Section Biological Physics
Fachverband Biologische Physik (BP)

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Overview of Invited Talks and Sessions

(lecture rooms H43 and H44; Poster B and D)

Invited Talks

BP 1.1	Mon	9:30–10:00	H43	**Physical Aspects of Evolutionary Transitions to Multicellularity** — •Raymond Goldstein
BP 1.2	Mon	10:00–10:30	H43	**Surfing genes: On the fate of neutral mutations in spreading populations** — •Oskar Hallatschek, David Nelson
BP 3.1	Mon	14:00–14:30	H43	**On the Timescales of Membrane Fusion** — •Rumiana Dimova
BP 5.1	Mon	10:30–11:00	H44	**Force induced strengthening of binding domains in specifically adhered vesicles** — •Ana-Suncana Smith
BP 9.1	Tue	9:30–10:00	H43	**Single molecule recognition in regulatory systems** — •Robert Ros
BP 9.2	Tue	10:00–10:30	H43	**Transcription by RNA Polymerase II** — •Stephan Grill, Eric Galburt, Martin Depken, Carlos Bustamante
BP 10.1	Tue	14:00–14:30	H43	**Supercoils and their Removal** — •Nynke Dekker
BP 12.1	Tue	10:30–11:00	H44	**The first micro seconds in the life of a nerve impulse** — •Fred Wolf
BP 22.1	Thu	9:30–10:00	H43	**DNA-based molecular machines and synthetic biology** — •Friedrich Simmel
BP 22.7	Thu	11:30–12:00	H43	**From biological towards artificial Molecular Machines** — •Thorsten Hugel
BP 23.1	Thu	14:00–14:30	H43	**The Physics of Neuronal Growth** — •Timo Betz, Daniel Koch, Josef Käs
BP 25.1	Thu	14:30–15:00	H44	**Mechanical amplification by sensory hair cells from the vertebrate ear** — •Pascal Martin
BP 27.1	Fri	10:30–11:00	H43	**From target search to travel bugs: scale free motion in biology** — •Dirk Brockmann

Invited talks of the joint symposium SYBM

See SYBM for the full program of the Symposium.

SYBM 1.1	Thu	9:30–10:00	H1	**Using Ice to Mimic Nacre: From Structural Materials to Artificial Bone** — •A. P. Tomsia, S. Deville, E. Saiz
SYBM 1.2	Thu	10:00–10:30	H1	**On the structure of biogenic $CaCO_3$** — •B. Pokroy
SYBM 1.3	Thu	10:30–11:00	H1	**Bio-Inspired Hybrid Materials from Block Copolymer Assemblies and Nanoparticle Co-assemblies** — •U. Wiesner
SYBM 1.4	Thu	11:15–11:45	H1	**Bio-Inspired Organic-inorganic Hybrid Materials** — •U. Steiner
SYBM 1.5	Thu	11:45–12:15	H1	**Structural, Nanomechanical, and Nanotribological Characterization of Human Hair Using Atomic Force Microscopy and Nanoindentation** — •Bharat Bhushan

Invited talks of the joint symposium SYNF

See SYNF for the full program of the Symposium.

SYNF 1.1	Wed	14:45–15:15	H1	**Depolymerization of microtubules by kinesins** — •Jonathon Howard
SYNF 1.2	Wed	15:15–15:45	H1	**Hydra Molecular Network Reaches Criticality at the Symmetry-Breaking Axis-Defining Moment** — Jordi Soriano, Cyril Colombo, •Albrecht Ott
SYNF 1.3	Wed	15:45–16:15	H1	**Morphogen Transport in Epithelia** — •Tobias Bollenbach
SYNF 1.4	Wed	16:15–16:45	H1	**Flocks, Herds and Schools - Physical Models of Animal Motion** — •Udo Erdmann
SYNF 1.5	Wed	16:45–17:15	H1	**Nonlinear transport processes in large-scale ecological networks** — •Bernd Blasius

Invited talks of the joint symposium SYPE

See SYPE for the full program of the Symposium.

SYPE 2.1	Thu	14:00–14:30	H37	**Coulomb and Flory: Fathers of SONS. Polyelectrolytes in Self Organized Nano Systems** — •Martien Cohen Stuart
SYPE 2.7	Thu	16:00–16:30	H37	**Bundling Phenomena in Semiflexible Polyelectrolytes** — •Christian Holm, Mehmet Sayar, Berk Hess
SYPE 3.1	Fri	10:30–11:00	H1	**Behaviour of polyelectrolyte solutions under confinement** — •Dominique Langevin, César Marquez, Heinig Peter, Dan Qu
SYPE 3.4	Fri	11:30–12:00	H1	**Polymers at Surfaces: Sticking and Gliding** — •Roland Netz

Sessions

BP 1.1–1.7	Mon	9:30–12:00	H43	**Evolutionary and Population Dynamics**
BP 2.1–2.4	Mon	12:15–13:15	H43	**Protein Function**
BP 3.1–3.12	Mon	14:00–17:15	H43	**Membranes and Interfaces**
BP 4.1–4.8	Mon	17:30–19:30	H43	**Protein Structure and Folding**
BP 5.1–5.8	Mon	10:30–13:00	H44	**Cell Adhesion**
BP 6.1–6.6	Mon	14:30–16:00	H44	**Biopolymer Conformation and Dynamics**
BP 7.1–7.7	Mon	16:15–18:00	H44	**Fibers and Bundles**
BP 8.1–8.6	Mon	18:00–19:30	H44	**Charge Transfer**
BP 9.1–9.11	Tue	9:30–13:00	H43	**Regulation and Signaling**
BP 10.1–10.6	Tue	14:00–15:45	H43	**DNA: supercoils, knots and melting**
BP 11.1–11.5	Tue	16:00–17:15	H43	**Micro- and Nanofluidics**
BP 12.1–12.6	Tue	10:30–12:15	H44	**Neuroscience**
BP 13.1–13.3	Tue	12:30–13:15	H44	**Photobiophysics**
BP 14.1–14.3	Tue	14:30–15:15	H44	**Chemotaxis**
BP 15.1–15.8	Tue	15:15–17:15	H44	**Biopolymer Solutions and Networks**
BP 16.1–16.58	Tue	17:00–19:30	Poster D	**Poster Session I**
BP 17	Wed	14:30–17:15	H1	**Symposium Nonlinear and Anomalous Transport in Complex Systems (SYNF)**
BP 18.1–18.5	Wed	14:00–15:15	H43	**Functionalized Nanoparticles**
BP 19.1–19.7	Wed	15:30–17:15	H43	**Biosensors and Biofunctionalized Systems**
BP 20.1–20.3	Wed	17:30–18:15	H43	**Novel Methods**
BP 21.1–21.4	Wed	18:15–19:15	H43	**High-Throughput Data and their Analysis**
BP 22.1–22.12	Thu	9:30–13:15	H43	**Molecular Machines**
BP 23.1–23.11	Thu	14:00–17:00	H43	**Cell Motility and Migration (in vitro and in vivo)**
BP 24.1–24.10	Thu	10:00–12:45	H44	**Cell Mechanics (in vivo)**
BP 25.1–25.9	Thu	14:30–17:00	H44	**Oscillatory Systems**
BP 26.1–26.49	Thu	17:00–19:30	Poster B	**Poster Session II**
BP 27.1–27.8	Fri	10:30–12:45	H43	**Nonequilibrium Processes and Self-Organisation**
BP 28.1–28.6	Fri	11:00–12:30	H44	**Biomedical Applications**

Annual General Meeting of the Section Biological Physics

Dienstag 19:30–20:30 H43

- Bericht

- Wahl
- Topics und Symposia 2008

BP 1: Evolutionary and Population Dynamics

Time: Monday 9:30–12:00 Location: H43

Invited Talk BP 1.1 Mon 9:30 H43

Physical Aspects of Evolutionary Transitions to Multicellularity — •Raymond Goldstein — Department of Applied Mathematics and Theoretical Physics, University of Cambridge, UK

An important issue in evolutionary biology is the emergence of multicellular organisms from unicellular individuals. The accompanying differentiation from motile totipotent unicellular organisms to multicellular ones having cells specialized into reproductive (germ) and vegetative (soma) functions, such as motility, implies both costs and benefits, the analysis of which involves the physics of buoyancy, diffusion, and mixing. In this talk, I discuss recent results on this transition in a model lineage: the volvocine green algae. Particle Imaging Velocimetry of fluid flows generated by these organisms show that they exist in the regime of very large Peclet numbers, where the scaling of nutrient uptake rates with organism size is highly nontrivial. In concert with metabolic studies of deflagellated colonies, investigations of phenotypic plasticity under nutrient-deprived conditions, and theoretical studies of transport in the high-Peclet number regime, we find that flagella-generated fluid flows enhance the nutrient uptake rate per cell, and thereby provide a driving force for evolutionary transitions to multicellularity. Thus, there is a link between motility, mixing, and multicellularity.

Invited Talk BP 1.2 Mon 10:00 H43

Surfing genes: On the fate of neutral mutations in spreading populations — •Oskar Hallatschek and David Nelson — Department of Physics, Harvard University, Cambridge, Massachusetts 02138, USA

Population expansions in space are common events in the demographic history of many species and have a strong impact on their genealogy. As compared to individuals in the wake, the pioneers in the wave front are usually much more successful in passing their genes on to future generations, not only because their reproduction is unhampered by limited resources but also because their offspring start out from a spatial position where they have good chances to keep up with the wave front (often by means of mere diffusion). Those pioneer genes have the chance to "surf" on the wave and the likelihood to do so will be the focus of the presentation. By means of simple experimental systems (E. Coli and Yeast), simulations and analytical considerations, we explore how the footprints of the successfully surfing genes may be used to infer past population expansions.

15 min. break.

BP 1.3 Mon 10:45 H43

A stochastic approach to group selection — •Arne Traulsen — Program for Evolutionary Dynamics, Harvard University, USA

A minimalist stochastic model of multi-level or group selection is discussed. A population is sub-divided into groups. Individuals reproduce; offspring are added to the same group. If a group reaches a certain size, it can split into two. Faster reproducing individuals lead to larger groups which split more often. It can be shown that this population structure acts as a suppressor of selection [1]. In this model, higher level selection emerges as a by-product of individual reproduction and population structure, allowing the evolution of cooperation. In a situation in which individuals interact with other members of the group in an evolutionary game which determines their fitness, one can derive a condition for the evolution of cooperation by group selection: if b/c> 1+ n/m then group selection favors cooperation [2]. The parameters B and c denote the benefit and cost of the altruistic act, while n and m denote the maximum group size and the number of groups. The model can be extended to more than two levels of selection and to include migration.

[1] A. Traulsen, A.M. Sengupta, and M.A. Nowak, J.Theor.Biol. 235, 393 (2005).

[2] A. Traulsen and M.A. Nowak, PNAS 103, 10952 (2006).

BP 1.4 Mon 11:00 H43

Stationary population distribution of quasispecies in fitness landscapes with multiple peaks — •Andrea Wolff and Joachim Krug — Universität zu Köln, Institut für theoretische Physik, Köln, Deutschland

We investigate the long time behaviour of the quasispecies model, as introduced by M. Eigen in 1971, in permutation invariant fitness landscapes. Examples include the multiplicative single peak Fujiyama landscape and a landscape with two peaks of different heights and widths. In the latter case, the competition between the two peaks leads to a first order 'selection transition' at which the population shifts discontinuously from one peak to the other. In contrast to the well-known delocalization transition occuring at the error threshold, the mutation rate at the selection transition does not scale with the sequence length N as $\mu \propto 1/N$. As a consequence, recently developed functional integral methods for estimating the largest eigenvalue of the evolution matrix in the limit $N \to \infty$ cannot be applied. Here we use direct diagonalization techniques to examine the nature of the selection transition and to find the correct scaling behaviour of the mutation rate with the sequence length.

BP 1.5 Mon 11:15 H43

Coexistence versus extinction in cyclic population models — •Tobias Reichenbach, Mauro Mobilia, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München, Theresienstrasse 37, D-80333 München

The maintenance of biodiversity under species coevolution is a central issue in modern theoretical biology. Cyclic dominance of species combined with local interactions of spatially distributed individuals has been identified experimentally as a potential mechanism, see e.g. B. Kerr, M. A. Riley, M. W. Feldman and B. J. M. Bohannan [Nature **418**, 171 (2002)]. We address these questions by studying theoretically a "rock-paper-scissors" model of three species that cyclically dominate each other. In the absence of spatial structure, fluctuations arising in finite populations are shown to have a drastic influence on the fate of the species and cause extinction. Arranging the individuals on a two-dimensional lattice and allowing only local interactions dramatically changes the situation. Spatial patterns form and ensure coexistence of all three species.

BP 1.6 Mon 11:30 H43

The Stability and Structure of Model Food Webs with Adaptive Behavior — •Satoshi Uchida and Barbara Drossel — Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstraße 6, D-64289, Darmstadt, Germany

We present results for the stability and structure of model food webs described by population dynamics and adaptive behavioural dynamics (adaptive foraging and predator avoidance). In particular the influence of the initial network topology (randomly connected or niche model), and the type of constraints on the adaptive behavior (linear or nonlinear) are investigated. We evaluated two kinds of stability, namely the proportion of species surviving after running population dynamics, and the species deletion stability, and we measured two types of network parameters - link density and trophic level structure. We show that the initial web structure does not have a large effect on the stability of food webs, but foraging behavior has a large stabilizing effect. It leads to a positive complexity-stability relationship whenever higher "complexity"implies more potential prey per species. The observed link density after population dynamics depends strongly on the presence or absence of adaptive foraging, and on the type of constraints used. We also show that the foraging behavior preserves the initial trophic level structure for random and niche webs, while the population dynamics destroys the initial trophic structure for random webs.

BP 1.7 Mon 11:45 H43

Influence of carrying capacity on stochastic predator-prey models — •Mauro Mobilia[1], Mark Washenberger[2], and Uwe Taeuber[2] — [1]Arnold Sommerfeld Center and Center for NanoScience, Ludwig-Maximilians-Universitaet Muenchen — [2]Virginia Polytechnic Institute and State University

We study a class of stochastic lattice predator-prey systems in the presence and the absence of restrictions on the number of particles per site. In the former case, the systems are characterized by an extinction threshold. On the other hand, when there is no site restrictions, the species always coexist in two dimensions. In both cases, by pointing

out similarities and differences, we carefully discuss the properties of the coexistence phases and of the correlated spatio-temporal structures which form in the course of the dynamics.

Refs: cond-mat/0606809 (accepted in J.Phys.:Condens. Matt.); Phys. Rev. E 73, 040903(R) (2006); q-bio.PE/0512039 (accepted in J.Stat.Phys.); q-bio.PE/0609039.

BP 2: Protein Function

Time: Monday 12:15–13:15 Location: H43

BP 2.1 Mon 12:15 H43

Reduced Molecular Models in (Bio)molecular Design — •Kay Hamacher — Max-Planck-Institut fuer Physik komplexer Systeme, Dresden

Apoptosis regulating proteins play an essential role in the development of organisms, immune responses and other cellular mechanisms. The BCL-2 protein family contains the BH3 motif, which was found to be of crucial importance in e.g. cancer. The isolated, unstructured BH3-peptide can be modified by a hydrocarbon linkage to regain function as was recently shown in experiment [1] and act therefore as a pharmacological active molecule. We show how an effective, coarse-grained model can be parametrized (using molecular dynamics simulations as well as density-functional theory computations) to investigate the stability effects of such covalent cross-linking. We explain why the peptide dynamics is crucial for the proper function of the linker and the resulting folding properties of the peptide. Long range stabilization effects can be shown by time series analysis techniques as well as by information theory motivated measures. The resulting model [2] is suitable for rational design of generic cross-linking systems *in silicio*.

[1] L.D.Walensky et al. Science **305**, 1466 (2004)

[2] K.Hamacher, A.Hübsch, J.A.McCammon. J. Chem. Phys. **124**, 164907 (2006)

BP 2.2 Mon 12:30 H43

Myoglobin solvated in glycerol-water mixtures: The interplay of solvent and protein dynamics. — •Florian Kargl[1], Helen Jansson[1], Felix Fernandez-Alonso[2], and Jan Swenson[1] — [1]Department of Applied Physics, Chalmers University of Technology, SE-41296 Göteborg, Schweden — [2]Rutherford Appleton Laboratory, Chilton, Didcot OX11 0QX, *United Kingdom

Water as the most abundant substance in all living organisms is essential for the functioning of proteins and a number of other biomolecules [1]. Despite numerous investigations on the relation of the water dynamics and the protein motion [2] the coupling of the solvent and the protein dynamics is still debated [3]. Here we report on quasielastic neutron scattering (QENS) measurements on myoglobin solvated in different mixtures of water and glycerol [4]. Varying the solvent composition and using selective deuteration allows us to emphasize different dynamical processes. We discuss mean square displacements revealing the onset of solvent and protein motions on the experimental time-scale and the nature of the dynamical processes derived from the measured dynamic structure factors.

[1] H. D. Middendorf, Physica B 226, 113 (1996).

[2] D. Vitkup et al., Nature struct. biol. 7, 34 (2000); M. Tarek et al., Phys. Rev. Lett. 88, 138101 (2002); P. W. Fenimore et al., P. Natl. Acad. Sci. 99, 16047 (2002).

[3] P. W. Fenimore et al., P. Natl. Acad. Sci. 101, 14408 (2004).

[4] F. Kargl, H. Jansson, F. Fernandez-Alonso, and J. Swenson (submitted)

BP 2.3 Mon 12:45 H43

Beitrag abgesagt — •XXX XXX —

BP 2.4 Mon 13:00 H43

Molecular Dynamics and Secondary Structure Behaviour of the C-Terminus of Vinculin that includes a Membrane Binding Anchor — Gerold Diez[1], •James Smith[1], Martin Stiebritz[2], and Wolfgang Goldmann[1] — [1]LPMT — [2]LS Biotechnik,FAU Erlangen

Vinculin (1066 residues) is a focal adhesion (FA) protein and has three lipid-binding sites, residues 935-978, 1020-1040 and 1052-1066. The first two regions are amphiphatic alpha-helices identified from sequence prediction and later revealed in crystal structures. The third putative lipid-binding region is unstructured and only experimental data has demonstrated that these C-terminal residues act as an essential anchor for membrane association. Our work investigates the molecular dynamical behaviour of the last twenty-one amino acids (residues 1045-1066), represented as a polypeptide in explicit solvent. Different formal charges for one acidic and five basic residues are altered, representing different pH and salt conditions. Our findings show that the polypeptide undergoes different anti-parallel ß-sheet formation. Two mutually exclusive beta-sheets are formed between residues 1047-1058 and between residues 1057-1064. It is likely that in vivo this bi-stable secondary structure behaviour would be influenced by local changes in ionic conditions. The results suggest a mechanism for favourable lipid-binding activation of the vinculin in presence of local ionic or pH gradients. We will investigate which of these two beta-sheets form favourable hydrogen bonds with the polar heads of phospholipids membrane models.

BP 3: Membranes and Interfaces

Time: Monday 14:00–17:15 Location: H43

Invited Talk BP 3.1 Mon 14:00 H43

On the Timescales of Membrane Fusion — •Rumiana Dimova — Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam, Germany

Membrane fusion is a vital process as it is involved in many cellular functions and stages of cell life like import of foodstuffs and export of waste, signaling between nerve cells, fertilization, and virus infection. In both the life sciences and bioengineering, controlled membrane fusion has many possible applications, such as drug delivery, gene transfer, chemical microreactors, or synthesis of nanomaterials.

Fusion dynamics is intriguing but microscopy observations with time resolution higher than several milliseconds have not been achieved until now. Using micromanipulation of giant unilamellar vesicles as model membranes one can directly observe membrane fusion. We induce the fusion of giant lipid vesicles in a controlled manner and monitor the fusion dynamics with a temporal resolution of 50 microseconds; see Haluska et al. Proc. Natl. Acad. Sci. USA. 103, 15841-15846 (2006). Two different approaches of inducing directed fusion are used: i) employing synthetic fusogenic molecules incorporated in the membranes, and ii) electrofusion. For both protocols, the opening of the fusion necks is very fast, with an average expansion velocity of centimeters per second. This velocity indicates that the initial formation of a single fusion neck can be completed in a few hundred nanoseconds.

BP 3.2 Mon 14:30 H43

Energy barriers for membrane fusion — •Andrea Grafmueller and Reinhard Lipowsky — Max-Planck-Institut of Colloids and Interfaces, Potsdam, Germany

The fusion of bilayer membranes and vesicles has been studied using Dissipative Particle Dynamics (DPD) simulations. A large number of fusion attempts between a vesicle and a planar membrane segment is monitored varying the area per lipid molecule which determines the initial membrane tension. Fusion events are observed with a high success rates at high tensions. For these successful events, the fusion time, i.e., the time from first contact between the bilayers until the opening of the pore, shows a strong, exponential dependence on the membrane

tension. The observed fusion process starts with the adhesion of the vesicle to the tense planar segment. Inter-bilayer flipflops disturb the bilayer order near the rim of the adhered area. Finally, the molecules in this disordered region reorganize into a small segment of a single (hemifused) bilayer, which ruptures at the edge. A detailed analysis of the observed fusion events reveals that these events are governed by at least two successive energy barriers.

BP 3.3 Mon 14:45 H43

What can be learned from a coarse-grained description of membrane fusion? — •Marcus Muller — Institut fuer Theoretische Physik, Georg-August Universitaet, Goettingen

Membrane fusion is a fundamental biological process of importance in fertilization, synaptic release, intracellular traffic, and viral infection. Coarse-grained models can contribute to our understanding of these collective phenomena in membranes [1] that evolve on a few nanometers and milliseconds.

We have carried out simulations of the fusion of tense apposed bilayers formed by amphiphilic molecules. The fusion pathway differs from the common stalk mechanism. Stalks do form between the apposed bilayers, but rather than expand radially to form an axial-symmetric hemifusion diaphragm and they promote the nucleation of small holes in their vicinity. Then, the stalk encircles a hole in one bilayer creating a diaphragm which ruptures to complete the fusion pore. The pathway give rise to mixing between both leaves of the bilayer and allow for transient leakage.

Self-consistent field calculations have be used to explored the role of lipid architecture and tension, and to calculate free energy barriers along the fusion path. We find that (i) successful fusion is found to be severely limited by the architecture of the lipids and that (ii) any mechanism which affects even modestly the line tension of a hole in a membrane affects greatly the ability of that membrane to undergo fusion.

[1] M. Müller, K. Katsov, and M. Schick, Phys. Rep. 434, 113 (2006)

BP 3.4 Mon 15:00 H43

Lipid Nanotubes for Probing Cell Membrane Reservoir — •Darius V. Köster[1], Pierre Sens[2], Christophe Lamaze[1], and Pierre Nassoy[1] — [1]Institut Curie, Paris, France — [2]ESPCI, Paris, France

Cells are exposed to mechanical stress due to shear flow (e.g. in veins and arteries) or stretching and relaxation (e.g. in muscle tissue). In this study, we study the mechanisms, which provide membrane integrity during these processes, since the membrane as a pure lipid bilayer would be fairly inextensible, and any stretching of it would lead to rupture. One important parameter to describe the cell membrane is its membrane tension, and it is reported that cells have membrane reservoirs, and regulate membrane tension. Pulling small tubes out of the cell membrane in using an optical trap allows us to probe these reservoirs and to measure the membrane tension. In combination with biological tools of cell modification (transfection and drug treatment) and fluorescence imaging we aim at identifying the compartments involved in membrane tension regulation. More specifically, in this work, we will focus on the role of caveolae, which are small membrane invaginations, in membrane tension buffering. To get a clear picture of their mechanical function, we will show that the interaction between membrane and cytoskeleton has to be investigated in details. Finally, we will propose that caveolae can indeed act as available membrane reservoirs for a cell membrane to accommodate sudden extend stress.

BP 3.5 Mon 15:15 H43

A novel method for measuring the bending rigidity of model lipid membranes by simulating tethers — •Vagelis Harmandaris and Markus Deserno — Max-Planck-Institute for Polymer Research*Max-Planck-Institute for Polymer Research, Theory Group, Mainz, Germany

The most common approach for measuring bending rigidities in simulations is from the spectrum of thermal shape fluctuations, which is the analogous of the experimental *flicker spectroscopy* technique. An alternative experimental method is to measure the tensile force needed to pull nanoscale bilayer tubes (tethers) from vesicles, since this force is proportional to the membrane's bending modulus and inversely proportional to the tube radius. Here, we show that this relation can be applied with even greater ease in computer simulations. Using a coarse-grained bilayer model developed recently [1], we efficiently obtain bending rigidities that compare very well with complementary measurements based on an analysis of thermal undulation modes. We furthermore illustrate that no deviations from simple quadratic continuum theory occur up to a radius of curvature comparable to the bilayer thickness [2].

References: 1. I.R. Cooke, K. Kremer and M. Deserno, Phys. Rev. E 72, 011506 (2005). 2. V. Harmandaris and M. Deserno, J. Chem. Phys. 125, 204905 (2006).

BP 3.6 Mon 15:30 H43

Shape and fluctuations of biphasic membrane vesicles — •Stefan Semrau[1], Timon Idema[2], Cornelis Storm[2], and Thomas Schmidt[1] — [1]Physics of life processes, Leiden institute of physics, Leiden university, The Netherlands — [2]Theoretical biophysics, Lorentz institute, Leiden university, The Netherlands

Heterogeneities in the cell membrane due to coexisting lipid phases have been conjectured to play a major functional role in cell signaling and traffic. Purely physical properties of such multiphase systems, such as the line tension and the bending moduli, are crucially involved in endocytocis and lipid trafficking, and determine the kinetics and asymptotics of phase separation. We have developed an analytical description of the vesicle shape of weakly budded biphasic vesicles and shown it to be in excellent agreement with numerical calculations and experiments. Our description allows for a reproducible and reliable systematic determination of the physical parameters of the membrane in the biologically relevant limit of weakly budded shapes. The parameters thus obtained allow us to determine an upper bound for the size of nanodomains in the plasma membrane of living cells.

BP 3.7 Mon 15:45 H43

Structure and dynamics of crystalline protein layers peripherally bound to supported lipid bilayers — •Christian Reich, Margaret Horton, Joachim Rädler, and Bert Nickel — Department für Physik, Ludwig-Maximilians-Universität, D-80539 München

We model peripheral membrane proteins at the surface of cell membranes using streptavidin and avidin bound to biotinylated lipids in a supported lipid bilayer (SLB) at the solid-liquid interface. Using X-ray reflectivity and simultaneous fluorescence microscopy, we characterize the structure and fluidity of a protein layer containing two-dimensional streptavidin crystals bound to a SLB. A single lipid bilayer provides a biologically-relevant environment for in-situ investigation of membrane-associated proteins interacting with lipids. Using continuous bleaching, we measure a 10-15% decrease in the fluidity of the SLB after protein layer formation. We propose that this reduction in lipid mobility is due to a small fraction ca. 0.04 of immobilized lipids bound to the protein layer that create obstacles to membrane diffusion. Fits to our X-ray reflectivity data show a ca. 40 Å thick layer of protein and we resolve the ca. 8 Å layer separating the protein layer from the bilayer. We suggest that the separation provided by this water layer allows the underlying lipid bilayer to retain its fluidity and stability. Finally, we show how complementary information can be obtained in neutron experiments at REFSANS (FRM2).

BP 3.8 Mon 16:00 H43

Curvature-mediated interactions between membrane proteins lead to aggregation and vesiculation — Benedict Reynolds, Gregoria Illya, Vagelis Harmandaris, Martin Müller, Kurt Kremer, and •Markus Deserno — MPI für Polymerforschung, Mainz, Germany

Cellular tasks such as endocytosis, vesiculation, and protein sorting, or the biogenesis of organelles such as the endoplasmic reticulum or the Golgi apparatus rely on significant protein-assisted membrane remodeling. Special curvature-sensitive proteins may both *experience* geometry-driven forces and, conversely, *induce* major changes in membrane shape and topology. But due to the lipid bilayer's bending stiffness, the latter requires the cooperative action of many individual proteins. The necessary protein aggregation is thought to be driven by specific interactions, but more generic mechanisms such as membrane mediated interactions are recently being discussed by biologists. I will show that the underlying physics of curvature forces is not as straightforward as it is sometimes assumed. Using large-scale coarse-grained membrane simulations I then demonstrate that even in the absence of direct protein interactions curvature-mediated forces alone provide a robust mechanism for aggregation and can subsequently trigger vesiculation.

BP 3.9 Mon 16:15 H43

Interplay of lateral diffusion and membrane fluctuations — •Ellen Reister-Gottfried and Udo Seifert — II. Institut für The-

oretische Physik, Universität Stuttgart, 70550 Stuttgart, Germany

Using a simulation scheme that numerically integrates both the equation of motion of a membrane and the Langevin equation of a particle diffusing freely along the curved surface of the membrane we study the interplay of membrane fluctuations and lateral diffusion. The energy of the membrane is given by the Helfrich Hamiltonian and its shape in the Monge gauge. In the regime where the relaxation time of membrane undulations with wavelength ξ is much smaller than the average time it takes a particle to cover the distance ξ, the particle experiences only averaged membrane quantities, such that a preaveraging approximation can be employed. We compare the diffusion coefficient projected on a flat reference plane –this is the typically measured quantity– obtained in previous analytical calculations that make use of this approximation with simulation results. Although the simulation scheme overcomes preaveraging, there is a surprisingly good agreement of analytical and simulation results even for parameter sets that do not meet the conditions for the preaveraging approximation. A detailed analysis of appropriate correlation functions using the simulation scheme explains the large validity range of the approximation.

BP 3.10 Mon 16:30 H43

Diffusion of nano-particles in model membranes — •Florian Rückerl, Carsten Selle, and Josef Käs — Universität Leipzig, Institut für Experimentelle Physik I, Abt. PWM

Langmuir monolayers are used as a simple membrane model in which partially charged nano-particles diffuse as model proteins. This system provides good control over obstacle sizes. The condensed domains within liquid phases that are found in the coexistence region exhibit a net dipole moment. The radial dependence of this electric dipolar field changes with the size of the domains from $E(|\mathbf{r}|) \propto 1/|\mathbf{r}|^3$ for a single dipole to $E(|\mathbf{r}|) \propto 1/|\mathbf{r}|$ for large domains ($R > 10\mu m$). The influence of this change on the particle diffusion was investigated by Monte Carlo simulations. The analysis shows that the particles are stronger confined at the domain border of smaller domains and that a change from two to one dimensional diffusion occurs.

We further investigate a more complex system, nano-particles diffusing on the surface of giant unilamellar vesicles composed of either a single lipid or a mixture of lipids: DOPC, DPPC and cholesterol. The latter systems exhibit $L_d - L_o$ coexisting phases which were shown to form curvature gradients in their bilayer surfaces. Therefore, the influence of the local membrane curvature on the diffusive behavior of the nano-particles can be investigated. A variety of lipid compositions and particles, $R = 34nm - 1.6\mu m$ with varying surface modifications, are used in order to to elucidate the interactions between nano-particles and lipids in bilayer membranes.

BP 3.11 Mon 16:45 H43

Dynamics of IP_3 receptor clustering on the endoplasmic reticulum — •Ronny Straube[1,2], Martin Falcke[1], and Michael Ward[3] — [1]Hahn-Meitner-Institut, Glienicker Str. 100, 14109 Berlin, Germany — [2]Max-Planck-Institut für Dynamik komplexer technischer Systeme, Sandtorstr. 1, 39106 Magdeburg, Germany — [3]Department of Mathematics, University of British Columbia, Vancouver, Canada

Motivated by the observation that IP_3 receptor channels (IP_3R) form clusters on the endoplasmic reticulum (ER) during ATP-induced calcium release [1], we calculate the reation rate of small diffusing molecules on a cylindrical membrane by taking into account the cylindrical topology of the tubular ER [2]. The reaction rate is obtained using the method of matched asymptotic expansions. For realistic parameter sets, our calculation predicts clustering rates in the experimentally observed range. Furthermore, it reveals how the cluster rate depends on the relevant system parameters such as the molecule size and the aspect ratio of the membrane. Based on our calculations of the reaction rate, we also study the dynamics of IP_3R clustering as it is triggered by an external calcium signal. A mean-field approach is used to determine the temporal evolution of the cluster-size distribution.

[1] Y. Tateishi et. al., Cluster formation of inositol 1,4,5-triphosphate receptor requires its transition to open state, J. Biol. Chem. 280(8), 6816-6822 (2005).

[2] R. S., Michael J. Ward and Martin Falcke, Reaction rate of small diffusing molecules on a cylindrical membrane, submitted to J. Stat. Phys.

BP 3.12 Mon 17:00 H43

Self-organization of exit sites in the endoplasmic reticulum in mammalian cells — •Matthias Weiss and Stephan Heinzer — Cellular Biophysics Group (B085), German Cancer Research Center, Im Neuenheimer Feld 580, 69120 Heidelberg

Exit sites (ES) are specialized membrane domains of the endoplasmic reticulum (ER) at which cargo proteins of the secretory pathway are packaged into small, COPII-coated vesicles. While the essential COPII proteins that are responsible for the emergence of the vesicles have been identified and characterized during the last decade, their binding kinetics and diffusion properties have remained elusive. Using high-resolution fluorescence microscopy techniques (photobleaching and correlation spectroscopy), we have dtermined the typical exchange time of COPII proteins at single ERES in vivo, the diffusion coefficients of the individual proteins in the cytoplasm as well as the cargo-dependent diffusion of ERES on the ER membrane. We also have quantified the spatial arrangement and size distribution of ERES in vivo. Based on these results, we propose a simple model for the self-organization of ERES that quantitatively matches the experimental data.

BP 4: Protein Structure and Folding

Time: Monday 17:30–19:30 Location: H43

BP 4.1 Mon 17:30 H43

MODELS FOR PROTEIN FOLDING — •PEDRO OJEDA[1], NAN-YOW CHEN[2], AURORA LONDONO[3], and MARTIN GARCIA[1] — [1]Theoretische Physik, FB 18, Universitaet Kassel, Kassel, Germany — [2]Institute of Physics, Academic Sinica, Nankang, Taiwan — [3]Department of Molecular Biology, IPICYT, S.L.P., Mexico

The problem of predicting the native structure of a protein for a given sequence is of great interest due to its relevance to many fields in Biology. Up to now two kinds of models were developed to qualitatively explain some aspects of the folding-problem, but the complete solution of the problem is still missing. One of those models is called *deterministic* because it considers all atoms and all interactions. The simulations require sophisticated computer resources. Another approach is called *stochastic* because it makes use of the so called Markov processess. This method has the advantage of requiring only a personal computer to obtain the solution.

In this work we employ Monte Carlo scheme and consider an *Off-lattice model* in which the degrees of freedom are the so-called Ramachandran angles. The potential energy is calculated as in PRL 96, 078103 (2006).

Using this method we were able to predict the native structure of diferent proteins.

BP 4.2 Mon 17:45 H43

Exact Solution of the RNA Folding Problem with Loop Entropy — •Thomas R. Einert, Paul Näger, and Roland Netz — Physikdepartment (T37), Technische Universität München, 85748 Garching, Deutschland

We discuss the equilibrium statistical mechanics of the secondary structure of an RNA molecule taking into account the loop entropy. We derive a recursion relation for the restricted partition $Z(N, M)$ function of an RNA of length N with M free backbone segments, M being a measure for the spatial extension of the molecule. The additional index M enables us to include loop entropy costs (characterized by the loop exponent c) and allows us to study stretching of the RNA. As an advantage over previous iterative formulations, our iteration equation can be solved in polynomial time. In the homopolymeric case, the recursion relation is solved analytically with generating functions methods. A phase transition is present only in the range $2 < c < 2.47...$ and is characterized by non-universal critical exponents . Explicit results for the force-extension curve are obtained.

BP 4.3 Mon 18:00 H43

Intrinsic structural properties of mesoscopic models for pro-

tein folding and aggregation — •Michael Bachmann[1,2], Stefan Schnabel[1], Christoph Junghans[1], and Wolfhard Janke[1] — [1]Institut für Theoretische Physik, Universität Leipzig, Augustusplatz 10/11, D-04109 Leipzig, Germany — [2]Computational Biology & Biological Physics, Lunds Universitet, Sölvegatan 14A, SE-223 62 Lund, Sweden

In this talk, the importance of mesoscopic models for soft materials is illustrated for folding processes of protein-like heteropolymers [1] and their aggregation [2]. In addition, it is shown that the conformational transitions accompanying folding and aggregation processes of naturally finite systems are similar to phase transitions, but not in a strict thermodynamic sense. In particular, the aggregation studies reveal the advantages of a microcanonical analysis, compared to the standard canonical approach.

[1] S. Schnabel, M. Bachmann, and W. Janke, Phys. Rev. Lett., in print; J. Chem. Phys., in print.

[2] C. Junghans, M. Bachmann, and W. Janke, Phys. Rev. Lett. **97**, 218103 (2006).

BP 4.4 Mon 18:15 H43

Analyzing knots in protein structures — •Virnau Peter[1], Mirny Leonid[2], and Kardar Mehran[3] — [1]Uni Mainz — [2]Harvard-MIT Division of Health Sciences and Technology — [3]Massachusetts Institute of Technology, Department of Physics

Although globular homopolymers display an abundance of knots (Virnau et al, J. Am. Chem. Soc. 127, 15102 (2005)), only about one in a thousand protein structures are knotted. Can this absence of entanglement be explained in terms of statistical mechanics or is there an evolutionary bias? Do knots in proteins serve a purpose and how do they actually fold? To elaborate on this, we will present an overview of knotted proteins from the current version of the Protein Data Bank (Virnau et al, PLOS Comp Biol 2, e122 (2006)). We will also discuss some particularly intriguing examples of this set and the evolutionary context in which knots appear.

BP 4.5 Mon 18:30 H43

Why are pi-helices so seldomly observed in proteins ? — Lars Ismer[1], Joel Ireta[2], and •Joerg Neugebauer[1] — [1]Max-Planck-Institut fuer Eisenforschung, Max-Planck-Strasse 1, D-40237 Duesseldorf — [2]Fritz-Haber-Institut, Faradayweg 4-6, D-14195 Berlin

Three different helical secondary structure motifs are observed in proteins: the alpha-, the 3-10-, and the pi-helix. While the alpha- and the 3-10-helix show occurences of about 80 % and 20 % respectively, the pi-helix is, however, only found in exceptional cases. The existing explanations herefore given in literature are rather qualitative and based on empirical assumptions. We here present a free energy analysis of infinitely long poly-L-alanine and -glycine helices which is based on DFT-GGA and the harmonic approximation and which is free of any empirical input parameters. We show, that the rarity of the pi-helix can be explained as an entropic effect, which is intrinsic and exists even in the absence of any environmental aspects, like solvents. By means of elasticity theory we show that the origin of the instability is due to geometric peculiarities of the pi-helix and independent of the amino acid sequence.

BP 4.6 Mon 18:45 H43

Protein structure reconstruction from a vectorial structure representation — •Katrin Wolff[1], Michele Vendruscolo[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstr. 8, 64289 Darmstadt, Germany — [2]Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge CB2 1EW, UK

We illustrate an approach to reconstruct the folded protein structure from its vectorial representation, a process which is indeed very similar to actual protein folding in the sense that it also employs a 1D quantity to determine the 3D folded structure. This has been prompted by the recent proof that the contact matrix of a protein structure can be reconstructed from its vectorial representation [1], from which the 3D structure can in turn be efficiently recovered [2]. Here, we take one step further and present a reconstruction procedure that uses directly a 3D structure description (the tube model [3]) and a cost function based on the vectorial structure representation. Although no full reconstruction has been achieved yet, the contact matrix overlap to the target structure reaches up to 75%. These simulations are used to investigate the 'energy landscape' of this model by means of enhanced sampling techniques including umbrella sampling. They provide a novel approach to investigate protein energy landscapes, which is conceptual different from usually applied Gō-type techniques.

[1] M. Porto *et al.*, Phys. Rev. Lett. **92**, 218101 (2004).
[2] M. Vendruscolo *et al.*, Fold. & Des. **2**, 295 (1997).
[3] T.X. Hoang *et al.*, Proc. Natl. Acad. Sci. USA **101**, 7960 (2004).

BP 4.7 Mon 19:00 H43

A generalized vectorial protein structure representation and its application in structure comparison — •Florian Teichert[1], Ugo Bastolla[2], and Markus Porto[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Hochschulstr. 8, 64289 Darmstadt, Germany — [2]Centro de Biología Molecular "Severo Ochoa", (CSIC-UAM), Cantoblanco, 28049 Madrid, Spain

A structural profile was recently proposed for single-domain protein structures [1]. We have extended this representation to include a consistent description of both single- and multi-domain folds [2], thus considerably broadening its applicability in bioinformatics. For one possible application, a so-called structure alignment scheme, we use this extended structural profile to compare three-dimensional protein folds and locate segments where similarities or differences exist. The benefit of our alignment scheme is that it is more general than existing algorithms. A first assessment shows that its performance is comparable with existing techniques. Yet, even more important, it constitutes a promising starting point for the analysis of structure/structure, sequence/structure, and sequence/sequence alignments within the same scheme.

[1] M. Porto, U. Bastolla, H.E. Roman, and M. Vendruscolo, Phys. Rev. Lett. **92**, 218101 (2004) *(4 pages)*.
[2] F. Teichert and M. Porto, Eur. Phys. J. B **54**, 131-136 (2006).

BP 4.8 Mon 19:15 H43

Electronic structure of proteins: extended building block model — •Volodymyr Maslyuk[1], Ingrid Mertig[1], Thomas Bredow[2], Michael Mertig[3], Denis Vyalikh[4], and Serguei Molodtsov[4] — [1]Martin-Luther-Universität Halle-Wittenberg, Fachbereich Physik, D-06099 Halle, Germany — [2]Institut für Physikalische und Theoretische Chemie, Universität Bonn, D-53115 Bonn, Germany — [3]Max-Bergmann-Zentrum für Biomaterialien, Technische Universität Dresden, D-01062 Dresden, Germany — [4]Institut für Festkörperphysik, Technische Universität Dresden, D-01062 Dresden, Germany

We report a novel approach for the calculation of the electronic density of states of proteins of huge biomolecules. The proposed model is based on the consideration of individual amino acids in the corresponding conformation of the peptide chain. The densities of sates (DOS) of the building blocks additively contribute to the electronic structure of the entire protein complex aligned at the charge-neutrality level [1] of the protein. The derived results agree well with experimental data obtained by means of photoemission (PE), resonant PE, and near-edge x-ray absorption spectroscopy. The model was applied to describe the electronic spectra of the surface protein layer (S-layer) of Bacillus sphaericus NCTC 9602. [1] H. Vázquez et al., Europhys. Lett. 65, 802 (2004); H. Vázquez et al., Appl. Surf. Sci. 234, 108 (2004); H. Vázquez et al., Phys. Rev. B 71, 041306(R)(2005).

BP 5: Cell Adhesion

Time: Monday 10:30–13:00 Location: H44

Invited Talk BP 5.1 Mon 10:30 H44

Force induced strengthening of binding domains in specifically adhered vesicles — •Ana-Suncana Smith — II. Institutut für Theoretische Physik,Universität Stuttgart

Specific adhesion between ligand-containing vesicles and receptor-functionalized substrates is an established model system for studying the initial stages of the cell recognition process and its control mechanisms. In order to provide a better understanding of the underlying physics emerging from recent experiments, and to allow for quantitative exploitation of this system, we develop a theoretical framework that accounts for the equilibrium state of adhesion. Therein, the macroscopic and microscopic aspects of the problem are successfully merged. Several mechanisms that control adhesion or induce de-adhesion are studied at the same level of theory. Particular attention is given to the problem of an externally applied force. In response to pulling, we predict passive strengthening of the adhesion, with the latter effect being significantly enhanced by the mobility of both binding partners.

BP 5.2 Mon 11:00 H44

Efficiency of Initiating Cell Adhesion in Hydrodynamic Flow — •Christian Korn[1,2] and Ulrich Schwarz[1] — [1]University of Heidelberg, Im Neuenheimer Feld 293, D-69120 Heidelberg, Germany — [2]Max Planck Institute of Colloids and Interfaces, D-14424 Potsdam, Germany

Motivated by the importance of cell adhesion under flow for various biological and biotechnological applications, we theoretically investigate the efficiency of initial binding between a receptor-coated sphere and a ligand-coated wall in linear shear flow. Using a Langevin equation that accounts for both hydrodynamic interactions and Browian motion, we numerically calculate the mean first passage time (MFPT) for receptor-ligand encounter. We study the influence of flow rate, receptor and ligand coverage, as well as receptor patch geometry on the MFPT. With increasing shear rate, the MFPT always decreases monotonically. Above a threshold value of a few hundreds, binding efficiency is enhanced only weakly upon increasing the number of receptor patches. Regarding receptor geometry, increasing height increases binding efficiency much stronger than increasing lateral size. This explains why white blood cells adhere to the vessel walls through receptor patches localized to the tips of microvilli, and why malaria-infected red blood cells form elevated receptor patches (*knobs*).

[1] C. Korn and U. S. Schwarz, *Phys. Rev. Lett.* **97**: 138103, 2006.

BP 5.3 Mon 11:15 H44

Adhesion of Membranes with Active Stickers — •Bartosz Rozycki, Thomas Weikl, and Reinhard Lipowsky — Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam, Germany

The adhesion of biological membranes has been theoretically studied for some time but primarily for equilibrium systems. Some of the adhesion proteins like integrins, however, are active molecules, which means that their conformational transitions are driven by external sources of energy such as ATP hydrolysis. These active, externally driven conformational transitions lead to local perturbations in interactions between membranes and keep the system away from equilibrium. We study the influence of these active processes on membrane adhesion in the framework of stochastic lattice models [1-3]. We show that the membrane adhesiveness exhibits a resonance as the rate of switching of the active adhesion molecules is varied [1,3].

[1] "Adhesion of Membranes with Active Stickers", Bartosz Rozycki, Reinhard Lipowsky, Thomas R. Weikl, Phys. Rev. Lett. 96, 048101 (2006). [2] "Adhesion of Membranes via Switchable Molecules", Bartosz Rozycki, Thomas R. Weikl, Reinhard Lipowsky, Phys. Rev. E 73, 061908 (2006). [3] "Stochastic Resonance for Adhesion of Membranes with Active Stickers", Bartosz Rozycki, Thomas R. Weikl, Reinhard Lipowsky, submitted to European Physical Journal E.

BP 5.4 Mon 11:30 H44

Investigation of erythrocytes cell-cell adhesion using holographic optical tweezers — •Achim Jung[1], Ingolf Bernhardt[2], Lyubomira Ivanova[2], Lars Kaestner[3], Peter Lipp[3], and Christian Wagner[1] — [1]Department of Physics, Saarland University, 66041 Saarbrücken, Germany — [2]Laboratory of Biophysics, Saarland University, 66041 Saarbrücken, Germany — [3]Institute for Molecular Cell Biology, Saarland University, 66424 Homburg, Germany

Prostaglandin E_2 (PGE_2) and lysophosphatidic acid (LPA) are released from activated platelets. Using fluorescence imaging, spectral imaging and the patch-clamp technique, we recently provided evidence that these lipid-mediators at physiological concentrations activate a non-selective cation-channel in human red blood cells (RBCs). This results in a Ca^{2+} influx and the consecutive intracellular Ca^{2+} concentration increase. Ca^{2+} increases elicits the Ca^{2+}-activated K^+ channel (Gardos channel) in the RBC membrane resulting in K^+ efflux and shrinkage of the cells. Therefore we have postulated that the PGE_2 and LPA responses of RBCs reveal a direct and active participation of these cells in blood clot formation. In order to test this hypothesis we set out to measure whether the intracellular Ca^{2+} increase leads to an adhesion force between individual RBCs. These measurements are making use of holographic optical tweezers based on a conventional fluorescence microscope. Experimentally the increase of the intracellular Ca^{2+} concentration was induced by the Ca^{2+} ionophore $A23187$.

15 min. break.

BP 5.5 Mon 12:00 H44

Quantification of Cell Adhesion Forces on Elastic Nanopattern Substrates — •Ilia Louban[1,2], Christine Selhuber[1,2], Stefan Gräter[1,2], and Joachim Spatz[1,2] — [1]Max-Planck-Institute for Metals Research, Dept. of New Materials and Biosystems, Heisenbergstr. 3, D-70569 Stuttgart — [2]University of Heidelberg, Biophysical Chemistry, INF 253, 69120 Heidelberg, Germany

Rigidity of the extracellular matrix (ECM) is one of the key properties in cell adhesion and cell migration. Its influence on cell adhesion forces is not quantitatively evaluated by biophysical means. Hydrogels, based on Poly(ethylene glycol) Diacrylate (PEG-DA), have been developed and tailored as synthetic ECM analog the last years. By changing the molecular weight of the PEG-DA macromolecules a variety of hydrogel elasticity are achieved. The Young's moduli (E) of available hydrogels span more than three orders of magnitude: from Petri-dish-like, stiff PEG-DA 700 (E = 6 MPa) to soft, gelatinous PEG-DA 20000 (E = 1 kPa). To promote cell adhesion, c(-RGDfK-) peptide functionalized, extended gold-nanopatterns are anchored on the surface of PEG-DA hydrogel. For adhesion experiments rat embryonic fibroblast are plated five to six hours on nanostructured hydrogel substrates. Cell adhesion forces are measured by detaching cells from the PEG-DA surface with tipless, biofunctionalized cantilever driven by an atomic force microscope. Forces are determined as a function of hydrogel stiffness and ligand patterning. The latter enables the quantification of cooperative processes on the molecular scale which govern cell adhesion phenomena.

BP 5.6 Mon 12:15 H44

Dynamic force spectroscopy on multiple bonds: evaluating rupture force histograms with a master equation model — •Thorsten Erdmann[1,3], Sebastien Pierrat[2], Pierre Nassoy[2], and Ulrich Schwarz[1] — [1]Center for Modelling and Simulation in the Biosciences (BIOMS),Universität Heidelberg, Im Neuenheimer Feld 293, 69120 Heidelberg, Germany — [2]Institut Curie, UMR 168, 26 rue d'Ulm, 75248 Paris Cedex 05, France — [3]Fom Institute for Atomic and Molecular Physics (AMOLF), Kruislaan 407, 1098 SJ Amsterdam, The Netherlands

We probe the dynamic strength of multiple parallel biotin-streptavidin adhesion bonds under linear loading using the biomembrane force probe setup for dynamic force spectroscopy. Using multiple rather than single bonds allows a more efficient evaluation of the experimental data. Measured rupture force histograms are compared to results from a master equation model for the stochastic dynamics of bond rupture under load. We extract the average number of bonds ruptured in each experiment as well as characteristic parameters of the adhesion bonds. The analysis shows that the peaks in the measured histograms are not simple multiples of the single bond values, but follow from a convolution procedure which generates different peak positions.

BP 5.7 Mon 12:30 H44

Vinculin head and tail fragments control adhesion forces and cell mechanics — •Claudia Tanja Mierke, Philip Kollmannsberger, Gerold Diez, Daniel Paranhos Zitterbart, Ben Fabry, and Wolfgang Goldmann — Biophysics, University of Erlangen, Germany

The focal adhesion protein vinculin consists of a head-domain and a tail-domain. Our aim was to quantify cell mechanics and the strength of cytoskeleton, focal adhesion complex and integrin receptor bonds in F9wt mouse embryonic carcinoma cells, vinculin knock-out, vinculin re-transfected and two vinculin-mutants: vinculin-knock-out cells transfected with head-fragment (vin-head) and tail-fragment (vin-tail). We measured rupture forces and creep responses by applying a staircase-like sequence of step forces between 0.5-10 nN to fibronectin-coated magnetic beads attached to the cells. All cells displayed power-law creep responses, J(t)=J0 (t/t0)b, and in most cases linear stress stiffening. The power-law exponent b was taken as a measure of molecular bond stability, with lower values corresponding to more stable bonds. The inverse creep modulus 1/J0 was taken as a measure of cell stiffness. Our results show a significant reduction in bond strength and bond number in vinculin knock-out cells and vin-tail cells. Cell stiffness was reduced in vinculin knock-out cells and vin-head cells. The effect of vin knock-out is more prominently in MEF than in F9 cells indicating cell-type specific differences. Our results show that the head-domain of vinculin is involved in adhesion strength and tail-domain in whole cell mechanics.

BP 5.8 Mon 12:45 H44

Directed cytoskeletal remodeling in response to integrin activation — •Carina Raupach, Claudia Tanja Mierke, Claus Metzner, and Ben Fabry — Zentrum für medizinische Physik und Technik, Universität Erlangen-Nürnberg

Binding of fibronectin-coated beads to the cell surface has been previously shown to trigger integrin clustering, recruitment of focal adhesion proteins, and directed cytoskeletal (CSK) remodeling (Galbraith *et al.* JCB (2002)). Moreover, these events have been shown to depend on bead size and bead binding time. To quantify CSK remodeling triggered by integrin activation, we measured the spontaneous motion of fibronectin-coated beads bound to carcinoma cells. We analyzed bead binding times ranging from 15 min to 7 h, and used beads with diameters of 0.5, 1, 2 and 4.5 μm. From the bead trajectories we computed the mean square displacement (MSD) and the persistence of motion, $p_\phi \in [-1, 1]$. For all bead sizes and binding times, the MSD followed a power law, $\Delta r^2(\Delta t) = D \cdot \Delta t^\beta + c$, with a motion that was superdiffusive ($\beta > 1$) and directionally persistent ($p_\phi > 0$ for $\Delta t > 3$ s). Persistence p_ϕ (for $\Delta t = 3$s) and β decreased monotonically with increasing bead binding time from a highly persistent and nearly ballistic behavior (at 15 min) to a more undirected and random behavior (at 7 h). With increasing bead size, persistence p_ϕ and β increased monotonically. These data show that directionally persistent CSK remodeling is highly dependent on bead size, and continues, although with declining persistence p_ϕ, for several hours after the initial integrin receptor activation through bead binding.

BP 6: Biopolymer Conformation and Dynamics

Time: Monday 14:30–16:00 Location: H44

BP 6.1 Mon 14:30 H44

Semiflexible polymers: Dependence on ensemble and boundary orientations — •Debasish Chaudhuri — MPIPKS Dresden, Noethnitzer Str. 38, 01187 Dresden

We show that the mechanical properties of a worm-like-chain (WLC) polymer, of contour length L and persistence length λ such that $t = L/\lambda \sim \mathcal{O}(1)$, depend both on the ensemble and the constraint on end-orientations. In the Helmholtz ensemble, multiple minima in the free energy near $t = 4$ persists for all kinds of orientational boundary conditions. The qualitative features of projected probability distribution of end to end vector depend crucially on the embedding dimensions.A mapping of the WLC model, to a quantum particle moving on the surface of an unit sphere, is used to obtain the statistical and mechanical properties of the polymer under various boundary conditions and ensembles. The results show excellent agreement with Monte-Carlo simulations.

BP 6.2 Mon 14:45 H44

DNA: From rigid base-pairs to semiflexible polymers — •Nils Becker[1] and Ralf Everaers[1,2] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden — [2]Laboratoire de Physique, ENS Lyon, 46, allée d'Italie, 69364 Lyon, France

The sequence–dependent elasticity of double-helical DNA on a nm length scale is captured by the rigid base–pair model, whose strains are the relative position and orientation of adjacent base–pairs. Corresponding elastic potentials have been obtained from all–atom MD simulation and from high–resolution structural data. On the scale of a hundred nm, DNA is successfully described by a continuous worm–like chain model with homogeneous elastic properties. These are characterized by a set of four elastic constants [1], recently measured on single molecules [2,3].

We present a theory that links these experiments on different scales by systematic coarse–graining. We find that the average elastic constants for random sequence DNA show reasonable agreement. However for short chains, the variability of structure and stiffness with sequence leads to large deviations from the average, including non-Gaussian bend angle distributions and elevated looping probabilities.

[1] J. F. Marko and E. D. Siggia, Biophys J 73, 2173, 1997
[2] T. Lionnet et al., Phys Rev Lett 96, 178102, 2006
[3] J. Gore et al., Nature 442, 836, 2006

BP 6.3 Mon 15:00 H44

Force-induced structural transitions in cross-linked DNA films — •Alexander André[1,2], Theo Fischer[1], Georg Maret[1], and Thomas Gisler[1] — [1]Universität Konstanz, Konstanz, Germany — [2]Université Louis Pasteur, Strasbourg, France

Single-molecule experiments have revealed that double-stranded DNA can be extended by about 60% beyond its natural contour length at nearly constant force [1,2]. The origin of this plateau in the force-extension curve is however still under debate, mainly since no direct structural information has so far been obtained from single overstretched DNA molecules. We propose an experimental approach to investigating the structure of overstretched DNA, using oriented DNA films obtained by wet-spinning. Randomly cross-linking DNA by intercalation compounds and covalent bonds between nucleobases results in elastomeric films which can be reversibly overstretched. We characterize the structure of these cross-linked films under mechanical load with X-ray diffraction and birefringence experiments.

[1] P. Cluzel, A. Lebrun, C. Heller et al., "DNA: An Extensible Molecule," Science 271, 792-794 (1996). [2] S. B. Smith, Y. Cui, A. C. Hausrath et al., "Stretching DNA beyond its B-form contour length," Biophys. J. 68, A250 (1995).

BP 6.4 Mon 15:15 H44

Fluctuating polymer rings — •Karen Winkler and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, D-80333 München, Germany

Geometric constraints have been proven to induce interesting behavior on polymers. We consider polymer bundles confined to a ring-like structure. This constraint causes an additional bending stiffness and coupling of bending and twisting modes. To describe polymer bundles we derived an analytic model for a semiflexible polymer ring with anisotropic bending stiffness and twist stiffness. This model predicts the mean square diameter of a ribbonlike ring thus giving a novel parameter to determine bending and twist stiffnesses of polymer bundles in experiments.

Furthermore the asymmetric shape of polymer rings with symmetric cross section is investigated over the whole range of flexibility by Monte Carlo simulations. For semiflexible polymers a scaling argument explains the change of the polymer's asphericity with increasing flexibility.

BP 6.5 Mon 15:30 H44

Conformation control of plasmid DNA on a solid substrate — •Wei Zhuang, Hua Liang, Nikolai Severin, and Jürgen P. Rabe — Institut für Physik, Humboldt University Berlin, Berlin, Germany

The conformation of single DNA molecules may be controlled by stretching them with optical tweezers [1] or an scanning force microscope (SFM) probe [2]. In recent work it has been demonstrated that a highly oriented pyrolytic graphite (HOPG) surface coated by self-assembled alkylamine amphiphiles can serve as a substrate on which single DNA molecules can be manipulated by an SFM probe [3]. A disadvantage of the above mentioned techniques is that they have to be applied to one molecule at a time. Here we describe a preparation of an amphiphile coated HOPG surface, on which the conformation of plasmid DNA can be fully controlled across the whole surface. By varying the concentration of amphiphiles on the surface, plasmid DNA molecules exhibit different conformations ranging from supercoiling, relaxed open circle, to overstretching. Particularly, when DNA molecules are adsorbed on 60% amphiphile sub-monolayer covered HOPG, upon mild annealing the DNA molecules can be overstretched up to 1.5 times of their B-form length due to steric repulsion between adjacent alkyl chains. It is suggested that a fully screened amphiphile-DNA complex is formed on the surface. The spontaneous overstretching of many DNA molecules at a time may become useful for the development of a fast processing genomic analysis chip. 1. S.B.Smith, et. al Science 271 (1996) 795 2. M.Rief, et. al Nat. Struct. Biol. 6 (1999) 346 3. N.Severin, et. al Nano Lett. 4 (2004) 577

BP 6.6 Mon 15:45 H44

How does a straight polymer relax? — •Benedikt Obermayer[1], Oskar Hallatschek[2], Erwin Frey[1], and Klaus Kroy[3] — [1]ASC und CeNS, LMU München — [2]Lyman Laboratory of Physics, Harvard University — [3]ITP, Universität Leipzig

Although the relaxation dynamics of semiflexible polymers from an initially straight conformation has been discussed extensively in the literature, this seemingly simple problem involves nontrivial physics that is not yet completely understood. This is partly due to the ambiguous meaning of "initially straight", for which various realizations are conceivable. The filament could be stretched (by optical tweezers, electric fields, elongational flows, ...), but it could also be quenched, i.e., prepared in an initial low-temperature environment. In all cases, the longitudinal contraction is driven by the same purely stochastic forces, yet the resulting deterministic growth laws for pertinent observables reflect for short times fundamental differences in the underlying relaxation processes. We present a comprehensive explanation how these differences emanate from the various realizations and how they give rise to universal long-time relaxation. Further, we compare our theoretical results to recent experiments and simulations, give suggestions on how to test our predictions, and comment on the choice of proper observables.

BP 7: Fibers and Bundles

Time: Monday 16:15–18:00 Location: H44

BP 7.1 Mon 16:15 H44

Finite bundle size in reconstituted cyotskeletal systems — •Mireille Claessens and Andreas Bausch — TUM, Physik Department E22, James Franck Straße, D-85747, Garching

In the presence of non-adsorbing polymer and/or multivalent counterions charged biopolymers such as F-actin, microtubules, or DNA have been reported to form an equilibrium phase of bundles with a well defined thickness. Even in vivo actin bundles formed by specific actin binding proteins (ABPs) appear with well defined diameters. The stabilization mechanism of such bundles is proposed to be similar to that of equilibrium colloid clusters; steric and short range electrostatic interactions or frustration within the bundles probably prevent charge neutralization and force the equilibrium bundle size to be finite.

We show that in the presence of the specific actin binding protein fascin actin filaments organize into bundles with well defined number of filaments in vitro. The total thickness is defined by the concentration of fascin and limited to a maximal size of about 20 filaments - independent of electrostatic interactions. Geometrical considerations indicate that competition between binding energy and bundle bending rigidity controls the bundle diameter. We discuss how arising frustrations or packing defects in the bundles could cause the bundle thickness to saturate.

BP 7.2 Mon 16:30 H44

Dynamics and statistical mechanics of semiflexible polymer bundles — •Claus Heussinger, Mark Bathe, and Erwin Frey — Arnold-Sommerfeld-Center, Ludwig-Maximilians Universität, München

Bundles formed from semiflexible polymers are ubiquitous in nature (e.g. filopodia) and many areas of technology (e.g. carbon nanotube bundles). Despite their simple structure, their mechanical and dynamical properties are only poorly understood. We set up an elastic energy functional that allows characterizing the dynamical and statistical mechanical properties of polymer bundles, in much the same way as the standard worm-like chain model does for single polymers. The key result of our analysis is that bundles must be characterized by a wave-number dependent persistence length $l_p(q)$ instead of just a single q-independent value. This finding is shown to have dramatic consequences not only on the static and dynamic fluctuation spectrum of an isolated bundle but also on the scaling behaviour of their entangled solutions as well as their cross-linked networks.

BP 7.3 Mon 16:45 H44

Fluctuation Dynamics of Grafted Microtubules — •Francesco Pampaloni[1], Katja Taute[2], Gianluca Lattanzi[3], and Ernst-Ludwig Florin[2] — [1]EMBL Heidelberg - Cell Biology and Biophysics Unit - Heidelberg, Germany — [2]Center for Nonlinear Dynamics - University of Texas at Austin - Austin, USA — [3]Department of Medical Biochemistry, Biology and Physics, University of Bari - Bari, Italy

Microtubules (MTs) are tubular protein filaments that constitute one of the main components of the cellular cytoskeleton. MTs are composed by a variable number of protofilaments (most frequently 13) made by the dimeric protein tubulin. MTs are highly optimized to a maximum of mechanical performance: the hollow cylindrical shape allows high strength and stiffness combined with a minimum of structural elements (tubulin dimers). Such features of MTs - light, flexible, and stiff at once - make them similar to versatile composite structures investigated by material scientists. Recent studies have shown that one key mechanical parameter, the persistence length, is subject to an unexpected dependence on the overall MT length. This has been attributed to the MT's large mechanical anisotropy on the molecular level. We performed a dynamical analysis of the thermal fluctuations of grafted MTs obtaining first mode relaxation times. Single-particle tracking was employed to measure the fluctuations of the free end of the filament. We found that relaxation times follow an L^2 instead of an L^4 dependence for short microtubules. This relation is shown to result from the length dependence of the persistence length.

BP 7.4 Mon 17:00 H44

Force regulation of microtubule dynamics in living cells — •Christian Tischer[1], Damian Brunner[2], and Marileen Dogterom[1] — [1]AMOLF, Amsterdam, Niederlande — [2]EMBL, Heidelberg, Deutschland

Microtubules are stiff biopolymers that self-assemble from tubulin proteins. Inside cells, microtubules are typically several micrometers long and form networks that are organized in a functional way. A unique property of microtubules is their ability to switch from a polymerizing to a depolymerizing state (so-called "catastrophes"). Investigating the intracellular regulation of this fascinating out-of-equilibrium behavior is crucial in order to understand how microtubules fulfill their important functions during cell division and cell morphogenesis. Here, we use the fission yeast (S. Pombe) to investigate regulation of microtubule catastrophes at the cell boundary. Fission yeast is an excellent model organism: it has a well defined cylindrical shape and contains only few microtubules whose dynamics can be readily followed with live-cell microscopy. Developing specialized image analysis methodology we were able to investigate the spatial and temporal distribution of microtubule catastrophes with unprecedented statistical accuracy.

Analyzing thousands of catastrophes in hundreds of cells, we provide strong evidence that compressive polymerization forces, arising from growth of microtubules against the cell boundary, indeed enhance the rate of catastrophes. This effect had been predicted by measurements on purified microtubules growing against artificial boundaries.

BP 7.5 Mon 17:15 H44

Force generation by growing filament bundles — •Jan Kierfeld, Torsten Kühne, and Reinhard Lipowsky — Max-Planck-Institut für Kolloid- und Grenzflächenforschung, Science Park Golm, 14424 Potsdam

Force generation by polymerizing bundles of semiflexible filaments, which are formed due to attractive filament interactions, is investigated theoretically using Monte-Carlo simulations and analytical arguments. If a compressive force is applied to the end of a bundle it can undergo a force-induced unbundling transition. A polymerizing bundle can generate forces either by a zipping mechanism, which converts adhesive energy into force, or by a polymerization mechanism, which converts the energy gain upon adding monomers into force. Limitations from the buckling instability of the bundle are discussed for both mechanisms.

BP 7.6 Mon 17:30 H44

The Influence of internucleosomal interaction and local structure on the geometry of large chromatin fibers — •René Stehr[1], Nick Kepper[2], Karsten Rippe[2], and Gero Wedemann[1] — [1]Fachhochschule Stralsund, System Engineering and Information Management, Zur Schwedenschanze 15, D-18435 Stralsund, Germany — [2]Kirchhoff-Institut für Physik, Molecular Biophysics Group, Ruprecht-Karls-Universität Heidelberg, Im Neuenheimer Feld 227, D-69120 Heidelberg, Germany

The structure of the genetic material plays a major role in the regulation of gene expression. In eukaryotic cells the DNA is folded with histone proteins into chromatin. The internal structure of chromatin at physiological ionic strength is unknown.

We utilize computer simulations to study both the effect of different interaction potentials betweeen nucleosomes as well as changes to the nucleosome geometry. Our analysis revealed that the previously used potentials (e.g. Gay-Berne potential) are not compatible with the formation of stable chromatin fibers under physiological potential strengths while other geometries do. Furthermore, we extended the "two angle" model for the description of the DNA-nucleosoe geometry.

The results of our analysis identify the internucleosomal interaction and the local geometry at the nucleosomes as key determinants for the organization of the chromatin fiber. Modifications of these parameters by biological factors could be used to control the accessibility of DNA in the fiber in vivo.

BP 7.7 Mon 17:45 H44

The 30nm chromatin fiber: As dense as it gets — •Martin Depken[1] and Helmut Schiessel[2] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden, Germany — [2]Instituut-Lorentz for Theoretical Physics, Leiden, The Netherlands

We address the problem of the structure of the 30nm chromatin fiber. By considering the packing of nucleosomes at the periphery of the fiber, together with their connections through the DNA linker backbone, we characterise the possible dense configurations without having to assume anything about the bending of the linker backbone. This results in a set of dense fiber configurations with properties that can be compared with experimental findings to determine possible structures.

BP 8: Charge Transfer

Time: Monday 18:00–19:30 Location: H44

BP 8.1 Mon 18:00 H44

Three-dimensional conductance mapping on living cells with scanning ion conductance microscopy — •Matthias Böcker[1,2], Joachim Wegener[3], and Tilman Schäffer[1,2] — [1]Center for Nanotechnology (CeNTech), Heisenbergstr. 11, 48149 Münster — [2]Physikalisches Institut, Wilhelm-Klemm-Str. 10, 48149 Münster — [3]Institut für Biochemie, Wilhelm-Klemm-Str. 2, 48149 Münster

A scanning ion conductance microscope (SICM) is based on an electrolyte-filled, tapered micropipette that acts as nanoscale current probe while being scanned over a sample surface. We used SICM to study the ion permeability of tissue-like cell layers with lateral resolution. For MDCK-II cells, we measured a larger ion conductance along the cell periphery in areas of cell-cell contacts, compared to that along the cell bodies. This suggests that ions mainly pass through the paracellular cleft between adjacent cells but not through the cellular plasma membrane.

In order to further refine these measurements, we implemented a novel three-dimensional imaging mode. In this mode, the micropipette is scanned in all three spatial dimensions over the sample surface while recording the ion conductance. The sample surface topography is tracked by using a complementary shear-force distance control with an optical readout. This allows us to create maps of ion conductance not only in a plane, but in a volume directly above the sample surface, revealing refined aspects of conductive sample properties.

BP 8.2 Mon 18:15 H44

Chemically driven electron tunnelling pumps — •Igor Goychuk — Universität Augsburg, Germany

The simplest mechanism for molecular electron pumps is discussed [1] which is based on nonadiabatic electron tunnelling and nonequilibrium conformational fluctuations [2,3]. Such fluctuations can be induced, e.g. by random binding of negatively charged ATP molecules to the electron-transferring molecular complex, their subsequent hydrolysis and the products dissociation. The pumping rate can be controlled by the ATP concentration in solution. Depending on the model parameters there may exist a critical ATP concentration for the pump to function. For realistically chosen parameters, the mechanism is shown to be robust and highly efficient. Such a mechanism is tentatively realised in nitrogenase protein complexes [4].

[1] I. Goychuk, Molecular Simulation **9**, 717 (2006) (Special Issue on Electron Transfer).
[2] I. A. Goychuk, E. G. Petrov, V. May, Phys. Rev. E **56**, 1421 (1997).
[3] I. Goychuk, P. Hänggi, Adv. Phys. **54**, 525 (2005).
[4] I. V. Kurnikov, A. K. Charnley, D. N. Beratan, J. Phys. Chem. B, **105**, 5359 (2001).

BP 8.3 Mon 18:30 H44

Electrostatic screening and energy barriers for ion translocation across low-dielectric membranes — •Andrey Cherstvy — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzerstrasse 38, D-01187 Dresden, Germany

We present exact solutions of the linear Poisson-Boltzmann equation for several problems relevant for ion translocation across low-dielectric membranes [1]. Our results are obtained for a finite Debye screening length, and they generalize the classical results for pure Coulombic electrostatics [2]. We calculate the electrostatic self-energy of an ion in the middle of a low-dielectric slab, its energy inside a cylindrical high-dielectric pore, and its energy inside a high-dielectric spherical jacket. We consider also the influence of negative charges distributed on the walls of the cylindrical pore. We show that ion self-energy barriers are considerably reduced due to screening of electrolyte. We compare our results with some numerical results for screened electrostatic interactions in ion channels and wide biological pores [3].

[1] A. G. Cherstvy, J. Phys. Chem. B, 110, 14503 (2006). [2] A. V. Parsegian, Nature (London), 221, 844 (1969). [3] P. C. Jordan et al., Biophys. J. 55, 1041 (1989).

BP 8.4 Mon 18:45 H44

Localization of electronic states of proteins probed by resonant photoemission — •Denis Vyalikh[1], Volodymyr Maslyuk[2], Andreas Kade[1], Alexander Kirchner[3], Anja Blüher[3], Ingrid Mertig[2], Michael Mertig[3], and Serguei Molodtsov[1] — [1]Institut für Festkörperphysik, Technische Universität Dresden, D-01062 Dresden, Germany — [2]Martin-Luther-Universität Halle-Wittenberg, Fach-

bereich Physik, D-06099 Halle, Germany — [3]Max-Bergmann-Zentrum für Biomaterialien, Technische Universität Dresden, D-01062 Dresden, Germany

The electronic structure of the biological system - regular two-dimensional bacterial surface protein layer (S layer) of Bacillus sphaericus NCTC 9602 - was investigated by resonant photoemission (PE) spectroscopy at the C 1s, N 1s and O 1s absorption edges. Resonant PE spectra taken in the vicinity of the C 1s absorption threshold exhibit an enhancement of the valence-band emission, indicating rather localized character of the lowest laying unoccupied orbitals. We have established kinetic energy shifts of the O- and N- KVV Auger lines across excitations of primarily electrons into the corresponding π^* resonances that can help to shed light on the electron transport properties in the extremely large biomolecules.

BP 8.5 Mon 19:00 H44

Hopping transport through nanowires: a unified approach to DNA charge transfer — Tobias Cramer, Sebastian Krapf, and •Thorsten Koslowski — Institut für Physikalische Chemie, Universität Freiburg, Albertsrasse 23a, D-79104 Freiburg im Breisgau

We address the problem of DNA charge transfer from a theoretical and numerical perspective. The electronic structure is described atomistically and chemically specific by an extended Su-Schrieffer-Heeger Hamiltonian that can be solved self-consistently [1]. The emerging potential energy surface exhibits the characteristics of small polaron formation. It can be analyzed to obtain the parameters relevant to Marcus' theory of thermally excited charge transfer. The findings are not only compatible with DNA photofragmentation experiments [2], but also provide an accurate description of charge transfer through bio-nano contacts. The resulting rate equations lead to a maximum current of 5 nA per A-DNA double strand upon the application of a potential of ± 2 V, a value comparable to recent experimental findings. In addition, we reproduce the overall shape of the experimental I-V curves and their pronounced dependence upon the DNA sequence [3].

[1] M. Rateitzak, and T. Koslowski, Chem. Phys. Lett. 377, 455 (2003)

[2] T. Cramer, S. Krapf, and T. Koslowski, J. Phys. Chem. B, 108, 11812 (2004); T. Cramer, A. Volta, A. Blumen, and T. Koslowski, J. Phys. Chem. B 108, 16586 (2004)

[3] T. Cramer, S. Krapf, and T. Koslowski, submitted for publication

BP 8.6 Mon 19:15 H44

Near-field optical imaging of a free-standing biological membrane under physiological conditions — •Nicole Neuberth[1], Michael Hermann[2], Joerg Wissler[1], Daniela Diessel[1], Dietmar Gradl[2], and Andreas Naber[1] — [1]Institut für Angewandte Physik, Universitaet Karlsruhe (TH) — [2]Zoologisches Institut II, Universitaet Karlsruhe (TH)

Nuclear pore complexes (NPCs) are supramolecular assemblies embedded in the nuclear envelope (NE) of a cell. They constitute a major gateway for the transport of molecules in and out of the nucleus. Though considerable insight has been gained into the signal-mediated translocation, it is still under debate in which way the structural properties of an NPC are related to its function as a "biological transport machine". We have recently demonstrated that SNOM provides a new possibility for an investigation of unfixed biological membranes [1]. For the intended transport studies, we improved the quality of our SNOM probe such that single molecule measurements with 30-nm-resolution are obtained routinely [2]. We developed a template based on cylindrical cavities in a photo-resist, and free-standing membrane patches are formed over the cavities by spreading the NE on the surface. We will present first near-field optical results of an unsupported nuclear membrane.

[1] C. Hoeppener et al., Biophys. J. 88, 3681 (2005).

[2] D. Molenda et al., Optics Exp. 13, 10688 (2005).

BP 9: Regulation and Signaling

Time: Tuesday 9:30–13:00 Location: H43

Invited Talk BP 9.1 Tue 9:30 H43

Single molecule recognition in regulatory systems — •Robert Ros — Experimental Biophysics, Physics Department, Bielefeld University, 33615 Bielefeld, Germany

Molecular recognition between proteins and nucleic acids is fundamental for many aspects of cellular regulation. For instance, a central issue for the regulation of gene expression is the specific recognition of DNA target sequences by transcription regulators. Furthermore, the protein expression of a cell can be regulated on the post-transcriptional level by the interaction of proteins with RNA. We are using atomic force microscopy (AFM) based force spectroscopy to investigate the interaction of proteins with DNA [1-4] and RNA target sequences at the single molecule level. For analyzing our force spectroscopy data, we apply and improve the concept of chemical bond heterogeneity [5], giving insights into the molecular binding mechanism and resulting in quantitative characterization of the interactions in terms of rate constants and dissociation lengths.

[1] F.W. Bartels et al.; J. Struct. Biol. 143: 145 (2003). [2] B. Baumgarth et al.; Microbiology 151: 259 (2005). [3] R. Eckel et al.; Ang. Chem. Int. Ed.44: 3921 (2005). [4] F.W. Bartels et al.; Biophys. J. (accepted). [5] Raible et al. ; Biophys.J. 90: 3851 (2006).

Invited Talk BP 9.2 Tue 10:00 H43

Transcription by RNA Polymerase II — •Stephan Grill[1,2,3], Eric Galburt[3,1], Martin Depken[1], and Carlos Bustamante[3] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden — [2]Max-Planck-Institut für molekulare Zellbiologie und Genetik, Dresden — [3]University of California, Berkeley

RNA polymerase II (RNAP II) is responsible for transcribing all mRNAs in eukaryotic cells in a highly regulated process that serves as a central control point for cellular function. We have investigated the transcription dynamics of single RNAP II molecules against force in the presence and absence of TFIIS, a transcription elongation factor that enables the enzyme to remove copy errors. Using a single-molecule dual-trap optical-tweezers assay, we found that the response of RNAP II to force is entirely determined by enzyme backtracking. We show that backtrack pause durations follow a $t^{-3/2}$ power law, implying that during backtracking RNAP II performs a random walk in discrete base-pair steps and suggesting that backtracks may account for most of RNAP II pauses. We discuss the implications of our results in light of an optimal balance between speed and accuracy in decoding the genetic information during transcription.

15 min. break.

BP 9.3 Tue 10:45 H43

Basal promoter activity of comK sets a switching-window into the K-state of Bacillus subtilis — •Madeleine Leisner[1,2], Joachim Rädler[1], and Berenike Maier[2] — [1]LMU, Department für Physik, LS Rädler, Geschwister-Scholl-Platz 1, Munic, Germany, — [2]WWU, Institut für allgemeine Zoologie und Genetik, Am Schlossplatz 5, Münster, Germany

Bacillus subtilis cell population divides into a competent fraction and a non-competent fraction in the stationary phase. The transition from the non-competent state (with basal ComK concentration) to the K-state (with high ComK concentration) behaves like a bistable switch. To determine factors that set the fraction of cells that switch into the K-state (K-fraction), we characterized the basal comK expression in individual non-competent cells and found a broad Gaussian distribution whose center shifted towards higher values before entry into stationary phase. Basal promoter activity increased exponentially, reached a maximum and decreased towards zero in the stationary phase. The intrinsic switching rate increased and decreased with a time lag. When switching was induced prematurely by down-regulation of ComK proteolysis, the K-fraction increased strongly. Our data supports a model in which the basal ComK concentration increases during the exponential phase and the fraction at the high end triggers the autocatalytic feedback for ComK transcription. Shut-down of basal promoter activity sets a 'time-window' for switching and is thus involved in determining the K-fraction in the bimodal population.

BP 9.4 Tue 11:00 H43

Yeast cell cycle: Stable network dynamics despite molecular fluctuations — •Stefan Braunewell and Stefan Bornholdt — Institute for Theoretical Physics, University of Bremen, Otto-Hahn-Allee, 28359 Bremen

Regulatory systems in living cells consist of many components, which interact through intricate cascades of molecular processes. In spite of the stochastic nature of these processes, a robust functioning of the regulatory machinery is required for the survival of the cell. On the basis of the model organism S. cerevisiae, we investigate the stability of the network dynamics under such noisy conditions [1]. We extend a recently proposed synchronous Boolean model of the yeast cell-cycle control network [2] to continuous time and allow for stochastic noise on the signal transmission times. Further we incorporate a low-pass filter to account for typical characteristics of transcriptional regulation. As a result, one finds that the cell-cycle network shows a remarkable stability against timing fluctuations and exhibits specific features that aid this stability.

[1] S. Braunewell and S. Bornholdt, Superstablity of the yeast cell cycle dynamics: Ensuring causality in the presence of biochemical stochasticity, J. Theor. Biol. (2006), doi:10.1016/j.jtbi.2006.11.012

[2] F. Li et al., The yeast cell-cycle network is robustly designed. Proc. Natl. Acad. Sci. USA (2004), 101(14):4781-4786

BP 9.5 Tue 11:15 H43

How general is the Boolean network approach for predictive models? A case study of the yeast cell-cycle. — •Maria Davidich and Stefan Bornholdt — Institute for Theoretical Physics, Bremen University, Bremen, Germany

Boolean networks once were a mere toy model analogy for how regulatory processes in living cells could in principle work [1]. However, today there are examples of Boolean networks predicting regulatory processes in living organisms as the cell-cycle control in yeast [2] or some developmental modules in Drosophila [3]. We here pose the question whether Boolean networks have the potential to provide a new general method for predicting biological regulatory networks and discuss this question by comparing alternative Boolean models for the yeast cell-cycle.

[1] Kauffman, S.A The Origins of Order: Self-Organization and Selection in Evolution (Oxford, UK: Oxford University Press), (2003).

[2] Li F, Long T, Lu Y, Quyang Q, Tang C. The yeast Cell-Cycle Network Is Robustly Designed. PNAS, April 6, 2004, vol. 101, no. 14, 4781-4786.

[3] Albert R, Othmer H.G. The topology of the regulatory interactions predicts the expression pattern of the Drosophila segment polarity genes. Journal of Theoretical Biology 223, 1-18 (2003).

BP 9.6 Tue 11:30 H43

Ca^{2+} signaling: order from disorder — •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 microscopic fluctuations, 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. We have measured oscillations of the cytosolic Ca^{2+} concentration in different cell types under different conditions. These oscillations 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 oscillations and the influence of Ca^{2+} buffer to specify the stochastic mechanism. It turns out that cells use array enhanced coherence resonance to create the wide spectrum of observed Ca^{2+} oscillations. Thus we demonstrate a first exampale of the constructive role of noise in cell signalling.

BP 9.7 Tue 11:45 H43

Hybrid models and simulations of intracellular calcium dynamics — •Sten Rüdiger — Hahn-Meitner-Institut, Glienicker Str. 100, 14109 Berlin

Intracellular calcium release is a prime example for the role of stochastic effects in cellular systems. Recent models consist of deterministic reaction-diffusion equations coupled to stochastic transitions of calcium channels. The resulting dynamics is of multiple time and spatial scales, which complicates far-reaching computer simulations. In this contribution we introduce a novel hybrid scheme that is especially tailored to accurately trace events with essential stochastic variations, while deterministic concentration variables are efficiently and accurately traced at the same time. We use finite elements to efficiently resolve the extreme spatial gradients of concentration variables close to a channel. We describe the algorithmic approach and we demonstrate its efficiency compared to conventional methods. Our single channel model matches experimental data by Mak et al. (PNAS 95, 15821, 1998) and results in intriguing dynamics if calcium is used as charge carrier. Random openings of the channel accumulate in bursts of calcium blips that may be central for the understanding of cellular calcium dynamics. We further discuss calcium release from clusters of channels and and the effects of calcium-binding proteins on the dynamics.

BP 9.8 Tue 12:00 H43

The Mechanism of Gene Repression Revealed by spFRET Investigations of TBP-NC2 Complexes — •Peter Schluesche[1], Gertraud Stelzer[2], Elisa Piaia[2], Christoph Braeuchle[1], Michael Meisterernst[2], and Don C. Lamb[1] — [1]Department for Physical Chemistry, Ludwig-Maximilians-University, Butenandtstr. 11, 81377 München — [2]GSF-National Research Center for Environment and Health, Department of Gene Expression, Marchioninistr. 25, 81377 München

The initiation of DNA transcription starts with the binding of the TATA-Box Binding Protein (TBP) to the gene promoter site on the DNA. The transcription can be inhibited by the regulatory protein Negative Cofactor 2 (NC2) which forms a complex with the DNA bound TBP and represses gene expression. Recent results of biochemical experiments suggest that the TBP becomes mobile along the DNA upon the binding of NC2. Thus, transcription inhibition by NC2 could be explained by the dislocation of TBP from the promoter site rather than by steric hindrances as currently thought. To test this hypothesis, we have performed fluorescence resonance energy transfer (FRET) experiments on single TBP-NC2 complexes bound to DNA using Total Internal Reflection Fluorescence Microscopy with dual color detection. TBP was labeled specifically with a FRET-donor molecule and a TATA sequence containing dsDNA was labeled with a FRET-acceptor. By observing fluctuations in the FRET efficiency of individual complexes upon NC2 binding, we confirmed the mobility of the TBP-NC2 complexes along the DNA.

BP 9.9 Tue 12:15 H43

Analysis of bacterial gene regulatory networks by time-lapse fluorescence microscopy — •Judith Leierseder[1], Georg Fritz[1], Kirsten Jung[2], and Joachim Rädler[1] — [1]Department für Physik, Ludwig-Maximilians-Universität München — [2]Department Biologie I, Ludwig-Maximilians-Universität München

The vision of artificial genetic circuits with well defined response functions to external signals requires a quantitative understanding and description of the function of gene regulatory networks. Gene expression is, however, not only determined by the mere network structure, but also influenced by stochastic effects that lead to significant cell to cell variations. The single cell studies that are thus required to resolve these variations are greatly facilitated by the use of the green fluorescent protein (GFP) as network output marker. Using semi-automated time-lapse fluorescence microscopy combined with quantitative image processing we measured expression kinetics for many single bacterial cells. For our model system, the pBAD/AraC module in Escherichia coli, we analyzed the response following different induction concentrations and compared the kinetics to a simple theoretical gene expression model of the network.

BP 9.10 Tue 12:30 H43

Detection of functional RNA in genomic sequences — •Bernd Burghardt and Alexander Hartmann — Institut für Theoretische Physik, Universität Göttingen

Some ten years ago it was believed that RNA mainly acts by transferring genetic information, i.e. essentially its primary structure is relevant. However, many RNAs provide functionality by its secondary and tertiary structure. Such non-coding RNA (ncRNA) is coded in genomic DNA sequences and includes well known types, e.g. tRNA and rRNA as well as recently discovered ones, e.g. miRNA. An important issue is, how to detect regions in the DNA which code for such functional RNAs, i.e. to distinguish it from gene-coding and other parts.

We present here a efficient numerical method to detect such functional RNAs in long RNA (or DNA) sequences. The method is based

on the ground-state calculations of RNA secondary structures for all subsequences up to a certain length. By analysing the average ground-state energy one gets strong evidence where such such functional RNA fragments are embedded.

BP 9.11 Tue 12:45 H43

Coarse-Grained Lattice Model for Molecular Recognition — •Hans Behringer, Andreas Degenhard, and Friederike Schmid — Fakultät für Physik, Universität Bielefeld, D-33615 Bielefeld

Equilibrium aspects of molecular recognition are investigated using coarse-grained models for the recognition process of two rigid biomolecules. To this end, a two-stage approach is adopted. First, the structure of the target molecule is fixed and learned by a probe molecule resulting in an ensemble of probe sequences. In a second step the recognition ability of the designed probe ensemble with respect to the chosen target sequence is tested by comparing the free energy of association with the previously fixed target structure and a different competing structure. Particular attention is paid to the influence of cooperative effects accompanying the association of the target biomolecule and the probe molecules. Cooperativity is found to enhance selectivity. In addition it is discussed how correlated hydrophobicity distributions affect the recognition ability.

Behringer, H., A. Degenhard, F. Schmid 2006, Coarse-Grained Lattice Model for Molecular Recognition, *Phys. Rev. Lett.* **97**, 128101.

BP 10: DNA: supercoils, knots and melting

Time: Tuesday 14:00–15:45 Location: H43

Invited Talk BP 10.1 Tue 14:00 H43

Supercoils and their Removal — •Nynke Dekker — Molecular Biophysics Group, Kavli Institute of NanoScience Delft University of Technology, Lorentzweg 1, 2628 CJ Delft, The Netherlands

The intertwining of the DNA strands further ensures DNA integrity by physically linking the individual chains. However, this poses a number of topological problems during the cell cycle. For example, the progressive unwinding of the DNA template during DNA replication and the segregation of multiply intertwined daughter DNA molecules require changes in the linkage of DNA strands and helices. Similarly, RNA transcription can produce local unwinding of the DNA helix behind the transcription complex and local overwinding of the duplex ahead. Such excess local winding, termed supercoiling, influences a number of important cellular processes such as gene expression, initiation of DNA replication, binding kinetics of sequence-specific proteins to their targets, and site-specific recombination. The degree of supercoiling is consequently carefully controlled by the cell. We will examine the inherent dynamics of supercoil removal from a physical perspective using single-molecule techniques, and illustrate the importance of efficient removal by demonstrating how it is hampered under the influence of chemotherapeutic drugs.

BP 10.2 Tue 14:30 H43

Sequence-specific Topological Changes of Single DNA Molecules by Human Topoisomerase I in the Presence of Chemotherapeutic Drugs — •Fabian Czerwinski[1,2], Daniel Koster[1], Ludovic Halby[3], Ulrich Schwarz[2], Paola B. Arimondo[3], and Nynke H. Dekker[1] — [1]Kavli Institute of Nanoscience, Delft University of Technology, The Netherlands — [2]Center for Modelling and Simulation in Biosciences (BIOMS), Universität Heidelberg, Germany — [3]UMR5153 CNRS, Paris, France

Human topoisomerase I relaxes the superhelical tension associated with DNA replication, transcription and recombination by generating a transient nick in the DNA duplex. This allows the DNA to swivel about the intact strand before religating. Topoisomerase I is the sole target of the camptothecin family of anticancer compounds which stabilize the covalent enzyme-DNA complex and slow down the removal of DNA supercoils leading to lesions that can induce cell death.

Real-time activity of topoisomerase I can be monitored using magnetic tweezers. Combining these with camptothecin-associated triple-helix formation permits, for the first time, sequence-specific detection of the intercalation of single camptothecins to the enzyme-DNA complex. The imposed sequence-specificity allows repeated interrogation of a well-defined interaction, more clearly exposing the underlying biophysical processes. In the presence of a single camptothecin, the swivel rate is lower for the removal of positive supercoils than for negative ones, in agreement with in vivo experiments showing an accumulation of positive DNA supercoils in drug-treated cells.

BP 10.3 Tue 14:45 H43

Dynamics of Knotted Polymers in Nanochannels — •Wolfram Möbius[1], Erwin Frey[1], and Ulrich Gerland[2] — [1]Arnold-Sommerfeld-Zentrum für theoretische Physik, LMU München — [2]Institut für theoretische Physik, Universität zu Köln

We study the dynamics of knotted linear polymers in narrow channels with widths comparable to the polymer's persistence length. We use a combination of extensive Brownian dynamics simulations and simplified stochastic models to determine the modes of knot motion. In particular, we focus on the dynamics of knot motion along the polymer and the modes of changes in the knot's configuration. Both aspects of the dynamics can be understood within a coarse-grained stochastic model. The coarse-grained model describes our simulations quantitatively without any free parameters. Furthermore, we determine the modes of knot disassembly and the scaling behavior of the mean unknotting time as a function of the total polymer length for initially small knots.

BP 10.4 Tue 15:00 H43

Segregation of flexible polymers in confinement — •Axel Arnold — AMOLF, Amsterdam, Niederlande

During the cell replication cycle of a bacterium, it is necessary for it to replicate its DNA and separate the two resulting DNA strings such that exactly one string goes to each of the two daughter cells. It is commonly believed that a not yet detected active process has to be involved in this separation. However, scaling arguments show that the confinement of two polymers in a pore alone leads to an entropy-driven segregation which resembles an active process. Here, MD simulation results are presented which confirm the scaling predictions for the segregation time.

BP 10.5 Tue 15:15 H43

DNA melting curves in a snapshot — •Philipp Baaske and Dieter Braun — Ludwig Maximilians Universität München, Center for NanoScience, Amalienstr. 54, 80799 München

We developed a new method for measuring DNA melting curves. It combines fluorescence microscopy with laser based heating of aqueous solutions. The technique allows to measure the stability of DNA in only 150ms.

A IR-laser is focused to a microfluidic chamber (thickness 20 microns) and generates a spatial temperature distribution on the length-scale of several 100 microns. All temperatures between Tmax (e.g. 90°C) and Tmin (e.g. 20°C) are realized simultaneously. With a CCD camera two images of the fluorescence are taken: one without the laser and one with the laser switched on. From them a melting curve can be derived. The time of 150ms between the images is long enough for equilibration of the temperature and short enough to prevent thermophoresis from affecting the measurement. The state of doublestranded DNA is measured with the use of intercalating dyes and dye-quencher pairs.

In the case of doublestranded DNA the measurements are conducted in nonequlibrium because of the slow hybridization dynamics. For the fast intramolecular DNA hairpin kinetics the new technique compares well with state of the art measurements like uv absorption.

We show the possibility to discriminate single nucleotide polymorphisms (SNPs) in only 150ms, proving the use of an all optical technique for stability analysis of biomolecules.

BP 10.6 Tue 15:30 H43

Distribution of bubble lengths in DNA — •Saul Ares[1] and George Kalosakas[2] — [1]Max Planck Institute for the Physics of Complex Systems, Noethnitzer Str. 38, 01187 Dresden, Germany — [2]Department of Materials Science, University of Patras, 26504 Patras, Greece

The distribution of bubble lengths in double-stranded DNA is pre-

sented for segments of varying GC content, obtained using the Peyrard-Bishop-Dauxois model at 310 K. We provide an analytical description of the obtained distribution in the whole regime investigated, i.e. up to bubble widths of the order of tens of nanometers. The decay lengths and characteristic exponents of this distribution show two distinct regimes as a function of GC content. The observed distribution is attributed to the anharmonic interactions within base-pairs. Moreover, the same distribution is predicted by the completely independent Poland-Scheraga theory, and thus our results settles a bridge between these two different theoretical descriptions of DNA.

BP 11: Micro- and Nanofluidics

Time: Tuesday 16:00–17:15 Location: H43

BP 11.1 Tue 16:00 H43

DNA Dielectrophoresis in Microfluidic Systems: Separation and Polarizability — •Henning Höfemann[1], Jan Regtmeier[1], Ralf Eichhorn[2], Dario Anselmetti[1], and Alexandra Ros[1] — [1]Bielefeld University, Biophysics & Applied Nanosciences, Universitätsstr. 25, 33615 Bielefeld, Germany — [2]Bielefeld University, Condensed Matter Theory, Universitätsstr. 25, 33615 Bielefeld, Germany

Electrophoresis (EP) and dielectrophoresis (DEP) represent an important tool for the manipulation of DNA in microfluidic systems. Recently, we have demonstrated that the DEP and EP forces can be exploited in tailored microfluidic systems to separate long DNA strands and to quantitatively access their polarizabilities [1]. The microfluidic device includes periodically arranged rows of posts generating DEP traps for DNA upon application of an AC voltage. Further an additional DC voltage invokes migration of DNA through the microchannel. The subtle interaction of the DNA with the created energy landscape, tuned by the parameters of the DC offset and AC conditions (amplitude and frequency) allows a precise control of the length dependent migration and trapping of DNA. Here, we extend our studies and demonstrate the length dependent migration of covalently closed circle DNA in a size range between 7 and 23 kpb including the quantitative deduction of DNA polarizabilities. Our future work is dedicated to the exploitation of this novel migration mechanism to the separation of DNA varying in length and conformation. [1] J. Regtmeier, T. T. Duong, R. Eichhorn, D. Anselmetti, A. Ros; Dielectrophoretic Manipulation of DNA: Separation and Polarizability, 2006, submitted

BP 11.2 Tue 16:15 H43

Self-propulsive motions of elastic filaments — •Hirofumi Wada and Roland Netz — Physics Department, TUM, Garching, Germany

Microbiology provides rich examples of self-propulsive motions in a viscous fluid, where inertia plays no role and the concept of momentum conservation does not work. In such a inertia-less limit, the Navier-Stokes equation is linearized, leading to the conclusion that geometrically reversible motion does not render any net thrust. Using hydrodynamic simulations, we study propulsive behavior of a few types of model-Stokesian swimmers with slender filaments, such as a rotating elastic rod and bistable helices. The generation of a shape change through an elastic instability or an active excitation results in a substantial forward thrust. The hydrodynamic efficiency, as well as its optimum condition, is examined in presence of thermal fluctuations. Its biological connection is also discussed.

BP 11.3 Tue 16:30 H43

Light Driven Microfluidics — •Franz Weinert and Dieter Braun — Noether Group on Dissipative Biosystems, LM-University Munich, Amalienstr. 54, D-80799 Munich, Germany

Microfluidics will play a major role for complex liquid manipulation in a wide variety of biological and chemical applications of the life sciences. In conventional microfluidics, liquid is pumped and switched through lithographically defined channels. Such microfluidic chips have to connect to a considerable complex interface for pumping, switching and providing the liquids.

We present an all-optical fluid flow control, which allows highly flexible and dynamic liquid handling, both in microfluidic channels and twodimensional gels. The fluid follows the arbitrary shaped path of an infrared laser scanning microscope without the need for microfluidic tubings and valves.

The physics behind is thermal expansion in a viscosity gradient, an effect previously not considered. We derive an analytical solution for the pump speed directly from the Navier-Stokes equations. Thermal relaxation is on the millisecond time scale and allows fast repetition of the laser spot movement. Pump speed rises quadratically for decreasing thickness, making the mechanism perfectly suitable for Nanofluidics. Under moderate conditions, pump speeds are 20 μm/s in a 2.5 μm thin water film. Notably, highly viscous liquids can be equally pumped. The novel mechanism allows highly miniaturized microfluidics under dynamic control without predefined channels.

BP 11.4 Tue 16:45 H43

Ionic currents in nanochannels and carbon nanotubes — •Christine Meyer, Jereon de Grebber, Vishal Merani, Derek Stein, Frank van der Heyden, Marc Zuiddam, Emile van der Drift, and Cees Dekker — Kavli Institute of Nanoscience, TU Delft, The Netherlands

The behaviour of electrolyte solutions in small confinements can differ a lot from bulk behaviour. This makes salt solutions in artificial nanofluidic channels an interesting subject for investigation.

Nanofluidic channels were fabricated using a sacrificial etch process. A sacrificial silicon layer that mimics the channel is covered with silicon oxide. Once the sacrificial layer is etched away selectively, a channel is created that we fill with an electrolyte solution. Using the same fabrication scheme, we plan to integrate a single-wall carbon nanotube as an ultimately small fluidic channel.

We investigated the ionic conductance of nanochannels as a function of salt concentration and found a saturation in the low-salt regime. With respect to the expected bulk conductance, the current in the saturation regime is enhanced. We can explain this by assuming that ions in the Debye layer, i.e. ions that screen surface charges, become the dominant charge carriers in this regime. If we can change the surface charge e.g. electrically, the conductance of the channel should change accordingly, which would lead to an "ionic transistor".

BP 11.5 Tue 17:00 H43

Thermophoretic Biomolecule Analytics — •Stefan Duhr and Dieter Braun — Ludwig Maximilians Universität München, Center for Nanoscience (CeNS), Amalienstrasse 54, 80799 München

Molecules drift along temperature gradients, an effect called thermophoresis, Soret-effect or thermodiffusion. We present a recently developed microscopic theory [1] based on solvation entropy. Stated in simple terms, the Soret coefficient is given by the negative solvation entropy, divided by kT. The theory predicts the thermodiffusion of polystyrene beads and DNA without any free parameters. This description holds as long as particles are in local thermodynamic equilibrium, which is valid for small molecules at moderate temperature gradients. Based on this theory, slight changes of surface properties on the molecular level lead to profound changes in thermophoretic behavior. We show experimental results for fast molecule characterization by thermophoresis. Thermal gradients provide a good tool to differentiate between DNA of different length within a few seconds, but they also allow for detection of biomolecule interactions. Thermophoresis may proof a very effective technique for biotechnological applications.

Reference: [1] S.Duhr and D.Braun, Why molecules move along a temperature gradient, PNAS, in press

BP 12: Neuroscience

Time: Tuesday 10:30–12:15 Location: H44

Invited Talk BP 12.1 Tue 10:30 H44

The first micro seconds in the life of a nerve impulse — •Fred Wolf — MPI for Dynamics and Self-Organization, 37073 Goettingen, Germany

The first micro seconds in the life of a nerve impulse

Neurons process and encode information by generating sequences of action potentials(APs). In the living brain, neurons operate under an intense synaptic bombardment causing strong and seemingly random fluctuations of their membrane potentials. Recent theoretical studies have revealed that under such conditions apparently minor modifications of the initiation dynamics of APs can dramatically change the nature of AP encoding (1-4). These studies have triggered a re-evaluation of the dynamics of AP generation in real nerve cells (3-5). Intriguingly, these studies indicate that (i) the actual dynamics of neuronal APs qualitatively deviates from the predictions of the canonical and widely accepted physiological model of AP generation, the Hodgkin and Huxley model, and that (ii) the AP dynamics appears to be optimized for the processing of fast varying signals (3,4). Here, I will discuss theoretical analyses of neuronal encoding, biophysical models, and in vitro experiments supporting the hypothesis that a direct cooperativity between sodium channel molecules within the neuronal membrane forms the origin of this unanticipated phenomenon.

(1) Fourcaud-Trocme et al. J.N. 23:11628 (2003) (2) Naundorf, Geisel, Wolf J.C.N. 18:297 (2005) (3) Naundorf, Wolf, Volgushev Nature 440:1060 (2006) (4) Naundorf, Wolf, Volgushev Nature, 445:E2 (2007) (5) MacCormick, Shu, Yu Nature 445:E1 (2007)

BP 12.2 Tue 11:00 H44

On the stationary state of a network of inhibitory spiking neurons — •Wolfgang Kinzel — Theoretische Physik, Universität Würzburg

The background activity of a cortical neural network is modeled by a homogeneous integrate-and-fire network with unreliable inhibitory synapses. Numerical and analytical calculations show that the network relaxes into a stationary state of high attention. The majority of the neurons has a membrane potential just below the threshold; as a consequence the network can react immediately - on the time scale of synaptic transmission- on external pulses. The neurons fire with a low rate and with a broad distribution of interspike intervals. Firing events of the total network are correlated over short time periods. The firing rate increases linearly with external stimuli. In the limit of infinitely large networks, the synaptic noise decreases to zero. Nevertheless, the distribution of interspike intervals remains broad.

BP 12.3 Tue 11:15 H44

Stimulation mechanisms of neurons in dissociated networks on wide planar electrodes — •A. Reiher[1], H. Witte[1], A. Krtschil[1], A. de Lima[2], A. Nörenberg[2], T. Voigt[2], and A. Krost[1] — [1]Inst. of Exp. Physics, Uni Magdeburg, PO Box 4120, 39016 Magdeburg — [2]Inst. of Physiology, Uni Magdeburg, Leipziger Str. 44, 39120 Magdeburg

Dissociated nerve cells from embryonic rat cerebral cortex form electrophysiologically active networks. If these networks are cultured on planar interdigitated gold electrodes, the stimulation conditions and the response of the cells can be analyzed. A blockade of synaptic activity in networks with antagonists to neurotransmitters glutamate and $GABA_A$ receptors offers the possibility to investigate the stimulation mechanism of isolated neurons. A significant parameter for stimulation is the lateral distribution of the field strength along the interface. Measurements and simulations of the field strength exhibited a geometry induced enhanced field strength along the electrode edges. Position dependent analysis of stimulated somata in synaptically blocked networks revealed a sporadic correlation between the number of excited neurons and the local electrical field strength. We varied the density of cell extensions along the electrode edges in specially designed networks to investigate whether the stimulation is realized via somata or dendrites and axons. After blocking the synaptic transmission, the stimulation is more efficient via dendrites and axons. We explain the excitation mechanism taking into account the geometrical distribution of cell extensions crossing electrode areas of high electric field strengths.

BP 12.4 Tue 11:30 H44

Modeling Neural Correlates of Selective Attention — •Hecke Schrobsdorff[1,2], Matthias Ihrke[1,3], Jörg Behrendt[1,3], Björn Kabisch[1], Marcus Hasselhorn[1,3], and Michael Herrmann[1,2] — [1]Bernstein Center for Computational Neuroscience Göttingen — [2]Institute for Nonlinear Dynamics — [3]Georg-Elias-Müller Institute, Göttingen University

In order to reveal cognitive mechanisms of selective attention, we study the paradigm of negative priming. In negative priming experiments, subjects have to discriminate a target from a distractor stimulus. While identical targets in two subsequent displays, the positive priming condition, leads to a speedup in reaction time, the opposite effect, a slowdown, is achieved if the former distractor becomes target in the actual display, called negative priming.

We model the process of discrimination by a dynamical systems approach with an adaptive threshold suppressing irrelevant stimuli. Our model perfectly explains phenomenological data, furthermore it makes predictions about behavior in rare stimulus configurations. Semantic representations of different stimuli are modeled by an activation level of cell assemblies. Therefore the model provides an interpretation of systematic variations of event related potentials from EEG recordings during negative priming trials.

BP 12.5 Tue 11:45 H44

Sequential Desynchronization of Clusters in Neural Networks with Partial Post-Spike Response — •Christoph Kirst[1,2] and Marc Timme[2,3,4] — [1]Faculty of Mathematics, University of Cambridge, CB3 0WA, United Kindom — [2]Network Dynamics Group, Max Planck Insitute for Dynamics and Selforganisation and — [3]Bernstein Center for Computational Neuroscience Göttingen, Bunsenstr. 10, 37073 Göttingen, Germany — [4]Center for Applied Mathematics, Theoretical and Applied Mechanics, Kimball Hall, Cornell University, Ithaca, NY 14853, USA

The response of a biological neuron to incoming signals strongly depends on whether or not it has just emitted a spike. Here we propose an analytically tractable network model of spiking neurons with partial post-spike response, that bridges between total charge conservation and total charge loss of supra-threshold inputs considered in previous models. For a rise of the membrane potential towards the firing threshold with a convex shape we find a sequence of desynchronization transitions between sets of admissable cluster states that is controlled by the strength of the post-spike response. We explain the mechanism underlying this transition and reveal similar phenomena in biophysically detailed models.

BP 12.6 Tue 12:00 H44

Non-invasive detection of human brain function using diffusing-wave spectroscopy — J. Li[1], F. Jaillon[1], G. Dietsche[1], T. Elbert[2], B. Rockstroh[2], G. Maret[1], and •T. Gisler[1] — [1]Universität Konstanz, Fachbereich Physik, 78457 Konstanz — [2]Universität Konstanz, Fachbereich Psychologie, 78457 Konstanz

Near-infrared light which is multiply scattered by biological tissue contains rich information on microscopic motions of scatterers deep within the tissue. The analysis of the speckle pattern fluctuations in terms of microscopic particle displacements is the basis of diffusing-wave spectroscopy (DWS), the extension of quasi-elastic light scattering to the regime of strong multiple scattering.

DWS was recently used to detect the activation of the human motor cortex upon somatosensory stimulation through the intact scalp and skull [1, 2]. Analyzing the measured autocorrelation functions of the scattered electric field a significant, hemispherically asymmetric acceleration of the cortical dynamics upon stimulation was found.

The origin of this accelerated dynamics has not entirely been clarified. In this contribution we present DWS measurements with a multispeckle detection setup which allows to follow non-stationary scatterer dynamics upon different stimulation protocols (motor, visual, and memory) with a temporal resolution of 26ms and to discriminate scatterer dynamics related to pulsation from other mechanisms.

[1] T. Durduran et al., Opt. Lett. 29, 1766-1768 (2004). [2] J. Li et al., J. Biomed. Opt. 10, 044002-1-12 (2005).

BP 13: Photobiophysics

Time: Tuesday 12:30–13:15 Location: H44

BP 13.1 Tue 12:30 H44

Fluorescence spectroscopy of single peridinin - chlorophyll a - protein light - harvesting complexes — •Stephan Wörmke[1], Sebastian Mackowski[1], Tatas Brotosudarmo[1], Christoph Bräuchle[1], Hugo Scheer[2], and Eckhard Hofmann[3] — [1]Department of Chemistry and Biochemistry and Center for Nanoscience, Ludwig-Maximilian-University, D-81377 Munich, Germany — [2]Department of Biology, Ludwig-Maximilian-University, D-80638 Munich, Germany — [3]Department of Biology, Ruhr-University Bochum, D-44780 Bochum, Germany

We report on single molecule spectroscopy studies of native and reconstituted peridinin - chlorophyll a - protein (PCP) light - harvesting complexes. In its native form PCP is a trimer of protein subunits, while the artificial complexes are of predominantly monomeric structure; they contain only two chlorophylls. We find that native PCP features better photostability and emits approximately 3 times more photons. The fluorescence trajectories detected for reconstituted complexes feature two intensity steps, each attributable to single chlorophyll fluorescence. During the consecutive bleaching of the chlorophylls, we do not observe any change in either the fluorescence frequency or the intensity of the remaining chlorophyll. This implies that the interaction between the fluorescing chlorophylls within the PCP monomer is extremely weak. The quite unique property allows us to independently monitor fluorescence of each of the chlorophylls and obtain valuable information about the energy splitting, spectral dynamics of the fluorescence and energy transfer from peridinins to chlorophyll.

BP 13.2 Tue 12:45 H44

Resonante Ramanspektroskopie an Photosystem I und II — •Katharina Brose[1], Norman Tschirner[1], Christian Thomsen[1], Athina Zouni[2] und Peter Hildebrandt[2] — [1]Institut für Festkörperphysik, TU Berlin, Deutschland — [2]Institut für Physikalische und Theoretische Chemie, TU Berlin, Deutschland

Pflanzen wandeln Photonenenergie mit Hilfe zweier photochemischer Komplexe, genannt Photosystem I und II, in chemische Energie um. Das Licht wird dabei von Pigmentkomplexen absorbiert und die Energie über Elektronenübergänge in das Reaktionszentrum des Photosystems geleitet. Dort wird die Energie zur Oxidation von H_2O zu O_2 und zur Reduktion von $NADP^+$ zu NADPH verwendet.

An belichteten und unbelichteten Proben wurden im sichtbaren und nahen infraroten Wellenlängenbereich resonante Ramanspektren aufgenommen und mit Hilfe einer Differenzmethode[1] ausgewertet. Ziel war die Untersuchung des Einflusses einzelner Pigmente (vornehmlich Carotine und Chlorophylle) innerhalb des Reaktionsablaufs für die verschiedenen Photosysteme.

[1] A. P. Shreve, N. J. Cherepy and R. A. Mathies, Appl. Spectrosc., 46, 707 (1992)

BP 13.3 Tue 13:00 H44

Light Guidance by Living Cells — •Kristian Franze[1,2], Jens Grosche[1], Serguei Skatchkov[3], Stefan Schinkinger[2], Detlev Schild[4], Ortrud Uckermann[1], Kort Travis[2], Andreas Reichenbach[1], and Jochen Guck[2] — [1]Paul-Flechsig-Institute of Brain Research, Universität Leipzig — [2]Soft Matter Physics, Universität Leipzig — [3]CMBN, Universidad Central de Caribe, Bayamon, USA — [4]DFG Research Center, Universität Göttingen

While cells are mostly transparent they are phase objects that differ in shape and refractive index. Any image that is projected through layers of cells will normally be distorted by refraction, reflection, and scattering. Strangely, the retina of the vertebrate eye is inverted with respect to its optical function and light must pass through several tissue layers before reaching the light-sensitive photoreceptor cells, with each photon having a chance of being scattered. Here we report how nature has optimized this apparently unfavourable situation. We investigated the optical properties of retinal tissue and individual Müller cells, which are radial glial cells spanning the entire thickness of the retina. We found that these cells act as optical fibers and guide light that would otherwise be scattered from the retinal surface to the photoreceptor cells. Their parallel arrangement in the retina is reminiscent of fiber-optic plates used for low-distortion image transfer. Thus, Müller cells seem to mediate the image transfer through the vertebrate retina with minimal distortion and low loss. This finding explains a fundamental feature of the inverted retina as an optical system and it ascribes a new function to glial cells.

BP 14: Chemotaxis

Time: Tuesday 14:30–15:15 Location: H44

BP 14.1 Tue 14:30 H44

Chemotaxis of Sperm Cells — •Benjamin Friedrich and Frank Jülicher — Max-Planck-Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, Dresden

Sperm cells swim towards the egg propelled by a flagellum which beats regularly. In many species sperm show chemotaxis, i.e. they move upwards a gradient of chemoattractant molecules released by the egg. Based on recent experiments on sea urchin sperm which indicate that the geometry of swimming trajectories is controlled by a signaling system in the sperm flagellum [1], we present a theoretical description of sperm chemotaxis. We discuss swimming trajectories in two and three dimensions in the presence of a chemoattractant source. From this discussion, we derive the necessary properties of the signaling system which ensure reliable motion towards the source.

[1] B. Kaupp *et al.*: NCB **5**,109 (2003)

BP 14.2 Tue 14:45 H44

Cytoskeletal dynamics in response to complex temporal signals — •Carsten Beta[1], Hellen Ishikawa[2], Till Bretschneider[2], Günther Gerisch[2], and Eberhard Bodenschatz[1] — [1]MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]MPI of Biochemistry, Martinsried, Germany

Understanding of cytoskeletal dynamics has seen a rapid advance through the use of fluorescent fusion proteins. Further progress in this field relies on experimental techniques to stimulate single cells with high temporal resolution. We combine microfluidic techniques with the photo-chemical release of caged signaling agents to expose cells to well-defined stimuli with changing temporal patterns. We apply this approach to quantify intracellular translocation of various fluorescently labeled cytoskeletal proteins in chemotactic *Dictyostelium* cells responding to complex temporal stimuli with cAMP.

BP 14.3 Tue 15:00 H44

Intracellular dynamics during directional sensing of chemotactic cells — •Gabriel Amselem, Eberhard Bodenschatz, and Carsten Beta — MPI for Dynamics and Self-Organization, Göttingen, Germany

We use an experimental approach based on the photo-chemical release of signaling molecules in microfluidic environments to expose chemotactic cells to well controlled chemoattractant stimuli. We apply this technique to study intracellular translocation of fluorescently labeled PH-domain proteins in the social ameba *Dictyostelium discoideum*. Single chemotactic *Dictyostelium* cells are exposed to localized, well defined gradients in the chemoattractant cAMP and their translocation response is quantified as a function of the external gradient.

BP 15: Biopolymer Solutions and Networks

Time: Tuesday 15:15–17:15 Location: H44

BP 15.1 Tue 15:15 H44

Protein Network Formation and Manipulation in Microfluidic Devices — •Heather Evans, Enkhtuul Surenjav, Craig Priest, Ralf Seemann, Stephan Herminghaus, and Thomas Pfohl — Max Planck Institute for Dynamics & Self-Organization, 37073 Goettingen

Microfluidic structures are particularly well-suited for controlled investigations of protein bundle and network formation. In addition to their ease of preparation and micrometer length scales, the myriad geometries and flow fields in such microdevices enable time-dependent investigations of non-equilibrium phenomena. We present studies of the blood clotting protein fibrin, a three-dimensional network formed from the enzymatic cleavage of fibrinogen monomers by the protein thrombin. Fibrin is a vital component of blood clots, and has been implicated in a variety of diseases. Real-time high resolution fluorescence microscopy and x-ray micro-diffraction are used to quantify supramolecular assembly and provide snapshots of the evolution of fibrin network formation. These techniques complement one another, providing information about fibrin assembly on length scales ranging from nanometers to micrometers. Specially designed microfluidic devices are also able to mechanically deform the fibrin networks within enclosed compartments. In this context, we report the influence of parameters, such as enzyme concentration and flow velocity, on fibrin network properties.

BP 15.2 Tue 15:30 H44

Contours and Thermal Fluctuations of Individual F-actin Filaments in Entangled Networks — •Marta Romanowska[1,2], Bernd Hoffmann[1], Norbert Kirchgessner[1], Margret Giesen[1], and Rudolf Merkel[1] — [1]Institute of Bio- and Nanosystems: Biomechanics, Research Centre Jüllich, 52425 Jülich, Germany — [2]Marian Smoluchowski Institut of Physics, Jagiellonian University Krakow, Reymonta 4, 30-059 Krakow, Poland

Recently significant scientific interest has been focused on the contours and fluctuations of isolated actin filaments. Moreover, rheological properties of F-actin solutions were characterized in detail. However, studies of the behavior of individual filaments within F-actin solutions are scarce.

To fill this gap, we analyze F-actin filaments in entangled networks by means of Confocal Laser Scanning Microscopy. From real-time observations of the Brownian motion time-averaged filament contours and the fluctuations around them are determined. Our system comprises of fluorescently labelled and phalloidin-stabilized reporter filaments embedded in a 3-D solution of unlabelled ones. Hence, the polymer conformations are determined by a competition of intrinsic filament stiffness and steric constraints induced by surrounding filaments. We investigate the effect of actin concentration as a parameter representing the strength of the confinement. Furthermore, we evaluate some static equilibrium properties of the filaments and compare our findings to theoretical results based on the wormlike chain model and the tube concept.

BP 15.3 Tue 15:45 H44

Dynamic Properties of individual F-Actin Filaments in 3D Networks — •masashi degawa, bernd hoffmann, rudolf merkel, and margret giesen — Forschungszentrum Juelich IBN4, 52425 Juelich Germany

The rigidity and dynamical properties of the cell cytoskeleton are determined by a 3D network of polymerized one-dimensional protein filaments, one of which is the actin filament (F-actin). The understanding of the thermodynamics of F-actin filaments is crucial for cell biophysics, specially within such a network. Whereas isolated F-actin is well described by the worm-like chain model [1], knowledge of thermodynamic properties of F-actin in networks is still scarce. Here we present first studies of F-actin within a 3D network where the presence of other filaments serves as an entropic constraint. We used partially TRITC-labeled networks of different concentration. The fluctuations of the labeled filaments were visualized with line-scan confocal scanning microscopy time images with a time resolution of 1 ms. We measure the time dependence of the filament fluctuations, which yield a concentration dependence of the crossover time in the time correlation function from isolated to constrained behavior of the individual F-actin. [1] L. Le Goff, O. Hallatschek, E. Frey, F. Amblard, Phys. Rev. Lett. 89, 258101 (2002)

BP 15.4 Tue 16:00 H44

Tube Radius in Entangled Networks of Semiflexible Polymers — •Hauke Hinsch, Jan Wilhelm, and Erwin Frey — Arnold Sommerfeld Center und CeNS, Department of Physics, Ludwig-Maximilians-Universität München

The mechanical properties of the cytoskeleton play an important role in many cellular functions like locomotion or adhesion. One of the cytoskeleton's dominant constituents is a network structure composed of the semiflexible polymer F-Actin. To connect the single polymer properties to the macroscopic behavior of the network, a single polymer is considered to be constrained to a tube established by neighboring filaments. Here we focus on the tube's diameter in entangled networks. While scaling laws for the tube diameter are well established, the absolute value is still under debate and different theoretical concepts and experimental measurements exist.

We present a new approach to the problem and have conducted extensive computer simulations to check the validity of our assumptions. A model of independent rods is used to describe the confinement of a single semi-flexible polymer in the network environment. A self-consistency approach allows us then to derive an absolute tube radius for the network as a function of several parameters and compare our results to experimental measurements.

BP 15.5 Tue 16:15 H44

Mechanics of bundled semiflexible polymer networks — •Oliver Lieleg[1], Mireille Claessens[1], Claus Heussinger[2], Erwin Frey[2], and Andreas Bausch[1] — [1]Lehrstuhl für Biophysik E22, Physik-Department, Technische Universität München, D-85747 Garching, Deutschland — [2]Arnold Sommerfeld Zentrum für Theoretische Physik und CeNS, Physik-Department, Ludwig-Maximilians-Universität München, D-80333 München, Deutschland

Cell shape, mechanics and motility are mainly determined by cross-linked and bundled actin networks. Despite their importance, the mechanical function of cross-linking molecules is not well understood. As in living cells many different actin binding molecules are used simultaneously, it is necessary to study their effect in in vitro systems. As we present here, above a critical concentration of the actin binding protein fascin, a solution of actin filaments organizes into a network of bundles. This structural transition is characterized by the competition between confinement energy and binding enthalpy. The mechanical response of the bundled network can be fully understood in terms of cross-linked bundles that consist of loosely coupled filaments and undergo non-affine bending undulations. Moreover, the mechanical properties of actin/fascin bundle networks can be described by a single pair of master curves over almost eight orders of magnitude in rescaled frequency. This remarkable finding can be attributed to the coarsening, self-similar network-structure.

BP 15.6 Tue 16:30 H44

Random Networks of Semiflexible Polymers — •Panayotis Benetatos and Annette Zippelius — Institut für Theoretische Physik der Universität Göttingen

We consider a fluid of semiflexible polymers modelled as identical wormlike chains with an excluded-volume interaction which prevents the system from collapsing. We introduce permanent cross-links which fix the tangent vectors of the corresponding filament segments to be parallel, and we treat them as quenched disorder which follows the Deam-Edwrads distribution. We present a semimicroscopic replica field theory of the formation of a random network. We show that, upon increasing the cross-link density in the fluid, an isotropic amorphous solid phase emerges in which the orientations of the chains are frozen in random directions. At a higher cross-link density, a different transition to an orientationally ordered phase is also possible.

BP 15.7 Tue 16:45 H44

Active and passive microrheology — •Daisuke Mizuno[1,2], Fredrick MacKintosh[1], and Christoph Schmidt[1,2] — [1]Department of Physics and Astronomy, Vrije Universiteit, Amsterdam, The Netherlands — [2]III. Physikalisches Institut, Fakultät f. Physik, Georg-August-Universität, Göttingen, Germany

We have developed active and passive, 1- and 2-particle microrheology (MR) using micron-sized colloidal particles as probes. Two laser beams focused through a microscope objective serve to both detect probe motion and exert controlled forces on the probes. Both active and passive MR can be done in a frequency range of 0.1Hz to 100 kHz. We compare results on model systems and discuss pros and cons of both technologies.

BP 15.8 Tue 17:00 H44

Modelling Non-Brownian Fluctuations in Stress Fiber Networks — •Claus Metzner, Carina Raupach, Daniel Paranhos-Zitterbart, and Ben Fabry — Biophysics Group, University of Erlangen, Germany

Microbeads attached to the intracellular actomyosin network show spontaneous fluctuations of non-thermal origin. Their motion is characterized by a transition from sub- to superdiffusive mean square displacement (MSD) with increasing lag time. This signature, associated with qualitative changes of the turning angle distribution, is reminescent of a particle diffusing in a potential well with slowly drifting minimum position. By solving this drifting well model analytically, we show that the complex statistical properties of the observed bead trajectories are captured by a small number of parameters.

Next we demonstrate numerically that a dynamic stress fiber network is a biologically plausible realization of drifting well behaviour. Essential features of the network include the formation of new fibers by actin polymerization, the building up of prestress by myosin cross-bridges, the elastic properties of the established fibers, and the reverse processes of fiber degradation. Here, noise caused by myosin activity represents the non-thermal driving force of the diffusion. Established fibers, adhering to the bead surface and connecting radially to the remaining network, form an elastic cage and create a plateau in the MSD. The occasional formation or degradation of bead-linked fibers gives rise to superdiffusive and directed motion on longer time scales.

BP 16: Poster Session I

Time: Tuesday 17:00–19:30 Location: Poster D

BP 16.1 Tue 17:00 Poster D

Preparation of dense arrays of end-tethered DNA on solid substrates — •hui li, juha koota, ina seuffert, alexander andré, georg maret, and thomas gisler — Fachbereich Physik, Universität Konstanz, 78457 Konstanz, Germany

We discuss various routes to produce dense end-tethered arrays of long-chain DNA molecules to solid substrates, using DNA carrying end groups such as biotin or thiol which specifically bind to surface-anchored streptavidin or gold.

Conventional end-tethering by adsorption of coiled DNA results in low tethering densities and mushroom-like conformations [1] due to the entropic repulsion of the coils. Using DC electric fields applied via conducting substrates such as gold or streptavidin-coated indium-tin oxide, DNA can be driven to the surface by electrophoresis. However, the high viscosity of the high DNA concentration near the surface dramatically slows down the tethering, resulting in only moderate enhancements of the tethering density.

As an alternative approach we exploit the liquid crystalline order in DNA solutions induced by osmotic stress [2] or by convective deposition onto a pinned contact line occurring in a "coffee ring" [3]. We investigate the effects of end-functionalization and end-tethering on liquid crystalline textures, and resulting tethering densities.

[1] R. Lehner, et al. Phys. Rev. Lett. 96 (2006), 107801.

[2] R. Podgornik, et al. Proc. Natl. Acad. Sci. USA 93 (1996), 4261-4266.

[3] I.I. Smalyukh, et al. Phys. Rev. Lett. 96 (2006), 177801.

BP 16.2 Tue 17:00 Poster D

Biological surfaces and their response to environmental stress — •Agnieszka Krol-Otwinowska, Karl Hieble, and Margret Giesen — Institute of Bio- and Nanosystems IBN-4, Research Centre Jülich GmbH, Germany

Biological surfaces form the interface between a living organism and the atmosphere. In addition, they mediate the response of a living organism to environmental stress by means of structural changes and chemical reactions. On the molecular scale, structural changes and chemical reactions generally involve changes in the local polarization of the electron charge density in the biological surfaces, which opens a pathway to study the response of biological surfaces to environmental stress from a surface scientist's perspective: Change in the local polarization of the electron charge density is the origin of the mechanical surface stress which is defined as the total work to enlarge the area of a solid surface by a certain amount. For the first time, we introduce measurements of the surface stress of biological surfaces under natural conditions and demonstrate that changes in the surface stress are sensitive indicators for the interaction of biological surfaces with their environment. As an example we present measurements of the surface stress of plant leaf wax layers and its dependence on climatic relevant parameters (gases, air humidity, UV-light).

BP 16.3 Tue 17:00 Poster D

Fast and Light-Efficient Wavefront Sensing — •Marcel Andreas Lauterbach, Markus Rueckel, and Winfried Denk — Max Planck Institute for Medical Research, Department of Biomedical Optics, Jahnstr. 29, 69120 Heidelberg, Germany

Adaptive Optics can improve the image quality of confocal/multi-photon microscopic images by correcting wavefront distortions of the excitation beam. The wavefront distortions can originate from the sample itself and must be measured for correction. The wavefront sensing should be light-efficient to allow fast correction and to avoid photodamage in the biological sample during the measurement process.

We developed an interferometer-based virtual modal wavefront sensor (VMWS) that can be configured to measure, for example, Zernike coefficients directly. This sensor is particularly light efficient. Including up to Zernike mode 21, aberrations can be determined with a precision of about 0.17 rad ($\lambda/37$) using low resolution (65 * 65 pixels) images and only about 400 photons total.

The VMWS uses Phase Shifting Interferometry (PSI), for which we developed a new scheme ("Nonlinear PSI" (NPSI)), which makes faster measurements possible. It allows an almost arbitrary reference phase shift during the interferogram recording. We especially investigated the case of a sinusoidal phase shift. We show results of wavefront measurements and the comparison with theoretical considerations and envision the applicability of the VMWS and NPSI to confocal/multi-photon microscopy. VMWS and NPSI are not limited to microscopy but should be applicable whenever a reference wavefront is available.

BP 16.4 Tue 17:00 Poster D

Energy Transfer between Photosynthetic Pigment-Protein Complexes in Model Membrane Systems — •Tobias Pflock[1], Manuela Dezi[2], Giovanni Venturoli[2], Jürgen Köhler[1], and Silke Oellerich[1] — [1]Experimentalphysik IV, Universität Bayreuth, D-95447 Bayreuth — [2]Dept. of Biology, University of Bologna, Italy

The photosynthetic unit (PSU) of purple bacteria represents a well known model system in photosynthesis research. It mainly consists of protein complexes, namely LH2 and LH1-RC, which contain photoactive pigment molecules harvesting solar light. The ring-shaped complexes are embedded in lipid membranes to form functional units that very efficiently transfer the excitation energy to the reaction center (RC). Therefore, the supramolecular organisation of the PSU within the biological membrane plays a significant role, and it is of particular interest to understand how the involved lipids contribute to the spatial arrangement of the membrane proteins.

In order to address this question systematically, we chose to reconstitute proteins into large unilamellar vesicles (LUV). This allows us to control the membrane lipid composition as well as the lipid-protein ratio. Selective excitation of the pigments embedded in LH2 rings by a pulsed laser makes it possible to determine the transfer efficiency to LH1-RC units directly via fluorescence lifetime measurements. Using a streak camera system we studied the fluorescence decay of reconstituted pigment-protein complexes to characterize excitation energy transfer from LH2 to LH1-RC complexes.

BP 16.5 Tue 17:00 Poster D

Lipid-mediated protein interactions in lipid bilayers — •Beate West and Friederike Schmid — Fakultät für Physik, Universität Bielefeld, Universitätsstr. 25, 33615 Bielefeld

Lipid-mediated interactions play a central role for the interactions between proteins in a lipid bilayer. The lipid bilayer as well as the proteins are simulated using a coarse-grained model.

We study how proteins influence the structure of the lipid bilayer at different temperatures, and, on the other hand, how the lipids influence the interactions of the proteins. To this end, we calculate the effective pair potential between the proteins with the method of umbrella-sampling.

BP 16.6 Tue 17:00 Poster D

Fluctuation-dissipation relation for colloidal particles in shear flow — •Thomas Speck and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

In equilibrium, the well-known fluctuation-dissipation theorem (FDT) connects the response of an observable with its auto-correlation function. For driven systems, breaking of detailed balance leads to dissipation and to the breakdown of the FDT. We have shown recently how to quantify this violation in terms of velocity correlations and how to restore then the original form of the FDT [1]. We investigate the violation function in the case of two interacting colloidal particles driven by shear flow and illustrate our results with numerical calculations.

[1] T. Speck and U. Seifert, Europhys. Lett. **74**, 391 (2006).

BP 16.7 Tue 17:00 Poster D

Cell shape-dependent forces at focal adhesions — •Sebastian Schmidt[1], Ilka Bischofs[2], and Ulrich Schwarz[1] — [1]University of Heidelberg, Im Neuenheimer Feld 293, D-69120 Heidelberg, Germany — [2]University of California at Berkeley, Department of Bioengineering, 717 Potter Street, Berkeley CA 94720, USA

Adhesion-dependent cells probe the mechanical properties of their environment by internally generated forces transmitted to the extracellular environment at sites of focal adhesions, with dramatic consequences for different physiological processes, including cell division and lineage specification. We introduce a mechanical model which allows to relate cellular forces applied to focal adhesions with their shape. Our model predicts that forces at focal adhesions are mainly determined by the line tension present in the cell contour. Both surface tension in the cell envelope and extracellular stiffness have an indirect effect by changing the geometrical arrangement through which the line tension acts. We also discuss the effect of tension-mediated reinforcement of the cell contour.

BP 16.8 Tue 17:00 Poster D

Energy transfer processes in a bisporphyrinic switch — •Jedrzej Szmytkowski[1,3], Robert Hauschild[1], Manfred Scholdt[1], Teodor Silviu Balaban[2,3], and Heinz Kalt[1,3] — [1]Univesität Karlsruhe (TH), Karlsruhe, Germany — [2]Forschungszentrum Karlsruhe, Institute for Nanotechnology, Karlsruhe, Germany — [3]Center for Functional Nanostructures (CFN), Karlsruhe, Germany

Energy transfer processes are the first step in light-harvesting and have been optimized in photosynthetic organisms. Artificial mimics are essential in understanding and controlling the efficiency with which after photon capture an energetic trap can be accessed. We have studied various bis-porphyrinic constructs, covalently attached to spacers such as a rigid steroidal skeleton or a terpyridine capable of undergoing a conformational switch from an extended "W" conformation into a more compact "U" form. The switching can be performed by addition of coordinating metals or of ditopic ligands. Singlet-singlet energy transfer was put into evidence by time-resolved fluorescence and the data have been analyzed using decay associated spectra (DAS). While in the steroidal systems a Förster-type energy transfer occurs, the rate and efficiency of the energy transfer can be influenced by the added ligand in the terpyridinc constructs.

BP 16.9 Tue 17:00 Poster D

Accuracy check of detection algorithms for fluorescent colloidal spheres by simulation — •Markus Gyger — Institute for Soft Matter Physics, University of Leipzig, Linnéstr. 5, 04103 Leipzig, Germany

In the discussion about like-charge attraction of colloidal spheres confined between parallel glass-plates there have been indications that the observed attraction is an artifact due to diffraction effects in optical video microscopy. We present a simulation technique which checks the accuracy of the detection algorithms for confined fluorescent colloidal particles and allows for determination of the difference between real and detected particle position in dependance on the interparticle separation. To that aim, images of interacting particles, whose positions were detected by different particle detection algorithms, were computer generated, simulating the image-taking process of digital video microscopy. Re-detecting the particle positions from the simulated images and comparing them with the originally detected positions provides some insight into the detection accuracy and systematic errors of the detection algorithms.

BP 16.10 Tue 17:00 Poster D

Brownian dynamics simulations of protein cluster assembly — •Jakob Schluttig and Ulrich Schwarz — University of Heidelberg, Im Neuenheimer Feld 293, D-69120 Heidelberg

Most proteins in the cell are active in complexes with two to several hundreds of components. Because only very small assemblies can be studied in an all-atom framework, coarse-grained approaches are required to model the association and dissociation dynamics of larger protein assemblies. We model proteins as spherical particles covered with few binding sites. Their motion is simulated with Brownian dynamics and binding is allowed to occur if two binding sites approach each other to a prescribed encounter length. The diffusion of clusters is treated using bead models for the hydrodynamics in the viscous regime. Using computer simulations, we measure the mean first passage times for the formation of clusters of different sizes.

BP 16.11 Tue 17:00 Poster D

Evolutionary emergence of complexity in model food webs — •Christian Guill and Barbara Drossel — Institut für Festkörperphysik, Technische Universität Darmstadt, Deutschland

Explaining the amazing diversity of ecological communities remains one of the greatest challenges in theoretical ecology. We investigate various mechanisms that promote the emergence of large and complex food webs in an evolutionary model that also includes population dynamics. Networks are created by starting from one species and external resources, followed by an iterated process of adding new species that are obtained by modifying existing species. Species are ordered on a one-dimensional niche axis, and links between them that represent feeding relationships are assigned according to the rules of the niche model (R.J. Williams, N.D. Martinez, 2000, Nature 404, 180-183). The average body size (or mass) of the species is assumed to increase with their position on the niche axis. The tested hypotheses for the promotion of complexity are the influence of different functional responses, adaptive behaviour, and body size effects that relate the metabolic rate of a species to its position on the niche axis. Adaptive foraging behaviour is found to be the key mechanism for the emergence of complex networks, while body size effects only determine the degree of complexity.

BP 16.12 Tue 17:00 Poster D

Nanotomography of Human Bone Based on Scanning Probe Microscopy — •Stephanie Röper[1], Christian Dietz[1], Sabine Scherdel[1], Anke Bernstein[2], Nicolaus Rehse[1], and Robert Magerle[1] — [1]Chemische Physik, TU Chemnitz, D-09107 Chemnitz — [2]Experimentelle Orthopädie, Martin-Luther-Universität Halle-Wittenberg, D-06097 Halle/Saale

Natural materials such as bone and teeth are nanocomposites of proteins and minerals, which exhibit a complex hierarchical structure ranging from macroscopic to molecular length scales. Scanning probe microscopy (SPM) based Nanotomography is a novel approach to image these materials. We focus on human bone which is first embedded in a methacrylate resin and then and then sectioned with the use of a microtome. For SPM based Nanotomography the specimen is ablated layer-by-layer by wet chemical etching and imaged with tapping mode scanning force microscopy after each etching step. From the resulting series of images the three-dimensional structure is reconstructed. The etching and imaging is done in-situ in a liquid cell of an SPM connected to reservoirs of etchants and water for flushing after each etching step. The flow of the different liquids is controlled with computer controlled valves which allow for an automated etching and measuring protocol. We will present first results of volume images of human bone and discuss our concepts for adjusting the imaging parameters to maintain a good imaging quality.

BP 16.13 Tue 17:00 Poster D

Dynamics of micro-capsules in shear flow using spectral methods — •Steffen Kessler, Reimar Finken, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Pfaffenwaldring 57/III, 70550 Stuttgart

Soft objects such as vesicles or micro-capsules in hydrodynamic Stokes flow present a challenging physical model system both from a theoretical and experimental point of view. We present a novel three dimensional numerical approach using spectral methods to simulate the dynamical behaviour of a micro-capsule in a linear shear flow. The shape of the membrane is expanded into a set of smooth basis functions. Using the balance between elastic and hydrodynamic forces and the no-slip boundary condition at the capsule membrane, we derive the equations of motion of the expansion coefficients. This set of coupled nonlinear equations is solved numerically. The mechanical properties of our capsule include resistance to shear, compression and bending. Different constitutive laws and arbitrary external flows can be employed in the code. A viscosity contrast between inner and outer fluid is permitted. We are able to observe relaxation into a stationary tank-treading state, which is also seen in experiments. Numerical results for the deformation and inclination angle agree well with theoretical predictions in the low shear rate limit. The spectral code is used to investigate capsule dynamics beyond the quasispherical approximation.

BP 16.14 Tue 17:00 Poster D

Interaction of Model Proteins in a Lipid Bilayer under Surface Tension — •Jörg Neder[1], Beate West[2], and Peter Nielaba[1] — [1]Department of Physics, University of Konstanz, 78457 Konstanz — [2]Department of Physics, University of Bielefeld, 33615 Bielefeld

Recently O. Lenz and F. Schmid [1] introduced a simple coarse-grained model to study lipid layers and their phase transitions. Using an extension of this model [2] we are investigating the influence of an applied surface tension to a bilayer membrane. One aim of our work is the comparison of lipid-mediated protein-protein interaction between the tensionless state of the bilayer and states with non-vanishing surface tension. Furthermore, we are interested in developing a method for calculating the chemical potential of incorporated model proteins.

[1] O. Lenz, F. Schmid, J. Mol. Liquids, **117**, 147 (2005)
[2] F. Schmid, et al., http://arxiv.org/pdf/physics/0608226

BP 16.15 Tue 17:00 Poster D

Nanoscale thermophoresis for bioanalysis on a chip — •Christoph Wienken and Dieter Braun — Emmy Noether Group at the Center of NanoScience (CeNS),, Ludwig Maximilian Universität München, Amalienstrasse 54, 80799 Munich, Germany

We explored a chip-based all electrical measurement scheme for thermophoresis on the nanoscale. Thermophoresis, also called Soret effect, is the movement of particles in a temperature gradient. It is sensitive to the particles' properties like charge and size.[1] Previously, measurements were carried out all optical. But for simpler and cheaper detection we now use a all electrical setup. By miniaturizing the setup to nanoscale we significantly increased the speed of the measurement.

In the experiment both heating and concentration measurements are realized electrically. We use a very narrow, miniaturized gold/gold capacitor covered with a nanoliter droplet. Applying a high frequency AC voltage to the capacitor creates a temperature gradient between the capacitor and its environment by ohmic heating of the solution. Due to this gradient particles move out of the capacitor and result in a changed conductivity of the analyte. The latter is detected in the current signal.

Our simulations show that the analysis results are obtained within milliseconds, much faster than existing methods. This is due to the highly localized resistive heating near the capacitor. The chip-based layout doesn*t require any precisely applied volumina but only a millimetre-sized droplet which covers the sensitive area.

[1] Stefan Duhr and Dieter Braun, PNAS 103, 19678-19682 (2006)

BP 16.16 Tue 17:00 Poster D

Sexual reproduction prevails in a world of structured resources in short supply — •Irene Ament[1], Barbara Drossel[1], and Stefan Scheu[2] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Deutschland — [2]Institut für Zoologie, Technische Universität Darmstadt, Deutschland

The maintenance of sexuality against the two-fold cost of sex is one of the most stunning problems in evolutionary biology. We present a model that is based on the availability of resources, which is the strongest factor determining the growth of populations. Key features of the model are that there is a broad spectrum of resources, that sexual reproduction sets in when resources become scarce, that only a few genotypes can coexist locally, and that resources regrow slowly. We show that under a wide range of conditions the sexual species outcompete the asexual ones. The asexual species win when survival conditions are harsh and death rates are high or consumer genotypes are so manifold that all resources are exploited to the same extent. These results are robust against modifications of the model, including various types of spatial structure.

BP 16.17 Tue 17:00 Poster D

Transport of phospholipids in the canalicular membrane of the hepatocyte — •Thomas Schwager[1], Hermann-Georg Holzhütter[2], and Andreas Herrmann[3] — [1]Charite, Augustenburger Platz 1, 13353 Berlin — [2]Institut für Biochemie, Charite, 10117 Berlin — [3]Institut für Biologie, Humboldt-Universität, 10115 Berlin

The bile is secreted by the hepatocytes from the liver of humans and other vertebrates. It plays an important role in the import of fat and in the export of cholesterol and xenobiotics. The hepatocytes pair to form a tiny canaliculus which transports the secreted bile. We present a mathematical model which contains the main molecular processes involved in the bile formation at the canalicular membrane. The membranes are modelled as a pair of regular hexagonal lattices, one of each representing the inner and the outer leaflet. The mobile constituents of the membrane may move along the lattice as well as between the leaflets, the so-called flip-flop. The interaction properties of the different particle species are characterized by affinities which influence the mobility of the particles. Although the model is very simple, it can quantitatively represent the known state of the canalicular membrane. It is applied to study the effect of perturbations of this reference state. Two examples of such perturbations: depletion of cholesterol and partial knock-out of the MDR3 transporter will be studied.

BP 16.18 Tue 17:00 Poster D

Stretching of a DNA/HU-protein complex in SMD simulations — •Carsten Olbrich and Ulrich Kleinekathöfer — International University Bremen (Jacobs University Bremen as of spring 2007), Campus Ring 1, 28759 Bremen, Germany

HU is a member of a family of prokaryotic proteins that interact with the DNA in a non-specific way. Its major function is the binding, compaction and stabilization of DNA. We applied steered molecular dynamic (SMD) simulations to DNA which is bonded to a HU protein and present some results in comparison with experiments done with optical tweezers. These show discrete steps during disruption. The goal is to analyze in detail these steps with the help of MD simulations.

BP 16.19 Tue 17:00 Poster D

Solution Behavior of Semiconductor-Binding Peptides — •Stefan Schnabel[1], Simon Mitternacht[2], Michael Bachmann[1,2], Anders Irbäck[2], and Wolfhard Janke[1] — [1]Institut für Theoretische Physik, University of Leipzig — [2]Complex Systems Division, Lund University, Sweden

Recent experiments have identified peptides with adhesion affinity for GaAs and Si surfaces. Here we use all-atom Monte Carlo (MC) simulations with implicit solvent to investigate the behavior in aqueous solution for four such peptides, all with 12 residues. At room temperature, we observe that all the four peptides are largely unstructured, which is consistent with experimental data. At the same time, it turns out that one of the peptides is structurally different and more flexible, compared to the others. This finding points at structural differences as a possible explanation for varying adhesion properties of the four peptides. An experimental test of this hypothesis is proposed.

BP 16.20 Tue 17:00 Poster D

Particle image correlation spectroscopy (PICS) — •Stefan Semrau and Thomas Schmidt — Physics of life processes, Leiden institute of physics, Leiden university, The Netherlands

Single-particle tracking (SPT) and image correlation microscopy (ICM) have been proven to be powerful tools for the investigation of local inhomogeneities in biological systems. Driven by recent discussions on the refinement of the classical fluid-mosaic model of the plasma membrane both tools were applied to elucidate the contribution of lipid organization and protein interactions to the behavior of signaling molecules. To overcome the drawbacks of both SPT and ICM we

have developed an analysis tool that combines both techniques and resolves correlations on the nanometer length and millisecond time scale (Semrau and Schmidt, Biophys. J., Vol. 92, 2007). This tool, adapted from methods of spatiotemporal image correlation spectroscopy, exploits the high positional accuracy of single-particle tracking. While conventional tracking methods break down if multiple particle trajectories intersect, our method works for arbitrarily large molecule densities and diffusion coefficients as long as individual molecules can be identified. It is computationally cheap and robust and requires no a priori knowledge about the dynamical coefficients. We demonstrate the validity of the method by Monte Carlo simulations and by application to single-molecule tracking data of membrane-anchored proteins in live cells. The results faithfully reproduce those obtained by conventional tracking: upon activation, a fraction of the small GTP-ase H-Ras is confined to domains of < 200 nm diameter.

BP 16.21 Tue 17:00 Poster D

Single molecule microscopy using focal plane illumination — •Jörg Ritter, Werner Wendler, and Ulrich Kubitscheck — Institute of Physical and Theoretical Chemistry, Bonn, Germany

Single molecule fluorescence microscopy performed in spatially extended samples severely suffers from a high fluorescence background. To overcome this problem we used a focal plane instead of the conventional epi-illumination. By means of a custom made cylindrical lens system (NA 0.33) we created a light sheet with a Rayleigh length of 37 μm, a FWHM width of 8.3 μm, and a FWHM thickness of 2 μm within the object plane of a detection objective lens. In this manner a simple optical sectioning microscope was created (Voie et al., 1993). The light sheet was produced inside a water chamber, where the sample was fixed within an agarose gel cylinder on a micrometer stage (Huisken et al., 2004). Fluorescence light was detected perpendicular to the illumination plane by a water-dipping microscope objective lens (60X, NA 1.0) and imaged onto an EMCCD. Only the plane of interest was illuminated and affected by photobleaching. Movement of the stage allowed the acquisition of 3D image stacks. Excitation in the focal plane only resulted in a striking reduction of fluorescence background. The axial resolution was determined by the light sheet thickness and the resolving power of the detection objective lens, and was determined as 1.35 μm FWHM at 680 nm (theoretical expectation, 1.17 μm). The penetration depth of the optical sectioning was limited by the working distance of the water-dipping microscope objective (2.5 mm).

BP 16.22 Tue 17:00 Poster D

Intranuclear dynamics of single mRNA molecules in living C. tentans salivary gland cell nuclei — •Roman Veith, Jan-Peter Siebrasse, and Ulrich Kubitscheck — Institute of Physical and Theoretical Chemistry, Bonn, Germany

The salivary glands of the dipteran Chironomus tentans provide an elegant model system for the analysis of specific messenger ribonucleoprotein particles, the Balbiani Ring (BR) mRNPs. BR mRNPs contain long RNA transcripts of roughly 35-40 kb in size, which possess a highly repetitive sequence. The diameter of the granular BR mRNPs is about 50 nm. Transcription and splicing of the BR mRNA and the formation of the BR particles was genetically and biochemically thoroughly investigated, and in several recent studies their intranuclear localisation in fixed glands was visualized by electron microscopy. However, up to now little was known about the intranuclear dynamics and mobility of the BR mRNPs. We analysed the intranuclear motions of BR particles in real-time by single particle tracking of fluorescence labelled BR mRNPs in living cell nuclei. Labelling was achieved in situ by nuclear microinjection of Cy5-conjugated oligonucleotides, which were complementary to the highly repetitive sequence on the BR mRNA. This approach generated fluorescent RNPs in vivo. Injection of control oligos and application of DRB proved that the labelling was specific. Using high speed single-molecule microscopy we analysed the intranuclear movements of the particles, and compared it to various model particles such as fluorescent microbeads, quantum dots and fluorescent dextrans.

BP 16.23 Tue 17:00 Poster D

Coarse-grained simulation studies of peptide-induced pore formation — •Gregoria Illya and Markus Deserno — Max Planck Institute for Polymer Research, Mainz, Germany

The interactions of cell membrane and antimicrobial peptides, which are amphiphilic molecules, can be very complicated. In the low concentration phase, antimicrobial peptides adsorb to the surface of the membrane, while in the high concentration phase, they insert across the membrane, resulting in the formation of pores. Despite being intensively studied experimentally, the mechanism of pore formation and its structure are remain disputed.

We investigate the interactions between lipid bilayers and amphiphilic peptides using a solvent free coarse-grained simulation technique. In our model, each lipid is represented by a 'hydrophilic' bead and three 'hydrophobic' beads. The amphiphilic peptide is modelled as a 'hydrophobic-hydrophilic' tube with 'hydrophilic' sites at the tube's ends.

It is observed that as the attractive interaction between peptides and lipids is successively increased, the preferred state of the peptide changes from desorbed to adsorbed to inserted. We show how several peptides which bind to the membrane surface cooperatively insert and subsequently induce the formation of pores.

BP 16.24 Tue 17:00 Poster D

Detecting lipid bilayer formation and expansion by a microfabricated cantilever array — Ioana Pera and •Jürgen Fritz — International University Bremen, D-28759, Bremen, Germany (Jacobs University Bremen, as of Spring 2007)

Biological applications of cantilever array sensors focus mainly on the detection of nucleic acids or proteins. We want to apply cantilever array sensors to the investigation of mechanical properties of lipid bilayers. Supported lipid bilayers formed on solid surfaces are model systems for cellular membranes and are often used as biosensor coatings. The investigation of mechanical properties of cellular membranes, e.g. their fluidity, rigidity, stretching and bending, can give novel insights into biological processes such as cell adhesion, exocytosis, or initiation of viral infection [1].

Here we report on lipid bilayer formation on the surface of microfabricated cantilevers and the related surface functionalizations [2]. Bilayer formation by vesicle fusion on top of cantilevers resulted in different bending strengths (between several 10 nm to several 100 nm) and bending directions (tensile or compressive) of the cantilevers. The bending depended mainly on the surface on which the bilayers were formed, i.e. if they were physisorbed on the silicon oxide or chemisorbed on the gold surface of cantilevers. First experiments on further modification of bilayers with the pore forming peptide melittin will be discussed.

[1] H.T. McMahon, J.L. Gallop, Nature 438 (2005) 590.
[2] J. Fritz, I. Pera, Langmuir 2006 (web release 09-Dec-2006).

BP 16.25 Tue 17:00 Poster D

Toxicologic impact of Carbon Nanotubes on Caco-2 cells — •Heike Kreher, Claus-Michael Lehr, and Marc Schneider — Universität des Saarlandes, Biopharmazie und Pharmazeutische Technologie, Campus Saarbrücken, Geb. A4 1 Postfach 151150, D-66041 Saarbrücken, Deutschland

Nanoparticles with most interesting properties for scientists and industry are Carbon Nanotubes (CNTs) which are stronger than steel at only 1/6th the weight and have higher current density than copper. For this reason CNTs are manufactured in a huge amount. In addition CNTs are produced in diesel engines of cars and in combusters. Thus it appears that humans are already exposed to CNTs in the air and it is important to know how these particles affect pulmonary cells and intestinal cells in terms of acute and long-term toxicity. After imaging of dispersed CNTs, we tested their influence in vitro on Caco-2 cells, which have morphological and biochemical similarity to the small intestinal columnar epithelium. We used standard assays to investigate the viability and the cytotoxicity respectively (LDH- and MTT-assays). Another important parameter, when considering the interaction of materials with epithelial layers is the barrier function itself. This was tested measuring the electrical resistance across the barrier (TEER values). To perform the tests, CNTs were suspended in medium in different concentrations and then the solutions were sonicated for 3 minutes. LDH test did not show any disturbance of the membrane integrity of the cells. Whereas MTT test showed a slight toxicity with increasing CNT concentration.

BP 16.26 Tue 17:00 Poster D

Biofilm adsorption on structured substrates — •Hubert Mantz[1], Christoph Gilow[1], Anthony Quinn[1], Karin Jacobs[1], Markus Bellion[2], and Ludger Santen[2] — [1]Saarland University, Experimental Physics, D-66041 Saarbrücken, Germany — [2]Saarland University, Theoretical Physics, D-66041 Saarbrücken, Germany

The aim of this experimental study is to shed light on the mechanism of biofilm adsorption. The behavior of biomolecules at surfaces plays

a fundamental role in a number of areas (e.g. the interaction between implant materials and human tissue) as structure of a protein is often closely related to its function.

Among a number of other factors, the complex process of protein adsorption is determined by surface properties. As a model system, a combination of structured substrates was used to isolate the contribution of different parameters (chemical composition, roughness, surface charge ...).

The adsorption kinetics of some proteins (amylase, lysozyme, albumin), as measured by in situ-ellipsometry have been compared to other techniques such as surface plasmon resonance and surface probe microscopy measurements.

The results have also been compared to Monte Carlo simulations, assuming conformational changes of the proteins with increasing surface coverage. Our results will be useful for the design of special (non-) adhesive biointerfaces.

BP 16.27 Tue 17:00 Poster D

Brownian dynamics of rods in a crowded environment — •Tobias Munk, Felix Höfling, Erwin Frey, and Thomas Franosch — Arnold-Sommerfeld-Center und CeNS, Ludwig-Maximilians-Universität München, Theresienstraße 37, 80333 München

Molecular crowding in the cell provides a heterogeneous, randomly structured medium. The properties of this environment strongly influence the diffusion of proteins and stiff polymers.

We have developed a theoretical model that mimics the essentials of this motion: A single spherical or rod-like object moves through a fixed array of hard-core obstacles. By means of Brownian dynamics simulations, we investigate the dynamics of the overdamped motion over nine decades in time and compare to a purely ballistic motion. For rods, interesting phenomena occur due to anisotropic friction and the coupling of rotational and translational degrees of freedom. In particular, we analyze predictions of the tube model.

BP 16.28 Tue 17:00 Poster D

Bacteriophage HK97 studied by nanoindentation — •Wouter H. Roos[1], Irena L. Ivanovska[1], John E. Johnson[2], and Gijs J. L. Wuite[1] — [1]Fysica van complexe systemen, Vrije Universiteit, 1081 HV Amsterdam, Niederlande — [2]Molecular biology, Scripps Research institute, La Jolla, CA, U.S.A.

After procapsids of bacteriophage HK97 have self-assembled, they mature and subsequently package dsDNA. The maturation process is accompanied by an expansion of the capsid, together with a crosslinking of the capsid proteins. We perform nanoindentation experiments using atomic force microscopy to probe the elastic properties of the HK97 shells at different states of maturation. We also determine the breaking force, i.e. the minimum force which is needed to deform the shell irreversibly.

BP 16.29 Tue 17:00 Poster D

Force generation in a filopodia model system — •Simone Köhler[1], Mireille Claessens[1], Michael Schleicher[2], and Andreas Bausch[1] — [1]TUM Physik Department E22, James Franck Straße, D-85747 Garching — [2]LMU Institute for Cell Biology, Schillerstraße, D-80336 München

Formins are multi-domain proteins with a highly conserved formin-homology domain 2, that can nucleate actin filaments from monomers alone and may even trigger filament growth by a processive capping mechanism. A formin of the slime mould *Dictyostelium discoideum*, dDia2, has been shown to be important for the formation, elongation and maintenance of filopodia. Fascin, an actin-bundling protein is essential for filopodial protrusion, too. For further understanding the interaction of these two proteins *in vitro* experiments have to be done.

We study the role of fascin on assembly rates and force generation by dDia2-induced actin polymerisation using total internal reflection fluorescence microscopy (TIRFM) as well as an *in vitro* motility assay. In the motility assay the force generated by actin polymerisation can be used to propell formin coated beads in a medium containing only purified proteins while TIRFM allows to follow the polymerisation of single actin filaments from dDia2 immobilized on a surface.

BP 16.30 Tue 17:00 Poster D

Ex-situ measurements of adsorbed protein layers — •Christof Weitenberg, Hubert Mantz, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbrücken, Germany

Measurements of biological tissue are usually done in situ, i.e. in solution. We investigated the possibility of an ex-situ determination of the thickness of lysozyme protein layers adsorbed to silicon oxide surfaces by means of ellipsometry. The expected shape of the adsorption kinetics and isotherms for different ionic strengths could be reproduced. Yet the time scale for adsorption appears to be much larger than for comparable in-situ measurements. We discuss the possible explanations for this behavior as well as assets and drawbacks of the applied ex-situ procedure.

BP 16.31 Tue 17:00 Poster D

Polymers in external fields — •Christian Sendner and Roland Netz — TU Muenchen, Physik Department, 85748 Garching

The dynamical response of polymers to external fields at finite temperature is investigated. We explicitly take hydrodynamic interactions in the limit of zero Reynolds number into account. The response of grafted DNA chains to alternating electric fields is examined, addressing important parameters like the bending rigidity. Terminally attached ligands change the dynamics of that system leading to possible biosensing applications [1]. In another project we analyze the influence of a solid–liquid interface on stiff polymers, driven parallel to the surface. This leads to a preferred orientation of the rod with respect to the wall, and gives rise to an effective repulsion away from the surface. We give scaling results for this long ranged repulsion in the high temperature limit. This purely hydrodynamic effect could lead to desorption transitions for short polymer chains which could be important for applications in the field of DNA chips.

[1] C. Sendner, Y.W. Kim, U. Rant, K. Arinaga, M. Tornow, and R. R. Netz, Phys. Stat. Sol. (a) 203 (14), 3476-3491 (2006)

BP 16.32 Tue 17:00 Poster D

Influence of spacer length and density on the vertical structures of supported membranes studied by neutron reflectivity — •Peter Seitz[1], Oliver Purrucker[2], Anton Förtig[3], Raimund Gleixner[4], Giovanna Fragneto[5], Rainer Jordan[3], and Motomu Tanaka[1,2] — [1]Physikalisch-Chemisches Institut, Universität Heidelberg, Germany — [2]Physik-Department E22, Technische Universität München, Germany — [3]Institut für Technische Chemie, Technische Universität München, Germany — [4]Max Planck Institute of Biochemistry, Martinsried, Germany — [5]Institut Laue-Langevin, Grenoble, France

We studied the structure of a new class of polymer-supported membranes, which are separated from the solid substrate via poly(2-methyl-2-oxazoline) spacers of defined length, functionalized with a surface coupling group and hydrophobic membrane anchors. The proximal leaflet was deposited via Langmuir-Blodgett transfer, followed by vesicle fusion to deposit the distal layer. Precise control of the polymer chain length and its lateral density enables the quantitative adjustment of the thickness and the viscosity of the polymer interlayer. Previously, we measured the membrane-substrate distance with fluorescence interference contrast microscopy (FLIC). To gain a deeper insight to the vertical structure of the membrane, we conducted specular neutron reflectivity experiments under a systematic variation of the spacer length and density, and calculated the static roughness and the volume fraction of water in the polymer interlayer.

BP 16.33 Tue 17:00 Poster D

Persistence length of semiflexible polymers and bending rigidity renormalization — •Petra Gutjahr, Reinhard Lipowsky, and Jan Kierfeld — Max Planck Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam, Germany

The persistence length of semiflexible polymers and one-dimensional fluid membranes is obtained from the renormalization of their bending rigidity. The renormalized bending rigidity is calculated using an exact real-space functional renormalization group transformation based on a mapping to the one-dimensional Heisenberg model. The renormalized bending rigidity vanishes exponentially at large length scales and its asymptotic behaviour is used to define the persistence length. For semiflexible polymers, our results agree with definitions based on the asymptotic behaviour of tangent correlation functions. Our definition differs from the one commonly used for fluid membranes, which is based on a perturbative renormalization of the bending rigidity.

BP 16.34 Tue 17:00 Poster D

Exact mean and variance of neuronal subthreshold voltage fluctuations driven by shot noise — •Lars Wolff and Benjamin Lindner — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Neurons are subject to a vast number of synaptic inputs from as many as tens of thousands of other cells. These inputs consist of spikes changing the conductivity of the target cell, i.e. they enter the neural dynamics as multiplicative shot noise. Up to now, only for simplified models like current-based (additive-noise) point neurons or models with Gaussian white noise input, exact solutions are available. We will present a method to calculate the exact time-dependent mean and variance for the voltage of a point neuron with conductance-based Poissonian shot noise and a passive membrane. The exact solutions show novel features (for instance, maxima of the moments vs time) and are in excellent agreement with numerical simulations. The theoretical analysis of subthreshold membrane fluctuations may contribute to a better comprehension of neural noise in general. It may also help devising schemes for the extraction of synaptic parameters or network parameters from voltage recordings.

BP 16.35 Tue 17:00 Poster D

Cellular Potts Model based simulation of endothelial network formation — •Martin Peglow and Heiko Rieger — Theoretische Physik, Universität des Saarlandes, PF 151150, D-66041 Saarbrücken

The Cellular Potts Model is a cell centered based Monte Carlo approach to development biology, focusing on intercellular adhesion forces. In an early stage of embryogenesis the capillary network, the first organ in vertebrates, is built to supply other tissues with oxygen and nutrients. Cells beeing self organized, there has to be a cell communication system which can describe the underlying mechanisms of vaculogenesis and angiogenesis. We study a theoretical model that describes chemotactic diffusion of growth factors, which are produced by autocrine cells and decay within the extracellular matrix. For a better understanding of this process, which has already been shown in vitro, we studied the influence of different strengths of a contact inhibited mechanism on the structure and shape of the network in 2d and 3d. Contact inhibition here means that chemotactic filopodia were supressed at cell-cell interfaces.

BP 16.36 Tue 17:00 Poster D

Remodelling of an arteriovenous vascular network during tumor growth and simulation of drug flow: A theoretical model — •Michael Welter and Heiko Rieger — Theoretische Physik, Universität des Saarlandes, PF 151150, D-66041 Saarbrücken

Tumor acquire sufficient oxygen and nutrient supply by coopting host vessels and neovasculature created via angiogenesis, thereby transforming a highly ordered network into chaotic heterogenous tumor specific vasculature. Vessel regression inside the tumor leads to large regions of necrotic tissue interspersed with isolated surviving vessels. A theoretical model is presented that captures these features in agreement with data from human melanoma. Extending our earlier work [K. Bartha and H. Rieger, J. Theor. Biol. 241, 903 (2006)] emphasis is put on realistic modeling of the vascular system by incorporating a stochastically grown hierarchical arteriovenous network, Fahraeus-Lindqvist and phase separation effects and refined tissue oxygen level computation. The irregularity of tumor vasculature has drastic effects upon potential drug delivery, therefore we also present results of simulations of a tracer substance flowing through the remodeled network.

BP 16.37 Tue 17:00 Poster D

Beitrag abgesagt — •XXX XXX —

BP 16.38 Tue 17:00 Poster D

Shift-Twist-Symmetry and pattern formation in the visual cortex — •Wolfgang Keil[1], Michael Schnabel[1,2], and Fred Wolf[1] — [1]Max-Planck-Institut for Dynamics and Self-Organization, Göttingen, D-37073 — [2]Bernstein Center for Computational Neuroscience, Göttingen

Neurons in the primary visual cortex preferentially respond to visual stimuli of a particular orientation. Across the cortex, these orientation preferences are arranged in quasiperiodic 2-D patterns, known as orientation maps. Biologically plausible symmetry assumptions have been used successfully to derive a theoretical model which accounts for the emergence of such patterns [1].

Recent measurements have revealed anisotropic coupling statistics in the underlying neural tissue [2], which require the reduction of symmetry in the original model. We discuss consequences of the remaining symmetry (shift-twist-symmetry) in pattern-formation models of the visual cortex. Focussing on the influence of linear and quadratic shift-twist-symmetric coupling terms in the corresponding amplitude equations, the attractors of the dynamics and their stability ranges are calculated. Statistical properties of the spatial arrangement of the emergent structures are compared with recent measurements in tree-shrews. Including additional linear terms improves the agreement with the data. The data exhibits significant signatures of higher-order statistics which are still to be explained by theoretical models.

[1] F. Wolf. Phys. Rev. Lett., 95,208701 (2005)
[2] W.H. Bosking, J. Neurosci., 17, 2112 (1997)

BP 16.39 Tue 17:00 Poster D

Detection of Coupling Directions in Multivariate Dynamical Systems with Applications to Tremor-Correlated Spike Activity in Parkinson's Disease — •Bjoern Schelter[1], Kathrin Henschel[1], Florian Amtage[2], Jan Vesper[3], Bernhard Hellwig[2], Carl Hermann Luecking[2], and Jens Timmer[1] — [1]FDM, Center for Data Analysis and Modeling, University of Freiburg, Germany — [2]Dpt. of Neurology and Neurophysiology, Neurozentrum, University of Freiburg, Germany — [3]Dpt. of Stereotactic Neurosurgery, Neurozentrum, University of Freiburg, Germany

Tremor in Parkinson's disease is a neurological disorder that manifests itself in involuntary oscillations of the upper limbs at a frequency of approximately 5 Hz. The aim of this study was to investigate the relation between tremor and spike activity in the subthalamic nucleus (STN) of patients with Parkinson's disease.

Data were obtained during stereotactic surgery on patients with Parkinson tremor. Muscular and neuronal spike activity was recorded simultaneously. Multivariate analysis techniques were applied to infer the underlying interdependence structure with particular emphasize on distinguishing direct and indirect interdependencies as well as the direction of the information flow. The techniques were successfully applied and our results support the hypothesis that synchronous neuronal activity in the STN contributes to the pathogenesis of Parkinsonian tremor.

BP 16.40 Tue 17:00 Poster D

Protein Adsorption kinetics monitored via SPR — •Hendrik Hähl, Hubert Mantz, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbrücken, Germany

The formation of protein layers on solid surfaces plays an important role in many biological processes. In our studies we focus on the adsorption of human saliva proteins. In the oral cavity, some of them can act as a medium for bacteria. The aim is to test the influence of the different contributions of the surface potential on the protein adsorption process.

Former investigations showed that the adsorption kinetics exhibits a different behaviour for different long-range van-der-Waals interactions (cf contribution of H. Mantz et al.). Now the influence of the short-range forces should also be tested.

By covering thin gold layers with self assembled monolayers of thiols with different headgroups, it is possible to tune the short-range forces acting on the adsorbing proteins. The growth of the protein layer is monitored via surface plasmon resonance. By the shift of the minimum in the reflectivity curves the thickness of the adsorbed layer can be measured. In combination with imaging ellipsometry this gives us major advantages in comparison with commercially available setups, e.g. the layer thicknesses can be compared directly.

BP 16.41 Tue 17:00 Poster D

Photobleaching in two-photon scanning fluorescence correlation spectroscopy — •Zdeněk Petrášek and Petra Schwille — Biotechnologisches Zentrum, Institut für Biophysik, TU Dresden

Two-photon Fluorescence Correlation Spectroscopy (FCS) takes advantage of the excitation being sufficiently localized, so that no confocal arrangement using a pinhole is necessary to create a well confined measurement volume. Although two-photon FCS has all the advantages well known from two-photon microscopy, signal-to-noise ratios lower than with one-photon excitation are usually achieved, a fact commonly attributed to optical saturation and photobleaching.

Scanning FCS (sFCS) combines the standard FCS with relative movement of the sample and the excitation beam. Although the information about diffusion kinetics is partially lost by scanning, sFCS can provide useful information on the role of photobleaching and saturation at high excitation intensities.

The measurements with circular-scanning sFCS indicate that photobleaching is the major factor responsible for the effects encountered at high excitation intensities, such as apparently shorter diffusion times and decrease of the autocorrelation amplitude $g(0)$. Furthermore,

sFCS reduces these effects and extends the range of excitation intensities where $g(0)$ is not affected by photobleaching, thus allowing measurements at higher molecular brightness and S/N ratio.

Numerical calculations show that photobleaching alone can explain the observed decrease of $g(0)$ and lower than expected fluorescence, without the need to consider saturation effects.

BP 16.42 Tue 17:00 Poster D

Mimicking E-cadherin mediated cell adhesion with synthetic lipid membranes — •Susanne Fenz and Kheya Sengupta — Institute of Bio- and Nanosystems 4: Biomechanics, Research Center Jülich, D-52425 Jülich, Germany

Mobility of cell adhesion molecules on the cell surface plays an important role in the formation of cell-cell adhesion. In order to distinguish active transport from passive diffusion we set up a biomimetic system. A supported bilayer decorated with the extracellular domain of the homophilic cell adhesion molecule E-cadherin (E-cad) mimics the surface of one cell and a vesicle that also exhibits E-cad acts as the other cell. The adhesion process is observed with reflection interference contrast microscopy (RICM) which enables us to reconstruct shape and fluctuations of the membrane. From these data membrane tension and adhesion energies can be calculated. We found that E-cad induced strong binding of the vesicle indicated by an increase of the adhesion energy and strong reduction of the fluctuations of the vesicles' membrane as compared to a negative control. Simultaneously we measured the change in the diffusion constant in the plane of the bilayer following adhesion of vesicles as a function of the adhesion strength.

BP 16.43 Tue 17:00 Poster D

Growth dependent alterations of the energy metabolism in neuronal cell cultures — •Jiraporn Luengviriya[1], Thomas Mair[1], Carina Helemeke[2], Katharina Braun[2], and Stefan C. Müller[1] — [1]Otto-von-Guericke-Universtität Magdeburg, Institut für Experimentelle Physik, Abteilung Biophysik, Universitätsplatz 2, 39106 Magdeburg, Germany — [2]Otto-von-Guericke-Universtität Magdeburg, Institut für Biologie, Lehrstuhl für Zoologie/Entwicklungsbiologie, Brenneckestr.6, 39118 Magdeburg, Germany

Glycolysis is an essential pathway of the energy metabolism in astrocytes which supplies energy-rich intermediates for neurons, via the so called lactate shuttle, in order to maintain the energy fuel of neurons. We investigated the energy state of cell cultures from the hippocampus of new born rats as a function of their growth state by spatiotemporal recordings of NAD(P)H-fluorescence. We stimulated the cells by local application of different chemicals and found, that cyanid inhibition of respiration leads to a pronounced increase of NAD(P)H fluorescence. This response was growth dependent and increased until about 15 days. Thereafter it decreased again. With the neurotransmitter NMDA as stimulus, we found also an increase of NAD(P)H-fluorescence, but now with 2 optima. The first one between day 6 and 12 and a second one between days 17 to 24. At the optimum of cyanid stimulation there was no response of the cellular NAD(P)H to NMDA. We interpret these data such, that there is a switch between glycolytic and respiratory energy metabolism during growth of these cells.

BP 16.44 Tue 17:00 Poster D

FRAP-Analysis of Protein Exchange Dynamics in Focal Adhesion Sites — •Christoph Möhl, Simone Born, Claudia Schäfer, Bernd Hoffmann, and Rudolf Merkel — Research Center Jülich GmbH, 52425 Jülich, Germany

Cell adhesion is an essential process for tissue integrity and cell movement. The adhesion process itself depends on clustered protein complexes called focal adhesion sites. These adhesion sites form a connection between the extracellular matrix and the actin cytoskeleton. Focal adhesions are characterized by a specific set of proteins such as integrins, regulatory kinases or proteins like vinculin, zyxin and VASP, bridging the integrins to actin fibers. In addition, focal adhesion sites can adapt in size and shape to cellular growth conditions. Thus, formation and release of focal adhesion sites are highly dynamic processes in moving cells but barely detectable when a cell is stationary. If various proteins additionally exchange in stable adhesion sites, and if such putative protein exchange dynamics goes along with the variable formation dynamics of whole adhesion sites is barely known.

Here, we present the analysis of protein exchange kinetics in focal adhesion sites of migrating and stationary cells by fluorescence recovery after photobleaching (FRAP). Experiments were performed with the GFP-labelled adhesion proteins vinculin, zyxin and VASP. The fluorescent label allowed the photobleaching of these proteins at distinct sites using a laser. By measuring the fluorescence recovery in the bleached area over time, we were able to examine significant differences between stable and dynamic adhesion sites.

BP 16.45 Tue 17:00 Poster D

Stochastic description of time delayed feedback oscillators — •Luis G. Morelli and Frank Jülicher — Max Planck Institute for the Physics of Complex Systems

Many cellular processes are regulated or driven by genetic oscillators, as in circadian clocks, the cell cycle, and patterning developing embryos. Due to the stochastic nature of gene expression, the period of such oscillations is subject to fluctuations. The precision of the oscillator can be characterized by the quality factor. We study the precision of genetic oscillators in a generic stochastic feedback system. We include the effects of amplification noise, arising for example from bursts of transcription and translation. We show that high quality is possible for certain parameter ranges even when the number of molecules is low and amplitude fluctuations are large.

BP 16.46 Tue 17:00 Poster D

Cooperativity of Integrin-mediated Adhesion on Nanopatterned Substrates — •Christine Selhuber[1,2], Thorsten Erdmann[3], Ulrich Schwarz[3], Horst Kessler[4], and Joachim Spatz[1,2] — [1]Universität Heidelberg, Physikalisch-Chemisches Institut — [2]Max-Planck-Institut für Metallforschung, Abteilung "Neue Materialien und Biophysik" — [3]Universität Heidelberg, BIOMS — [4]Technische Universität München, Department Chemie

Surfaces of defined adhesion properties are required for a physical and quantitative understanding of cell adhesion in vivo. In this work, biofunctional nanopatterns are employed, which allow adhesion ligands to be positioned in a quasi-hexagonal lattice. Such nanopatterns are used to investigate integrin-mediated cell adhesion, which is a highly complex biological process and essential for numerous cell functions. With nanopatterns the distance between adjacent single integrin binding sites is precisely defined. Recent cell culture experiments have revealed that this distance strongly affects cell adhesion and the formation of adhesion clusters, known as focal contacts. To quantify the adhesion cluster formation for different integrin binding site spacings, cell adhesion forces were studied using atomic force microscopy (AFM). The experiments demonstrate that an integrin binding site spacing of 70 nm and more prevents the cooperative formation of early adhesion clusters in initial adhesion. In long-term adhesion studies, after several hours of cell adhesion, it turned out that focal contact formation cooperatively increases the local adhesion strength. The obtained results were related to theoretical models on adhesion cluster stability.

BP 16.47 Tue 17:00 Poster D

Nonlinear Elasticity of Entangled Actin Networks — •Christine Semmrich[1], Klaus Kroy[2,3], and Andreas Bausch[1] — [1]Lehrstuhl für Biophysik E22, TU München, Deutschland — [2]Institut für Theoretische Physik, Universität Leipzig, Deutschland — [3]Hahn-Meitner-Institut, Berlin, Deutschland

The strain hardening of crosslinked actin networks is currently attracting lots of attention as a paradigm for essential mechanical properties of living cells. The elasticity of such crosslinked networks can vary by more than one order of magnitude in dependence of the applied stress. This has been attributed to the nonlinear mechanical behaviour of single filaments. In contrast, the mechanical response of purely entangled actin is often reported to be shear thinning. By means of different rheological approaches we are able to investigate the nonlinear response of purely entangled actin networks. Interestingly, under standard conditions a strain hardening occurs below a critical temperature while above this critical temperature strain softening is reported. Moreover, this transition is highly dependent on the buffer salt concentration. We suggest a simple theoretical model based on the interaction potential between single actin filaments including temperature and salt dependent effects to rationalize this behaviour.

BP 16.48 Tue 17:00 Poster D

Driven transport through channels: Interaction effects — •Martin Körner[1], Mario Einax[1], Philipp Maass[1], and Abraham Nitzan[2] — [1]Institut für Physik, Technische Universität Ilmenau, 98684 Ilmenau, Germany — [2]School of Chemistry, The Sackler University of Science, Tel Aviv University, Tel Aviv 69978, Israel

Ionic transport through biological membranes is often modelled by

one-dimensional hopping processes between binding sites supplied by a channel protein. This leads to a theoretical description in terms of a bridge that connects two particle reservoirs at different chemical potentials and along which particles can be transported by nearest neighbour hopping processes between sites at different energy levels. Using Monte-Carlo simulations, numerical solutions of the underlying master equation and analytical approximation methods, we study the current-voltage characteristics, current fluctuations and correlation effects in dependence of the chemical potential difference between the reservoirs. In particular the influence of the inhomogeneity of site energies and of the interactions between the particles is discussed.

BP 16.49 Tue 17:00 Poster D

Dynamic light scattering of F-actin solutions — •Jens Glaser and Klaus Kroy — Inst. f. Theoretische Physik, Universität Leipzig, PF 100920, 04009 Leipzig

A network of the semiflexible polymer actin forms an integral part of the eucaryotic cell's cytoskeleton. Structural properties of F-actin solutions can be determined by dynamic light scattering (DLS). While the method is usually successfully applied to determine the size of flexible polymers, a consistent determination of the persistence length of actin has not yet been achieved.

We report measurements of the persistence length by a comprehensive analysis of DLS data, which are in agreement with values obtained by different techniques for unstabilized actin filaments. Collective effects of F-actin networks are also analyzed and they give estimates e.g. of the tube diameter of the filaments which confirm current predictions of the tube model of semiflexible polymers.

BP 16.50 Tue 17:00 Poster D

Untersuchungen tiefenaufgelöster elektrischer Eigenschaften im Kortex von Mongolischen Wüstenrennmäusen — M. Kruse[1], M. Deliano[2], H. Witte[1], F.W. Ohl[2], •A. Reiher[1], A. Krtschil[1] und A. Krost[1] — [1]Inst. Exp. Physik, Uni Magdeburg, 39016 Magdeburg — [2]Leibniz Institut für Neurobiologie, 39008 Magdeburg

Biomedizinisch motivierte Untersuchungen der Stromquellendichte-Verteilung im Gehirn gehen von einer isotropen Verteilung der Leitfähigkeit im Gewebe aus. Diese Annahme ist mit großer Wahrscheinlichkeit falsch; aufgrund des geschichteten Aufbaus des Kortex ist eine Variation der tangentialen und der radialen Leitfähigkeit zu erwarten. Deshalb wurden im rechten primären auditorischen Kortex von Mongolischen Wüstenrennmäusen tiefenaufgelöste impedanzspektroskopische Untersuchungen vorgenommen. Dabei wurden drei 50μ m dicke Wolframdrähte als Elektroden benutzt, die in tangentialer Richtung jeweils 200μm entfernt waren. Eine Elektrode war 200μm in radialer Richtung verschoben. Durch diese Anordnung kann die räumliche Organisation des Leitfähigkeitstensors durch Triangulation bestimmt werden. Es wurden Impedanzmessungen (20Hz und 1MHz) mit einer örtlichen Tiefenvariation von 30μm aufgenommen. Auf der Grundlage einer intensiven Elektrodencharakterisierung und Analyse der Impedanzspektren wurde ein Ersatzschaltbild zur Identifizierung der Gewebeeigenschaften entworfen. Durch Ableitungsuntersuchungen und histologische Verfahren konnten Änderungen im dielektrischen Verhalten speziellen Schichten zugeordnet werden.

BP 16.51 Tue 17:00 Poster D

Single Molecule Unzipping of Coiled-Coils: The role of neck/hinge interactions for the regulaton of fungal kinesins — •Elisabeth Wasner, Thomas Bornschlögl, and Matthias Rief — Physik Departement E22, Technische Universität München, James-Franck-Straße, 85748 Garching, Germany

A model for the regulation of motor activity in fungal kinesins suggests important amino acid interactions between the hinge and the neck coiled-coil. The hinge sequence follows the neck and shows no specific tertiary structure. It contains an aromatic tryptophan that is strongly conserved among fungal kinesins.

In this AFM experiment, we try to answer the following question: Does the hinge contribute to the stability of the neck in fungal kinesins?

For this reason, three similar proteins were constructed: All of them contain ddFLN 1-5 domains, a well-investigated leucine zipper (based on GCN4-p1) followed by the Neurospora crassa kinesin neck. These constructs dimerize and are crosslinked by a cysteine that replaces the last d-position of the neck coiled-coil. Two of the constructs additionally contain the hinge - in one of it, the hydrophobic tryptophan has been replaced by a hydrophilic glutamine.

The corresponding protein unfolding and refolding force-extension curves can be interpreted by an equilibrium model und therefore the stability profile along the coiled-coil can be read off.

BP 16.52 Tue 17:00 Poster D

Time-Resolved Spectroscopy on Flavoproteins — •Florian Spreitler[1], Astrid Pelzmann[2], Ortwin Meyer[2], and Jürgen Köhler[1] — [1]Experimentalphysik IV and BIMF, Universität Bayreuth, Universitätsstrasse 30, 95447 Bayreuth, Germany — [2]Mikrobiologie, Universität Bayreuth, Universitätsstrasse 30, 95447 Bayreuth, Germany

Flavoproteins are of great importance in nature because they function in several life-sustaining processes, such as cellular respiration, redox biochemistry, purine metabolism and the oxidation of CO. Their common cofactor flavin adenine dinocleotide (FAD), which can be bound in a covalent or non-covalent fashion, is thought to be fine-tuned by the respective protein matrix both in its redox properties and the exposure of certain atoms to the solvent.

Our main objective is to study the fast photophysics of FAD in different enzymes and enzyme mutants on timescales between 1 ps and 10 ns using a streak camera setup. The work will also resolve structure-function relationships of the FAD binding site during catalysis and at different states of reduction.

We are presenting first results from pure FAD in solution and the FAD cofactor of two structurally similar molybdo iron-sulfur flavoproteins, which are the [CuSMoO2] CO dehydrogenase from *Oligotropha carboxidovorans* and the [MoSO2] xanthine oxidase from bovine milk.

BP 16.53 Tue 17:00 Poster D

Investigtion of the first stepsat the CNTF mediated signal transduction by means of fluorescence correlation spectroscopy (FCS) in living cells — •Eva Wallhäusser[1], Felix Neugart[1], Andrea Zappe[1], Deborah Buk[2], Lutz Graeve[2], Carsten Tietz[1], and Jörg Wrachtrupp[1] — [1]3. Physikalisches Institut, Universität Stuttgart, Stuttgart — [2]Institut für Chemische Biologie und Ernährungswissenschaften, Universität Hohenheim, Stuttgart

The investigation of signal transduction in living cells is an important step to understand what is happening in the body during the signal transduction and possibly influence several diseases in the case of a malfunction within the signalling cascade. Due to the tiny concentration of most of the signalling components a very sensitive method like FCS is necessary. In this work the first steps of signal transduction of the cilliary neutrophic factor (CNTF) by the CNTF-receptor complex were investigated. The complex is considered of three components, namely, CNTF-receptor itself, LIF-receptor and gp130. Measuring the diffusion constant of this different GFP-labeled receptors allows us to show if some parts of the receptor are pre-associated.

BP 16.54 Tue 17:00 Poster D

Improving the Functionality of DNA Layers on Gold by Electrically Induced Desorption — •Jelena Knežević[1], Kenji Arinaga[1,2], Ulrich Rant[1], Erika Pringsheim[1], Marc Tornow[1], Shozo Fujita[2], Naoki Yokoyama[2], and Gerhard Abstreiter[1] — [1]Walter Schottky Institut, Technische Universität München, Am Coulombwall 3, 85748 Garching — [2]Fujitsu Laboratories Ltd., 10-1 Morinosato-Wakamiya, Atsugi 243-0197, Japan

Self-assembled DNA layers on solid surfaces have been of great interest and widely introduced to various techniques for bio-molecular investigations. Recently, it has been recognized that the molecular packing density within the DNA layer crucially determines the functionality of the nucleic acids, for instance, the efficiency to hybridize to complementary targets. In this contribution, we describe a novel protocol to adjust the density of oligonucleotide layers by electrical means. At first a densely packed layer is immobilized onto a gold surface, in a second step, a fraction of the DNA molecules are desorbed from the surface by applying a series of electrochemical potentials. By monitoring steric interactions (hindrance) among the nucleic acids within the layer using optical means it is possible to evaluate the packing density in-situ and in real-time. We discuss several parameters which govern the desorption process (desorption potentials, DNA length, competitive adsorbents, etc.) and prove that the method allows a fine-tuning the DNA coverage. Finally, we demonstrate that layers prepared by electro-desorption retain their full bio-functionality by showing that dilute DNA layers exhibit hybridization efficiencies of approx. 100%.

BP 16.55 Tue 17:00 Poster D

How depletion forces affect the organisation and mechan-

ics of actin bundles — •Philipp von Olshausen, Oliver Lieleg, Mireille Claessens, and Andreas Bausch — Lehrstuhl für Biophysik E22, TU München

To organise actin filaments (F-actin) in bundles cells make use of many different types of actin binding proteins (ABPs). In vitro, the bundles' mechanical properties are strongly dependent on ABP type and density. However, in the crowded environment of a cell depletion forces might become important in filaments organisation, since they are known to strongly bundle F-actin. Thus it is an interesting question if cells can use ABPs to tune bundle mechanics and prevent the formation of stiff structures. Different microscopic techniques and an in vitro system of F-actin, ABPs and the depletion agent PEG-6k enable us to shed light on the interplay of specific ABPs and unspecific depletion forces in the process of actin bundling.

BP 16.56 Tue 17:00 Poster D

Electrostatics of DNA complexes with cationic lipids — •Andrey Cherstvy — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzerstrasse 38, D-01187 Dresden, Germany

We present exact solutions of Poisson-Boltzmann equation for several problems relevant to electrostatics (el) of DNA complexes with cationic lipids [1]. We calculate the el potential and energy for lamellar and inverted hexagonal phases, concentrating on effects of dielectric boundaries. Our results for energy of complexes is in good agreement with known numerical solutions [2]. We calculate compressibility modulus B of lamellar phase and compare it with the experimental data [3]. We suggest a new scaling relation for B as a function of DNA-DNA separation. Also, we treat charge-charge interactions across, along, and in between two low-dielectric membranes. We calculate the strength of el interactions of 1D DNA smectic layers across lipid membrane to treat DNA correlations in neighboring layers in lamellar complexes. We discuss some aspects of 2D DNA condensation and DNA-DNA attraction in DNA-lipid lamellar phase with multivalent cations. We analyze equilibrium DNA-DNA separations in condensed lamellar phase [4] and in 3D DNA condensates [5] using the theory of el interactions of DNA helical charge motifs developed recently [6-8].

[1] A.G. Cherstvy, in press. [2] D. Harries, et al., BJ 75 159 (1998). [3] T. Salditt, et al., PRE 58 889 (1998). [4] I. Koltover, et al., PNAS 97 14046 (2000). [5] E. Raspaud, et al., BJ 88, 392 (2005). [6] A.A. Kornyshev et al., PRL 82 4138 (1999). [7] A.G. Cherstvy, et al., JPCB 106 13362 (2002). [8] A.G. Cherstvy, et al., JPCB 108 6508 (2004).

BP 16.57 Tue 17:00 Poster D

Disordered ocular dominance maps by inter-map coupling — •Lars Reichl[1,2], Siegrid Löwel[3], and Fred Wolf[1,2] — [1]MPI für Dynamik und Selbstorganisation, Göttingen — [2]Bernstein Center for Computational Neuroscience, Göttingen — [3]Friedrich-Schiller-Universität , Jena

In the visual cortex of cats, orientation preference (OP) maps and ocular dominance (OD) maps are spatially irregular. Many models, e.g. [1], predict the formation of spatially periodic cortical maps. Recently it was found that irregular maps can be stabilized by long-range interactions in pattern formation models [2]. Because OD and OP maps are geometrically coupled, we studied whether such a coupling can transfer spatial irregularity from OP to OD maps. To this end we contructed dynamical pattern forming models in which we can continuously vary the strength of the inter-map coupling. The solutions of these models were investigated using coupled amplitude equations for the active Fourier modes of the two patterns. If the coupling enters at seventh order in these equations there is a limit in which the back-reaction of the OD dynamics onto the dynamics of the OP map is negligible. In the uncoupled case, OP maps are pinwheel rich and spatially aperiodic whereas OD maps consist of spatially periodic parallel stripes. Above a critical coupling strength the OD stripe solutions become unstable towards solutions showing a disordered layout. [1] Koulakov, Neuron 29, 519 (2001) [2] Wolf, PRL, 95:208701 (2005) [3] Hübener et al. J. of Neuroscience 17:9270 (1997)

BP 16.58 Tue 17:00 Poster D

Floppy modes: low-energy elastic excitations of stiff polymer networks — Claus Heussinger, •Boris Schaefer, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics, LMU Muenchen, Theresienstrasse 37, 80333 Muenchen

Stiff polymers, unlike their flexible counterparts, have a highly anisotropic elastic response, where the low-energy elastic excitations are of bending nature, while stretching deformations are energetically highly unfavourable. Based on this scale separation between bending and stretching mode we analyze the elasticity of *networks* of stiff polymers in terms of the "floppy-mode"concept. A floppy mode defines a deformation field that is constructed by requiring polymer end-to-end distances to stay constant during the course of deformation. As a consequence, stretching deformations are avoided and network elasticity is exclusively due to the bending mode. Singular value decomposition of the kinematic matrix is used to construct the orthonormalized set of floppy modes, which may be viewed as the direct analog to the set of vibrational eigenmodes in networks of central force springs.

BP 17: Symposium Nonlinear and Anomalous Transport in Complex Systems (SYNF)

Time: Wednesday 14:30–17:15 Location: H1

See SYNF for the full program of the Symposium.

BP 18: Functionalized Nanoparticles

Time: Wednesday 14:00–15:15 Location: H43

BP 18.1 Wed 14:00 H43

Phosphorescence quenching in the vicinity of gold nanoparticles — •Thomas Soller[1], Moritz Ringler[1], Thomas Arno Klar[1], Jochen Feldmann[1], Michael Wunderlich[2], Yvonne Markert[2], Hans-Peter Josel[2], Alfons Nichtl[2], and Konrad Kürzinger[2] — [1]Photonics and Optoelectronics Group, Department of Physics and CeNS, Ludwig-Maximilians-Universität München — [2]Roche Diagnostics GmbH, Nonnenwald 2, Penzberg

Gold nanoparticles alter the radiative and nonradiative decay rates of nearby dye molecules, resulting either in a decreased or increased luminescence intensity. While the effects of gold nanoparticles on surrounding fluorophores have been investigated thoroughly, there are no corresponding studies dealing with the influence of gold nanoparticles on the luminescent properties of phosphors. Especially for applications in biosensing, phosphors are particularly suitable, as they allow to cut off autofluorescence.

We have investigated the influence of gold nanoparticles on the radiative and nonradiative decay rates of two different phosphorescent dyes. The phosphors are attached to the nanoparticles via a biomolecular recognition reaction. Time-resolved luminescence spectroscopy reveals an increase of the radiative as well as the nonradiative rate in all regarded phosphor/gold nanoparticle hybrid systems. The increase in the radiative rate is outweighed by the more prominent enhancement in the nonradiatve rate, thus a luminescence quenching occurs.

BP 18.2 Wed 14:15 H43

Nanodiamonds as Photostable Fluorophoric Lable in Living Cells — •Felix Neugart, Carsten Tietz, Fedor Jelezko, and Jörg Wrachtrup — 3. Physical Institute, Pfaffenwaldring 57, University of Stuttgart, 70550 Stuttgart

Many processes in living cells could be promoted by investigation on a single molecule level such as single particle tracking. Dye molecules, especially auto fluorescent proteins, are limited by photobleaching, semiconductor quantum dots are toxic for cells. Nanodiamonds are non-toxic and show a bright non bleaching fluorescence. The origin of the fluorescence are colour centres, these are defects in the diamond lattice. The surface can be functionalized to bind to proteins or other particles of interest. With a size of down to 5 nm nanodiamonds are

comparatively small. For our experiments we prepared diamonds (50 nm and 125 nm crystallites) with NV-centres emitting around 700 nm where living cells show a low autofluorescence. Defects at the surface of the nanodiamonds cause aggregation of the diamonds in physiological buffer solutions. To clean the surface of the nanodiamonds from graphite and other impurities the crystallites were penetrated by strong acids. Acid treated nanodiamonds stay in the buffer in stable colloidal solution. We inserted the nanodiamonds into cells by microinjection or by endocytosis. The diamonds could be detected by fluorescence as well as refraction.

BP 18.3 Wed 14:30 H43

Core-Shell Nanoparticle Layers for Label-Free Biosensing in Array Format — •Reiner Dahint[1], Elka Trileva[1], Hatice Acunman[1], Ulrike Konrad[1], Martin Zimmer[1], Volker Stadler[2], and Michael Himmelhaus[1] — [1]Angewandte Physikalische Chemie, Universität Heidelberg — [2]DKFZ Heidelberg

A novel complex material has been prepared with combined biological and optical functionalities. It consists of biofunctionalized gold-coated nanoparticles self-assembled on surfaces, which locally change their optical absorption properties in response to biospecific interactions. For the preparation of the layers, nanoparticles of about 400 nm in diameter are self-assembled on a gold-coated substrate to form a random-close-packed monolayer. Afterwards, the nanoparticle layer is covered with a metal film by deposition of gold colloid prior to an electroless plating step. The resulting surface exhibits a pronounced optical extinction upon reflection of white light. When organic molecules bind to the surface, the peak position of this extinction shows a strong red-shift. It is demonstrated that sensitivity towards molecule adsorption can be significantly enhanced compared to conventional surface plasmon resonance based techniques. By immobilizing a pattern of different peptides on the nanoparticle layers and reacting the surface with specific antibodies label-free detection of biospecific interactions in array format has been shown. In the future we intend to immobilize high-density peptide libraries on the nanoparticle layers by combinatorial synthesis to facilitate in situ, parallel, time-resolved, and label-free screening of biospecific binding processes.

BP 18.4 Wed 14:45 H43

Polymer-coated inorganic nanocrystals with a defined number of functional groups — •Ralph Sperling, Marco Zanella, and Wolfgang Parak — Ludwig-Maximilians-Universität München, Center for NanoScience, Amalienstr. 54, 80799 München, Germany

Inorganic hydrophobic nanoparticles of different materials such as Au, CdSe/ZnS, CoPt etc. can be coated with an amphiphilic polymer to yield particles that are stable in aqueous solution.

The carboxylic groups on the surface of the polymer shell serve as anchor points for further chemical functionalization. Ligand molecules with amino groups can be covalently bound to the particles. Poly(ethylene glycol) (PEG) is an inert biocompatible polymer that is known to decrease unspecific binding of particles to surfaces and to increase the colloidal stability at physiological salt concentrations. With bifunctional PEG molecules, the particles can be modified with additional functional groups such as amines, thiols, maleimides etc.

By the increase in size, the binding of the PEG molecules to the particles can be monitored by gel electrophoresis and other techniques. If the molecular weight of the PEG molecule is high enough, conjugates of nanoparticles with one, two, and three PEG molecules per nanoparticle can be separated using gel electrophoresis. In this way the PEG molecules act as spacers that allow the sorting of nanoparticles with a discrete number of functional groups, in order to eliminate uncontrolled inter-particle crosslinking in further experiments.

BP 18.5 Wed 15:00 H43

Surface-enhanced Raman scattering (SERS) in single gold nanoparticle dimers — •Moritz Ringler[1], Alexander Schwemer[1], Joachim Stehr[1], Alfons Nichtl[2], Konrad Kürzinger[2], Gunnar Raschke[1], Richard T. Phillips[3], Thomas A. Klar[1], and Jochen Feldmann[1] — [1]Photonics and Optoelectronics Group, Physics Department and CeNS, Ludwig-Maximilians-Universität, 80799 Munich, Germany — [2]Roche Diagnostics GmbH, Nonnenwald 2, D-82372 Penzberg, Germany — [3]Cavendish Laboratory, University of Cambridge, Madingley Road, Cambridge CB3 0HE, United Kingdom

We have used protein-ligand interaction to link gold nanoparticles to dimers that have a well-defined SERS hot spot in the inter-particle gap. The dimer geometry is observed through Rayleigh scattering while the hot spot is probed via Raman spectroscopy. Surface-enhanced Raman emission from the dimer hot spot can be excited when the polarization of the Raman laser beam is parallel to the dimer axis. SERS spectra fluctuate both in shape and amplitude, and Raman emission and Rayleigh scattering spectra are strongly correlated.

BP 19: Biosensors and Biofunctionalized Systems

Time: Wednesday 15:30–17:15 Location: H43

BP 19.1 Wed 15:30 H43

Dependence of DNA/Dendrimer Nanoscale Structures on pH and Composition — •Rolf Dootz and Thomas Pfohl — MPI for Dynamics and Self-Organization, Bunsenstraße 10, 37073 Göttingen

DNA condensation by nanoscale objects represents the process by which the genetic information is packed and protected. Moreover, using artificial nanoscale 3D structures leads to novel DNA-containing nanostructures which exhibit great potential not only as genetic but also as generic materials possessing many valuable functional and material properties. However, a profound knowledge of the manifold DNA organization factors is still missing. Here, the self-assembly behavior of DNA and PAMAM dendrimers generation 6 (P6) is studied as a function of the overall complex composition and the pH of the solution, which is known to affect the dendritic structure and charge significantly. The complexation is found to result in DNA condensation through which the dendrimer-bound DNA chains are aggregated significantly to form ordered structures. At low pH values, a liquid crystalline phase is formed which shows a weak dependence of the complex composition. At high pH values, increasing the dendrimer fraction first results in a condensed nematic phase in which the locally oriented DNA chains do not exhibit a coherent positional order. Subsequently, the condensed DNA structure transforms into a long-range ordered dual lattice phase which has not been described previously. To rule out the nature of the observed phases, the evolution of the interaction between P6 and DNA is studied accomplishing hydrodynamic focussing experiments in crossed microchannel devices.

BP 19.2 Wed 15:45 H43

Development of a Biosensor Device Comprising Functionalized Silicon-On-Insulator (SOI) Structures for the Specific Detection of Proteins — •Bernhard Wunderlich, Petra Neff, and Andreas Bausch — Lehrstuhl für Biophysik E22, TU München, 85747 Garching, Germany

Recently, a new Silicon-on-Insulator (SOI) based thin film resistor for chemical and biological sensor applications was introduced. Its response against pH changes and variations of the salt concentration was measured and compared to the theoretical predictions. It has been shown that this sensor is highly sensitive to variations of the surface potential evoked by the adsorption of small amounts of charged molecules.

We use this sensor device for the label-free detection of proteins. The passivation of the native silicon oxide surface by either physical adsorption of proteins or covalent binding of silane is presented. Different strategies for further functionalizations of the sensor surface with molecules for biomolecular recognition have been evaluated, including the deposition of lipid monolayers with incorporated metal chelate lipids and covalent immobilization of antibodies onto the sensor. Results of the specific detection of proteins by affinity reactions are discussed and compared to the results obtained from fluorescence and ellipsometry measurements.

As the device is based on standard semiconductor technologies, the SOI-based biosensor is well suited for parallelization needed in high throughput applications. We present a sensor device including several sensitive areas suitable for parallel and differential detection.

BP 19.3 Wed 16:00 H43

Impact of Peptide Structure on Semiconductor Binding — •Stefan Schnabel[1], Simon Mitternacht[2], Michael Bachmann[1,2], Anders Irbäck[2], and Wolfhard Janke[1] — [1]Institut für Theoretische Physik, University of Leipzig — [2]Complex Systems Division, Lund University. Sweden

We applied simulated tempering and multicanonical Monte Carlo methods to an all-atom protein model to investigate the thermodynamical behavior of four selected peptides, each consisting of 12 residues, in aqueous solution. By recent experiments it is known that all of the four peptides tend to bind well at a GaAs surface, while only one shows good adhesion to Si. In the simulations we also observed a structural anomaly for this peptide. Since this difference is not induced by a different amino acid content, we conjecture that structural properties play an important role in the adhesion process and propose further experiments to verify this hypothesis.

BP 19.4 Wed 16:15 H43

Chemical Grafting of Biphenyl Self-Assembled Monolayers on Diamond for the Electro-Addressing of Proteins — •Simon Lud[1], Florian Spirkl[1], Marin Steenackers[2], Rainer Jordan[2], Paola Bruno[3], Dieter M. Gruen[3], Stefan Neppl[4], Peter Feulner[4], Jose A. Garrido[1], and Martin Stutzmann[1] — [1]Walter Schottky Institut, Technische Universität München — [2]Lehrstuhl für Makromolekulare Stoffe, Technische Universität München — [3]Materials Science Department, Argonne National Laboratory — [4]Physics Department E20, Technische Universität München

We have explored the formation of self-assembled monolayers (SAMs) of 4'-nitro-1,1-biphenyl-4-diazonium tetrafluoroborate (NBD) onto ultrananocrystalline diamond (UNCD) thin films. In contrast to the established method to modify diamond and diamond like substrates by electrografting, the SAM was formed from the saturated solution of NBD in acetonitrile by spontaneous chemical grafting. Atomic force microscopy (AFM), X-ray photoelectron spectroscopy (XPS), cyclic voltammetry (CV), and near edge X-ray absorption fine structure spectroscopy (NEXAFS) have been used to verify the direct covalent attachment of the 4'-nitro-1,1-biphenyl (NB) SAM on the diamond substrate via stable C-C bonds. The results confirm the presence of a very stable, homogeneous, and dense monolayer. Quantitative analysis by XPS, NEXAFS, and CV has confirmed the presence of a densely packed monomolecular layer with a grafting density of 4.5-5.3 x 10^{-10}mol/cm^2, equivqalent to a nominal area of 31-37 Å^2/molecule.

BP 19.5 Wed 16:30 H43

Desorption of Spider Silk Proteins from Surfaces with an AFM studied by Molecular Dynamics — •Dominik Horinek and Roland Netz — Physik Department, Technische Universität München, 85748 Garching

Protein adsorption is important in many biological phenomena like biomineralization or cardiovascular diseases. This adsorption is governed by electrostatic forces, and by nonelectrostatic dispersion and hydrophobic forces. Recently, it was discovered that polymer adsorption is dominated by nonelectrostatic contributions even for charged substrates. We present classical molecular dynamics simulations of protein adsorption, which account for electrostatics, dispersion, and hydrophobic forces.

Spider silk proteins, which do not form secondary structure in solution, are good model compounds for computer simulation studies of protein-surface interactions. We study the desorption of spider silk proteins from hydrophobic and hydrophilic surfaces with an AFM with different pulling rates. On hydrophobic surfaces, we show that equilibrium desorption forces can be calculated by molecular dynamics, whereas thermal equilibrium is not reached when pulling off a hydrophilic surface.

We compare our modeling results with recent AFM experiments. The equilibrium desorption forces are analyzed in the context of hydrophobic and van der Waals forces, which are important for phenomena like protein folding. We also discuss friction effects, which are seen for fast pulling rates.

BP 19.6 Wed 16:45 H43

Membrane-Grafted Hyaluronan Films: a Well-Defined Model of Glycoconjugate Cell Coats — •Ralf Richter and Joachim Spatz — Heidelberg University & MPI for Metals Research (Stuttgart)

Many cells endow themselves with a carbohydrate-rich pericellular coat, which is particular in many respects. It is amazingly thick (up to several micrometers), extremely hydrated, self-assembled and highly dynamic. These coats play a crucial role in the general protection of the cell, act as a mediator in the communication with its environment, and are vital in structuring its surrounding. A prominent example of such an intriguing self-organized edifice is the hyaluronan-rich coat around chondrocytes. The elucidation of the self-organization and functional properties of these coats constitutes a considerable challenge, due to the complex dynamics of the living cell and due to the coat's highly hydrated nature.

We have developed simplified models of the pericellular coat that are confined on solid supports. Such confinement makes them amenable to investigations with a wide range of biophysical characterization techniques. The end-grafting of hyaluronan (HA) on a solid-supported lipid membrane is an example of a bottom-up approach, with which we create well-controlled models with tuneable complexity that mimic various aspects of the pericellular coat. We present novel experimental approaches to characterize the formation kinetics, thickness, mechanical properties and permeability of hyaluronan-based films. Ultimately, we expect to gain novel information about the relationship between the coat's composition, supramolecular structure and biological function.

BP 19.7 Wed 17:00 H43

Spatially and temporally varying magnetic, biocompatible substrates for induction of cell differentiation — •Juliane Issle, Martin Loichen, and Uwe Hartmann — Institute of Experimental Physics, University of Saarland, 66123 Saarbruecken, Germany

The main goal of the here presented work is to develop a method to induce (stem-) cell differentiation by means of surface-cell interaction. The setup consists of three parts: the biomolecules, magnetic beads as carriers for the biomolecules and a magnetic carrier substrate.

Magnetic nanobeads of an average diameter of 250 nm are commercially available with different surface groups, like carboxylic or amino groups. The magnetic core consists of 20 nm magnetite crystals kept together by means of a dextran matrix. Magnetization curves show that they are superparamagnetic. Cell type specific biomolecules can be covalently bound to the reactive surface groups of the nanobeads. As magnetic carrier substrates out-of-plane magnetized garnet films with particular domain structure are used as they appeared to be biocompatible. The domain structure can be changed using perpendicular or parallel external magnetic fields. As long as the set up is kept in liquid environment (cell culture medium) the nanobeads can follow the domain changes, once they are deposited onto the domain walls.

This opens the opportunity to change the structure of the substrate in vitro and to investigate the influence of topographical as well as chemical substrate changes on cell growth and differentiation. The physical properties of the described setup are analyzed mainly by AFM and MFM, fluorescence microscopy, magnetometry and SEM.

BP 20: Novel Methods

Time: Wednesday 17:30–18:15 Location: H43

BP 20.1 Wed 17:30 H43

The optical cell rotator: An approach to single cell tomography. — •Moritz Kreysing[1], Anatol Fritsch[1], Tobias Kiessling[1], Jochen Guck[2], and Josef Käs[1] — [1]Institute for Soft Matter Physics, Universität Leipzig, Linnéstr. 5, 04103 Leipzig — [2]University of Cambridge, Department of Physics, JJ Thomson Avenue, Cambridge, CB3 0HE, GB

Although optical trapping techniques have become essential in the field of micromanipulation of biological samples during the last decades, all related attempts to control the orientation of biological cells perpendicular to the optical axis of a microscope were unsatisfactory.

With our work we present for the first time a laser tool to hold, continually rotate and stably orient individual biological cells. The so called "optical cell rotator" is based on a dual beam laser trap but due

to a modified beam geometry extended by a potential for the cells' orientation. The generation of this potential could be achieved by the excitation of high order modes in a polarization-maintaining optical fiber resulting in a steadily transported asymmetric beam profile.

Experiments with erythrocytes and HL60 cells clearly show that suspended cells orient one-to-one correlated to a rotation of this laser beam almost instantaneously and can thus be observed under any angle. Our method combined with confocal laser microscopy and modern tomography software promises imaging of individual suspended cells and even separated cell organelles with isotropic resolution.

BP 20.2 Wed 17:45 H43

Nonlinear vibrational microscopy with coherent anti-Stokes Raman scattering — •Christoph Heinrich, Alexander Hofer, Stefan Bernet, and Monika Ritsch-Marte — Division for Biomedical Physics, Innsbruck Medical University, Müllerstraße 44 A-6020 Innsbruck, Austria

It is well known that the intrinsic ability of molecules to rotate and vibrate can be utilized to obtain spectroscopic resolution. Commonly used methods like Raman and infrared spectroscopy have, however, crucial shortcomings in microscopy. Infrared microscopy yields a lack of resolution due to the long excitation wavelengths whereas Raman microscopy does only deliver a weak signal. Coherent anti-Stokes Raman scattering (CARS) microscopy has emerged as new microscopic method a few years ago combining both, high resolution and an intense signal. High resolution is guaranteed through the blue shifted anti-Stokes signal making it also easy to separate it form the excitation laser beams and fluorescence by means of a short pass filter. The coherent signal is enhanced compared to the linear Raman effect due to stimulated emission and constructive interference in the direction determined by the phase matching condition. A drawback unfortunately is a frequency independent nonresonant background always accompanying the resonant signal. Wide-field CARS microscopy presented in this contribution is a non-scanning approach that allows high speed imaging. Latest results and prospects will be discussed.

BP 20.3 Wed 18:00 H43

Surface Plasmon Excited Nanolight Sources — •Dominic Zerulla, Brian Ashall, and Michael Berndt — UCD Dublin, School of Physics, Dublin 4, Ireland

Presented here is a project to develop novel apertureless nanolight sources which would find applications in many innovative devices. In particular, they will be the basis of novel lightsources which will combine beyond diffraction limit resolution with a currently unattainable high photon flux. In brief, the creation of these sources is based on the phenomenon of Surface Plasmon excitation on complex nanostructures. The topographic design of the nanostructures creates a 3-dimensional highly focused electromagnetic field distribution.

The tailor-made structure arrays have been designed on the basis of our theoretical predictions and have been fabricated using e-beam lithography. The layout of the individual nanostructures is not necessarily rotationally symmetric but can have a threefold symmetry axis or even more complex symmetry. The nanostructure are arranged in form of an array.

The light emission and Surface Plasmon resonances from these arrays are currently been investigated in the far-field and the near-field. Additionally, an investigation into the polarisation dependence of the intensities of the diffracted patterns from the above mentioned nanostructured arrays will be discussed. The generation of these highly focused, controllable and localized electromagnetic fields will permit currently unattainable imaging resolution to drive advances in the critical biomedical sector.

BP 21: High-Throughput Data and their Analysis

Time: Wednesday 18:15–19:15 Location: H43

BP 21.1 Wed 18:15 H43

Competitive DNA Hybridization: Experimental Results and Conclusions for Microarray Experiments — •Timo Mai[1], Wolfgang Michel[1], Philipp Baaske[2], Thomas Naiser[1], and Albrecht Ott[1] — [1]Physikalisches Institut, Universität Bayreuth, 95440 Bayreuth — [2]present address: Lehrstuhl für Experimentelle Physik - Biophysik, LMU München, 80539 München

We experimentally approach the complex multi-component hybridization to microarrays by a simple system: A two-component mixture in solution consisting of a perfect match (PM) and a mismatch (MM) oligonucleotide competing for a immobilized probe sequence. We first characterize the binding of PM and MM separately in single hybridization experiments. We deduce rate constants and confirm them with values extracted from analysis of the temperature dependent hybridization signal. From this we predict the time course of hybridization of PM and MM when in competition for surface binding sites and compare with our competitive hybridization experiments.

This is useful for understanding the process of MM displacement by the PM and attaining an estimate for the specificity and the detection limit of microarray experiments.

BP 21.2 Wed 18:30 H43

Optical Study of DNA surface hybridization reveals DNA surface density as a key parameter for interpretation of microarray data — •Wolfgang Michel, Timo Mai, Thomas Naiser, and Albrecht Ott — Experimental Physics 1, University Bayreuth, Germany

We investigate the kinetics of DNA hybridization reactions on glass substrates, where one 22mer strand (bound-DNA) is immobilized via phenylene-diisothiocyanate linker molecule on the substrate, the dye-labeled (Cy3) complementary strand (free-DNA) is in solution in a reaction chamber. We use total internal reflection fluorescence (TIRF) for surface detection of hybridization. As a new feature we perform a simultaneous real-time measurement of the change of free-DNA concentration in bulk parallel to the TIRF measurement. We observe that the free-DNA concentration decreases considerably during hybridization. We show how the standard Langmuir kinetics needs to be extended to take into account the change in bulk concentration and explain our experimental results. Connecting both measurements we can estimate the surface density of accessible, immobilized bound-DNA. We observe that the fluorescent signal from the surface ceases to be proportional to the number of dye-labeled molecules on the surface for surface-densities of hybridized molecules above 5*10ˆ11 molecules/cmˆ2. We discuss the implications with respect to DNA microarray detection.

BP 21.3 Wed 18:45 H43

Decomposing gene expression profiles using sparseness and nonnegativity via genetic optimization — Kurt Stadlthanner[1], •Elmar Lang[1], Ana-Maria Tomé[2], Carlos Puntonet[3], and Fabian Theis[4] — [1]Institute of Biophysics, University of Regensburg, Germany — [2]DETI/IEETA, Universidade de Aveiro, Portugal — [3]Dep. Arqitectura y Tecnología de Computadores, Universidad de Granada, Spain — [4]MPI for Dynamics and Self-Organisation, Göttingen, Germany

Nonnegative matrix factorization (NMF) has proven to be a useful tool for the analysis of nonnegative multivariate data. Gene expression profiles naturally conform to assumptions about data formats raised by NMF. However, its cost function is known to have a rather high indeterminacy concerning the component signals extracted. Hence we consider an extension of the NMF algorithm that provides unique solutions whenever the underlying component signals are sufficiently sparse. However, the resulting fitness function is discontinuous and exhibits many local minima, hence we use a genetic algorithm for its optimization. The algorithm is first applied to toy data in order to investigate its statistical properties. Application to a microarray data set related to Pseudo-Xanthoma Elasticum (PXE) then shows that the proposed algorithm performs superior when compared to standard methods with respect to the estimated PXE-related gene clusters.

BP 21.4 Wed 19:00 H43

Efficient dimension reduction of large-scale biomedical time-series — •Fabian Theis — MPI for Dynamics and Self-Organisation, Göttingen, Germany

Dimension reduction considers the question of removing a noise subspace from a larger multivariate signal. It is a key preprocessing step in

contemporary biomedical data analysis for example of EEG or fMRI. Classically, a signal is differentiated from noise by having a higher variance, and algorithms such as principal component analysis (PCA) remove the low-variance components thereby failing to capture signals that are deteriorated by noise of similar or stronger power.

In order to perform noisy dimension reduction, either higher-order statistics of the data or additional information such as temporal structure may be used. The former methods assume i.i.d. signals, whereas the latter deal with the more realistic assumption of a multivariate 'colored' (in contrast to white) stochastic process. The proposed method, denoted by colored subspace analysis (CSA), distinguishes signal from noise by nontrivial autocovariances. The goal of CSA is to find such a projection onto a signal subspace of minimal dimension. We can prove that the signal subspace is unique, and an efficient algorithm can be proposed. Its complexity is in the order of twice the order of PCA, with an optional accuracy factor. The feasibility of the algorithm is illustrated when applied to fMRI. Independent of data dimension, a task-related subspace is robustly identified. In contrast, the necessary dimension of the PCA-based signal subspace is not invariant under increasing number of captured MRI frames.

BP 22: Molecular Machines

Time: Thursday 9:30–13:15 Location: H43

Invited Talk BP 22.1 Thu 9:30 H43

DNA-based molecular machines and synthetic biology — •Friedrich Simmel — Department Physik, LMU München, Geschwister-Scholl-Platz 1, 80539 München

The unique biophysical and biochemical properties of DNA molecules can be utilized to artificially construct machine-like molecular devices. These devices can perform simple mechanical tasks, controllably bind and release molecules, they can be used as autonomous biosensors, or as active units of switchable materials.

A 'natural' way to control DNA-based devices is to utilize RNA effector molecules rather than DNA. These RNA effectors can be transcribed from artificial 'genes' which in turn can be put under the control of gene regulatory elements. This allows for the construction of genetic control circuits for DNA devices. For example, the action of molecular machines can be made dependent on environmental stimuli by use of appropriate transcriptional logic gates. Coupling DNA devices to transcription also opens up the possibility to realize molecular machines which respond to the presence of naturally occuring RNA molecules.

BP 22.2 Thu 10:00 H43

Bidirectional cargo transport by two species of molecular motors — •Melanie Muller[1], Stefan Klumpp[2], and Reinhard Lipowsky[1] — [1]Max Planck Institute of Colloids and Interfaces, Potsdam-Golm, Germany — [2]Center for Theoretical Biological Physics, University of California San Diego, USA

Long-range intracellular transport is based on molecular motors that pull cargos along cytoskeletal filaments. One type of motor always moves in one direction, e.g. conventional kinesin moves to the microtubule plus end, while cytoplasmic dynein moves to the microtubule minus end. However, many cellular cargos are observed to move bidirectionally, involving both plus-end and minus-end directed motors. We present a stochastic 'tug-of-war' model for which motors work independently and are only coupled via the mechanical interaction with their common cargo. Depending on the motor parameters (such as microtubule affinity or stall force), we obtain three distinct types of motility behaviour of the cargo: no significant motility, stochastic switching between fast plus and minus end motion, and stochastic switching between all three types of motion. In the parameter range which leads to switches between fast plus and minus end motility, the motors appear to act in a cooperative way in spite of the underlying tug-of-war.

BP 22.3 Thu 10:15 H43

Microtubule crosslinking triggers the directional motility of Kinesin-5 — Lukas C. Kapitein[1], Benjamin H. Kwok[2], Tarun M. Kapoor[2], Erwin J.G. Peterman[1], and •Christoph F. Schmidt[1,3] — [1]Department of Physics and Astronomy and Laser Centre, Vrije Universiteit, De Boelelaan 1081, 1081 HV Amsterdam, The Netherlands — [2]Laboratory of Chemistry and Cell Biology, The Rockefeller University, New York, NY 10021, USA — [3]III. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany

Tetrameric kinesin-5 motor proteins are needed for eukaryotic cell division. Assembly and maintenance of the spindle is a highly controlled process. Some kinesins have been found to be cargo-activated, but for a tetrameric motor such was Eg5 it is not obvious how a corresponding mechanism could function. Here we examine factors that influence the switching of Eg5 between the a directional and a diffusive mode, varying buffers and microtubule-binding geometries. We found that at moderate ionic strength, Eg5 moves directionally. In contrast, at higher ionic strength Eg5 diffuses along microtubules without directional bias. Remarkably, under these conditions Eg5 still moves directionally when bound between two microtubules. In the spindle, this functional specialization might allow Eg5 to diffuse on single microtubules without hydrolyzing ATP until the motor gets activated by binding another microtubule.

BP 22.4 Thu 10:30 H43

Kinesin's network of chemomechanical motor cycles — •Steffen Liepelt and Reinhard Lipowsky — Max-Planck-Institute of Colloids and Interfaces, Science Park Golm, 14424 Potsdam

Using the chemical energy released by the hydrolysis of ATP, the molecular motor kinesin moves processively along microtubules. A single motor step is caused by the coupling of conformational changes and filament-binding that is described by the chemomechanical cycle.

We will discuss a general network theory that is based on the distinct chemical states of the motor and on the recent observation that stepping occurs as a single event and is not built up by sub-steps. The necessity of a network theory including several motor cycles comes with the fact, that kinesin is able to walk backwards even at small concentrations of the ATP hydrolysis product ADP, which is inconsistent with the conventional picture of a single chemomechanical cycle.

In our theory, the motor's behavior is governed by the competition of two chemomechanical motor cycles which determine the motor's stall force. A third cycle becomes important for large ADP concentrations. The theory provides a quantitative description for the functional dependencies of different motor properties as observed in single molecule experiments.

BP 22.5 Thu 10:45 H43

Optimal flexibility for conformational transitions in macromolecules — •Richard Neher[1], Wolfram Möbius[1], Erwin Frey[1], and Ulrich Gerland[2] — [1]Arnold-Sommerfeld-Center for Theoretical Physics, LMU München — [2]Institute for Theoretical Physics, Universität zu Köln

Conformational transitions in macromolecules often involve the rotation of extended lever-like structures. We show, that the transition rate is drastically accelerated by a flexible hinge in the lever and that the transition is fastest at an optimal stiffness of the hinge. Near the optimal stiffness, the rate decreases only weakly when cargo is attached to the lever, which might be exploited by molecular motors. To describe our simulation data, we generalize the Kramers-Langer theory to configuration dependent mobility matrices.

BP 22.6 Thu 11:00 H43

Spontaneous wave propagation in muscle fibres. — •Stefan Günther[1,2] and Karsten Kruse[1,2] — [1]Universität des Saarlandes, Theoretische Physik, 66041 Saarbrücken, Germany — [2]Max-Planck-Institut für Physik komplexer Systeme, 01187 Dresden, Germany

Coupled to an elastic element, molecular motors can spontaneously oscillate. In cilia and flagella an ensemble of such oscillatory elements leads to regular wave patterns. In order to gain insight into the mechanism generating these waves, we study chains of sarcomeres. A sarcomere is the elementary force generating unit of a muscle and contains motors as well as elastic elements. Single sarcomeres have been found to oscillate spontaneously [1] and waves of contraction are generated in sarcomere chains [2]. We analyse the dynamics of such chains by using a microscopic sarcomere model. Using parameter values obtained from

single molecule experiments, we find quantitative agreement between our calculations and the experiments. By coarse-graining our description we can relate the parameters of a phenomenological description to the microscopic parameters.

[1] Yasuda, Shindo, and Ishiwata, Biophys. J. 70 (1996)
[2] Sasaki et al, J. Muscle Res. Cell Motil. 26 (2005)

15 min. break.

Invited Talk BP 22.7 Thu 11:30 H43

From biological towards artificial Molecular Machines — •Thorsten Hugel — Biophysics (E22) and Institute for Medical Engineering (IMETUM), Technical University Munich, Garching, Germany

A thorough understanding of nature's fascinating molecular machines will not only help to develop better drugs, but should also guide the construction of man-made Nanosystems, especially if they have to function in physiological conditions. I will report on latest insights into DNA-packaging by the bacteriophage Phi29 portal import motor [1] and on the mechanism of the molecular chaperone HSP90 [2]. Most experiments were performed on the single molecule level, especially by single-molecule force spectroscopy and single-molecule fluorescence. In addition, I will demonstrate how peptide-based synthetic material is capable of energy conversion at the molecular level and could therefore be the basis for biomimetic molecular machines.

[1] T. Hugel, et al., PLoS Biol 5(3): e59 (2007)
[2] H. Wegele, et al., Rev. Physiol. Biochem. Pharmacol 151, 1 (2004)

BP 22.8 Thu 12:00 H43

Single-molecule fluorescence resonance energy transfer studies of RNA polymerase II — •Jens Michaelis[1,2], Joanna Andrecka[1], Florian Brückner[3], and Patrick Cramer[1,3] — [1]Ludwig-Maximilians-Universität München, Department Chemie und Biochemie, Butenandstr.11, 81377 München — [2]Center for Nanoscience, CeNS — [3]Ludwig-Maximilians-Universität München, Gene Center

The crystal structure of the elongation complex of the complete 12 subunit RNA polymerase II (Pol II) reveals incoming template and non-template DNA, a seven base pair DNA/RNA hybrid, and three nucleotides each of separating DNA and RNA. Albeit, longer oligomers were used in preparation, the exit pathway of the nascent RNA could not be observed, presumably due to the inherent flexibility.

To determine the position of the nascent RNA, we have measured the distances between several known points on the Pol II elongation complex and the RNA using single pair fluorescence resonance energy transfer (sp-FRET). For a given position on the RNA we have measured three distances to known positions within the elongation complex, in order to map the unknown RNA position by triangulation. We have determined the position of the end of a 17-nt, 20-nt and 23-nt RNA thus mapping the exit pathway of the RNA product. As the RNA grows longer, we observe binding of to the dock domain and dynamical repositioning of the RNA.

BP 22.9 Thu 12:15 H43

Stepsize of the two rotary motors of FoF1-ATP synthase monitored by single-molecule FRET — Monika Düser, Nawid Zarrabi, Rolf Reuter, Dongmei Ji, Frank-Mario Boldt, and •Michael Börsch — 3. Physikalisches Institut, Universität Stuttgart, Pfaffenwaldring 57, 70550 Stuttgart

FoF1-ATP synthases are the membrane-embedded enzymes in mitochondria, chloroplasts and bacteria which supply cells with the chemical 'energy carrier' adenosine triphosphate, ATP. The enzyme consists of two coupled counteracting rotary motors. The Fo motor is driven by the electrochemical potential difference of protons across the membrane and has 10 proton binding sites. However, the isolated F1 motor can be driven by ATP hydrolysis and rotates in 120° steps in opposite direction. We investigate the elastic energy storage within FoF1 caused by the symmetry mismatch of the two motors (10-step versus 3-step per 360° turn) using time resolved single-molecule Förster resonance energy transfer, FRET. Therefore we have introduced pairs of two fluorophores at several positions within the Escherichia coli enzyme using eGFP-fused subunits and specific amino acid labeling. To switch-on and control the ATP production of an individual FoF1-ATP synthase we recently developed local electrochemical proton generation at the tip of a nanoelectrode in the confocal detection volume. Multiparameter FRET data provide insights into the varying stepsize of the Fo motor during ATP synthesis, and into the action mode of the non-competitive inhibitor aurovertin which modulates the rotary motion during ATP hydrolysis.

BP 22.10 Thu 12:30 H43

Stochastic thermodynamics of the single F_1-ATPase molecules — •Alexander Kovalev[1], Florian Werz[1], Michael Börsch[1], Dirk Bald[3], Tim Schmiedl[2], Udo Seifert[2], Jörg Wrachtrup[1], and Carsten Tietz[1] — [1]3rd Institute of Physics, Stuttgart University, Stuttgart, Germany — [2]II. Institute for Theoretical Physics, Stuttgart University, Stuttgart, Germany — [3]Department of Structural Biology, Vrije Universiteit Amsterdam, Amsterdam, Netherlands

A water soluble part of the whole transmembrane protein F0F1-ATP synthase, F1-ATPase, is a rotary motor driven by ATP hydrolysis. The back rotation of F1-ATPase induces ATP synthesis. Due to the 3 fold symmetry the central subunit of F1-ATPase rotates in three steps pausing during ATP-binding. The single molecule study allows us to reconstruct the distribution of the rate constants, which seems to be higher compared to ensemble measurements. We have determined different statistical quantities characterizing dynamical properties of F1-ATPase transition rates between its three states. A fluctuation theorem relating the forward and backward steps was verified on single trajectories using the 3-state model. That gives us opportunity to describe F1-ATPase behaviour using stochastic thermodynamics theory. The time dependent conditional probabilities for F1-ATPase to be in a certain state were compared with solution of the master equations. The 3-states model trajectories were simulated to estimate the statistical errors.

BP 22.11 Thu 12:45 H43

Data Analysis with Hidden Markov Models on a single rotary motor FoF1-ATP synthase — •Nawid Zarrabi, Monika Düser, and Michael Börsch — 3. Physikalisches Institut, Pfaffenwaldring 57, Universität Stuttgart, 70569 Stuttgart

The formation of ATP from ADP and phosphate is the major reaction that provides the 'chemical energy' for living organisms. This reaction is performed by a stepwise internal rotation of subunits of the enzyme FoF1-ATP synthase. We modeled the stepwise subunit rotation of the ATP synthase with Hidden Markov Models (HMM) and evaluated those models with confocal single-molecule fluorescence resonance energy transfer (FRET) data [1,2]. To monitor the capability of the HMM approach we generated single molecule data of freely diffusing enzymes in liposoms by a Monte-Carlo-simulation. Thereby we included the intensity fluctuations due to Brownian motion. The rotary catalysis of the ATP synthase was described by a Markov process with predefined rates for forward and backward steps. The aim of the data analysis method was the determination of dynamic parameters of ATP synthase, i.e. the occurrence of substeps depending on the ATP concentration.

References: [1] B. Zimmermann, N. Zarrabi, M. Diez, P. Gräber, M. Börsch, (2005) EMBO J. 24:2053-2063. [2] M. G. Düser, N. Zarrabi, Y. Bi, B. Zimmermann, S. D. Dunn, M. Börsch (2006) Proc. of SPIE 6062:89-104.

BP 22.12 Thu 13:00 H43

Regulation of a chimeric Eg5head/DmKHC tail motor protein — •Stefan Lakämper[1], Mikhail J. Korneev[2,3], Stefanie Reiter[1], Lukas C. Kapitein[3], Erwin J.G. Peterman[3], and Christoph F. Schmidt[1] — [1]III. Physikalisches Institut, Georg-August-Universität, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany — [2]ASML, De Run 6501, 5504 DR Veldhoven, The Netherlands — [3]Department of Physics and Astronomy and Laser Centre, Vrije Universiteit, De Boelelaan 1081, 1081 HV Amsterdam, The Netherlands

We have constructed a chimeric motor protein using the head and neck portion of the mitotic Eg5 kinesin and the tail protion of a kinesin 1 (DmKHC). This chimeric motor maintains characteristic features of the slow mitotic Eg5, but it is dimeric instead of tetrameric and the regulation by the opposing pair of heads is eliminated. This allowed us to study directly the inhibition of the dimer function by the small drug monastrol.

BP 23: Cell Motility and Migration (in vitro and in vivo)

Time: Thursday 14:00–17:00 Location: H43

Invited Talk BP 23.1 Thu 14:00 H43

The Physics of Neuronal Growth — •Timo Betz, Daniel Koch, and Josef Käs — Institut for Soft Matter Physics, University of Leipzig, Germany

The correct development of the central nervous system requires accurate and reliable neuronal network formation, a process accomplished by a highly dynamic structure at the tip of a growing neurite, called the growth cone. To find its proper target, each growth cone integrates chemical and mechanical signals, and converts these signals into changes of its active polymeric cytoskeleton. To understand these fundamental growth processes, we quantified the physical properties of a growth cone, like traction forces, viscoelastic properties and actin dynamics, and found that growth cones show unique features with respect to other motile cell types.

We show that bistable stochastic fluctuations between growth and retraction phases determine the direction of neuronal growth, and that these fluctuations are dominated by bistable modes of actin polymerization. Furthermore, the viscoelastic properties of the growth cone are combined with the measured actin dynamics to calculate the active internal and external forces generated by the growth cone. Integrating these data suggests that growth cones utilize physical processes like stochastic signal amplification and unique mechanical properties to build an organism's intricate nervous system. Moreover, our measurements provide the base to understand the complex interplay between actin polymerization, active internal forces and substrate adhesion that finally results in nerve regeneration and neuronal network formation.

BP 23.2 Thu 14:30 H43

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

The growth cone, a highly motile sensory structure at the tip of an advancing neurite, plays a fundamental role in the wiring of neuronal connections during development, nerve regeneration, and in neuronal plasticity. The dynamics of the leading edge is governed by actin polymerization and can be described as a bistable stochastic process which means polymerization is either turned on or off. Furthermore, the direction taken by the growth cone is introduced by the orientation of the filopodia which are force sensitive actin filament bundled structures that emerge from the leading edge. In actively extending growth cones, a laser spot placed at the leading edge affects the direction taken by the growth cone. However, optical control is not achieved in non-extending growth cones with polymerization mostly turned off which sets a natural limit for optical neuron guidance. The analysis of optically induced turning events reveals that the applied optical forces lead to filopodia reorientation. We hypothesize that the filopodia are coupled back into the central region and in a lever arm like fashion change the extension of the leading edge.

BP 23.3 Thu 14:45 H43

Glial Cell Stiffness as Guidance Cue for Neurons — •Kristian Franze[1,2], Timo Betz[1], Yunbi Lu[1,2], Johannes Bayer[3], Melike Lakadamyali[3], Paul Janmey[4], and Josef Käs[1] — [1]Soft Matter Physics, Universität Leipzig — [2]Paul-Flechsig-Institute of Brain Research, Universität Leipzig — [3]CNLD, University of Texas, Austin, USA — [4]Inst. Medicin & Engineering, University of Pennsylvania, Philadelphia, USA

Neuronal migration is a fundamental event during development. Neurons travel from the ventricular zone, the place of their origin, to the cortical plate, bridging distances that can be a multiple of their length. Radial glial cells, which are cells that connect the ventricular zone with the opposing cortical surface with two long, radial processes, are known to guide neuronal migration. Neurons attach to these cells and precisely follow their processes, even if they are significantly bent. No biochemical guidance cues have been identified for this behavior and simple diffusive gradients cannot explain how neurons follow the bent glial shape. We found that in vitro neurons actively probe their mechanical environment. They retracted their processes and reextended them in a random direction when mechanical stresses exceeding ˜300 Pa opposed their leading edge. This threshold corresponds to the maximum substrate stiffness that neurons could visibly deform. Interestingly, radial glial cells were softer than 300 Pa, suggesting that their mechanical properties may facilitate neuronal radial migration in the developing brain. This is in sharp contrast to the current opinion that neuronal guidance is solely based on biochemical signaling.

BP 23.4 Thu 15:00 H43

Symmetry breaking in actin gels - Implications for cellular motility — •Karin John, Philippe Peyla, and Chaouqi Misbah — Université Joseph Fourier Grenoble, Laboratoire de Spectrométrie Physique, BP 87 - 38402 St.-Martin-d'Hères, France

The physical origin of cell motility is not fully understood.

Recently minimal model systems have shown, that polymerizing actin itself can produce a motile force, without the help of motor proteins. Pathogens like Shigella or Listeria use actin to propel themselves forward in their host cell.

The same process can be mimicked with polystyrene beads covered with the activating protein ActA, which reside in a solution containing actin monomers. ActA induces the growth of an actin gel at the bead surface. Initially the gel grows symmetrically around the bead until a critical size is reached. Subsequently one observes a symmetry breaking and the gel starts to grow asymmetrically around the bead developing a tail of actin at one side. This symmetry breaking is accompanied by a directed movement of the bead, with the actin tail trailing behind the bead. Force generation relies on the combination of two properties: growth and elasticity of the actin gel.

We study this phenomenon theoretically within the framework of a linear elasticity theory and linear flux-force relationships for the evolution of an elastic gel around a hard sphere.

Conditions for a parity symmetry breaking are identified analytically and illustrated numerically with the help of a phasefield model.

BP 23.5 Thu 15:15 H43

A Biomimetic System Modeling Active Lamellipodial Network Dynamics — •Florian Huber, Björn Stuhrmann, and Josef Käs — Institute for Soft Matter Physics, University Leipzig, Linnéstr. 5, D-04103 Leipzig, Germany

Many different cell types (e.g., keratocytes or fibroblasts) show directed motion (motility), a process driven by the assembly of Actin protein at the leading front of the cell, the lamellipodium. Although the details of polymerization regulation by accessory proteins differ between cell types, several important features are conserved throughout the eukaryotic kingdom. The key molecular players involved in these processes have been identified and have already been used to generate *in vitro* Actin network growth. While existing assays are sufficient to explain intracellular bacteria propulsion, they are not adequate to describe crawling cell motility extensively. The required next step towards cellular conditions is to confine the polymerizing Actin gel to nanostructured cell-sized chambers. This approach restricts the protein pool available and thus allows to mimic for the first time the self-sustaining character of the lamellipodia machinery.

Our setup will allow the observation of the system's response to controlled variation of various biochemical and physical parameters. Numerical simulations will be used to extract constitutive equations from experimantal data on dynamic distributions of the various protein species. Mechanical properties will be analyzed using passive microrheology. This model system represents a novel means to explore biomechanical mechanisms forming the basis of cell motility.

BP 23.6 Thu 15:30 H43

Investigation of Filopodial Mechanics and Dynamics — •Brian Gentry[1], Michel Gögler[1], Marie-France Carlier[2], and Josef Käs[1] — [1]Universität Leipzig, Linnestr. 5, Leipzig, Germany — [2]CNRS, LEBS, 1 Avenue de la Terrasse, Gif-sur-Yvette, France

The actin cytoskeleton is a complex system that dynamically reorganizes its structure to produce forces that drive the leading edge of a cell membrane outward. Filopodia emerge from local reorganization of the dense lamellipodial filament network. Stiff bundles are essential to produce protrusive forces, so we study their mechanical properties. We directly measure actin bundle bending stiffness in vitro, providing information about crosslinker and bundle characteristics. Formation of long, unbranched bundles also requires that fiber ends be protected from capping. Formin is an end-binding molecule which is capable of

nucleating and driving the polymerization of actin polymers in vivo, remaining bound simultaneously to both fiber and substrate. We are studying formin in a controlled, reconstituted system to help elucidate its precise functions as considered in recent models. Both experiments use a state-of-the-art laser tweezer to track the position of a bead attached to an actin filament bundle, allowing us to measure critical buckling and motor-driven forces. The formin measurements are the first for an end-tracking motor and will lend new insight into the underlying dynamics of its operation. Our setup allows us to take a novel approach to the study of filopodial component's properties-bundles which provide stiffness and a molecular engine which produces adequate forces such that protrusion can occur.

BP 23.7 Thu 15:45 H43

Dynamics of receptor-ligand binding and filopodial retraction in phagocytosis — •Alexander Rohrbach[1] and Holger Kress[2,3] — [1]University of Freiburg, Germany — [2]EMBL, Heidelberg, Germany — [3]present address: Yale University, New Haven, USA

Phagocytosis is the process by which bacteria are internalized into macrophages. This process, which is a central mechanism in the immune system, was so far mainly investigated by conventional light and electron microscopies. However, its mechanical properties were barely known up to now. We used optical tweezers-based microscopy to investigate the mechanics of phagocytosis. The motion of an optically trapped bead was tracked interferometrically in 3D with nanometer precision at a microsecond timescale.

The measurement of the thermal bead fluctuations during the binding to the cell membrane enabled the observation of individual receptor-ligand bond formation. These observations were in agreement with Brownian dynamics simulations of the binding process. By inducing binding of beads to filopodia, we found that filopodia act as cellular tentacles: They retract a few seconds after binding and pull the bound beads towards the cell. The observation of discrete F-actin dependent 33-nanometer steps during retraction led to the hypothesis that an actin-based molecular motor plays an important role in the retraction. Force-velocity measurements revealed the mechanical properties of this putative motor. A model for the force-dependent motor kinetics confirming these results was developed.

BP 23.8 Thu 16:00 H43

Keratocyte migration as active Brownian motion: Experiments and theory — •Simon Flyvbjerg Tolic-Norrelykke and Frank Julicher — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Fish keratocytes constitute a popular model system for the study of cell migration. Keratocytes are highly mobile cells that live on the outside of fish-scales where they are thought to be involved in wound healing and repair.

We will present some recent experimental findings and theoretical results for the migration of individual keratocytes in two dimensions. Cells were tracked as they migrated on a glass surface in the absence of external stimuli and parameters were extracted from the time-series of positions, allowing for the construction of an equation of motion. In contrast to other existing models for migration, these cells turned out to be best described in terms of an active Brownian process. In active Brownian processes internal energy is converted into motion, leading to a preferred speed that is different from zero and velocity histograms with a characteristic donut shape. Analytical expressions for observable parameters are derived and compared to the experimental data as well as to results from simple simulations.

BP 23.9 Thu 16:15 H43

driving forces in cell motility, motors versus polymerization — •Claudia Brunner, Michael Gögler, Allen Ehrlicher, and Josef Käs — Universität Leipzig, Linnestr 5, 04103 Leipzig

A cell's ability to move is fundamental for various functions in nature, such as morphogenesis, immune response, and the invasiveness of cancer. On the molecular level, actin polymerization and molecular motors, such as myosin, are involved in cell motility but the mechanism as a whole is not very well understood. Here we present direct measurements of the forward forces generated at the leading edge of the lamellipodium and at the cell body of rapidly translocating fish keratocytes. Our SFM-based technique uses the vertical and lateral deflection of the cantilever to directly measure the maximal forward force of whole cells by stalling them. Through selective manipulation of molecular components by addition of different drugs, the stall forces and the velocity correlation can be compared to elucidate the importance of different force generating processes, such as polymerization and molecular motors.

BP 23.10 Thu 16:30 H43

Role of viscosity and surface tension of zebrafish embryonic tissues in tissue flows during gastrulation — •Eva-Maria Schoetz[1,2], Tigran Bacarian[3], Malcom Steinberg[4], William Bialek[4], Carl-Philipp Heisenberg[1], Ramsey Foty[5], and Frank Julicher[2] — [1]MPI-CBG, Dresden — [2]MPI-PKS, Dresden — [3]UCI, USA — [4]Princeton University, USA — [5]UMDNJ, USA

At the onset of gastrulation in zebrafish, complex flows and cell movements occur, which are not well understood. Here, we study the material properties of zebrafish embryonic tissues which are important for the tissue dynamics. We found that these tissues behave viscoelastic and exhibit liquid-like properties on long time scales. They relax internal stress caused by compressive forces or, in the absence of external forces, round up and fuse into spheres to minimize their free surface. Quantitative differences in the adhesivity between different types of tissues result in their immiscibility and sorting behavior analogous to that of ordinary immiscible liquids. When mixed, cells segregate into discrete phases, and the position adopted correlates with differences in the aggregate surface tensions for these phases. Surface tensions were measured with a tissue surface tensiometer. Aggregates were compressed and their force response and shape were recorded as a function of time. From the analysis of the force-relaxation curves, we determined the surface tensions, relaxation times, tissue viscosities and shear moduli. Furthermore, by 4D-cell tracking, we measured kinetic parameters such as cell speed, directionality and persistence of cell movement.

BP 23.11 Thu 16:45 H43

Continuum Description of Growing Cellular Tissues — •Thomas Bittig[1], Ortrud Wartlick[2], Anna Kicheva[2], Marcos González-Gaitán[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 28, 01187 Dresden, Germany — [2]Department of Biochemistry and Department of Molecular Biology, Geneva University, Sciences II, Quai Ernest-Ansermet 30, 1211 Geneva 4, Switzerland

During the development of multicellular organisms, organs grow to well-defined shapes and sizes. The mechanisms that coordinate the proliferation and movement of cells in growing tissues remain still unclear. In order to study cellular movement in a growing epithelium, we developed a continuum description which considers the time evolution of a local cell density in two or three dimensions. We describe the tissue as a viscous fluid in which active stresses are generated by cell division. We consider situations where cell division is randomly oriented and where a preferred orientation of cell division exists. We perform numerical studies of this macroscopic description using a discrete model on a cellular level. Our descriptions can be used as a basis for the study of the transport of signaling molecules through growing tissues as e.g. in the growing Drosophila wing disc, a precursor of the fly wing.

BP 24: Cell Mechanics (in vivo)

Time: Thursday 10:00–12:45 Location: H44

BP 24.1 Thu 10:00 H44

Nonlinear creep measurements in living fibroblasts — •Philip Kollmannsberger, Claudia T. Mierke, and Ben Fabry — ZMPT, Biophysics Group, University of Erlangen-Nuremberg

The linear viscoelasticity of adherent cells and biological tissue is characterized by a wide distribution of relaxation times and shows a power-law creep response or a power-law viscoelastic spectrum over several decades of time or frequency. In addition, single cells and tissue exhibit a highly nonlinear stress-strain relationship. The viscoelastic behavior of cells in the non-linear regime is unknown, however, but is of particular interest to test different conflicting theories. Here we measured the viscoelastic behavior of a variety of adherent cells in the linear and non-linear regime using magnetic tweezers with real-time force feedback. We imposed a staircase-like sequence of 1 nN force steps up to a maximum force of 10 nN onto 4.5 μm fibronectin-coated magnetic beads bound to the cytoskeleton via integrins. For each stress level σ, the differential creep response of single cells followed a power law: $J(\sigma,t) = J_0(\sigma)(\frac{t}{t_0})^b$, however the differential creep modulus $J_0(\sigma)$ decreased with stress, equivalent to stress stiffening. The power-law creep exponent b showed no systematic stress dependence, although in some cells b increased at high forces, consistent with yielding and disruption events. Static stress stiffening is predicted by models of semiflexible polymers and can be modelled using Fung's theory of quasilinear viscoelasticity for biological tissues, whereas a speed-up of relaxation processes due to yielding and structural changes is consistent with soft glassy rheology.

BP 24.2 Thu 10:15 H44

Cellular pattern formation by strain-mediated active switching — •Raja Paul and Ulrich Schwarz — University of Heidelberg, Im Neuenheimer Feld 293, D-69120 Heidelberg, Germany

Using Monte Carlo simulations, we investigate the time evolution of the force generated by an ensemble of cells placed initially at random in the extracellular matrix (ECM). The ECM is modelled as a two-dimensional cable network with triangular or square lattice geometry and the cells are modelled as force contraction dipoles. We observe various patterns depending on prestrain, geometry, boundary conditions, elastic moduli, cell density, density of ECM crosslinks and temperature. Recent experiments of cellular assembly in a clamped collagen matrix show that force increases with time. This observation can be explained in our model by considering a strain mediated switching of cells into the active state and subsequent contraction from an initial quiescent state.

BP 24.3 Thu 10:30 H44

Modelling the spatially inhomogeneous contraction of stress fibers — •Achim Besser and Ulrich Schwarz — University of Heidelberg, INF 293, D-69120 Heidelberg, Germany

The contractile activity of cells is often associated with stress fibers, which are contractile bundles of actin filaments crosslinked by α-actinin and the motor protein myosin II. At their ends, they are attached to the extracellular environment through cell-matrix contacts called *focal adhesions*. Upon contraction, elastic deformations along the fibers have been observed experimentally to be inhomogeneous. We suggest that these spatial differences arise from biochemical signals originating from the focal adhesions. Stress fibers are modeled as a periodic arrangement of springs, dashpots and contractile elements. Contractile activity is coupled to the diffusible biochemical signal. We solve our model in a continuum approximation and show that it results in the experimentally observed deformation pattern.

BP 24.4 Thu 10:45 H44

High Resolution Mapping of Cell Mechanics (in Vivo) Using Digital Pulsed Force Mode — •Michael Holzwarth[1], Alexander Gigler[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University, D-89069 Ulm, Germany — [2]Present address: Section Crystallography, University of Munich, Theresienstrasse 41/II, D-80333 Munich, Germany

Local mechanical properties of living cells have been investigated by means of AFM, using Digital Pulsed Force Mode (DPFM). The DPFM images the surface while probing its mechanical properties locally. At least one force curve is recorded for each point of the scanned area. Thus, more than 500,000 curves have been recorded and completely evaluated for each single experiment.

The glass-like substrate served as an online reference material for calibration purposes. First, the force trajectories were corrected for the viscous drag force in the liquid environment. Secondly, the curves within the region of the substrate were phase corrected to compensate for the time lag of the signal in the setup assuming a purely elastic response of the reference material. Finally, all the force traces have been corrected by using this calibration and evaluated according to common continuum-elastic models.

The resulting images allow the assignment of values of Young's modulus, local adhesion and hysteretic behaviour at a high lateral resolution all over the cell body. The procedure of our measurement and the corresponding signal correction strategy of the automated data evaluation will be shown.

BP 24.5 Thu 11:00 H44

Rate of stress increase during cell spreading on substrates with different matrix rigidity — •Daniel Paranhos Zitterbart, Claudia T. Mierke, Thorsten M. Koch, and Ben Fabry — ZMPT, Biophysics Group, Universität Erlangen

For most cell types, adhesion, spreading and tension generation are crucial for cell survival. These processes are strongly influenced by the rigidity of the extracellular matrix: Cells spread more and faster, and generate higher tension on more rigid substrates. We report simultaneous measurements of cell spreading and traction generation during adhesion of MDA-MB-231 breast carcinoma cells onto collagen coated polyacrylamid gels. The Youngs modulus of the gels was tuned between 1500 ('soft') and 6000 ('hard') Pa. The evolution of cell tractions was computed from the gel deformation measured every 30 sec by tracking the displacements of fluorescent beads ($\varnothing 0.5\mu m$) embedded at the gel surface. As a robust estimate of total force generation, we computed for each cell the elastic strain energy U stored within the gel. As expected, cells generated a higher maximum strain energy $U = 1.01pJ$) and spread more ($A = 6002 \pm 961\mu m^2$) on harder gels compared to softer gels ($U = 0.20pJ, A = 3012 \pm 492\mu m^2$). When the strain energy vs. time data of individual cells were normalized by spreading area, they collapsed onto a single relationship, regardless of gel stiffness. These data extend earlier findings of a proportionality between cell spreading and tension generation (Reinhard-King, Biophys J 2005) and show that individual cells exhibit a constant rate of stress increase during early adhesion events regardless of the substrate rigidity.

15 min. break.

BP 24.6 Thu 11:30 H44

Cell elasticity as a function of actin expression — •Carsten Stüber and Josef Käs — Institute of Experimental Physics I, University of Leipzig, Germany

The deformation response to an external force of an eurkaryotic cell mainly depends on its cytoskeletal composition. Theoretical models have been introduced to quantify the concentration dependence of the different cytoskeletal components to the elastic strength of cells. Verifying the models experimentally, the optical stretcher, a two beam optical trap, is used to elongate fibroblast cells. These fibroblasts are transfected with GFP-actin, which leads to an overexpression of actin within the cell and allows to determine the actin concentration using fluorescence image analysis. The dependence of the elasticity on the actin concentration of fibroblasts shows a softening of the cell with increasing number of actin filaments.

BP 24.7 Thu 11:45 H44

Active mechanical stabilization of the viscoplastic intracellular space of Dictyostelia cells by microtubule-actin crosstalk — •Doris Heinrich and Erich Sackmann — Department für Physik, Ludwig-Maximilians-Universität, Geschwister-Scholl-Platz 1, 80539 München, Germany

We investigated the micro-viscoelasticity of the intracellular space of Dictyostelium discoideum cells by evaluating the intracellular trans-

port of magnetic force probes and their viscoelastic responses to force pulses of 20-700 pN. The role of the actin cortex, the microtubule (MT) aster and their crosstalk is explored by comparing the behaviour of wild type cells, myosin II null mutants, latrunculin A and benomyl treated cells. The MT coupled beads perform irregular local and long range directed motions which are characterized by measuring their velocity distributions (P(v)). The correlated motion of the MT and the centrosome are evaluated by microfluorescence of GFP-labeled MTs. P(v) can be represented by log-normal distributions with long tails and it is determined by random sweeping motions of the MTs and by intermittent bead transports parallel to the MTs. The viscoelastic responses are strongly non-linear and are mostly directed opposite or perpendicular to the force, showing that the cytoplasm behaves as an active viscoplastic body with time and force dependent drag coefficients. Force-balance is established by the mechanical coupling between the soft microtubules and the viscoelastic actin cortex, providing cells with high mechanical stability despite the softness of the cytoplasm.

BP 24.8 Thu 12:00 H44

Single fibroblast viscoplasticity: elastic stiffening and kinematic hardening — •Pablo Fernandez[1,2], Pramod Pullarkat[1], and Albrecht Ott[1] — [1]Universität Bayreuth, Germany — [2]Present address: Technische Universität München, Germany

The deep biological relevance of mechanics is well illustrated by features such as cell locomotion, contractility, and mechanotransduction. The advent of single-cell rheology brings hope of a physical understanding of these phenomena. We report that the mechanical response of single 3T3 fibroblasts to uniaxial extension in the 1–100% range obeys a remarkably simple and robust phenomenology. Below 10% deformation cells exhibit a previously reported, stress-stiffening master relation probed with sinusoidal oscillations. Beyond 10% stretch, deformations at a constant rate in a 0.03–3 μm/s range always exhibit pure plastic flow. The plastic deformation translates the elastic region, a behaviour known as kinematic hardening. Fixing the cells abolishes the plastic response. Then the force-length relation shows dramatic stiffening, the integral of the previously described master-relation. Thus 2 key features summarise fibroblast mechanical behaviour: exponential elastic stiffening and viscoplastic kinematic hardening.

BP 24.9 Thu 12:15 H44

Physical description of mitotic spindle orientation during cell division — •Andrea Jiménez-Dalmaroni[1], Manuel Théry[2], Victor Racine[2], Michel Bornens[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden, Germany — [2]Institut Curie, CNRS UMR144, Compart. et Dynamique Cellulaire, 26 rue d'Ulm 75248, Paris, France

During cell division, the duplicated chromosomes are physically separated by the action of the mitotic spindle. The mitotic spindle is a dynamic structure of the cytoskeleton, which consists of two microtubule asters. Its orientation defines the axis along which the cell divides. Recent experiments on dividing cells, which adhere to patterned substrates, show that the spindle orientation depends on the spatial distribution of cell adhesion sites. Here we show that the experimentally observed spindle orientation can be understood as the result of the action of cortical force generators acting on the spindle microtubules. We assume that the local activity of force generators is controlled by the spatial distribution of cell adhesion sites determined by the particular geometry of the adhesive substrate. We develop a simple physical description of the spindle mechanics, which allows us to calculate the torque acting on the spindle, as well as the energy profile and the angular distribution of spindle orientation. Our model accounts for the preferred spindle orientation, as well as the full shape of the angular distributions of spindle orientation observed in a wide variety of patterns. We conclude that, based on a few simple assumptions, we can provide a quantitative description of the spindle orientation.

BP 24.10 Thu 12:30 H44

Beyond the Rim: The Viscoelastic Pericellular Coat — •Heike Boehm, Joachim Spatz, and Jennifer Curtis — Max-Planck-Institute for Metals Research, Department New Materials & Biosystems & University of Heidelberg, Department of Biophysical Chemistry

Most mammalian cells are surrounded by an optically-transparent layer of highly hydrated polysaccharides and proteins, the pericellular coat (PCC). The most vital component is a linear, flexible polyelectrolyte: hyaluronan, which is synthesized directly on the outer cell membrane. Different proteins can bind to the hyaluronan and thus anchor it to the cell membrane, stiffen and/or crosslink it. The resulting viscoelastic coat plays a vital role in cell migration, proliferation and various diseases like cancer and arthritis.

Few studies quantitatively examine the PCC's mechanical properties induced by structural or compositional reorganization. We perform microrheology studies to determine the viscoelasticity and define the impact of proteins and glycosaminoglycans on the structure of the PCC. Information about the structure of the polymer matrix can thus be gained by observing the diffusion of a particle embedded in the PCC of living cells (passive microrheology). With our holographic optical tweezers (HOT) setup we can create a dynamic array of traps, that enable us to carefully place several beads at different sides of a living cell simultaneously and to measure or apply forces ranging from femtonewtons to 10's of piconewtons (active microrheology).

BP 25: Oscillatory Systems

Time: Thursday 14:30–17:00 Location: H44

Invited Talk BP 25.1 Thu 14:30 H44

Mechanical amplification by sensory hair cells from the vertebrate ear — •Pascal Martin — Institut Curie recherche\CNRS - Laboratoire PCC (UMR168), 26 rue d'Ulm 75005 Paris, France

The dazzling sensitivity and frequency selectivity of the vertebrate ear rely on mechanical amplification of small sounds by hair cells, the sensory receptors of the inner ear that transduce mechanical stimuli into electrical signals that will then be received by the brain. As revealed by spontaneous oscillations and forms of mechanical excitability in response to force steps, the hair bundle that adorns each hair cell is both a mechano-sensory antenna and a force generator. To study active hair-bundle motility, we use flexible glass micro-fibers to stimulate mechanically in vitro a single hair bundle from the bullfrog's sacculus. We find that an oscillatory hair bundle amplifies its response to small stimuli at frequencies near that of the spontaneous oscillation. By combining measurements of force-displacement relations with Ca2+ iontophoresis, we show that the location of a bundle's operating point within its nonlinear force-displacement relation controls the type of movements observed. We have developed a simple theoretical description that can account for the various incarnations of active hair-bundle motility. There, mechanical activity stems solely from myosin-based adaptation, the process by which molecular motors (myosins) in the hair bundle set the open probability of mechano-sensitive ion channels at steady state. By taking intrinsic hair-bundle fluctuations into account, we could reach quantitative agreement between calculated and experimentally measured response functions.

BP 25.2 Thu 15:00 H44

Biophysics of Drosophila Audition — •Björn Nadrowski, Jörg Thaddäus Albert, and Martin Cornelius Göpfert — Zoologisches Institut, Universität Köln, Weyertal 119, 50923 Köln

In Drosophila, hearing is mediated by the antenna. Stimulus forces acting on the antennal receiver are coupled to dedicated neurons that comprise the molecular machinery for mechanosensory transduction, adaptation and amplification. Because the action of this machinery is reflected in the receiver's mechanics, the latter can be used to probe the molecular mechanisms that bring about hearing in an intact ear . These mechanisms are now shown to closely resemble those that are at work in hair cells in vertebrate ears. Based on the gating-spring model of transduction in vertebrate hair cells, we have developed an extended, symmetric gating-spring model that takes the fly's anatomy into account. This model explains the ear's performance, including the receiver's mechanics and the electrical response of the afferent nerve. These findings suggest that while the auditory anatomies are vastly different, the mechanisms that promote fly and vertebrate hearing are functionally equivalent and, possibly, evolutionarily conserved.

BP 25.3 Thu 15:15 H44

Mobility of Min-proteins in Escherichia coli by fluorescence correlation spectroscopy — Giovanni Meacci[1], Jonas Ries[2], •Elisabeth Fischer-Friedrich[1], Nicoletta Kahya[2], Petra Schwille[2], and Karsten Kruse[1] — [1]Max-Planck Institute for the Physics of Complex Systems, Nöthnitzer Str. 38, 01187 Dresden, Germany — [2]TU-Dresden, Biotec, Am Tatzberg 47-51, 01307 Dresden, Germany

In the bacterium Escherichia coli, positioning of the division site involves pole-to-pole oscillations of Min-proteins.

Different oscillation mechanisms based on cooperative effects between Min-proteins and the exchange of Min-proteins between the cytoplasm and the cytoplasmic membrane have been proposed.

However, the parameters characterising the dynamics of the Min-proteins in vivo are not known. Therefore, it has been difficult to compare the models quantitatively with experiments.

We have now performed in vivo measurements of the mobility of Min-proteins using fluorescence correlation spectroscopy.

Two distinct time-scales are visible in the correlation curves. While the faster time-scale can be attributed to cytoplasmic diffusion, the slower time-scale could result from diffusion of membrane-bound proteins or from protein exchange between the cytoplasm and the membrane.

We discuss implications of the measured values for the oscillation mechanism.

BP 25.4 Thu 15:30 H44

Nuclear oscillations during sexual reproduction in yeast — Sven Vogel and •Iva Tolic-Norrelykke — Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

When two cells of the fission yeast *Schizosaccharomyces pombe* mate, the cell nucleus oscillates from one end of the cell to the other with a period of about 5 minutes and a total duration of a few hours. The biological significance of the nuclear oscillation seems to be in facilitating the spatial alignment of homologous chromosomes.

We set out to determine which forces drive the nuclear oscillation and how the force generation is spatially and temporally regulated. The nuclear oscillation is dependent on astral microtubules (MTs) radiating from the spindle pole body and on cytoplasmic dynein, a minus end directed MT motor. By cutting single MTs using laser nanosurgery, we can distinguish between different models of force generation and identify a subset of MTs that are responsible for nuclear oscillation. Our data provide direct evidence that the main forces contributing to the nuclear oscillation are pulling forces, which are typically generated at the cell ends, and that the event of force generation is driven by the interaction of forward-extending MTs with the cell end cortex.

BP 25.5 Thu 15:45 H44

Waves of gene expression in vertebrate segmentation — •Luis G. Morelli[1], Saul Ares[1], Leah Herrgen[2], Christian Schröter[2], Andrew Oates[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max Planck Institute of Molecular Cell Biology and Genetics

During vertebrate development, the body axis segments sequentially from the head to the tail of the embryo. This process is driven by genetic oscillators together with a moving determination front that slows down and arrests the oscillators. As a result, waves of gene expression propagate along the body axis. We propose a theoretical description based on coupled phase oscillators that describes the patterns of gene expression observed in experiments, both in wild type and mutants. Based on experimental evidence our description introduces a frequency profile, together with a moving boundary that describes axis elongation. To account for the time it takes for signaling molecules to be produced and exported to the cell membrane we include a time delay in the coupling. We derive analytical expressions for the wavelength of the patterns and the period of oscillations.

BP 25.6 Thu 16:00 H44

A bidomain threshold model of intracellular calcium release — •Rüdiger Thul[1], Stephen Coombes[1], and Greg D. Smith[2] — [1]School of Mathematical Sciences, University of Nottingham, Nottingham, NG7 2RD, UK — [2]Department of Applied Sciences, The College of William and Mary, Williamsburg, Virginia, 23187, USA

We introduce a bidomain threshold model of intracellular calcium release. By the explicit construction of travelling wave solutions we are able to probe the dependence of wave speed on physiologically important parameters, including the rate of calcium pumping between the endoplasmic reticulum and the cytosol. Importantly we develop a linear stability analysis that predicts the onset of front instabilities, leading to the emergence of waves that propagate in a back-and-forth manner. Direct numerical simulations are used to confirm our travelling wave predictions.

BP 25.7 Thu 16:15 H44

Spontaneous shape oscillations in non-adherent fibroblasts — •Pramod Pullarkat — University of Bayreuth, Bayreuth-95440, Germany

Fibroblast cells which are maintained in suspension exhibit a dynamic shape instability resulting in sustained, periodic oscillations. This instability is due to the active, contractile nature of the cortical actin layer in these cells. We will discuss experiments aimed at understanding this dynamic instability. We will show how myosin motor activity and signaling via extracellular calcium plays a role in this process. We will also reveal some remarkable similarities between the oscillatory dynamics and the commonly observed blebbing dynamics in cells. Finally a 'working model' will be proposed for the observed phenomena.

BP 25.8 Thu 16:30 H44

Velocity oscillations in polymerizing actin networks — •Azam Gholami[1], Martin Falcke[1], and Erwin Frey[2] — [1]Hahn-Meitner-Institut, Abteilung Theorie, Glienicker Str. 100, D-14109 Berlin, Germany — [2]Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstrasse 37, D-80333 München, Germany

Force generation by semiflexible polymers is versatilely used for cell motility. The leading edge of lamellipodia of crawling cell is pushed forward by a polymerizing actin network and bacteria move inside cells by riding on a comet tail of growing actin filaments. In vivo systems are complemented by in vitro assays using plastic beads and lipid vesicles that, when coated with appropriate proteins, move much the same way as the pathogens. We present a simple theoretical description for actin-based motility. We show that cooperative attachment and detachment of actin filaments to the obstacle, polymerization of the filaments free ends and cross-linking of the actin network lead to spontaneous oscillations of the obstacle velocity.

BP 25.9 Thu 16:45 H44

Dynamics of Phase Singularities in Cardiac Tissue — •Amgad Squires[1,2], Gisa Luther[2], Robert Jr. Gilmour[1], Eberhard Bodenschatz[2], and Stefan Luther[2] — [1]Department of Biomedical Sciences, Cornell University, NY — [2]Max Planck Institute for Dynamics and Self-Organization, Goettingen, Germany

Many spatially extended, nonlinear systems exhibit spatio-temporal chaos in terms of irregular wave fronts or turbulent spiral dynamics. Examples can be found in systems as diverse as Rayleigh-Bénard convection, liquid crystals and excitable media. An example of the latter is cardiac tissue. Here, spiral waves and subsequent wave breaks correspond to an electro-mechanical malfunction of the heart. Spiral wave cores and breakup correspond to phase singularities or defects. We investigate the dynamics of these objects using numerical simulations and arterially perfused canine wedge preparations.

We use an automated phase transformation method that can identify and track these objects from onset to termination of an arrhythmic episode. The system is robust to noise and can be used in vivo and in silico. It has been used to study various arrhythmias as well as a recently proposed far-field defibrillation protocol. Singularity detection and tracking allows us to analyze the interaction of singularities with each other and with external stimuli, in both space and time, and to characterize the complexity of spatiotemporal states. In light of these methods, we discuss current hypotheses of cardiac fibrillation.

BP 26: Poster Session II

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

BP 26.1 Thu 17:00 Poster B

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

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

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

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

BP 26.2 Thu 17:00 Poster B

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

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

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

BP 26.3 Thu 17:00 Poster B

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

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

BP 26.4 Thu 17:00 Poster B

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

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

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

BP 26.5 Thu 17:00 Poster B

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

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

BP 26.6 Thu 17:00 Poster B

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

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

BP 26.7 Thu 17:00 Poster B

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

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

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

BP 26.8 Thu 17:00 Poster B

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

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

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

BP 26.9 Thu 17:00 Poster B

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

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

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

BP 26.10 Thu 17:00 Poster B

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

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

BP 26.11 Thu 17:00 Poster B

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

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

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

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

BP 26.12 Thu 17:00 Poster B

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

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

BP 26.13 Thu 17:00 Poster B

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

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

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

BP 26.14 Thu 17:00 Poster B

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

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

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BP 26.15 Thu 17:00 Poster B

Artificial Chloroplasts from Giant Unilamellar Vesicles —

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

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

BP 26.16 Thu 17:00 Poster B

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

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

BP 26.17 Thu 17:00 Poster B

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

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

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

BP 26.18 Thu 17:00 Poster B

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

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

BP 26.19 Thu 17:00 Poster B

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

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

BP 26.20 Thu 17:00 Poster B

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

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

BP 26.21 Thu 17:00 Poster B

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

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

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

BP 26.22 Thu 17:00 Poster B

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

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

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[2] W. Im and B. Roux, J. Mol. Biol. 319, 1177 (2002).
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BP 26.23 Thu 17:00 Poster B

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

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

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

BP 26.24 Thu 17:00 Poster B

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

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

BP 26.25 Thu 17:00 Poster B

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

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

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

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

BP 26.26 Thu 17:00 Poster B

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

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

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

BP 26.27 Thu 17:00 Poster B

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

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

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

BP 26.28 Thu 17:00 Poster B

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

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

the visual nerve.

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

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

BP 26.29 Thu 17:00 Poster B

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

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

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

BP 26.30 Thu 17:00 Poster B

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

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

BP 26.31 Thu 17:00 Poster B

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

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

BP 26.32 Thu 17:00 Poster B

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

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

BP 26.33 Thu 17:00 Poster B

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

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

BP 26.34 Thu 17:00 Poster B

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

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

BP 26.35 Thu 17:00 Poster B

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

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

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

BP 26.36 Thu 17:00 Poster B

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

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

BP 26.37 Thu 17:00 Poster B

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

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

BP 26.38 Thu 17:00 Poster B

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

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

BP 26.39 Thu 17:00 Poster B

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

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

BP 26.40 Thu 17:00 Poster B

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

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

BP 26.41 Thu 17:00 Poster B

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

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

BP 26.42 Thu 17:00 Poster B

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

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

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

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

It seems conceivable that living cells could control protein motion

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

BP 26.43 Thu 17:00 Poster B

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

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

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

BP 26.44 Thu 17:00 Poster B

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

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

BP 26.45 Thu 17:00 Poster B

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

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

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

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

BP 26.46 Thu 17:00 Poster B

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

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

BP 26.47 Thu 17:00 Poster B

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

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

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

BP 26.48 Thu 17:00 Poster B

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

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

BP 26.49 Thu 17:00 Poster B

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

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

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

BP 27: Nonequilibrium Processes and Self-Organisation

Time: Friday 10:30–12:45 Location: H43

Invited Talk BP 27.1 Fri 10:30 H43

From target search to travel bugs: scale free motion in biology — •Dirk Brockmann — MPI for Dynamics and Self-Organization, Göttingen, Germany

Numerous physical, biological and social systems exhibit anomalous diffusion, i.e particles or mobile agents perform stochastic motion that violates the key features of ordinary Brownian motion. Superdiffusion is typically a consequence of a lack of scale in the spatial increments, the distribution of which follows an inverse power-law with divergent second moment. For these processes the term Lévy flight has been coined and the utilisation fractional diffusion equations turns out to be a key theoretical framework to describe these systems. Lévy flights exhibit particulary interesting behavior when they evolve in heterogeneous environments and when superdiffusion is a consequence of the topological complexity of the system. I will give an overview of recent discoveries of this type of topological superdiffusion and similar processes in a variety of biological systems ranging from facilitated target location of proteins on folding heteropolymers, optimal saccadic scanpaths in human eye-movements, the geographic trajectories of banknotes to current research on the dispersal of travel bugs. These are tagged items that are part of geocaching, a worldwide kind of GPS treature hunt. I will allude to similarities between these systems, discuss there differences and provide a general theoretical framework for the description of topologically superdiffusive systems.

BP 27.2 Fri 11:00 H43

Dynamics of rod-like macromolecules — •Felix Höfling[1,2], Erwin Frey[1], and Thomas Franosch[1] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department für Physik, Ludwig-Maximilians-Universität München, Theresienstraße 37, 80333 München — [2]Hahn-Meitner Institut, Abteilung Theorie, Glienicker Straße 100, 14109 Berlin

Nature as well as modern technology presents us a variety of heterogeneous materials ranging from porous rock over gels to the inner structure of eukaryotic cells. Macromolecules being immersed in such materials exhibit a host of phenomena including Brownian motion, anomalous diffusion, fractal dynamics and a peculiar zig-zag motion.

The emergence of anomalous transport can be understood as a consequence of spatial heterogeneities and excluded volume within a minimal model [1]. We have extended this model to capture essential properties of the dynamics of a rod moving between randomly distributed, fixed rods. For long rods, strong entanglement effects lead to a suppression of rotational diffusion, while at the same time, they enhance center-of-mass diffusion [2].

Our results from Molecular Dynamics simulations allow for a detailed comparison with the tube model. Further, they give insight into the origin of the zig-zag motion and the effect of enhanced diffusion.

[1] F. Höfling, T. Franosch, E. Frey, *Phys. Rev. Lett.* **96,** 165901 (2006).

[2] F. Höfling, Ph. D. thesis, Ludwig-Maximilians-Universität München (2006).

BP 27.3 Fri 11:15 H43

Directed Brownian motion of non-spherical particles — •Susan Sporer, Christian Goll, and Klaus Mecke — Institut für Theoretische Physik, Universität Erlangen-Nürnberg, Staudtstrasse 7, 91058 Erlangen

Mesoscopic particles, such as molecular motors, embedded in a fluid are expected to perform symmetric thermal fluctuations around a mean position. A net transport in a preferred direction is not possible in thermal equilibrium without applying a temperature gradient or an external force which breaks the spatial symmetry. However, directed Brownian motion is possible if the particle is a-symmetric and the system is prohibited from relaxation in thermal equilibrium. A non-equilibrium state can be sustained by stopping the particle at periodic sites along a filament. After releasing the relaxation process towards a Maxwellian velocity distribution has a preferred direction which causes a directed motion due to the particle asymmetry. Even motion against a small fluid drift is possible. The relaxation process, the directed motion and its dependence on the particle shape are analyzed analytically. The results are compared to molecular dynamics simulations.

BP 27.4 Fri 11:30 H43

The Einstein relation generalized to non-equilibrium — •Valentin Blickle[1], Thomas Speck[2], Christoph Lutz[1], Udo Seifert[2], and Clemens Bechinger[1] — [1]2. Physikalisches Institut, Universität Stuttgart — [2]II. Institut für Theoretische Physik, Universität Stuttgart

Thermodynamics and classical statistical mechanics are not able to describe processes far from equilibrium. Recently, several exact theoretical relations, e.g. Jarzynski equation [1] and other fluctuation theorems were derived for this regime. We focuss on the Einstein relation, a prominent example of the fluctuation dissipation theorem, connecting the diffusion constant and the mobility which is violated beyond linear response. In our experiment we test its recent theoretical generalization [2] to the non-equilibrium regime. With video microscopy we observe the motion of a driven Brownian colloidal particle trapped within a torroidal 3d laser trap. Additionally we can modulate the laser intensity, imposing a stationary potential onto the torus. Using the measured particle trajectory we determine an integral over velocity correlation functions which quantifies the violation of the Einstein relation. The fact that this integral cannot be neglected demonstrates that in our experiment we are probing a regime which is far from thermal equilibrium and beyond linear response.

[1] C. Jarzynski, *Phys. Rev. Lett.* **78**, 2690 (1997).

[2]T. Speck, U. Seifert, *Europhys. Lett.* **74**, 391 (2006).

BP 27.5 Fri 11:45 H43

Optimal finite-time processes in stochastic thermodynamics — •Tim Schmiedl and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, 70550 Stuttgart

For a small system like a colloidal particle or a single biomolecule embedded in a heat bath, we ask for the optimal protocol of an external control parameter minimizing the mean work required to drive the system from one given equilibrium state to another in a finite time. The emphasis on a finite time is crucial since for infinite time the work spent in any quasi-static process is equal to the free energy difference of the two states. For finite time the mean work is larger and will depend on the protocol. Knowing the optimal protocol could inter alia improve the extraction of free energy differences from finite-time path sampling via the Jarzynski relation both in numerical schemes and in experimental studies.

In general, the optimal protocol obeys an integro-differential equation. We derive explicite solutions both for a moving harmonic laser trap and a time-dependent strength of such a trap. In both cases, the optimal protocol exhibits finite jumps both at the beginning and the end of the process. We expect such jumps to be generic even for nonharmonic potentials.

BP 27.6 Fri 12:00 H43

Self-organization in systems of treadmilling filaments — •Konstantin Doubrovinski and Karsten Kruse — Universität des Saarlandes, Postfach 151150, D-66041, Saarbrücken

The polymerization and depolymerization of cytoskeletal filaments plays an important role in many subcellular processes. It can produce forces and lead to effective filament transport. An example of the latter is provided by treadmilling, which occurs when subunits are added one end at the same rate as they are removed at the other. Addition and removal of subunits is influenced by a large number of proteins. In fish melanophores such porteins are coupled to color pigments. There, treadmilling filaments and polymerization affecting proteins can self-organize into states of agglomerated or dispersed pigments which allows the fish to change color. A theoretical treatment of such systems is difficult as distributions of filaments lengths must

be taken into account. We present a new mesoscopic approach which allows for numerical as well as analytical analysis. We find a multitude of patterns such as asters, traveling fronts and solitary waves. We apply this formalism to melanophores and point out possible implications for cell locomotion.

BP 27.7 Fri 12:15 H43

Mean-field transition in two dimensional self-propelled particle systems with different alignment mechanisms — •Fernando Peruani[1,2], Andreas Deutsch[1], and Markus Baer[3] — [1]Technische Universitaet Dresden, Dresden, Germany — [2]Max Planck for the Physics of Complex Systems, Dresden, Germany — [3]Physikalisch-Technische Bundesanstalt, Berlin, Germany

We study the emergence of collective effects in two-dimensional systems of self-propelled particles interacting locally through a liquid crystal-based alignment mechanism. In the model particles are driven with a constant absolute velocity and align their direction of motion to the local director. We show through extensive simulations that there is a continuous kinetic phase transition for sufficient low directional noise and high enough density. Moreover, we propose an effective mean-field equation and show that this approach correctly describes the the scaling of the order parameter vs. noise intensity. Similar arguments follow for the ferromagnetic alignment. These findings strongly suggest that self-propelled particles exhibit kinetic mean-field-type transitions in which the critical noise depends explicitly on the density and the alignment mechanism.

BP 27.8 Fri 12:30 H43

Cell morphology in growing tissues — •Reza Farhadi Far[1], Jens-Christian Röper[2], Suzanne Eaton[2], and Frank Jülicher[1] — [1]Max-Planck-Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, Dresden — [2]Max-Planck-Institute for Molecular Cell Biology and Genetics, Pfotenhauer Straße 108, Dresden

We present a theoretical study of the morphology and topology of cell packing in a two dimensional tissue. Using a vertex model, we represent each cell by a polygon and take into account cell elastic properties, line tension due to adhesion with neighboring cells as well as contractility of the cell. We present a phase diagram of the model and study the topology and morphology of the cell packing in the presence of cell division. We find three distinct types of tissue morphology, depending on parameter values. We compare our calculations to observed cell packings in the wing-disc of the fruit fly *Drosophila*.

BP 28: Biomedical Applications

Time: Friday 11:00–12:30 Location: H44

BP 28.1 Fri 11:00 H44

Can Polymer Physics Help Cellular Biomedicine? — •Josef Käs — Abt. f. Physik weicher Materie, Fak. f. Physik u. Geowiss., Universität Leipzig

The cytoskeleton, an intracellular polymeric scaffold, stabilizes and organizes biological cells. As a compound of highly dynamic protein filaments and active nano-sized molecular motors it mechanically senses a cell's environment and generates forces for cellular motion sufficiently strong to push rigid AFM-cantilevers out of the way. The study of the cytoskeleton from a polymer physics perspective with novel optical micro- and nano-manipulation techniques, scanning force microscopy, time lapse image analysis of intracellular processes, and modern genetic manipulation methods leads to results, which simultaneously promote physics and medicine (diagnosis as well as therapy). The extremely sensitive polymeric properties of single cells' cytoskeletons measured with the laser-based Optical Stretcher distinguish different cell types and monitor cellular changes such as cancer progression and stem cell differentiation proving recent theories on semiflexible polymers. Cellular motion required for neuronal plasticity and nerve regeneration - but also found in cancer metastasis - inspire the emerging field of active polymer networks. The resulting, novel perception of cell migration will impact therapies to reduce metastatic aggressiveness and inspire new strategies for nerve regeneration.

BP 28.2 Fri 11:15 H44

Bildgebende Zweiphotonen Fluoreszenz zur Untersuchung von Hautschädigung durch Laserstrahlen — •Andreas Garz[1], Christian Spitz[1], Andreas Krink[2], Hans Peter Berlien[2] und Ralf Menzel[1] — [1]Universität Potsdam — [2]Elisabeth Klinik, Berlin

Zweiphotonenangeregte Fluoreszenz mit Anregung im nahen Infrarot ist für die Darstellung von Gewebezuständen besonders geeignet, da die Anregungsstrahlung mit geringer Störung ins Gewebe eindringen kann. Bei Beschränkung auf endogene Fluorophore kommt man ohne Markierungsfarbstoffe aus und die Messmethode ist in vivo einsetzbar. Diese Technik hat sich bereits in der Mikroskopie mit subzellulärer Auflösung zur Bildgebung bewährt, da durch die nichtlineare Intensitätsabhängigkeit eine optische Biopsie in der Fokalebene ähnlich wie bei konfokaler Mikroskopie möglich ist.

Bei geringerer Auflösung und größeren Bildausschnitten von einigen Millimetern eröffnen sich neue Möglichkeiten, da der Bezug zu örtlich variierenden Krankheitsbildern oder Schädigungen hergestellt werden kann. Demonstriert wird die Untersuchung der schädigenden Wirkung von Erbium-Laserstrahlung auf gesunder Haut.

Gefördert durch das BMBF und den VDI-TZ

BP 28.3 Fri 11:30 H44

CXCR2 determines invasiveness, traction forces and cytoskeletal dynamics of tumor cells — •Claudia Tanja Mierke, Philip Kollmannsberger, Daniel Paranhos Zitterbart, Carina Raupach, and Ben Fabry — Biophysics, University Erlangen, Germany

Tumor cells consist of populations with different capacities to invade and different CXCR2 expression. We tested the hypothesis that highly invasive tumor cells reorganize their cytoskeleton more rapidly and can generate higher tractions than less-invasive cells. We isolated a highly- and a low-invasive variant of MDA-MB-231 carcinoma cells (231-high/-low) with a 5-fold difference in CXCR2 expression. Invasiveness was analysed in a collagen gel. Cytoskeletal dynamics was determined from the creep response of cells and from spontaneous nanoscale-movements of magnetic particles. Step forces from 1-10 nN were applied to fibronectin-coated beads. Bead displacement vs. time followed a power-law. The exponent was taken as a measure of cytoskeletal dynamics, with low values corresponding to a solid-like, static and high corresponding to a liquid-like, dynamic behavior. 231-high cells had a substantially higher exponent compared to 231-low cells. Spontaneous bead motion showed significantly more superdiffusive behavior in 231-high compared to 231-low cells. Tractions measured during adhesion onto collagen-coated gels showed that 231-high cells generate 8x higher contractile forces compared to 231-low cells. In summary, the ability of tumor cells to remodel their cytoskeleton and to generate high tractions seems be key factors for metastasis formation.

BP 28.4 Fri 11:45 H44

Ellipsometric studies on protein adsorption kinetics — •Christoph Gilow[1], Hubert Mantz[1], Anthony Quinn[1], Karin Jacobs[1], Markus Bellion[2], and Ludger Santen[2] — [1]Saarland University, Experimental Physics, D-66041 Saarbrücken, Germany — [2]Saarland University, Theoretical Physics, D-66041 Saarbrücken, Germany

Adsorption processes of proteins play an important role in many biomedical systems. Examples are the protein films on teeth or tissue compatibility.

From a physical point of view these processes raise a number of challenging questions, e.g., which substrate properties (chemical composition, roughness,...) have an impact on protein adsorption.

We investigated the adsorption kinetics of several salivary proteins in a liquid environment on tailored substrates by means of ellipsometry and found a new type of adsorption kinetics. A comparison to extensive Monte Carlo simulations strongly suggests that long-range contributions to the surface potential lead to conformational changes of the protein on the surface which are responsible for the observed unusual kinetics of the amylase.

BP 28.5 Fri 12:00 H44

Strain Energy during Tumor Cell Invasion in 3-D Collagen Gels — •Thorsten Koch, Claudia Mierke, Daniel Paranhos Zitterbart, Stefan Münster, and Ben Fabry — Friedrich-Alexander-Universität Erlangen-Nürnberg - Zentrum für Medizinische Physik und Technik - Lehrstuhl für Physikalisch-Medizinische Technik - Henkestraße 91 - D-91052 Erlangen

Cells cultured on 2D rigid substrates behave differently from cells suspended in a 3D connective tissue matrix, e.g. in 3D cells exhibit a more elongated morphology, less pronounced stress fiber formation, and marked differences in focal adhesion composition. In this study we compared the strain energies resulting from forces exerted on 2D vs. 3D extracellular matrices by MDA-MB-231 breast carcinoma cells. Cells were plated on the surface of 2D polyacrylamide hydrogels (Young's modulus $E = 1.5$ and 6 kPa), or 3D collagen gels ($E = 50$ Pa), and allowed to spread onto, or invade into, the gels for two days. Gel deformation was quantified by tracking the 3D positions of embedded fluorescent beads (ø 1 μm). The undeformed state was obtained by disrupting the actin cytoskeleton and hence force transmission with Cytochalasin-D (4 μM). The strain energy, calculated from displacements of beads between the initial and final states, was $U = 1.01$ pJ ($E = 6$ kPa) and $U = 0.2$ pJ ($E = 1.5$ kPa) on 2D gels. Surprisingly, cells in a soft 3D matrix generated significantly higher strain energy $U = (1.8 \pm 0.2)$ pJ ($n = 47$). These results demonstrate that tumor cells can exert substantial forces on surrounding tissue during invasion that cannot be inferred from traction measurements in 2D.

BP 28.6 Fri 12:15 H44

Analysis of radiation-induced damages of DNA molecules by means of SFM and gel-electrophoresis — •Mihail Brezeanu, Frank Träger, and Frank Hubenthal — Institute of Physics and Center for Interdisciplinary Nanostructure Science and Technology - CINSaT, Universität Kassel, Germany

Studying radiation-induced damages in DNA molecules is important to understand the processes that occur in radiotherapy and DNA repair. The most serious damages of DNA molecules are double-strand breaks (DSB), i.e. the rupture of both DNA strands in the range of a few base pairs and single-strand breaks (SSB), when one of the DNA strands is broken. In this contribution we present our recent analysis of radiation-induced damages in phiX174 plasmids after X-ray and carbon-ion irradiations. The percentages of plasmids with DSBs, SSBs, and multiple strand breaks, i.e. linear fragments (LF), have been determined as a function of radiation dose by means of scanning force microscopy (SFM) and gel-electrophoresis measurements. The results show an increase of the DSBs percentage from initially 0% to 12.5% after X-ray irradiation, while after carbon ion irradiation 19% of DSBs have been found for the same applied dose of 1 kGy. In addition, a detailed SFM analyses revealed that the distribution of LF after irradiation with C-ions contains a significant higher amount of small fragments in the range from 50 nm to 700 nm, compared to the X-rays, while a clear reduction of large fragments has been observed. The results explain, for example, why the DNA repair rate after carbon ion irradiation is much lower that for X-rays at the same dose.