AKB 30 Poster Session I

Time: Monday 15:30–18:00 Room: P1

AKB 30.1 Mon 15:30 P1

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

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

AKB 30.2 Mon 15:30 P1

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

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

AKB 30.3 Mon 15:30 P1

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

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

AKB 30.4 Mon 15:30 P1

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

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

AKB 30.5 Mon 15:30 P1

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

Natural materials such as bone and teeth are nanocomposites of proteins and minerals, which exhibit many levels of complex structure from macroscopic to microscopic length scale. Nanotomography is a novel approach to image such complex structures. We focus on bovine bone, which is first embedded in a methacrylate resin and then microtomed. For Nanotomography the specimen is ablated layer-by-layer by wet chemical etching and imaged with scanning force microscopy after each etching step. From the resulting series of images the three-dimensional structure is reconstructed. Finding a proper etching method for both components, the mineral platelets and the collagen matrix is the first requirement for successful Nanotomography imaging. On our poster we will present our results on etching experiments with oxidizing solutions.

AKB 30.6 Mon 15:30 P1

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

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

AKB 30.7 Mon 15:30 P1

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

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

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

AKB 30.8 Mon 15:30 P1

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

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

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

AKB 30.9 Mon 15:30 P1

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

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

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

AKB 30.10 Mon 15:30 P1

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

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

AKB 30.11 Mon 15:30 P1

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

A fundamental property of mammalian cells is their motility, which correlates with the metastatic behavior of cancer cells. Thus detection of cell motiliy is important for understanding the metastatic process and developing clinical measurements for diagnosis and treatment of cancer. We report a new approach to expose cell motility using the quartz crystal microbalance (QCM). The QCM is known as an excellent and sensitive tool to follow adsorption in liquid environment like the attachment and spreading of mammalian cells. The technique is based on a quartz resonator sandwiched between two metal electrodes that are used to excite mechanical shear displacements of the piezoelectric quartz disks electrically. Measuring cell motility is done by evaluating the noise of the cell-covered quartz crystal in the resonant frequency response produced by active formation and breakage of noncovalent bonds as well as volume changes that might be produced by periodic contraction of actin stress fibers. We show how the QCM could be used to monitor shape fluctuations of living cells with a prospective application as an assay for biological activity of cells as found in metastasis of tumor cells. The QCM provides a quantitative means to monitor mechanical vibration of cells with amplitudes in the nanometer regime at high time resolution and might be used to distinguish between malign and benign cells.

AKB 30.12 Mon 15:30 P1

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

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

AKB 30.13 Mon 15:30 P1

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

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

AKB 30.14 Mon 15:30 P1

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

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

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

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

AKB 30.15 Mon 15:30 P1

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

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

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

AKB 30.16 Mon 15:30 P1

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

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

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

AKB 30.17 Mon 15:30 P1

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

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

AKB 30.18 Mon 15:30 P1

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

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

AKB 30.19 Mon 15:30 P1

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

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

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

AKB 30.20 Mon 15:30 P1

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

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

AKB 30.21 Mon 15:30 P1

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

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

AKB 30.22 Mon 15:30 P1

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

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

AKB 30.23 Mon 15:30 P1

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

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

AKB 30.24 Mon 15:30 P1

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

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

AKB 30.25 Mon 15:30 P1

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

Phase separation and lipid-protein interactions are important processes occurring in cell membranes. Useful model systems are single supported lipid bilayers, which retain to a high extent the properties of real cell membranes. We use a novel microfluidic setup that allows to employ complementary methods such as high resolution synchrotron reflectivity and fluorescence microscopy on the same sample [1]. These two dictinct but highly complementary methods allow for the first time to get a full micro- and nanoscopic picture of membrane properties such as structure, packing density, homogeneity and fluidity.
Current research topics in our group focus on the molecular arrangement of complex lipid mixtures in supported membranes and their transport properties. Recent results are presented.
[1] C. Reich et al., Rev. Sci. Instr. 76, 095103 (2005)

AKB 30.26 Mon 15:30 P1

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

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

AKB 30.27 Mon 15:30 P1

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

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

AKB 30.28 Mon 15:30 P1

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

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

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

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

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

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

AKB 30.31 Mon 15:30 P1

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

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

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

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

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

A previously proposed mathematical model [1] based on a simplified scheme of Th1–Th2 regulation mediated by the cytokine network which describes the population dynamics of allergen-specific naive T-cells, Th1

and Th2-cells, autocrine and cross-suppressive cytokines, and allergen is closer investigated. The model provides a theoretical explanation of the switch from a Th2 dominated response to a Th1 dominated response to allergen in allergic individuals as a result of a hyposensitization therapy.

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

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

AKB 30.34 Mon 15:30 P1

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

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

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

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

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

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

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

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

AKB 30.36 Mon 15:30 P1

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

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

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

AKB 30.37 Mon 15:30 P1

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

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

AKB 30.38 Mon 15:30 P1

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

Detailed information about the interactions between virus particles and living cells can be obtained by visualising and tracking individual virus particles in real time. For the investigation of HIV entry, we have developed a novel, dual-colour HIV derivative that allows us to distinguish between complete viruses and those that have undergone fusion. We are observing the infection pathway of these particles using a dual-colour microscope. The microscope is based on wide-field microscopy with laser excitation and ultrasensitive fluorescence detection. The laser beams are guided through a vibrating, multimode optical fiber to remove interference fringes in the image plane, creating a very homogenous excitation profile. Improved depth resolution is achieved using a Köhler illumination scheme. The excitation sources are interleaved such that green and red fluorophores are excited on alternate images, and the emitted light is further spectrally separated onto two regions of the camera. This set up removes cross-talk between the two fluorescent labels, and allows us to distinguish broad-spectrum cellular autofluorescence from the viral signals and to correct for it.

AKB 30.39 Mon 15:30 P1

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

Due to its high sensitivity fluorescence correlation spectroscopy is suited to investigate processes in live cells where the endogenous concentration of the participating molecules are low, e.g., in many signaling cascades. Here, FCS is used to unravel dynamics of the membrane re-

ceptors TNFR1 and TNFR2 which play important roles in apoptotic signaling pathways. Although structurally similar in their transmembrane domains both receptors behave markedly different in the cell membrane. Upon binding of the ligand TNF the diffusion constant of TNFR2 is reduced from 3.3×10^{-9} to 0.8×10^{-9} cm^2/s. Experiments on receptors without its binding domain in the cytoplasm show that interaction of the receptor signaling complex with immobile parts of the cellular interior is not responsible for the reduction in diffusion rate. Rather it appears that the TNFR2 receptor attaches to slowly diffusing membrane microdomains after stimulation. Using a new set-up for cross-talk free FCCS with the fluorophore pair CFP and YFP it was shown that there is no pre-association behavior of TNFR2 before stimulation.

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

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