev[2], and Helmut Grubmüller[1] — [1]MPI biophysik. Chemie, Göttingen — [2]Freie Universität, Berlin

Fluorescence anisotropy experiments in combination with site-directed fluorescent labeling offer the chance to locally probe protein conformation and dynamics. To study how information on the protein dynamics can be extracted from the fluorescence anisotropy of a bound dye, we performed molecular dynamics simulations of an Alexa488 dye covalently bound to the loop connecting the A- and B-helix of bacteriorhodopsin. The fluorescence anisotropy decay predicted by the simulation agrees well with the experimental results. The simulation revealed two depolarization processes with a rotational correlation time of about one nanosecond, which are due to the loop flexibility and slow conformational dye dynamics and which cannot be separated by experiment alone. Analysis of the correlation between the dye and the protein motions provides an atomistic description of the part of the protein dynamics, that is actually observed in the experiment. Furthermore, comparison of simulations with and without bound dye enabled us to test the inevitable assumption that in the experiment the influence of the dye on the protein dynamics is negligible. Indeed, only minor deviations in the loop flexibility were seen, thus providing solid theoretical grounds for the usual interpretation of the measurements.

AKB 200.38 Di 17:00 Poster TU C

Scanning Probe Microscopy Investigations of the Oriented Attachment and Membrane Reconstitution of His-tagged Cytochrome c oxidase to a Gold Electrode — •Dirk Mayer[1], Andreas Offenhäusser[1], Kenichi Ataka[2], and Joachim Heberle[2] — [1]Forschungszentrum Jülich, ISG-2: Institute for Bio and Chemosensors, Jülich, Germany — [2]Forschungszentrum Jülich, IBI-2: Structural Biology, Jülich, Germany

Many of the vital functions of cells are maintained by membrane proteins, which for instance selectively control the transfer of ions, biological signal molecules and energ. The high complexity of biological transmembrane machineries with respect to their structure (consisting of many subunits), the reduced periodicity (scalablility) and the multistep reaction paths makes the assignment of structure and function a challenging task. Monolayers of reconstituted membrane proteins supported by solid surfaces can be applied to modern surface analyzing methods. We are giving an account of a novel approach, combining the modification of a metal surface by attaching a Ni- NTA moiety with the reconstitution of the oriented and detergent solubilized proteins in a lipid bilayer. We employed surface-enhanced infrared absorption spectroscopy and scanning probe techniques for deriving a detailed description of the whole solid surface supported immobilization and reconstitution reaction path.

AKB 200.39 Di 17:00 Poster TU C

Near-field-THz-Imaging with high power cw-radiation — •Bruno Gompf, Michael Gerull, Tobias Müller, and Martin Dressel — 1.Physikalisches Institut, Universität Stuttgart

There is an increasing interest in THz-imaging especially of biological and medical samples. But until now, most of the work done in this field is based on time-domain techniques using ultrafast laser pulses. The inherent disadvantages of this broadband method are the low intensity and poor energy resolution. In combination with a near-field arrangement time-domain techniques have the additional problem that small apertures always act as high pass filters on broad-band radiation. We have developed a near-field spectrometer operating in the THz-range between 30 GHz and 1.4 THz, where we use backward-wave oscillators (BWO) as continuous-wave sources, which supply highly monochromatic ($\Delta\nu/\nu = 10^{-6}$) and coherent radiation with an output power of up to 300 mW. This instrument allows to record THz-images with a high spatial and spectroscopic resolution with an acquisition time of about 10 ms/pixel.

AKB 200.40 Di 17:00 Poster TU C

Development of a biosensor device on functionalized Silicon on Insulator (SOI) structures for the specific detection of proteins — •Simon Lud, Cornelia Neunteufel, Petra Neff, Michael Nikolaides, M. Fischer, and Andreas Bausch — Lehrstuhl für Biophysik E22, TU München, 85747 Garching, Germany

To handle the vast number of possible interactions between different molecules, detection systems must be able to screen many different in-

teractions in parallel. Further on, in order to account for the different physical properties of the involved molecules, the detector must have a tunable sensitivity.

We present a device based on standard semiconductor technology which enables the selective and quantitative detection of biomolecular interactions. The sensor is based on hydrophobized Silicon-On-Insulator (SOI) substrates and is functionalized by a monolayer of lipids with incorporated metal chelate lipids. Both reversible charging of the chelate headgroup with divalent nickel ions and the specific binding of proteins was detected In addition, it was possible to detect charge differences between both peptides and proteins quantitatively. The sensor response is modelled within the standard Poisson-Boltzman theory and thus an average effective charge of different peptides and proteins can be determined. As the device is based on standard semiconductor technologies the SOI based Biosensor is well suited for parallelization needed in high throughput applications.

AKB 200.41 Di 17:00 Poster TU C

A Simple Scheme for Rapid 3D Orientation Determination of the Emission Dipole of Single Molecules — •Johannes Hohlbein[1] and Christian G. Hübner[2] — [1]Max Planck Institute of Microstructure Physics, Weinberg 2, 06120 Halle — [2]Martin Luther University Halle-Wittenberg, Department of Physics, Hoher Weg 8, 06120 Halle

One of the unique features of single molecule absorption and emission is their anisotropy due to the well-defined transition dipole(s) for both processes allowing the determination of the molecule's orientation. While polarization-resolved techniques are usually capable to detect only a projection of the transition dipole, several methods have been proposed in order to determine the full three-dimensional orientation. Here, we report on a new detection scheme that allows for a shot-noise limited determination of the emission dipole orientation utilizing an annular mirror, a polarizing beam splitter in conjunction with three detectors in a scanning confocal optical microscope.

AKB 200.42 Di 17:00 Poster TU C

Molecular dynamics simulations of aquaporin channels — •Jochen Hub und Bert de Groot — Max-Planck-Institut für biophysikalische Chemie, Computational Biomolecular Dynamics Group, Am Fassberg 11, 37077 Göttingen

Aquaglyceroporins (AQPs) constitute a large family of integral membrane proteins that facilitate efficient and specific passive permeation of water and/or small alcohols across biological membranes in response to osmotic gradients. Members of these channels have been found in organisms ranging from bacteria to mammals. In humans they are expressed in tissues as diverse as kidney, red blood cells, brain, and eye lens.

Within the last years substantial progress has been made in understanding the permeation mechanism through AQPs, however questions regarding their selectivity for different solutes remain challenging.

We present "real time"molecular dynamics simulations of permeation through a recently discovered AQP channel in the malaria parasite Plasmodium falciparum (PfAQP). PfAQP shows the unusual behavior of high water *and* glycerol permeation which makes it an interesting target to investigate the molecular mechanisms of channel selectivity.

Since glycerol uptake via PfAQP is essential for the biogenesis of the parasite's glycerolipids, the long term focus is the design of a specific inhibitor for PfAQP as a novel potential anti-malaria agent.

AKB 200.43 Di 17:00 Poster TU C

Wirkung von Funkwellen auf Bäume und andere Pflanzen — •Jette Dröse und Irene Pundt — Institut für Umweltphysik, Universität Heidelberg, INF 229, 69120 Heidelberg

In Deutschland werden und wurden in den letzten 10 Jahren mehr als 80000 Mobilfunksendeanlagen aufgestellt. Europaweit führt die Intensivierung der bisherigen Mobilfunk Netze sowie des zukünftigen UMTS-Netzes zu einer deutlichen Erhöhung der gepulsten Mikrowellenstrahlung in der Atmosphäre. Gleichzeitig sind in den meisten Ländern Europas zunehmende Waldschäden zu beobachten. In Italien, Spanien und Frankreich ist der Anteil der gesunden Bäume in den letzten 10 Jahren um 30 Prozent gesunken auf nur noch 20 Prozent in Italien und Spanien bzw. 35 Prozent in Frankreich (Europäischer Waldschadensbericht, 2004, http://www.icp-forests.org/Reports.htm). Als Ursachen für die sog. neuen Waldschäden werden der Saure Regen, Ozon, der Klimawandel sowie verschiedene Kleinstlebewesen (Borkenkäfer) genannt. Es wird vielfach vermutet, dass auch Mikrowellenstrahlung (Rundfunk, Radar, Richt-, Mobilfunk) für Waldschäden mitverantwortlich ist. Wir geben einen Überblick über Ergebnisse bisheriger Untersuchungen, die sich mit dem Einfluss von Mikrowellen auf Bäume und Pflanzen beschäftigen.

AKB 200.44 Di 17:00 Poster TU C

Kinetics of Solid-Phase DNA Hybridization — •Timo Mai, Thomas Naiser, Wolfgang Michel, Philipp Baaske, and Albrecht Ott — Physikalisches Institut, Universität Bayreuth, 95440 Bayreuth

Solid-phase hybridization of DNA oligonucleotides is of growing importance because of the advances in DNA microarray technology.

We apply two distinct strategies both commonly used in DNA microarray experiments: Immobilization of pre-fabricated oligonucleotides and light directed in-situ synthesis. We investigate kinetics of hybridization on glass substrates using evanescent field excitation and fluorescence labelling of oligonucleotides. A FRET technique is used to account for contributions of nonspecific adsorption to the substrate during the hybridization process. We discuss the impact of these different methods of immobilization on hybridization kinetics.

AKB 200.45 Di 17:00 Poster TU C

Einkopplung externer elektrischer Pulse in Hefezellkulturen zur gezielten Beeinflussung des Stoffwechsels — •A. Reiher[1], S. Günther[1], A. Krtschil[1], H. Witte[1], A. Krost[1], C. Warnke[2], T. Mair[2] und S.C. Müller[2] — [1]Inst. für Exp. Physik, Abt. Halbleiterepitaxie, Universität Magdeburg, PF 4120, 39016 Magdeburg — [2]Inst. für Exp. Physik, Abt. Biophysik, Universität Magdeburg, PF 4120, 39016 Magdeburg

Wir zeigen, wie mittels einer elektrischen Stimulation über eine planare Mehrelektroden-Anordnung gezielt das Stoffwechselgleichgewicht von Hefezellen beeinflusst werden kann, was sich durch eine Verringerung eines detektierten NADH-Fluoreszenzsignals nachweisen lässt. Die Elektroden-Anordnung besteht aus zwei in sich greifenden Gold- Titan-Elektroden auf einem Glassubstrat. Es werden die Einkoppeleigenschaften für systematisch variierte Spannungspulse in die Hefezellkultur (bei Variation der Form, Dauer und Höhe der Spannungspulse, isolierte oder metallische Elektrode) untersucht. Die genutzte Elektrodenanordnung weist einen optimalen Puls- höhenbereich von 10 V bis 15 V auf, wobei die Einsatzspannung für die induzierten Stoffwechselveränderungen zwischen 4-5 V liegt. Diese Abhängigkeiten werden systematisch für verschiedene Elektrolyten (variierte Molarität bzw. pH-Wert) aufgezeigt, um die Physik der Pulsübertragung und -einkopplung in die Zellen zu verstehen.

AKB 200.46 Di 17:00 Poster TU C

Biochemical synthesis of periodic DNA nanotemplates — •Stefan Beyer und Friedrich C. Simmel — Department Physik, LMU München, Geschwister-Scholl-Platz 1, 80539 München

Rolling circle amplification (RCA), a biochemical method established in genetics and biosensing, can be used to produce DNA building blocks for the self-assembly of nanostructures. In RCA, small circular single-stranded oligonucleotides serve as templates for the polymerization of the complementary strand. The polymerase (phi29 DNA polymerase) used for this process has a unique strand displacement activity. This allows it to continue with the polymerization process after the completion of one cycle without unbinding from the substrate. After one polymerization cycle the leading strand is removed and another cycle begins. The result of many of such cycles is a long single DNA strand with a repetitive sequence. Such a strand can be functionalized by hybridization with biotinylated DNA strands complementary to the repetition unit. The resulting DNA nanotemplate can be used to align biotin-binding nanoparticles (streptavidin or anti-biotin conjugates) into one-dimensional arrays. The constructs are analyzed by atomic force microscopy, scanning electron microscopy, gel electrophoresis and fluorescence microscopy. RCA proves to be a very simple, efficient and inexpensive way to create long periodic DNA sequences which can serve as templates for linear structures composed of nanoobjects.

AKB 200.47 Di 17:00 Poster TU C

Osmotically induced water permeation through gramicidin and derivatives studied by computer simulations. — •Guillem Portella and Bert L. de Groot — Max Plank Institute for Biophysical Chemistry, Computational Biomolecular Dynamics Group Am Faßberg 11, 37077 Göttingen, Germany

Full atomistic molecular dynamics simulations provides deeper understanding of the microscopic energetic and structural determinants underlying permeation through molecular membrane channels. Gramicidin A has been used as a model channel extensively both experimentally and computationally. Here, we focus particularly on the efficient simulation of an osmotically induced water flux. So far, different methods have been developed to derive permeation rates from simulations: continuous-time random model aproximation from equilibrium simulations or external forces acting on molecules as a result of the osmotic gradient. We chose to explore a method that attempts to mimick the true situation in vitro or in vivo as closely as possible, namely by introducing a true osmotic gradient. This is achieved by a solute concentration gradient across the membrane. As membrane simulations are usually carried out using periodic boundary conditions, this creates a challenge to the simulation of osmotic gradients, as they would normally be balanced by diffusion across the periodic boundaries. In order to alleviate this problem, we created two different water compartments (with different solute concentrations) by simulating two bilayers, which allows to efficiently study osmotically induced permeation, as has recently been demonstrated for carbon nanotubes.

AKB 200.48 Di 17:00 Poster TU C

Mapping the Thermoplasma proteome - structural proteomics studies by free-flow electrophoresis and cryo-electron tomography — •Christine Kofler, Istvan Nagy, Stephan Nickell, Marius Boicu, and Wolfgang Baumeister — Max Planck Institut für Biochemie, Molekulare Strukturbiologie

Thermoplasma acidophilum is a thermoacidophilic archaeon whose genome is completely known. To carry out proteomic analysis on this organism we use cell lysates which are fractionated using free-flow electrophoresis (FFE). The FFE separates the cytoplasmic proteins according to their isoelectric point. Single fractions are then investigated by means of cryo-electron tomography (cryo-ET) which allows to obtain three-dimensional (3-D) structural information of vitrified biological specimens at a resolution of 2-4 nm. Additionally, the contents of the single fractions are characterised by polyacrylamide gel electrophoresis and mass spectrometry. The knowledge of the 3-D structure and the determination of the identity of different proteins will enable us to generate a library of templates which is used as an input for pattern recognition algorithms designed to search electron tomograms of whole ice-embedded cells. The final aim of these studies is to locate and quantify the different macromolecular assemblies within 3-D reconstructions of intact *T. acidophilum* cells.

AKB 200.49 Di 17:00 Poster TU C

Solid State 31P-NMR Investigations of Different Calcium Phosphates — •Inderchand Manjubala[1], Sergey Maltsev[2], Christian Jaeger[2], and Peter Fratzl[1] — [1]Max-Planck Institute for Colloids and Interfaces, Department of Biomaterials, 14424 Potsdam, Germany — [2]Bundesanstalt für Materialforschung und -prüfung, Projektgruppe I.3903, Richard Willstaetter Str. 11, D-12489 Berlin, Germany

Synthetic hydroxyapatite and carbonated apatite have been used widely as bone substitute ceramic material as they resemble the natural bone apatite. In this study in-situ formation of biphasic calcium phosphate ceramic consisting of a mixture of hydroxyapatite and tricalcium phosphate in various ratios is synthesized under microwave irradiation. The amount of TCP increases as the Ca/P ratio decreases. 31P solid-state nuclear magnetic resonance (NMR) with magic-angle spinning (MAS) was used to determine the structure of the various synthetic calcium phosphates in comparison with X-ray diffraction. The XRD study reveals biphasic structure with hydroxyapatite and tricalcium phosphate phase and the amount of TCP increases as Ca/P ratio decreases. The Ca/P was also estimated from EDAX analysis.

AKB 200.50 Di 17:00 Poster TU C

Fluorescence spectroscopy of DNA nanodevices — •Andreas Reuter and Friedrich C. Simmel — CeNs und Department für Physik, Geschwister-Scholl-Platz 1, 80539 München

DNA tweezers consist of three branches of single stranded DNA, one of which is labelled with a fluorescence resonance energy transfer (FRET) pair. The three single strands form two double-stranded arms of 18 base pairs or roughly 6.1 nm length connected by a short hinge. The two duplex arms can be pulled together by the addition of a fourth single stranded DNA. In this case the dyes are in close proximity and FRET is very efficient. For the open configuration of the tweezers the average distance between the dyes was determined to be around 6 nm which corresponds to a mean opening angle between the duplex arms of 60°. However this value represents an average value over many possible configurations.

We perform single pair FRET experiments on three different configurations of the tweezers: fully stretched, where the dyes are separated by 40 base pairs, opened and closed. The width of the distribution of FRET efficiencies contains important information about the flexibility of the DNA nanodevice.

AKB 200.51 Di 17:00 Poster TU C

Complex and dynamic estrogen receptor-α interactions in living cells revealed by diffusion-time distribution analysis — •Michael Prummer, Hanna Jankevics, Paulina Izewska, Horst Pick, Kirsten Leufgen, and Horst Vogel — Laboratory of Physical Chemistry of Polymers and Membranes, Institute of Chemical Sciences and Engineering, Swiss Federal Institute of Technology (EPFL), CH-1015 Lausanne, Switzerland

Specific binding of ligands induce characteristic mobility patterns of human estrogen receptor-α (ER) in living breast cancer cells. These patterns were determined by analyzing the distribution of diffusion times obtained from fluorescence correlation spectroscopy experiments of ER conjugated to yellow fluorescent protein (YFP). The highly mobile ER in untreated cells slowed down in the presence of agonist and partial antagonist. The reduced mobility was accompanied by the formation of multiple discrete states in a broad distribution of diffusion times, where different states were observed for different ligands. This new finding reveals that ER forms a limited number of complexes with different mobility and varying population by dynamic interaction with many other nuclear components with well defined interaction times. Our approach to examine ER interactions at native expression levels opens up new routes to elucidate hormone-dependent transcription regulation and allows for the detection and distinction of pharmacologically and toxicologically active compounds. Diffusion time distribution analysis has the potential to become a general approach to monitor physical properties of biochemical networks in living cells.

AKB 200.52 Di 17:00 Poster TU C

Monitoring individual odorant receptors in cultured mammalian cells — •Michael Prummer, Valerie Jacquier, Horst Pick, and Horst Vogel — Laboratory of Physical Chemistry of Polymers and Membranes, Institute of Chemical Sciences and Engineering, Swiss Federal Institute of Technology (EPFL), CH-1015 Lausanne, Switzerland

The olfactory system is a highly specialized chemo-sensor recognizing a myriad of compounds at very low concentrations. Human odorant receptors (ORs) constitute a multi-gene family of G-protein coupled receptors with about 450 members. Although many putative ORs have been cloned, the expression in heterologous systems has been complicated by the failure of these proteins to translocate efficiently to the plasma membrane. Here, single-molecule detection is an appropriate tool allowing for the investigation of single ORs in the membrane of living cells. Human OR17-40 was enzymatically labeled with Cy5 and expressed in HEK293 cells where ligand-induced Ca-signaling and internalization proved its structural integrity and the existence of a functional secondary messenger system. Single-molecule tracking wide-field microscopy was utilized to record trajectories of ORs, which were analyzed in terms of the microscopic diffusion coefficient of each molecule, and the probability distribution of the mean-square displacement, averaged over many molecules. Current investigations are focused on how the mobility of ORs is influenced by ligand activation. The ultimate goal is to monitor the fate of individual ORs from their resting state through ligand binding until desensitization occurs.

AKB 200.53 Di 17:00 Poster TU C

The effect of biological variability on spatiotemporal patterns in a chain of biochemical oscillators: numerical simulations and Eigenvalue analysis — •Tetyana Morokhovska and Marc-Thorsten Hütt — Bioinformatics Group, Department of Biology, Darmstadt University, Schnittspahnstr. 3-5, D-64287 Darmstadt

Noise has an important effect on spatiotemporal patterns in biological systems. In contrast to noise, biological variability (or disorder) is a static system property. Nevertheless it can have dynamical implications, as the magnitude and the statistical properties of the biological variability influence the capabilities of the elements to synchronize or form patterns. We study such influences in a chain of coupled nonlinear oscillators, each

of which can be thought of as a simple form of oscillating biochemical reaction. In addition to numerical simulations, where spatiotemporal patterns are quantified with methods from information theory, we also present results on Eigenvalue distributions, which arise from biological variability in the system's parameters.

The simulations show that under certain conditions an increase in variability can induce spatial waves and complex spatiotemporal patterns. In particular, it is seen that the mutual information quantifying the complexity of the spatiotemporal patterns can depend resonantly on variability.

Eigenvalues for this system are studied both numerically and with algebraic methods based on Sturm sequences and the Routh-Hurwitz criterion. We show that certain aspects of the spatiotemporal patterns can be understood qualitatively on the level of Eigenvalue distributions.

AKB 200.54 Di 17:00 Poster TU C

Watching conformational changes of pigment-protein complexes by optical single-molecule spectroscopy — •Silke Oellerich[1,2], W.P.F. de Ruijter[2], R.J. Cogdell[3], J. Köhler[1], and T.J. Aartsma[2] — [1]Experimentalphysik IV, Universität Bayreuth — [2]Dept. of Biophysics, Leiden University, The Netherlands — [3]Dept. of Biochemistry, University of Glasgow, Scotland

Pigment-protein complexes of photosynthetic purple bacteria are an interesting model system for studying pigment-pigment interactions as well as pigment-protein interactions. These interactions strongly affect the spectral properties of the complex. Changes or even fluctuations in these interactions result in spectral changes, which can be followed by optical single-molecule spectroscopy. Low-temperature fluorescence-excitation spectra of individual bacterial light-harvesting 3 complexes (LH3), which consists of 27 bacteriochlorophyll a pigments, provide a detailed picture about the influence of locally restricted changes in the pigment-protein interaction on the spectral properties of the entire complex.

AKB 200.55 Di 17:00 Poster TU C

Theoretical investigations of radiation damage in protein crystals produced by X-rays — •Melanie Zehnder, Ivan Vartaniants, and Edgar Weckert — HASYLAB at DESY, Notkestrasse 85, 22607 Hamburg

The data quality and the achievable resolution in X-ray crystal-structure analysis of protein crystals is limited by radiation damage in many cases. The aim of the investigation is a better quantitative understanding of the damage caused by the absorbed photon and the subsequent processes in proteins by Monte-Carlo simulations.

The dominating inelastic interaction for X-ray photons of usual energies with an atom in the protein is the photo-effect, in which photoelectrons with nearly the incoming photon energy and low energy Auger-electrons are created. At higher energies the Compton scattering becomes more and more dominant. In this case an electron of few keV is produced and most of the energy is kept by the photon. For normal protein crystal sizes of around 0.3 mm this photon interacts in general just once. In contrast, the produced electrons have a high inelastic cross-section, so that the resulting electron cascade has a high damage-potential.

By means of a Monte-Carlo approach the electron cascade and the spatial distribution of ions and excited atoms produced by inelastic interactions are analyzed in order to obtain more quantitative information of the damage. Furthermore, the average time for a cascade produced by each photon is evaluated. One of the aims of these investigations is to find the optimum data collection energy dependent on a given chemical composition.

AKB 200.56 Di 17:00 Poster TU C

Modelling the Structure and Optical Properties of the Rhodopsin Chromophore — •Minoru Sugihara[1], Marko Schreiber[2], Peter Entel[1], and Volker Buss[2] — [1]Theoretical Physics, University of Duisburg-Essen — [2]Theoretical Chemistry, University of Duisburg-Essen

Modelling the Rhodopsin Chromophore with QM/MM: Four available X-ray structures of rhodopsin show a considerable variety of the chromophore geometry despite the similarity of the chromophore binding pocket. Based on the recent two crystal structures obtained by Okada [1,2], we have re-investigated the chromophore geometry applying QM/MM methodology. Our results show that the different chromophore geometries converge to practically one identical structure, which shows strong bond alternation and is twisted, in addition to the ionone ring, in the region undergoing photoisomerization [2].

Calculation of the Optical Properties with Ab-Initio Method: (CASPT2) Using the calculated chromophore geometry inside the binding pocket the absorption maximum of the chromophore was calculated. Two factors were considered: the internal distorsion and the presence of the counterion. We find that the first excited state is weakly red-shifted (ca. 20nm) due to the deformation of the chromophore and is strongly blue-shifted (ca. 100nm) in the presence of the counterion [3].

[1] T. Okada, et al. Proc. Natl. Acad. Sci. USA, 99 (2002) 5982. [2] T. Okada, et al. J. Mol. Biol. 342 (2004) 517. [3] M. Schreiber, et al. J. Chem. Phys. 23 (2003) 12045

AKB 200.57 Di 17:00 Poster TU C

Analysis of spatio-temporal patterns of the energy metabolism in a yeast extract by Karhunen - Loève decomposition — •Satenik Bagyan, Ronny Straube, Thomas Mair, and Stefan Müller — Otto-von-Guericke-Universität Magdeburg, Institut für Experimentelle Physik, Abteilung Biophysik, Universitätsplatz 2, 39106 Magdeburg, Germany

Glycolytic degradation of sugar is the primary pathway for the generation of energy in living cells and shows non-linear, oscillatory reaction kinetics, which is mediated by an autocatalytic reaction. Coupling of non-linear reaction kinetics with diffusion leads to the formation of glycolytic waves. We used an open spatial reactor to investigate the spatio-temporal pattern formation during glycolysis in the yeast extract. The dynamics of glycolytic waves in the open spatial reactor is changing over time from ordered (circular- or spiral- shaped waves) to more complex structures. To elucidate the mechanisms leading from ordered to complex behaviour, we analysed the dynamics of the spatio-temporal patterns with a Karhunen-Loève decomposition. We found that the early behavior of the patterns can be reconstructed with only 2 modes, but the later states require more modes for reconstruction. This indicates that during the initial states the patterns are dominated by periodic forces whereas at later states some kind of spatial desynchronization takes place.

AKB 200.58 Di 17:00 Poster TU C

Electric field induced perturbation of the energy metabolism of living yeast cells — •Ch. Warnke[1], T. Mair[1], S.C. Mueller[1], A. Reiher[2], A. Kritschl[2], H. Witte[2], and A. Krost[2] — [1]Otto-von-Guericke Universität Magdeburg, Inst.Exp.Phy., Abt.Biophysik — [2]Otto-von-Guericke Universität Magdeburg, Inst.Exp.Phy., Abt.Halbleiterepitaxie

Electric fields are often used for biophysical or biomedical treatment of biological cells, e.g. cell fusion or killing of cells. Despite these important applications, there are only a few data about the possible mechanisms that determine the electrosensitivity of biological cells. Since electrostimulation always induces depolarization of biomembranes, an impact of the energy metabolism is obvious due to the regeneration of electrochemical gradients by the expenditure of cellular energy. We have constructed a new electrical interface for local stimulation of biological cells with variable duration and amplitude. When applying short lasting electrical pulses to yeast cells, we find a direct response of the energy metabolism (measured by NADH-fluorescence) to these pulses. A sudden and fast decrease in NADH is followed by a slower recovery of the fluorescence signal. We attribute these changes to the immediate break down of ATP as a consequence of the regeneration of the membrane potential (AT-Pases) and the slower regeneration of ATP by glycolysis and respiration. We present a first kinetic analysis of this behaviour and basic characterization of the phenomenon.

AKB 200.59 Di 17:00 Poster TU C

Characterization of Cellular Protein Distributions Using *Karhunen-Lòeve* Decompositon — •Ronny Straube[1], Stefan C. Müller[1], Ronald Koop[2], and Walter Schubert[2] — [1]Abteilung Biophysik, Otto-von-Guericke-Universität Magdeburg, 39106 Magdeburg, Germany — [2]MelTec GmbH, Leipziger Str. 44, 39120 Magdeburg, Germany

Immuno-fluorescence microscopy is a widely used technique to visualize the location of proteins on a cellular level. This method is based upon the interaction of fluorochrome labeled antibodies with antigens. In general, it is limited by the number of simultaneously usable fluorochrome labeled antibodies due to problems concerning the spectral separability of the fluorescence signals.

Recently, this limitation has been overcome by using a repetitive method (called *MELK* [1]) where many different antigens can be vi-

sualized on the same sample of cells. Thereby, it becomes now possible to study combinatorial patterns of protein distributions based on series of fluorescence intensity images of a high spatial resolution.

We use the *Karhunen-Lòeve* decomposition to characterize the cellular distributions of 18 human surface antigens on an ensemble of peripheral blood leukocytes (PBL's). By analyzing the mode structure we find that some antigens tend to aggregate while others prefer to separate. We also investigate the reproducibility of the *MELK* patterns.

[1] Patentnummer (Deutschland): 197 09 348.5-52, W. Schubert, "Automatisches Multi-Epitop-Ligand-Kartierungsverfahren", MelTec GmbH, 1997

AKB 200.60 Di 17:00 Poster TU C

Potential and limitations of DNA microarrays from a single-molecule point of view — •Beate Sick and Keith Harshman — DNA Array Facility, Universitaet Lausanne, CH-1015 Lausanne

DNA microarrays are a high-throughput technology which provide a snapshot of the transcriptome of some ten thousand genes in parallel. Since the native RNA expression levels in a cell can span a range of 6 orders of magnitude, it is desirable to cover the same dynamic range in one microarray experiment. In order to approach this goal several components in a microarray experiment have still to be optimized. In this contribution we assess physical limitations of DNA microarray experiments and include technical boundaries and biological variability. We discuss the observed limited reproducibility and dynamic range of typical microarray data from homemade spotted arrays and from commercial platforms (Affymetrix). The ultimate lower detection limit is reached when a single target gene transcript binds to a probe feature, provided the instrumentation has single-molecule sensitivity. On the other hand, the total number of binding sites for transcripts on each feature, which is determined for instance by the feature size, defines the ultimate upper detection limit. From these theoretical considerations the accessible dynamic range is evaluated for different existing platforms. In an outlook the impact of further miniaturization of microarrays on the dynamic range will be discussed.

AKB 200.61 Di 17:00 Poster TU C

Response of ion currents across the cell membrane to excitation with high-frequency electrical fields — •Michael Olapinski[1], Andrea Brüggemann[2], Michael George[2], Stephan Manus[1], Niels Fertig[2], and Friedrich C. Simmel[1] — [1]Sektion Physik and Center for Nanoscience, Universität München, Geschwister-Scholl-Platz 1, 80539 München — [2]Nanion Technologies GmbH, Pettenkoferstr. 12, 80336 München

Due to the intrinsically large RC time constants of the measurement setup, classical patch-clamp techniques are limited in time resolution. They are therefore not suitable for the application of high-frequency (HF) electrical signals and for the study of fast processes coupling to the ion transport dynamics.

Our setup combines a patch-clamp on-a-chip system with an open-end coaxial probe that is positioned a few tenths of a millimeter above the investigated cells. Ion currents through the cell membrane are measured in whole-cell configuration while high-frequency fields are applied at frequencies between 100 MHz and 50 GHz and at power levels up to +25dBm.

Preliminary results obtained on rat basophil leukaemia (RBL) cells containing potassium channel $K_{ir}2.1$ suggest that the ion current is sensitive to the applied HF field in specific frequency ranges and depends on the presence of potassium ions and the applied membrane potential. Temperature measurements of the solution do not show any significant temperature rise.

AKB 200.62 Di 17:00 Poster TU C

Nanomechanical Cantilevers: Versatile, Label-free Biosensors — •Joachim Köser and Felice Mauro Battiston — Concentris GmbH, Davidsbodenstrasse 63, CH-4056 Basel, Switzerland

Nanomechanical cantilever sensors are a promising, label-free technology for the detection of biomolecules and the measurement of biomolecular interactions. They allow the real-time study of processes occurring at biological interfaces. Cantilevers are small silicon beams, which are fixed to a solid support at one end and move freely at the other end. They support two complementary sensing principles: While their resonance frequency depends on the mass load, changes in surface stress are reflected by the bending of the cantilevers. Surface stress can forces from conformational changes upon ligand binding or nucleic acid hybridization as well as protein denaturation or misfolding. Further biophysical properties, such as repulsion/attraction of molecules at the sensor surface, or binding of substances from the analyte can be monitored with the appropriate equipment.

We will present novel instrumental developments, which allow reliable, user-friendly measurements with cantilever sensors and open the door for a wider range of applications of this technology in basic research and biochemical analysis. Recent data obtained with our new cantilever sensor platform "Cantisens Research"will be presented.

AKB 200.63 Di 17:00 Poster TU C

Design of Novel GaAs/Peptide Hybrids Using Molecular Dipole Engineering — •Klaus Adlkofer[1], Tomoyuki Morita[2], Daniel Gassull[1], Shunsaku Kimura[2], and Motomu Tanaka[1] — [1]Lehrstuhl für Biophysik E22, Technische Universität München, James-Franck-Strasse, D-85748 Garching, Germany — [2]Department of Material Chemistry, Graduate School of Engineering, Kyoto University, Japan

Combination of low-dimensional semiconductors and bio/organic molecular constructs includes a large potential towards the design of new functional material. The primary aim of this study exists in design of novel hybrid materials by combination of GaAs semiconductors and functional peptide helices with a large macromolecular dipole. The quality of the optimized monolayers was examined by measuring the film thickness with ellipsometry. When LipoL16B was grafted on GaAs, the film showed a lot of defects, which can be attributed to the weaker reactivity of disulfide coupling group. However, grafting of the peptides with thiol coupling groups (AcSL8B and AcSL16B) resulted in film thickness which agrees very well with the length of the peptide helices. Topography of the engineered surface was studied by AFM, confirming that the peptide monolayer is as smooth as the native GaAs surfaces. Furthermore, the orientation of the helical peptides was evaluated by FTIR. The established functionalization protocols can be transferred onto near-surface semiconductor nano-structures with GaAs cap layers such as quantum dots (QDs) and two-dimensional electron gases (2DEGs).

AKB 200.64 Di 17:00 Poster TU C

Multi-Frequency EPR studies on Quinoprotein Ethanol Dehydrogenase:Characterization of the novel PQQ cofactor — •Robert Bittl[1], Christopher Kay[1], Bina Mennenga[2], and Helmut Görisch[2] — [1]Institut für Experimentalphysik, Fachbereich Physik, Freie Universität Berlin, Arnimallee 14, 14195 Berlin, Germany — [2]Fachgebiet Technische Biochemie, Institut für Biotechnologie, Technische Universität Berlin, 13353 Berlin, Germany

Pyrroloquinoline quinone (PQQ) is one of several quinone cofactors utilized in a class of dehydrogenases, known as quinoproteins. The quinoprotein methanol dehydrogenase (MDH) is among the best-characterised PQQ-dependent enzymes thus far. MDH has an $\alpha 2\beta 2$ tetrameric structure with each β-subunit folded around the surface of an α-subunit. The PQQ cofactor is bound to a Ca2+ ion and sandwiched between a tryptophane residue and an unusual eight-membered disulfide ring structure formed from adjacent cysteine residues.

Here we describe the first detailed characterization of the enzyme-bound PQQ in both wild type and mutant proteins lacking the disulfide ring, using multi-frequency/resonance EPR methods. Thus, we have determined the principal values of the rhombic g-tensor [1], and from pulsed ENDOR experiments at X-Band and W-Band, supported by DFT calculations, we have determined and assigned many of the proton hyperfine couplings. From HYSCORE experiments, the hyperfine couplings from the two nitrogens in the cofactor could be determined.

[1] C. W. M. Kay, B. Mennenga, H. Görisch and R. Bittl, FEBS Lett 564 (2004) 69-72.

AKB 200.65 Di 17:00 Poster TU C

A grating based detection platform for multi-color fluorescence correlation spectroscopy — •Markus Burkhardt, Katrin G. Heinze, 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 via Brownian diffusion. From these fluctuations, concentrations, diffusion and binding coefficients are easily obtained. Simultaneous monitoring of biomolecular species, labeled with spectrally distinct fluorophores, has proven to reveal inter- and intramolecular mechanisms both in vitro and in vivo.

We have developed a continuously tunable, filterless multi-color detection unit for FCS. Our tailored platform, using a grating instead of the classical dichroic mirror cascade, allows for accommodation of up to 15 detection channels covering the entire visible spectral range. As a proof of principle, we successfully demonstrate simultaneous FCS of four distinct fluorescent quantum dots being mixed in aqueous solution. Grating-based detection allows for spectral high-resolution FCS and is a feasible tool for quantitative investigation of complex biomolecular dynamics on a single molecule level.

AKB 200.66 Di 17:00 Poster TU C

Design of functional carbohydrate clusters for control of dynamic cell adhesion — •Jochen Oelke[1], Andreea Banu[1], Richard R. Schmidt[2], Achim Wixforth[3], and Motomu Tanaka[1] — [1]Dept. Phys. E22, TU München, D-85748 Garching, e-mail: mtanaka@ph.tum.de — [2]Dept. Chem., Univ. Konstanz, D-78457 Konstanz — [3]Dept. Phys., Univ. Augsburg, D-86135 Augsburg

The general goal of this work is the design of functional micro- and nano-clusters of ligands through controlled self-assembling processes at the interface, and their use as a new platform to control adhesion of bacteria under defined shear stresses.
As functional ligands, we synthesize a new class of fluorinated glycolipids bearing mannose or gal(1→4)-α-gal moieties. The fluorocarbon segment is used in order to induce de-mixinig due to the immicibility with the hydrocarbon segment, whereas the sugar part is responsible for the recognition with bacteria (for example mannose for enteroaggregative bacteria). As the first step, formation of these clusters was studied at the air/water interface, followed by deposition onto solid surfaces. The strength of bacterial adhesion, we determine the critical shear field required for the cell detachment (dissociation rate) by coupling the functionalized surface to two micro-fluidic systems: (a) conventional capillary flow chambers, and (b) "flat-fluidics" using surface acoustic waves (SAWs).

AKB 200.67 Di 17:00 Poster TU C

Characterization of High-K Coatings on Silicon Chips in Electrolyte for Capacitive Stimulation of Nerve Cells — •Frank Wallrapp und Peter Fromherz — Max Planck Institute of Biochemistry, Martinsried, Germany

Non-invasive capacitive stimulation of neurons is commonly achieved from silicon chips insulated by a thin layer of SiO_2. Higher capacitances of the chips however would facilitate stimulation. We therefore replaced SiO_2 by the high-k materials HfO_2 and TiO_2. Capacitance and leakage current were measured in an electrolyte-insulator-silicon (EIS) configuration. Considering leakage current and biocompatibility, HfO_2 and TiO_2 both proved to be as suitable for neuronal stimulation as SiO_2. Due to the higher capacitance, TiO_2 is superior in applications. For all materials, the dielectric constant, interfacial layer thickness and charge trapping properties were examined. The capacitance vs. voltages (CV) curves of SiO_2 and HfO_2 were explained by standard metal-insulator-semiconductor (MIS) theory. Those of TiO_2 exhibited some unique features which we were able to rationalize by treating the TiO_2 explicitly as a wide band-gap semiconductor. The new high-k coated chips have opened up the way to new applications, e.g. opening voltage-gated channels in HEK293 cells and stimulating rat brain slices.

AKB 200.68 Di 17:00 Poster TU C

Capacitive stimulation of recombinant voltage-gated Na^+ channels on a silicon chip — •Ingmar Schön and Peter Fromherz — Dept. Membrane and Neurophysics, MPI of Biochemistry, Martinsried, Germany

To understand and optimize capacitive excitation of neurons from silicon microstructures, it is necessary to study the response of defined voltage-gated ion channels to voltage transients applied to a chip.

The model system comprises HEK293 cells stably transfected with $rNa_V1.4$ sodium channels. The cells were cultured on a silicon chip insulated with a thin layer of hafnium oxide and coated with fibronectin. Voltage transients were applied to the chip. They were chosen such that capacitive coupling gave rise to a stationary negative voltage in the narrow extracellular space between chip and cell. The resulting changes of sodium current through the attached membrane were recorded at constant intracellular voltage using whole-cell patch clamp.

We succeeded in capacitive gating of $rNa_V1.4$ channels. The evoked sodium current was sensitive to pharmacological agents LqhαIT (slowed inactivation) and TTX (channel blocking). Numerical simulations were in good agreement with the experiments. However, sufficient coupling strength required an electrolyte with rigorous reduced conductance.

AKB 200.69 Di 17:00 Poster TU C

A versatile two-photon fluorescence laser scanning microscope for single molecule applications — •Zdeněk Petrášek and Petra Schwille — Biotechnologisches Zentrum der TU Dresden; Institut für Biophysik; Tatzberg 47 - 51; 01307 Dresden; Germany

An imaging system with optical beam scanning, two-photon excitation and fluorescence detection has been constructed. The setup consists of a Ti:Sapph laser and a commercial inverted microscope to which a home-built scanning and detection unit is attached. The fluorescence signal can be detected in two channels with the light separation based on wavelength or polarization. The time-resolved detection allows simultaneous measurement of fluorescence decay kinetics (sub-ns timescale) and FCS (sub-μs to $>s$ timescale) with the access to the complete photon sequence. The combination of imaging, pulsed excitation and fast detection allows fluorescence lifetime imaging (FLIM) to be performed.

The design focus has been on the freedom of control over the scan mirror movement. An arbitrary scanning pattern can be programmed, thus allowing scanning-FCS techniques to be employed. Scanning-FCS is especially suitable for investigation of slowly diffusing or stationary chromophores (FCS, cross-correlation). Since it is the laser beam and not the sample stage that is being moved, mechanical stability of the sample is maintained.

AKB 200.70 Di 17:00 Poster TU C

Acute Brain Slices on Silicon Chips: From Capacitive Stimulation to Recording with Field Effect Transistor Array — •Christian Stangl and Peter Fromherz — Max Planck Institute of Biochemistry, Dept. Membrane- and Neurophysics, Am Klopferspitz 18, D-82152 Martinsried

Silicon chips with arrays of capacitive stimulators and field effect transistors provide a novel approach in investigating the brain. Previous studies demonstrated the non-invasive stimulation and recording on cultured brain slices. Now for the first time acutely dissected brain slices have been used to record evoked neuronal field potentials.

Dead cell layers on the surface of acute slices, caused by the cutting procedure, complicate both capacitive stimulation and coupling with transistors. We treated this problem by simulating the distribution of evoked field potentials within the slice. The calculated profiles fit to data from conventional extracellular microelectrode measurements.

Capacitive stimulation and recording with field effect transistors are possible with the use of acute brain slices in spite of the dead cell layers. With this novel non-invasive approach we could probe neuronal projections in hippocampal slices as well as the neuronal plasticity of the hippocampus.

AKB 200.71 Di 17:00 Poster TU C

Single Molecule Anisotropy Measurements in Lipid Bilayers — •Jakob C. Schweizer, Zdeněk Petrášek, and Petra Schwille — Biotechnologisches Zentrum der TU Dresden; Institut für Biophysik; Tatzberg 47-51; 01307 Dresden; Germany

Fluorescence widefield microscopy was combined with polarization optics in order to study the fluorescence polarization of single biomolecules. The fluorescence emission was split by a wollaston prism, providing spatially displaced images for the parallel and perpendicular polarization components, respectively. From these images, fluorescence anisotropy values were calculated.

A common cause for fluorescence depolarization, among others, is rotational diffusion. Initial measurements were performed in which orientation and rotational diffusion of flourescent dyes in supported lipid bilayers in different membrane phases were investigated. In these systems, the orientation of transition dipoles of the used dyes was shown to be restricted to two dimensions. The Perrin equation for such a two-dimensional system was deduced. Fluorescence anisotropy values from ensemble measurements and single molecule-measurements were compared. The investigation of rotational diffusion on the single molecule level is expected to yield a deeper insight into the structure and dynamics of biological systems.