Overview of Invited Talks and Sessions
(lecture rooms ZEU 250 and ZEU 260; poster P3)

Plenary Talks related to BP

PV III Mon 9:15–10:00 HSZ01 Linear and Non-linear Mechanics of Biopolymer Networks — ●DAVID A. WEITZ

PV XIII Tue 8:30– 9:15 HSZ01 Pushing the Envelope in Biological Imaging — ●ERIC BETZIG

Invited Talks

BP 1.1 Mon 10:15–10:45 ZEU 250 High throughput microscopy for systems biology: from genome-wide profiling to the analysis of protein complexes — ●JAN ELLEMBERG

BP 2.1 Mon 10:15–10:45 ZEU 260 Protein Structure and Dynamics from Low-Resolution Data — ●GUNNAR F. SCHROEDER

BP 4.1 Mon 14:00–14:30 ZEU 260 Single-molecule detection of DNA repair in real-time — ●TERENCE STRICK

BP 5.1 Mon 14:00–14:30 ZEU 250 Are biomechanical changes necessary for tumor progression? - The impact of cell mechanics on cancer development — ●MAREIKE ZINK

BP 15.1 Tue 10:15–10:45 ZEU 250 Single-molecule mechanics: theory, analysis, interpretation — ●OLGA DUDKO

BP 16.1 Tue 10:15–10:45 ZEU 260 The dynamic organization in the membrane of a G-protein-coupled receptor is related to its functional state — ●LAURENCE SALOME

BP 18.1 Tue 14:00–14:30 ZEU 250 Amyloid at the nanoscale: single molecule and ensemble studies of amyloid-lipid interactions — ●VINOD SUBRAMANIAM

BP 20.1 Wed 10:15–10:45 ZEU 250 Quantitative universality and non-local interactions in neural pattern formation — ●MATTHIAS KASCHUBE


BP 22.1 Wed 15:00–15:30 ZEU 250 The interplay between actin dynamics and membrane tension determines the shape of moving cells — ●KINNERET KEREN

BP 25.1 Thu 10:15–10:45 ZEU 260 Bacterial Games — ●ERWIN FREY

BP 27.1 Thu 14:00–14:30 ZEU 250 Inelastic Mechanics of Biopolymer Networks — ●KLAUS KROY


BP 34.1 Fri 10:15–10:45 ZEU 260 Super-resolution fluorescence imaging of cellular structure and dynamics — ●MARKUS SAUER

Invited talks of the joint symposium SKM-SYBE
See SKM-SYBE for the full program of the symposium.

SKM-SYBE 1.1 Fri 10:30–11:00 TRE Ma Microbial evolution in spatially-structured environments — ●ARJAN DE VISser

SKM-SYBE 1.2 Fri 11:00–11:30 TRE Ma Correlated mutations: Facts or artifacts? — ●AMNON HOROVITZ
SKM-SYBE 1.3 Fri 11:30–12:00 TRE Ma Macroscopic laws in bacterial genome evolution — Erik van Nimwegen

SKM-SYBE 1.4 Fri 12:00–12:30 TRE Ma The role of horizontal gene transfer in the evolution of bacterial genomes — Paul Higgs

Sessions

BP 1.1–1.9 Mon 10:15–13:00 ZEU 250 Statistical Physics in Biological Systems I (joint DY, BP)
BP 2.1–2.9 Mon 10:15–13:00 ZEU 260 Protein Structure & Dynamics
BP 3.1–3.9 Mon 10:30–13:00 ZEU 222 Biopolymers and Biomaterials I (with CPP)
BP 4.1–4.10 Mon 14:00–17:00 ZEU 260 DNA & DNA Enzymes
BP 5.1–5.9 Mon 14:00–16:45 ZEU 250 Tissue Dynamics & Developmental Processes
BP 6.1–6.11 Mon 14:00–17:00 HÜL 186 Statistical Physics of Biological Systems II (joint DY, BP)
BP 7.1–7.25 Mon 17:15–20:00 P3 Posters: Statistical Physics in Biological Systems
BP 8.1–8.9 Mon 17:15–20:00 P3 Posters: Protein Structure & Dynamics
BP 9.1–9.9 Mon 17:15–20:00 P3 Posters: DNA & DNA Enzymes
BP 10.1–10.13 Mon 17:15–20:00 P3 Posters: Tissue Dynamics & Developmental Processes
BP 11.1–11.14 Mon 17:15–20:00 P3 Posters: Single-Molecule Biophysics
BP 12.1–12.18 Mon 17:15–20:00 P3 Posters: New Technologies
BP 13.1–13.17 Mon 17:15–20:00 P3 Posters: Biological Membranes
BP 14.1–14.13 Mon 17:15–20:00 P3 Posters: Neurobiophysics, Theoretical Neuroscience, Sensory Transduction
BP 15.1–15.9 Tue 10:15–13:00 ZEU 250 Single-Molecule Biophysics I
BP 16.1–16.9 Tue 10:15–13:00 ZEU 260 Biological Membranes I
BP 17.1–17.3 Tue 10:30–12:10 HSZ 201 Biophysics I: Bionics and Biomaterials (joint AG jDPG, BP)
BP 18.1–18.4 Tue 14:00–15:15 ZEU 250 Single-Molecule Biophysics II
BP 19.1–19.5 Tue 14:00–15:15 ZEU 260 Biological Membranes II
BP 20.1–20.9 Wed 10:15–13:00 ZEU 250 Neurobiophysics
BP 21.1–21.9 Wed 10:15–13:00 ZEU 260 Biopolymers and Biomaterials II (with CPP)
BP 22.1–22.9 Wed 15:00–17:45 ZEU 250 Physics of Cells I
BP 23.1–23.10 Wed 15:00–17:45 ZEU 260 Biopolymers and Biomaterials III (with CPP)
BP 24.1–24.10 Thu 10:15–13:00 ZEU 250 Physics of Cells II
BP 25.1–25.9 Thu 10:15–13:00 ZEU 260 Statistical Physics in Biological Systems III (joint DY, BP)
BP 27.1–27.10 Thu 14:00–17:00 ZEU 250 Physics of Cells III
BP 28.1–28.10 Thu 14:00–16:45 ZEU 260 Statistical Physics in Biological Systems IV (joint DY, BP)
BP 29.1–29.27 Thu 17:15–20:00 P3 Posters: Biopolymers & Biomaterials
BP 30.1–30.33 Thu 17:15–20:00 P3 Posters: Physics of Cells
BP 31.1–31.4 Thu 17:15–20:00 P3 Posters: Biological Machines & Motor Proteins
BP 32.1–32.9 Thu 17:15–20:00 P3 Posters: Other Topics in Biological Physics
BP 33.1–33.9 Fri 10:15–13:00 ZEU 250 Biological Machines & Motor Proteins
BP 34.1–34.9 Fri 10:15–13:00 ZEU 260 New Technologies
BP 35.1–35.4 Fri 10:30–12:30 TRE Ma SYBE: Statistical Physics and Biological Evolution

Annual General Meeting of the Biological Physics Division

Wednesday 18:00–19:00 ZEU 260

- Bericht
- Wahl des Stellvertretenden Sprechers
- Verschiedenes
BP 1: Statistical Physics in Biological Systems I (joint DY, BP)

**Invited Talk**

**BP 1.1 Mon 10:15 ZEU 250**

High throughput microscopy for systems biology: from genomewide profiling to the analysis of protein complexes

---

**JAN ELENBERG** — EMBL, Heidelberg, Germany

Despite our exponentially growing knowledge about the human genome, we do not know all human genes required for some of the most basic functions of life, such as cell division. Furthermore we do not know how the proteins encoded by these genes work together to carry out the underlying cellular processes. We have developed high throughput microscopy platforms to systematically identify and characterize the function of their encoded proteins. For gene identification, we have integrated methods for gene silencing by RNA interference with phenotyping by time-lapse microscopy and computational image processing into one high throughput pipeline. This technology platform allowed us to carry out a genomewide profiling of each of the ~21 000 human protein-coding genes by two day live imaging of fluorescently labeled chromosomes. Quantitative image analysis identified hundreds of human genes involved in several basic biological functions including cell division, migration and survival. Computational clustering of the phenotypic signatures of cell division genes allowed us to group them into different categories and make predictions about their function. To analyze the predicted function of proteins in phenotypic clusters, we are currently developing high throughput fluorescence microscopy and biophysical methods to systematically study their localization, interactions and assembly in the physiological context of the living cell.

**BP 1.2 Mon 10:45 ZEU 250**

The flow field of an individual bacterium and its implications for cell-cell and cell-surface interactions

---

**KNOT DRESCHE**1, **JÖRN DUNKEL**1, **LUIS CHERNOV**2, **SUOV GANGULY**3, and **RAYMOND GOLDSTEIN**1 — 1DAMTP, University of Cambridge, Wilberforce Road, Cambridge CB3 0WA, UK — 2Department of Physics, University of Arizona, 1118 E 4th St, Tucson, AZ 85721, USA

Swimming bacteria create microflows that have been commonly assumed to play an important role in their pair-interactions and during scattering with surfaces. Here, we present the first direct measurement of the bacterial flow field generated by individual *E. coli*. Our experiments allow us to infer the relative importance of fluid dynamics and noise for cell-cell and cell-surface scattering. We find that rotational diffusion due to thermal and intrinsic stochasticity drowns the effects of long-range hydrodynamic pair-interactions, implying that physical interactions between bacteria are dominated by steric collisions and near-field lubrication forces. This closely links collective motion in bacterial suspensions to self-organization in driven granular systems, assemblies of biofilaments, and animal flocks. We further conclude that long-range fluid dynamics is negligible for the scattering of bacteria with surfaces. However, once a bacterium has aligned with the surface through an inelastic collision and swims along the surface at a distance of less than two microns, the self-generated flow traps the bacterium and large fluctuations in orientation are needed to escape. Since our results are based on purely mechanical properties, they are expected to apply to a wide range of bacteria.

**BP 1.3 Mon 11:00 ZEU 250**

The energy-speed-accuracy tradeoff in sensory adaptation

---

**GANHUI LAN**1, **PABLO SARTORI**2, **SILKE NEUMANN**2, **VIKTOR SOURKIN**3, and **YUTAI TU**1 — 1IBM T. J. Watson Research Center, Yorktown Heights, NY 10598, USA — 2Max Planck Institute for the Physics of Complex Systems, Dresden 01187, Germany — 3Zentrum für Molekulare Biologie der Universität Heidelberg, Heidelberg, Germany

Adaptation is a fundamental function of living systems. The benefits of adaptation in sensory systems are well known, but its costs remain poorly understood. By analyzing a stochastic model of the generic feedback circuit responsible for sensory adaptation, we show that adaptation processes are inherently dissipative and continuous energy consumption is required to stabilize the adapted state. We derive a universal relation among energy dissipation rate, adaptation speed, and the maximum adaptation accuracy from our model. We demonstrate how this general energy-speed-accuracy (ESA) relation applies to the *E. coli* chemosensory system, where hydrolysis of the S-adenosylmethionine (SAM) molecules drives the near-perfect adaptation of the system and maintains its high sensitivity in a wide range of backgrounds. We identify the key requirements for an adaptive network to achieve its maximum accuracy with a given energy budget. These requirements are met in the *E. coli* chemotaxis pathway, making it highly efficient. Moreover, direct measurements confirm that adaptation slows down as cells gradually de-energize in medium without nutrients.
interacting drug pair, conflicts are resolved by linearly interpolating the two single drug responses, while for the antagonistic drug pair, the drug that has the stronger impact on growth dominates the transcriptional response. Importantly, for a given drug pair, the same strategy of conflict resolution is used for almost all genes. These results provide a recipe for predicting gene expression responses to drug combinations, which may lead to a more rational design of combination treatments.

**BP 1.7** Mon 12:15 ZEU 250

Modelling the dynamics of micro-swimmers ●EVA BARESSEL and RUDOLF FRIEDRICH — Institute for Theoretical Physics, University of Münster, Wilhelm-Klemm-Str. 9, D-48149 Münster

The motion of self-propelled flagellated bacteria consists of two different modalities: "running" if all flagella rotate counter-clockwise or "tumbling" if at least one flagellum rotates clockwise. As a model for these bacterial motors we consider the dynamics of an ensemble of swimming objects which are composed of two rigidly connected point vortices. The single objects are able to show translational or rotational movement depending on the circulations of the single point vortices. We discuss the collective behaviour for several of these objects and the resulting velocity fields by means of numerical calculations.

**BP 1.8** Mon 12:30 ZEU 250

Onset of Collective Motion due to Escape and Pursuit

●PAWEŁ ROMANCUZK,1 VISHWESA GUTTA2, LUTZ SCHIMANSKY-GEIER,1 and IAIN D. COUZIN2 — 1Department of Physics, Humboldt Universität zu Berlin, Germany — 2Department of Ecology and Evolutionary Biology, Princeton University, USA

Recent studies suggest that noncooperative behavior such as cannibalism may be a driving mechanism of collective motion in mass migrating insects such as desert locusts [1]. We have shown in a biologically motivated model of individuals interacting via escape and pursuit interactions associated with cannibalism the emergence of large scale collective motion [2]. Furthermore we were able to reproduce experimental results and make specific prediction from our modelling approach [3]. Here we focus on a generalized model of self-propelled particles interacting via selective attraction or repulsion to approaching or moving-away individuals. We identify conditions for large scale collective motion in our model and discuss the onset of collective motion as an evolutionary stable strategy (ESS) in the context of mass migration of desert locusts under threat of cannibalism.


**BP 1.9** Mon 12:45 ZEU 250

Spontaneous spiking in presence of an autaptic feedback loop — YUNYUN LI1, GERHARD SCHMID1, PETER HÄNGGI, and LUTZ SCHIMANSKY-GEIER2 — 1Universität Augsburg, Germany — 2Humboldt Universität zu Berlin, Germany

The effect of intrinsic channel noise on the dynamics of a neuronal cell with a delayed feedback loop is investigated [1]. The loop is based on the so-called autapse phenomenon in which dendrites establish not only connections to neighboring cells but as well to its own axon. The modeling is achieved in terms of a stochastic Hodgkin-Huxley model containing such a built in delayed feedback. The fluctuations stem from intrinsic channel noise, being caused by the stochastic nature of the gating dynamics of ion channels. The delayed feedback manifests itself in the occurrence of bursting and a rich multimodal interspike interval distribution, exhibiting a delay-induced reduction of the spontaneous spiking activity at characteristic frequencies. Moreover, a specific frequency-locking mechanism is detected for the mean interspike interval distribution of Münster, Wilhelm-Klemm-Str. 9, D-48149 Münster

**BP 2: Protein Structure & Dynamics**

Time: Monday 10:15-13:00

**Invited Talk**

BP 2.1 Mon 10:15 ZEU 260

Protein Structure and Dynamics from Low-Resolution Data — GUNNAR F. SCHRÖDER — Forschungszentrum Jülich

Structure determination of large proteins and protein assemblies is a major challenge in molecular biology. Experiments, such as X-ray crystallography or single particle Cryo-EM, on such complex systems often yield only low resolution (> 4 Å) data, which are not sufficient to fully determine atomic structures. The refinement of approximate initial models is typically significantly harder than at high resolution. We present an approach that makes use of additional prior information on homologous structures which guides the refinement and dramatically improves the obtained structures.

Single-particle Cryo-EM yields images of individual proteins in potentially different conformations and therefore yields a wealth of information on structural dynamics. This information is however very difficult to extract since each image is extremely noisy. The common approaches to reconstruct three-dimensional density maps average out any structural heterogeneity and the information on the dynamics is lost. We show how principal protein motions can be reconstructed from the variation contained in the single particle images.

BP 2.2 Mon 10:45 ZEU 260

Mechanism of signal transduction of the LOV2-Jo-photosensor from Avena sativa — EMANUEL K. PETER, BERNHARD DICK, and STEPHAN A. BAUREL — Fakultät für Chemie und Pharmazie, Universität Regensburg, 93040 Regensburg, Deutschland

Fusion proteins containing light-activatable protein domains possess great potential as molecular switches in cell signaling and for controlling enzymatic reactivity. This has recently been impressively demonstrated in living cell experiments through connecting the blue light-activatable LOV2-Jo-protein domain from phototropin1 of Avena sativa (AsLOV2-Jo) with the Rac1-GTPase, responsible for regulating the morphology and motility of metazoan cells. However, a target-oriented development of fusion proteins in conjunction with the AsLOV2-Jo-photosensor is still very challenging, because a detailed understanding of its signal transduction pathway on a molecular level is still lacking. In this presentation we elucidate the mechanism of signal transduction of this photosensor on a molecular level, which opens new perspectives for the creation of light-activable molecular switches and enzymes [1].


BP 2.3 Mon 11:00 ZEU 260

Concurrent Enzymatic Reactions as a Source of Bistability in Single Protein Modification Cycles — RONNY STRAUBE — MPI for Dynamics of Complex Technical Systems, Magdeburg, Germany

It is well known that reversible protein modifications can generate ultrasensitivity when the modifying enzymes operate in saturation [1]. They can also exhibit bistability if the substrate protein is antagonistically modified at multiple sites [2]. However, in the mathematical description of such mechanisms it is often neglected that the activity and/or substrate affinity of the modifying enzymes (e.g. kinase and phosphatase) is often itself regulated through reversible binding of allosteric effectors which can interact convert the respective enzyme species between a high and a low catalytic activity form. Here, I show that the concurrent action of different activity forms of an antagonistic enzyme pair can generate a bistable system response already at the level of a single protein modification cycle, i.e. without the requirement for multisite modifications. In contrast to other mechanisms [1,2] bistability is predicted to occur even when substrate molecules and enzymes are present in equal amounts. I further show that the same mechanism is also applicable to two component systems which are the most simple signal transduction systems in bacteria. Since the formation of enzyme sub populations is difficult to avoid both in vivo and in vitro concurrent enzymatic reactions might be a ubiquitous source for generating bistability in biological systems. [1] A. Goldbeter and D. E. Koshland Jr. J. N. Acad. Sci. USA, 103, 6840 (1981). [2] N. I. Markевич, J. B. Hoek and B. N. Khodolenko J. Cell Biol. 164 553 (2004).

BP 2.4 Mon 11:15 ZEU 260
Lateral Diffusion and Correlation of Membrane Anchored Proteins — *Wasm Abullalian*, Andreas Hartel, Nicola Jones, Markus Engstler, and Motomu Tanaka —  
1Department of Cell and Developmental Biology, Würzburg University, Germany  
2Faculty of Biology, University of Würzburg, Germany  
Many Glycosylphosphatidylinositol (GPI)-anchored proteins are found on the plasma membrane of eukaryotic cells. For example, GPI-anchored Variant Surface Glycoprotein (VSG) is among the most abundant cell-surface proteins in trypanosoma protozoa, playing important roles in viability and defense against the host immune system. The lateral mobility of lipids and membrane proteins in the plane of membranes can affect their function. The lateral correlation and coupling of membrane proteins are studied by Grazing Incidence Small Angle X-ray Scattering (GISAXS) and high energy X-ray reflectivity (XRR) at the air/water and solid/water interfaces. Although this has been a challenge due to the low contrast in the scattering length density of proteins, we have successfully detected the two membrane anchored proteins using XRR and GISAXS: (i) engineered recombinant avidin coupled to biotinylated lipids, and (ii) GPI-anchored VSG purified from trypanosoma. XRR results revealed the uniform coupling/incorporation of proteins to the membrane surface, while the form- and structure factors of the proteins in the plane of membranes have been determined by GISAXS.

15 min. break

BP 2.5 Mon 11:45 ZEU 260 Using Graph Measures to Observe Complex Formation in Multiparticle Simulations — Florian Lauch1,2 and Thamer Geyer3  
1Center for Bioinformatics, Saarland University, Saarbrücken — 2Dep. of Bioengineering and Therapeutic Sciences, UC San Francisco, CA, USA  
Modern simulation techniques are beginning to study the dynamic assembly and disassembly of multi-protein systems. In these many-particle simulations it can be very tedious to monitor the formation of specific structures such as fully assembled protein complexes or virus capsids above a background of monomers and partial complexes. However, such analyses can be performed conveniently when the spatial configuration is mapped onto a dynamically updated interaction graph. On the example of Monte Carlo simulations of spherical particles with either isotropic or directed mutual attractions we demonstrate that this combined strategy allows for an efficient and also detailed analysis of complex formation in many-particle systems.

BP 2.6 Mon 12:00 ZEU 260 Asymmetric folding pathways and transient misfolding in a coarse-grained model of proteins — Katrin Wolfl, Michele Vendruscolo, and Markus Portos — 1Institute for Condensed Matter and Complex Systems, University of Edinburgh, UK  
2Department of Chemistry, University of Cambridge, UK  
3Institut für Theoretische Physik, Universität zu Köln, Germany  
We investigate free energy landscapes and protein folding pathways in a coarse-grained protein model. Our model’s two primary characteristics are a tube-like geometry to describe the self-avoidance effects of the polypeptide chain, and an energy function based on a one-dimensional structural representation which specifies the amino acids’ connectivity for any given conformation. Such an energy function, rather than favouring the formation of specific native pairwise contacts, promotes the establishment of the native connectivity for each amino acid. Specifically, we look at the free energy landscape of the villin headpiece domain (Protein Data Bank (PDB) id. 1und) and show that in its distinctive asymmetry it resembles that found in computationally more demanding atomistic molecular dynamics studies [1]. That the asymmetry is indeed a specific feature of the villin headpiece domain is demonstrated by studying the free energy landscape of another small three-helix bundle protein (PDB id. 1vd0), for which we find an essentially symmetric free energy landscape [2].

2K. Wolff et al., submitted

BP 2.7 Mon 12:15 ZEU 260 Impact of compatible solutes on the water structure and the structural organization of lipid monolayers — Jens Smitte1, Rakesh Kumar Harishchandra2, Oliver Rubner1, Hans-Joachim Gall2, and Andreas Heuer1 — 1Institut für Physikalische Chemie, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany  
2Institut für Biochemie, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany  
We have performed Molecular Dynamics simulations of ectoine, hydroxyectoine and urea in explicit solvent. Special attention has been spent on characterizing the local ordering of the water molecules around these compatible solutes. Our results indicate that ectoine and hydroxyectoine are able to bind more water molecules than urea on short scales. Furthermore we investigated the number and appearance of hydrogen bonds between the molecules and the solvent. The simulations show that some specific groups in the compatible solutes are able to form a pronounced ordering of the local water structure. Additionally, we have validated that the charging of the molecules is of main importance. Furthermore we show the impact of a locally varying salt concentration. Experimental results are shown which indicate a direct influence of compatible solutes on the liquid expanded-liquid condensed phase transition in DPPC monolayers. We are able to identify a variation of the local water pressure around the compatible solutes by numerical calculations as a possible reason for an experimentally observed broadening of the phase transition.

BP 2.8 Mon 12:30 ZEU 260 Simulation of protein charge inversion by trivalent metal ion binding — Sara Leibbrandt1, Felix Rosens-Runge2, Fajun Zhang3, Nina Fischer2, Oliver Kohlbracht2, Sophie Weggler2, Michael Ziller2, Andreas Hildebrandt2, Elena Jordan2, and Frank Schreiber1 — 1Institut für Angewandte Physik, Universität Tübingen — 2Zentrum für Bioinformatik, Universität Tübingen — 3Zentrum für Bioinformatik, Universität des Saarlandes  
Experiments indicate that the effective charge of proteins in solution can be inverted by high valent metal ions [1]. In addition, X-ray diffraction data show that metal ions bind to negatively charged carboxyl groups on the protein surface. In order to elucidate the binding of trivalent metal ions, two simulation approaches were carried out in the dilute protein limit for the case of Y3+. Firstly, a classical protonation titration approach was adopted to trivalent ion systems [2]. This approach yields binding probabilities for the binding sites of the protein. The effective charge of the protein as a function of yttrium concentration was calculated at different concentrations of monovalent salt. The results are in accordance with the experimentally observed phase transition in protein solution from the dissolved to the condensed phase. Secondly, a classical molecular dynamics simulation was performed, yielding the dynamic binding behavior of yttrium to the protein. With this approach, also the binding of several carboxylic groups to one yttrium ion is observed, which is consistent with the crystallographic findings. [1] Zhang et al., Proteins, 78:3450, 2010; [2] Zhang et al., Phys Rev Lett, 101:148101, 2008

BP 2.9 Mon 12:45 ZEU 260 Water soluble chlorophyll (Chl) binding protein (WSCP) of higher plants as model system for the investigation of pigment-pigment and pigment-protein interactions — Franz-Josef Schmitt1, Jörg Pieper2, Christoph Theis1, Inga Trostmann3, Harald Paulsen3, Thomas Renger1, Hans Joachim Eichler1, Thomas Friedrich1, and Gernot Renger3 — 1Berlin Institute of Technology, Germany  
2University of Tartu, Estonia  
3Johannes Gutenberg University Mainz, Germany  
4Johannes Kepler University Linz, Austria  
Spectroscopic studies on pigment-pigment and pigment-protein interactions of Chl a and b bound to the recombinant class Ia WSCP from cauliflower are presented. Two Chls form a strongly excitedly coupled open sandwich dimer within the tetrameric protein matrix giving rise to an upper excitonic state with a large oscillator strength. Fluorescence lifetime measurements show that the unusually high photostability of Chls bound to WSCP most probably originates from a diffusion barrier to interaction of molecular oxygen with Chl triplets. The spectra are well described by a Chl dimer modulated by the protein environment. These findings are in good agreement with recent hole-burning and fluorescence line narrowing results.

The presented results illustrate the great potential of WSCP as a model system for systematic experimental and theoretical studies on the functionalization of Chls by the protein matrix. It opens the way for the application of pigment-protein complexes as photo-switchable protein coatings of medical drugs.
Topical Talk

BP 3.1 Mon 10:30 ZEU 222
Crystalline combine amorphous and crystalline mineral to build a functional tooth structure — Barbaras Aichlmayer1, Shemuel Bentov2,3, Ali Al-Sawalmih1, Adimurthy Mas1, Paul Zaslansky1, Peter Fratzl1, Amir Sagi4,5, and Amir Berman2,6
1 Department of Biomatierials, Max Planck Institute of Colloids and Interfaces, 14424 Potsdam, Germany — 2Department of Biotechnology Engineering, Ben-Gurion University of the Negev, 84105, Israel — 3Department of Life Sciences, Ben-Gurion University of the Negev, 84105, Israel — 4 The National Institute for Biotechnology in the Negev, Israel

Various strategies allow for the formation of functional tooth structures including examples as different as the self-sharpening teeth of sea-urchins and our durable human teeth. The freshwater crayfish Cherax quadricarinatus follows a unique approach of using amorphous and crystalline minerals to build the molar extension of its mandible, which serves as an efficient grinding tool. Mechanical properties with an astonishing similarity to human teeth are achieved by the combination of an enamel-like layer of oriented fluorapatite crystals and a graded structure of chitin and amorphous mineral with an increasing phosphate/carbonate ratio. The composition and structure of the crayfish molar, in the amorphous state of the art techniques such as Raman imaging, synchrotron X-ray diffraction and micro-CT, are related to its mechanical properties and discussed with respect to the role of the calcium phosphate, which allows for the formation of the hard, crystalline coating and also helps to stabilize the amorphous mineral.

BP 3.2 Mon 11:00 ZEU 222
Structure-property relationships of natural silk fibers as studied by time-resolved Fourier-Transform Infrared Spectroscopy (FTIR) — Roxana Ensi1, Periklis Papadopoulos2, and Friedrich Kremer1,2 Institut für Experimentelle Physik I, Leipzig, Germany — 2Max-Planck-Institut für Polymerforschung, Mainz, Germany

Polarized IR-spectroscopic and mechanical measurements are combined to analyse the conformational changes in hydrogenated and partially deuterated major ampullate spider silk of Nephila edulis[1]. Crystal stress can be measured from the frequency shift of main-chain vibrations. The results show that in both states of silk a serial arrangement between the crystalline and amorphous phase dominates the nanostructure. The determination of the molecular order parameters of the different moieties proves that the amide hydrogen exchange is a selective process, taking place at the surface of β-sheet nanocrystals, implying that these regions are accessible by water[2]. The mechanical properties are changing dramatically when the fiber is wet due to the fact that the pre-stress of the chains interconnecting the nanocrystals is irreversibly released. A three-component combined model of crystals in serial arrangement with amorphous chains and a fraction of chains bypassing them can describe all aforementioned states of spider silk[3]. [1] P. Papadopoulos, R. Ene, I. Weidner, F. Kremer Macromol. Rapid Commun. 30 (2009). [2] R. Ene, P. Papadopoulos, F. Kremer Polymer 51, (2010) [3] R. Ene, P. Papadopoulos, F. Kremer, Soft Matter 5 (2009)

BP 3.3 Mon 11:15 ZEU 222
Mechanical properties of fiber-fiber bonds in paper studied by atomic force microscopy — Franz Schmied1, Wolfgang Fischer1,2, Ulrich Hirs1,2, Robert Schienknecht1,2, and Christiaan Teich1,2
1 Institute of Physics, University of Leoben, 8700 Leoben, Austria — 2Institute for Paper, Pulp and Fiber Technology, Graz University of Technology, 8010 Graz, Austria — 3Institute of Solid State Physics, Graz University of Technology, 8010 Graz, Austria — 4CD-Laboratory for Surface Chemical and Physical Fundamentals of Paper Strength, Graz University of Technology, 8010 Graz, Austria

Paper has been used as a packaging material and for printing purposes for a long time, however a fundamental quantitative understanding for the mechanisms of paper strength has not yet been worked out. A sheet of paper is a network of individual single fibers extracted from wood. During the production cycle, these single fibers need to approach close enough to form bonds between each other. The resulting network is then called paper. Here, we present a comprehensive AFM investigation of single fibers as well as fiber-fiber bonds to achieve a deeper insight into the various mechanisms [1] that bind two single pulp fibers together. Beside morphological investigations, we present force versus distance curves to study the separation of two bonded fibers as distance and force controlled experiments. With these experiments it is possible to learn more about the mechanical properties of single fiber-fiber bonds. Supported by Mondi and the Christian Doppler Research Society, Vienna, Austria. [1] Lindström, T. et al., Proc. 13th Fundamental Research Symp, 2005.

BP 3.4 Mon 11:30 ZEU 222
Influence of temperature on the morphology of casein micellar films — Ezzeлин Mevtalli1, Alexander Dietert2, Joseph Adelsberger2, Robert Cuhrt2, Ulrich Kulzer3, and Peter Müller-Buschbaum1,7

Casein micelles for non-food applications such as coatings, adhesives and cosmetics are the main drive to study casein micelles structure in the thin film format. The effect of temperature on the structure of casein micelle films is investigated using grazing incidence small angle neutron scattering (GISANS). GISANS has proved sensitivity to micellar structure due to a high contrast imparted by an outer shell of D2O on the objects [1]. At different temperatures, various average micelle sizes with large size distribution are due to an aggregation behavior of the casein proteins. For freshly prepared samples, the average micelle size is increasing from about 80 to 120 nm with increasing temperatures from 5 to 35 °C. Aged casein micelles films for 100 days at room temperature indicate a continuous structural reorganization. The continuous aggregation between hydrated micelles in the film to reach equilibrated structures explains the high stability of casein-based coatings and adhesives by the ability to adapt itself to varying environmental conditions. [1] E. Mevtalli et al., Langmuir 25, 4124 (2009)

BP 3.5 Mon 11:45 ZEU 222
Thermodynamics of chondroitin sulfate solutions using field-theoretic methodologies — Stephan A Baeurle1, Michael G Kiewel2, Elena S Makarova2, and Evgenii A Nogovitsyn1
1 Department of Chemistry and Pharmacy, Institute of Physical and Theoretical Chemistry, University of Regensburg, Universitätstr. 31, D-93053 Regensburg, Germany — 2Institute of Solution Chemistry, Russian Academy of Sciences, 153045 Ivanovo, Russia

Articular cartilage is predominantly composed of chondroitin sulfates, which are known to affect in a decisive way the mobility and flexibility of our joints. Progress in understanding their frictional-compressive properties of the molecules needs further development of reliable experimental data and the multitude of controlling parameters, influencing their structure and properties under physiological conditions. Here, we discuss the thermodynamic response of aqueous chondroitin sulfate solutions to changes in the monomer and added salt concentrations, using a recently developed field-theoretic approach beyond the mean-field level of approximation (S.A. Baeurle et al, Polymer 50, 1805-1813 (2009)). We compare our calculation results to experimental as well as molecular modeling data, and demonstrate that our field-theoretic approach provides useful estimates for important physical properties, affecting their frictional-compressive behavior.

BP 3.6 Mon 12:00 ZEU 222
The swelling/stability effect of hyaluron on a lipid multilayer system — Martin Kreuzer1, Markus Stoobl1, Matthias Reinhardt2, Reiner Dahnt1, and Roland Steitz2
1 Universität Heidelberg, Physikalisches Chemisches Institut, 69120 Heidelberg, Germany — 2 Helmholtz-Zentrum Berlin GmbH, 14109 Berlin, Germany

Hyaluron (HA) is a high molecular weight polysaccharide. HA is involved in a wide range of processes in the human body, such as wound healing, severe stress, tumor progression and invasion. It was possible to show, that HA also stabilizes lipid multilayer systems at physiological conditions: Neutron reflectometry measurements, carried out at V6 of BioRef neutron reflectometer at the Helmholtz-Zentrum Berlin, in excess D2O verified, that a oligomannial DMPC lipid bilayer coating remains stable on a silicon substrate at 21°C in its ordered state (Ld2).
with a d-spacing of 66Å, but detaches almost completely at 38°C in its chain-disordered Lo state from the solid support - the origin of the loss of the oligolamellar DMPC bilayer stack at 38°C is unclear. By contrast oligolamellar lipid bilayers remain stable on a substrate at 38°C when incubated with a solution of HA in D2O. In an independent experiment, an oligolamellar lipid bilayers stack was measured against a solution of 3mg/mL HA in D2O. The sample was investigated shortly after incubating at 21°C and after raising sample temperature to 38°C. The oligolamellar lipid layer remained stable on the substrate, but an immense swelling occurred until a d-spacing of 209Å is reached. We will discuss a possible mechanism of the transformation of the oligolamellar lipid system with incubation time.

BP 3.7 Mon 12:15 ZEU 222
Influence of the intercalating fluorescent dye YOYO-1 on DNA properties — •Katrin Günther1, Ralph Seidel2, and Michael Meisel3 — 1Technische Universität Dresden, Institut für Physikalische Chemie, Mess- und Sensortechnik, 01069 Dresden, Germany — 2Technische Universität Dresden, Biotechnology Center, Tatzeberg 47-51 01307 Dresden, Germany
Fluorescent dyes of the cyanine family are widely used for staining DNA in order to explore the statistical-mechanical properties and the dynamical behaviour of DNA, even though their impact on the mechanical and structural properties has not been reliably quantified so far.

The influence of the bis-intercalating fluorescent dye YOYO-1 on the mechanical and structural properties of the molecule duplex is investigated in a wide range of staining ratios. Magnetic tweezers were used to measure the persistence and the contour length as well as the dye-induced unwinding of DNA molecules. The ionic conditions were found to considerably affect the stability of YOYO-1 binding to DNA. In contrast to other intercalating dyes, we found the persistence length remaining constant independent on the amount of bound YOYO-1.

BP 3.8 Mon 12:30 ZEU 222
Stiffening effect of cholesterol on large unilamellar vesicles based on POPC — •Thomas Hellweg1, Laura Rodriguez-Arriaga2, Ivan Lopez-Montero2, Bela Farago3, and Francisco Monroy2 — 1Universität Bielefeld, PC III, Universitätstr. 25 33615 Bielefeld, Germany — 2Universidad Complutense, 28040 Madrid, Spain — 3ILL, 6 rue Jules Horowitz, BP 156, F-38042 Grenoble Cedex 9, France
In the present contribution the center of mass diffusion and shape fluctu-ations of unilamellar POPC vesicles are studied by means of neutron spin-echo (NSE) in combination with dynamic light scattering (DLS).

The intermediate scattering functions were measured for several dif-ferent values of the momentum transfer q and for different cholesterol contents in the membrane. The combined analysis of NSE and DLS data allows the calculation of the bending elastic constant K of the bilayer. A stiffening effect monitored as an increase of K with increasing cholesterol molar ratio is evidenced from these measurements [1]. At high values of q apparently intermonolayer friction modes can be resolved using NSE [2]. The presented approach could also be applied to study the influence of membrane proteins on K or of substances like e.g. Gramicidine.


BP 3.9 Mon 12:45 ZEU 222
Investigation of L-Cysteine in aqueous solution using the RIXS-map approach — •Frank Meyer1, Lothar Weinhardt2, Monika Blum3, Marcus Barth4, Regan Wilks5, Wanni Yang6, Clemens Heske7, and Friedrich Reinert6 — 1Exp. Physik VII, Universität Würzburg — 2Department of Chemistry, University of Nevada Las Vegas, USA — 3Solar Energy Research, Helmholtz-Zentrum Berlin für Materialien und Energie GmbH — 4Advanced Light Source, Lawrence Berkeley National Laboratory, USA
Amino acids are the building blocks of many biologically relevant macro-molecules. Consequently, their electronic structure is of fundamental interest and hence has been the topic of many studies. Most investigations focus on solid-state samples, the study of amino acids in their native (i.e. aqueous) environment with core-level spectroscopy has only become possible as a result of the development of specialized experimental set-ups. In combination with a high-transmission soft x-ray spectrometer, our liquid flow through cell allows us to measure two-dimensional resonant inelastic x-ray scattering (RIXS) maps of liq-uids and solutions. RIXS maps display the x-ray emission intensity as a function of emission and excitation energy and hence provide a comprehensive picture of the electronic structure of the investigated material.

In this contribution, we will present RIXS maps of aqueous cysteine solutions at various pH values. We observe a significant impact of the pH value and evidence for proton dynamics on the time scale of the RIXS process. The results are compared to RIXS and photoemission measurements of cysteine in films and of related molecules.

BP 4: DNA & DNA Enzymes

Invited Talk
BP 4.1 Mon 14:00 ZEU 260
Single-molecule detection of DNA repair in real-time — •Terence Strick1, Kevin Howan1, Nigel Savery2, Seth Darst3, and MM2F PPT Consortium4 — 1CNRS Institut Jacques Monod Paris, France — 2University of Bristol, UK — 3Rockefeller Institute, NY, USA — 4Erasmus Univ., Rotterdam
We describe the bottom-up reconstruction of DNA repair pathways using single-molecule nanomanipulation methods. This allows us to observe in real-time the initial steps of DNA repair and build up kinetic models for repair processes. We discuss a variety of DNA repair systems and show in which ways these systems are mechanosensitive or not.

BP 4.2 Mon 14:30 ZEU 260
Partitioning of RNA polymerases in bacterial cells — •Stefan Klumpp1, Marco Mauri1, and Terence Hwa2 — 1Max Planck Institute of Colloids and Interfaces, Potsdam — 2University of California, San Diego
How frequently a gene is transcribed depends not only on its regula-tion, but also on the availability of the necessary molecular machinery, RNA polymerases (RNAPs) and their associated factors. The concen-tration of free RNAPs and factors, i.e. those that are available for the initiation of transcription, depends also on the demand by other genes, such that genes may compete for the transcription machinery.

We used a model for the partitioning of RNAPs into several func-tional classes to address the effect of this competition [1]. The model has been tested against existing experimental data for the growth-rate dependence of constitutive transcription and the effects of RNAP over-expression. We find that the competition of genes for RNAPs generally plays a minor role, because a pool of RNAPs non-specifically bound to DNA buffers against such effects. For sigma factors, the component of the transcription machinery required for promoter recognition and binding, however, competition seems to play an important role and may actively be modulated by the cell during global switches in the gene expression program, such as in stress responses.


BP 4.3 Mon 14:45 ZEU 260
A model for the degradation of messenger RNA in bacteria — •Carlus Denese, Angelo Valleriani, and Reinhard Lipowsky — Max-Planck-Institut für Kolloid- und Grenzflächenforschung, De-partment of Theory and Bio-Systems, Potsdam, Germany
In a cell, the amount of messenger RNA (mRNA) is kept in balance by the processes of transcription and degradation. In the bacterium E. coli, the stability of mRNA is limited due to the action of protein complexes called the degradosome. They consist of several endo- and exonucleases which cooperatively degrade the mRNA chain until it is eventually fully recycled.

In this contribution, we present a theoretical model that takes into account the stochastic nature of this process. To build the model, we have assumed that in bacteria the main degradation pathway is ini-tiated by endonucleolytic cleavage, according to the standard view in
the field. It exploits the fact that the coverage of mRNA with ribosomes depends on the age of the transcript and that ribosomes shield the transcript against degrading proteins.

One consequence of the model is that the mean lifetime of the transcripts decreases with the length of the coding sequence. This conclusion is in agreement with many experimental half-life measurements. We will show a comparison of our model to experimental half-life data and critically discuss the nature of these data.

Type III restriction enzymes sense the relative orientation of their distant target sites and cleave DNA only if at least two of them are situated in an inverted repeat. The communication process is strictly dependent on ATP hydrolysis catalyzed by their superfamily 2 helicase domain. Given the similarity to Type I restriction enzymes which couple ATP hydrolysis to directed motion on DNA, unidirectional loop translocation has been the suggested communication mechanism for Type III enzymes. Based on magnetic tweezers single-molecule cleavage experiments and ATPase measurements we suggest an alternative inter-site communication mechanism using 1D diffusion along the DNA contour. In order to verify this hypothesis we directly visualized the motion of Q-dot labeled Type III restriction enzymes along DNA. For this we used a setup that combines magnetic tweezers with total internal reflection fluorescence microscopy. The enzymes undergo a diffusive motion along DNA, capable of scanning kb distances per second. We also found that the affinity of the enzymes to non-specific and specific DNA is regulated by the presence of ATP, suggesting that ATP hydrolysis acts as a trigger for diffusion. Thus Type III restriction enzymes are the first DNA-modifying enzymes which communicate target site orientations over long distances via 1D diffusion.

15 min. break.

Development of an inter-nucleotide potential for DNA based on Density Functional theory — ▪ Maria Fyta, Greg Lakatos, Pierfrancesco Rosini, Amanda Peters, Simone Melchiona, and Effthimios Kaxiras

Department of Physics and School of Engineering Sciences, University of California, Cambridge, MA, USA — ▪ Physics Department, Technical University of Munich, 85748 Garching, Germany — ▪ Laboratory for Multiscale Modeling of Materials, EPFL, Lausanne, Switzerland — ▪ Istituto Applicazioni Calcolo, CNR, Rome, Italy

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

Type III restriction enzymes use 1D diffusion to communicate the relative orientation of their distant target sites — ▪ Friedrich W. Schwarz, Julia Töth, Kaira van Abeele, Mark D. Szczelkun, and Ralph Seidel

1 BIOTEC TU-Dresden — 2 University of Bristol, UK

Unfolding mechanisms and the free energy landscape of the DNA i-motif — ▪ Jens Smitak and Andreas Heuer

Institut für Festkörperphysik, TU Darmstadt

Inspired by detailed cell-biological data on the dynamics of DNA replication during S phase, we present a stochastic model of DNA replication dynamics that allows for a quantitative comparison between model parameters and data.

Further important model features are the induced initiation of replication in the vicinity of replication forks and a limitation of the number of replication forks due to the limited availability of essential replication proteins.

Probing the elasticity of DNA on short length scales by modeling supercoiled DNA under tension — ▪ Robert Schöpfel, Helge Brutzer, Oliver Müller, Ralph Seidel, and Gero Weidemann

1 University of Applied Sciences Stralsund, 18435 Stralsund, Germany — ▪ Biotechnology Center Dresden, University of Technology Dresden, 01062 Dresden, Germany

The worm-like-chain (WLC) is the most commonly used theoretical model for modeling the elasticity of DNA. However, recently alternative so-called sub-elastic chain (SEC) models [1] were proposed that predict for large deflections a higher flexibility than the usual harmonic model. So far, no unambiguous verification of these models has been obtained since probing the elasticity of DNA on short length scales remains challenging. Here, we address this question by modeling single-molecule experiments on different types of DNA. We present a theoretical model of an isolated DNA molecule in an ideal solvent that predicts for large deflections a higher flexibility than the usual harmonic model. So far, no unambiguous verification of these models has been obtained since probing the elasticity of DNA on short length scales remains challenging. Here, we address this question by modeling single-molecule experiments on different types of DNA. We present a theoretical model of an isolated DNA molecule in an ideal solvent that predicts for large deflections a higher flexibility than the usual harmonic model. So far, no unambiguous verification of these models has been obtained since probing the elasticity of DNA on short length scales remains challenging. Here, we address this question by modeling single-molecule experiments on different types of DNA. We present a theoretical model of an isolated DNA molecule in an ideal solvent that predicts for large deflections a higher flexibility than the usual harmonic model.

We investigated the translocation of single protein molecules (RecA, Peroxiredoxin and EcoRI) bound to dsDNA through a solid-state nanopore controlled by optical tweezers and an electric field (nanopore force spectroscopy). During threading, we found distinct asymmetric force signals depending on the protein charge, the DNA elasticity and the counter-ionic screening [1]. A theoretical model of an isolated charge on an elastic polyelectrolyte strand experiencing an anharmonic force signals depending on the protein charge, the DNA elasticity and the counter-ionic screening [1]. A theoretical model of an isolated charge on an elastic polyelectrolyte strand experiencing an anharmonic force signals depending on the protein charge, the DNA elasticity and the counter-ionic screening [1]. A theoretical model of an isolated charge on an elastic polyelectrolyte strand experiencing an anharmonic force signals depending on the protein charge, the DNA elasticity and the counter-ionic screening [1]. A theoretical model of an isolated charge on an elastic polyelectrolyte strand experiencing an anharmonic force signals depending on the protein charge, the DNA elasticity and the counter-ionic screening [1]. A theoretical model of an isolated charge on an elastic polyelectrolyte strand experiencing...

The interplay of mutations and electronic properties in disease-associated genes — CHI-TIN SHI1,2, STEPHEN A WELLS3, CHING-LIN HSU4, YUN-YIN CHENG1, and RUDELF A RÖMER3
1Department of Physics, Tsinghua University, 100084 Beijing, China — 2Department of Physics, National Taiwan University, Taipei, Taiwan — 3Dept. of Physics and Center for Theoretical Sciences, 30013 Hsinchu, Taiwan — 4Dept. of Physics and Center for Scientific Computing, University of Warwick, Gibbet Hill Road, Coventry, CV4 7AL, UK

The electronic properties of DNA molecules are believed to play a crucial role in many phenomena taking place in living organisms, for example the detection of DNA lesions by base excision repair (BER) of glycosylases such as Endonuclease III and MutY and the regulation of tumor-suppressor genes such as p53 by detection of oxidative damage. However, the reproducible measurement and modelling of charge migration through DNA molecules at the nanometer scale, in vitro or in vivo, remains a challenging and controversial subject even after more than two decades of research. We present and analyze 162 disease-associated genes from a variety of medical databases with a total of almost 20000 known pathogenic mutations, a significant difference in the electronic properties of the population of pathogenic mutations compared to the set of all possible mutations. Comparison of the results for different models of charge transport suggests that it is the electronic properties of the coding strand rather than the conduction of the double helix, that is significant.

BP 5: Tissue Dynamics & Developmental Processes

Time: Monday 14:00–16:45
Invited Talk
BP 5.1 Mon 14:00 ZEU 250
Are biomechanical changes necessary for tumor progression?
- The impact of cell mechanics on cancer development — MAREIKE ZINCK, ANATOL FRITSC, TOBIAS KISSLING, K. DAVID NSETU, STEVE PAWLZAK, FRANZISKA WETZEL, and JOSEF KAS — Abteilung Physik der weichen Materie, Fakultät für Physik und Geowissenschaften, Universität Leipzig, Leipzig, Germany
With an increasing knowledge in tumor biology an overwhelming complexity becomes obvious which roots in the diversity of tumors and their heterogeneous molecular composition. Nevertheless in all solid tumors malignant neoplasia, i.e. uncontrolled growth, invasion of adjacent tissues, and metastasis, occurs. Physics sheds some new light on cancer by approaching this problem from a fundamental, material perspective. Recent results indicate that all three pathomechanisms require changes in the active and passive cellular biomechanics. Malignant transformation causes cell softening for small deformations which correlates with an increased rate of proliferation and faster cell migration. The tumor cell's ability to stain harden permits tumor growth against a rigid tissue environment. A highly mechanosensitive, enhanced cell contractility is a prerequisite that tumor cells can cross its tumor boundaries and that this cells can migrate through the extracellular matrix. Insights into the biomechanical changes during tumor progression may lead to selective treatments by altering cell mechanics. Such drugs would not cure by killing cancer cells, but slow down tumor progression with only mild side effects and thus may be an option for older and frail patients.

BP 5.2 Mon 14:30 ZEU 250
Blood flow and blood cell interactions and migration in microvessels — MITCH FEDOSOU, JULIA FORNLEHTNER, and GERHARD GOMPER — Forschungszentrum Juelich, Institute of Solid State Research, Juelich 52425, Germany
Blood flow in microcirculation plays a fundamental role in a wide range of physiological processes and pathologies in the organism. To understand and, if necessary, manipulate the course of these processes it is essential to investigate blood flow under realistic conditions including deformability of blood cells, their interactions, and behavior in the complex microvascular network which is characteristic for the microcirculation. We employ the Dissipative Particle Dynamics method to model blood as a suspension of deformable cells represented by a viscoelastic spring-network which incorporates appropriate mechanical and rheological cell-membrane properties. Blood flow is investigated in idealized geometries. In particular, migration of blood cells and their distribution in blood flow are studied with respect to various conditions such as hematocrit, flow rate, red blood cell aggregation. Physical mechanisms which govern cell migration in microcirculation and, in particular, margination of white blood cells towards the vessel wall, will be discussed. In addition, we characterize blood flow dynamics and quantify hemodynamic resistance.

BP 5.3 Mon 14:45 ZEU 250
Cell flow reorients planar cell polarity in the developing wing epithelium of the fly — DOUGLAS B. STAPLE1, REZA FARHADIPAR2, BENNOIT AIGOUY2, ANDREAS SAGNER2, JENS-CHRISTIAN RÖSER2, SUZANNE EATON2, and FRANK JÜLICH1 — 1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany
Epithelia are two-dimensional sheets of cells. Cell polarity in epithelia typically forms large scale aligned patterns in the plane of the tissue. In the Drosophila wing, an important model system for the study of epithelial organization, this planar polarity is reflected in the pattern of wing-hairs and in the distribution of planar cell polarity (PCP) proteins at earlier stages during development. Here we investigate the mechanisms underlying the dynamic reorganization of planar cell polarity in the Drosophila wing using a combination of theory and experiment. Experimentally, we perform time-lapsed imaging during pupal development in order to extract both the time-dependent distribution of PCP proteins, and also the spatially and temporally inhomogeneous cell flow field in the tissue. The pattern of PCP proteins is found to reorient during development. We decompose the velocity field into patterns of local shear, compression, and rotation rates. Given the time-dependent shear and rotation rates and an experimentally measured initial condition, the time-evolution of the polarity pattern is computed using a phenomenological hydrodynamic theory, and is found to be consistent with the experimentally observed time-evolution.

BP 5.4 Mon 15:00 ZEU 250
Fluidization of tissues due to cell division and apoptosis — JONAS RANFT1,2, MARKUS BASAN1, JENS ELFERT1, JEAN-FRANÇOIS JOANNY1, JACQUES PROST3, and FRANK JÜLICH1 — 1Institut Curie, 26 rue d’Ulm, 75005 Paris, France — 2Max-Planck-Institut für Physik Komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden, Germany — 3ESPCI, 10 rue Vauquelin, 75005 Paris, France
Throughout development, tissues grow due to continuous cell division. In later stages, tissues can reach a homeostatic state in which cell division and cell death balance on average. In addition to genetic regulation, the mechanics of tissues play an important role in these processes. We develop a continuum description of tissue dynamics in order to account for the stress distribution and cell flows on large scales [1]. In the absence of cell division and apoptosis, we consider the tissue to behave as an elastic solid. Cell division and apoptosis introduce stress sources which in general are anisotropic. By combining cell number balance with dynamic equations for the stress source, we show that the tissue effectively behaves as a visco-elastic fluid with a relaxation time set by the rates of division and apoptosis. We find that close to the homeostatic state, the compressional modulus of the tissue vanishes on long time scales. We discuss the effects of fluctuations in cell division and apoptosis and compare our results to simulations of multicellular systems. This approach can be extended to a two-component description of tissues that takes the extracellular fluid explicitly into account.

actomyosin cell cortex in which biochemical pathways regulate active stress. We present a mechanism in which a single diffusing species up-regulates active stress, resulting in steady flow and concentration patterns. We also discuss general pattern-formation behaviors of reaction diffusion systems placed in active fluids.

15 min. break.

BP 5.6 Mon 15:45 ZEU 250
General analysis of mathematical models for bone remodeling
— Martin Zum桑de1, Dirk Steffn1, Stefan Siegmund1, and Thiilo Giessl1 — Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany. — Department of Mathematics, Dresden University of Technology, 01062 Dresden, Germany.

Bone remodeling is a complex process by which the skeleton of vertebrates is rebuilt continuously throughout their life. It is based on the interplay of two cell types, bone-resorbing osteoclasts and bone-forming osteoblasts and regulated by various cytokines, hormones and other signaling agents. In this work, we apply the method of generalized modelling to systematically analyze a large class of mathematical models of bone remodeling that are based on ODEs. Our analysis shows that the precursors of osteoblast play an important role in the regulation of bone remodeling. Further, we find that stability of the steady state, which is required in the physiological state, is not a self-evident property of the models. In contrast, the parameter regime that is most likely realized in nature based on experimental input is situated close to bifurcation lines, marking qualitative changes in the dynamics. Although proximity to a bifurcation facilitates adaptive responses to changing external conditions, it entails the danger of losing dynamical stability. These dynamical transitions can possibly be related to diseases of bone such as Paget's disease.

BP 5.7 Mon 16:00 ZEU 250
Oct4 kinetics predicts cell lineage patterning in the early mammalian embryo — Nicolas Plachita1, Tobias Bollenbach1,2, Shirley Fraser1, Scott E. Fraser1, and Periklis Pantazis1 — California Institute of Technology, Pasadena, CA, USA. — Harvard Medical School, Boston, MA, USA. — IST Austria, Klosterneuburg, Austria.

Transcription factors (TFs) are central to sustaining pluripotency in mammalian development. Here, we establish a fluorescence decay after photoactivation (FDAP) assay to quantitatively study the nuclear transport kinetics of Oct4, a key TF controlling pre-implantation development in the mouse embryo. Combining FDAP measurements with a physical description of nuclear transport, we reveal that each cell in a developing mouse embryo exhibits one of two distinct Oct4 kinetic profiles, before there are any morphologically distinguishable differences or outward signs of lineage patterning. By tracing the lineages of the cells in these two distinct sub-populations, we find that Oct4 kinetics predict lineages of the early embryo. Cells in which FDAP reveals slower Oct4 kinetics are much more likely to contribute to the pluripotent cell lineage which creates the inner cell mass and later gives rise to the fetus. In contrast, cells with faster Oct4 kinetics contribute almost exclusively to the extra-embryonic lineages which later form the placenta. Our findings identify Oct4 nuclear transport kinetics, rather than differences in total expression levels, as a predictive measure of cell lineage patterning in the early mouse embryo.

Reference: N. Plachita et al., Nature Cell Biology, accepted.

BP 5.8 Mon 16:15 ZEU 250
Mechanotaxis in the brain — Kristian Frangze1,2, Hanno Svoboda3, Pouria Mosayyedi3,1, Andreas Christ1,3, James Fawcett1,3, Christine Holt1,3, and Jochen Geck1 — Department of Physics, Argonne National Laboratory, Argonne, U.S. — Department of Physiology, Development and Neuroscience, Theoretical Physics Group, University of Manchester, UK.

Biophysics is just beginning to unravel important physical problems in biology and medicine that have been mostly overlooked for decades. While neuroscience has mainly focused on biochemical and molecular biological aspects of neuronal migration and growth, virtually nothing is known about mechanical aspects. Here we show that both neurons and glial cells, the basic building blocks of nerve tissue, respond to mechanical stimuli in their environment. Mechanosensing involves the application of forces driven by the interaction of actin and myosin II, and intracellular calcium signaling. Using culture substrates incorporating gradients of mechanical properties, we found that neuronal axons are repelled by stiff substrates while activated glial cells are attracted toward them. Applying a modified scanning force microscopy technique, we found mechanical gradients in the nerve tissue along which neurite growth varies. Hence, our data suggest that cell growth and migration in the central nervous system are not only guided by chemical signals - as it is currently assumed - but also by the nerve tissue's mechanical properties.

BP 5.9 Mon 16:30 ZEU 250
Dynamics of axenial reproduction in planarians — Bryan Lincoln, Sofia Quinodoz, and Eva-Maria Schotte — 170 Carl-Icahn Laboratory, Princeton University, Princeton, NJ, USA.

Planaria research has undergone a recent resurgence due to the development of molecular tools, the Planarian genome project and database resources. Despite the resulting progress in planarian biology research, an extensive study of their physical properties remains to be undertaken. We have developed a method to collect a large amount of data on the dynamics of clonal reproduction in the freshwater planarian S.mediterranea. The capability of planarians to regenerate from a minuscule body part on the order of 10000 cells is based on a homogeneously distributed stem cell population that comprises ~30% of all cells. Due to this stem cell contingent, planarians can further reproduce spontaneously by dividing into a larger head and smaller tail piece, which then will rebuild the missing body parts, including a central nervous system, within about a week. Time-lapse imaging allows us to characterize the fission process in detail, revealing its developmental stages and capturing the critical moment of rupture. A traction force measurement setup is being developed to allow us to quantify the forces planarians exert on the substrate during reproduction, a macroscopic analog to the Traction Force Microscopy setups used to determine local cellular forces. We are particularly interested in the molecular processes during division and the interplay between tissue mechanics and cell signaling.

BP 6: Statistical Physics of Biological Systems II (joint DY, BP)

BP 6.1 Mon 14:00 HÜL 186
Collective dynamics in the cytoskeleton and swimming bacteria — Falko Ziebert1, Martin Zumsande1, Sumanth Swaminathan1, Shawn Ryan1,4,5, Leonid Berlyand4, and Igor Aranson5 — PCT - UMR CNRS Gulliver 7083, ESPCI, Paris, France. — 2Physikalisches Institut, Universität Freiburg. — 3Engineering Sciences and Applied Mathematics, Northwestern University, Evanston, U.S. — 4Department of Mathematics, Pennsylvania State University, U.S. — 5Materials Science Division, Argonne National Laboratory, Argonne, U.S.

Collective dynamics in active biological materials has attracted much attention in recent years. I will focus on select topics on two systems: i) semi-dilute cytoskeletal solutions where molecular motors induce self-organization of filaments and ii) collective swimming of bacterial solutions. In the first system I propose a model for the semi-dilute case, i.e. the regime of multi-filament interactions. I discuss the order of the isotropic-polar nematic transition - which can not be determined by macroscopic models - as well as the influence of motor fluctuations on the ordering and the respective defect patterns that form. In case of bacterial solutions, recent experimental studies evidenced a decrease in viscosity as a function of density/volume fraction of swimmers in case of pushers (e.g. B. subtilis). In contrast, pullers (e.g. chlamydomonas) lead to an increase in viscosity. To rationalize these findings we performed simulations and analytical work, demonstrating that the viscosity reduction in case of pushers is related to the onset of large-scale collective motion due to interactions between swimmers.
Stochastic models, subject to external forcing, can capture the regular oscillatory patterns of childhood epidemics, such as measles and whooping cough, but so far the mechanisms generating these patterns have not been well understood. We study the stochastic susceptible-infected-recovered (SIR) model with time-dependent forcing using analytic techniques which allow us to disentangle the interaction of stochasticity and external forcing. The model is formulated as a continuous time Markov process, which is decomposed into a deterministic dynamics together with stochastic corrections, by using an expansion in inverse system size. The forcing induces a limit cycle in the deterministic dynamics, and with the use of Floquet theory, a complete analysis of the fluctuations about this time-dependent solution is given. This analysis is applied when the limit cycle is annual, and after a period-doubling when it is biennial. The comprehensive nature of our approach allows us to give a coherent picture of the dynamics which unifies past work, but which also provides a systematic method for predicting the periods of oscillations seen in both whooping cough and measles epidemics.

**BP 6.3 Mon 14:45 HÜL 186**

**Strong Noise Effects in one-dimensional Neutral Populations**

— **Luca Dall’Ast** 1, Fabio Caccioli 2, and Deborha Brege 1

1ICTP, Trieste, Italy — 2Santa Fe Institute, Santa Fe, NM

The dynamics of well-mixed biological populations is studied using mean-field methods and weak-noise expansions. Similar methods have been applied also in spatially extended problems, relying on the fact that these populations are organized in colonies with a large local density of individuals. We provide a counterexample discussing a one-dimensional neutral population with a negative frequency-dependent selection. The system exhibits a continuous phase transition between genetic fixation and coexistence that is unexpected from weak-noise arguments. We show that the behavior is a non-perturbative effect of the internal noise that is amplified by presence of strong correlations (strong-noise regime).

**BP 6.4 Mon 15:00 HÜL 186**

**Active colloidal suspensions exhibit orientational order under gravity**

— **Mihaela Enculescu** and Holger Stark —

Technische Universität Berlin, Institut für Theoretische Physik, Hardenbergstr. 36, 10623 Berlin

Recently, the steady state of an active colloidal suspension under gravitational field was studied experimentally in [J. Palacci et al., Phys. Rev. Lett. 105, 088304 (2010)]. It was found that the sedimentation length depends strongly on the velocity of the active Brownian particles. We present a theoretical analysis for the sedimentation of an active colloidal suspension. We find that the change of the sedimentation length is coupled to a partial alignment of the suspension with the mean swimming direction oriented against the gravitational field. Our approach starts from Langevin equations of non-interacting active particles, from which a Smoluchowski equation for the particle distribution is derived. We determine the stationary particle distribution both numerically and by perturbation theory. It agrees very well with the experimental data. The predicted anisotropy in the particle orientation distribution is found to depend on the particle activity, as well as on the gravitational force.

**BP 6.5 Mon 15:15 HÜL 186**

**Fluctuations of intracellular filaments**

— **Sue-Ine Kristin Weber** and Ludger Santen —

Department of Theoretical Physics, Saarland University, Saarbrücken, Germany

The cytoskeleton is an inhomogeneous network of polar filaments consisting of, amongst others, microtubules. These highly dynamic biopolymer filaments are involved in a wide variety of biological processes such as cell division and intracellular transport. Although they are very rigid and form a stiff structural network, it has been shown that they typically exhibit significant bending on all length scales. In this work we describe microtubules as semi-flexible polymers and investigate their fluctuations under thermal and non-thermal forces by means of computer simulations and phenomenological approaches.

**BP 6.6 Mon 15:30 HÜL 186**

**Modelling the African Trypanosome with stochastic rotation dynamics**

— **Subh Banu** and Herbert Spohn —

Institut für Theoretische Physik Technische Universität Berlin

The dynamics of microorganisms in a viscous fluid has recently received considerable attention in the physics community. It has been reported that the African Trypanosome makes use of hydrodynamic flow fields to evade attack from antibodies in the blood stream. The spindle-shaped flexible cell body of the African Trypanosome possesses some bending rigidity due to its cytoskeleton. A single flagellum runs from the thicker posterior end to the thinner anterior end of the cell body and is firmly attached to it. By propagating a wave along the flagellum from the anterior to the posterior end, the trypanosome moves forward. However, the details of this propulsion mechanism is still under debate. Our goal is to study a model trypanosome in its viscous environment. We model the cell body and the flagellum as a network of very fine Oedudepsicted by springs and also include some resistance to bending. A bending wave passing through the flagellum propels the trypanosome. We simulate the flow field around the model trypanosome using the method of stochastic rotation dynamics, which is an effective solver for the Navier-Stokes equations but also includes thermal fluctuations. We will demonstrate how the model trypanosome is coupled to the effective fluid particles of stochastic rotation dynamics. We will also discuss the propulsion mechanism of the microorganism and demonstrate that our modeling reproduces different shape conformation observed in experiments.

**BP 6.7 Mon 15:45 HÜL 186**

**Explicit Expressions for the Mean First Passage Time of a Diffusing Molecule in Different Two-Dimensional Geometries**

— **Ronnny Straube** —

Systems Biology Group, Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany

The mean first passage time (MFPT) of a diffusing molecule is an important quantity that describes the first encounter between the molecule and a distant target site. For signaling molecules the MFPT can have a strong influence on the dynamics of a system. In this talk, we will explore the inverse problem of a significance of the MFPT. We will present a formula for the MFPT in terms of an associated Neumann function whose regular part can be evaluated analytically. The formula is applicable for any two-dimensional geometry and also includes some resistance to bending. A bending wave passing through the flagellum propels the trypanosome. We simulate the flow field around the model trypanosome using the method of stochastic rotation dynamics. We will also discuss the propulsion mechanism of the microorganism and demonstrate that our modeling reproduces different shape conformation observed in experiments.
clusters.

We also show that, by applying confining boundary conditions, a self-organization of the network toward a polarized structure is induced, even without explicit regulation and interactions. The polarity, can lead to separation of particle species adjacent to the enclosing geometry. The underlying mechanism can be understood by a linear theory similar to electrostatics. Finally we are discussing active transport phenomena on realistic cellular structures.


Modeling the adsorption of biofilms — Olef Leiding and Ludger Santen

The very first step of the formation of a biofilm at a surface, the adsorption of proteins, is investigated. Therefore a colloid model is used, in which proteins are described as polydisperse spheres interacting with each other via the framework of the DLVO theory – including steric repulsion, van der Waals and electrostatic interactions. Furthermore an internal degree of freedom, modelled as a change of geometry, is used to represent different conformations of a protein at the surface.

In qualitative agreement with experimental results, the adsorption kinetics of the initial biofilm formation were reproduced by means of Monte Carlo simulations [1,2]. The adsorption kinetics can be divided into three intervals: Initially the adsorption is limited by the flux of particles to the surface. At low concentrations the proteins spread at the surface in order to optimize the binding to the surface. At higher concentrations the adsorbed proteins are compacted due to particle-particle interactions and finally the surface coverage saturates. These dynamical regimes can be identified in experimental and theoretical investigations of the adsorbed amount. The comparison between experimental and theoretically generated biofilms is completed by a detailed analysis of the point patterns connected to the adsorbed particles, which is carried out by means of integral measures.


Boundary-induced polarity of random intra-cellular filament networks and vesicle agglomerations — Philip Greulich and Ludger Santen

The distribution of nutrients and metabolic products within cells is crucial for cell function. It is performed by active directed transport of vesicles along polarized intracellular filaments, mediated by motor proteins.

We present a model that captures basic features of active vesicle transport on randomly evolving filaments. The filaments form disordered random networks. Filament-filament interactions are neglected and dynamics are homogeneous and isotropic. Due to these symmetries, there is no net bias of filament orientations for periodic boundary conditions. However, symmetry breaking by confining boundary conditions induces a self-organization towards a polarized structure. This occurs despite unbiased dynamics and the absence of external gradients. It leads to a separation and accumulation of vesicle species, following the geometry of the cell volume. The phenomenon can be theoretically understood by using an analogy to Electrostatics. For realistic geometries the model reproduces vesicle agglomerations as can be experimentally observed.

Quorum sensing by yeast cells — André Weber, Yuriy Prokazov, Thomas Mair, Werner Zuschrotter, and Markus Hauser

Glycolysis is a central pathway in the energy metabolism of cells, and it have been reported for Bacillus subtilis.

We consider the thermally activated fragmentation of a homopolymer chain, which can exhibit strongly non-Markovian behavior on the timescale of interest. In our model the dynamics of the intact chain is a Rouse one until a bond breaks and bond breakdown is considered as a first passage problem over a barrier to an absorbing boundary. Using the framework of the Wilemski-Fixman approximation we calculate activation times of individual bonds for free and grafted polymer chains. We show that these times crucially depend on the length of the chain and the location of the bond yielding a minimum at the free chain end. Going beyond the Wilemski-Fixman approximation we show that a generalized form of the renewal equation for barrier crossings serves to improve the quantitative agreement between numerical simulations and analytical predictions.

Universal clustering properties in bacteria — Fernando Pernot, Joern Starkschall, Vladimir Jakovlevic, Lotte Sogaard-Andersen, Marks Bak, and Andreas Deutsch

Collective behaviour of individual cells marks the outset of the transition to multicellularity. This transition is thought to rely on some specific intercellular communication between cells. In this talk, we will show that the transition from single cell to collective behaviour in a Myxococcus xanthus mutant can be understood as a dynamical self-assembly process where no biochemical communication is required. The transition is characterized by a scale-free cluster size distribution that emerges at a critical cell density. The experimental data is consistent with predictions from a mathematical model in which bacteria are described as self-propelled rods with merely steric interactions. Our findings provide a universal mechanism for pattern formation in bacteria that only depends on the physical properties of the system, in particular, on cell shape and cell density. Interestingly, similar results have been reported for Bacillus subtilis.

Species deletion stability of model food webs that include allometric scaling and adaptive foraging — Lotte Heckmann, Christian Gull, and Barbara Droesser

Ecosystems are subjected to various types of perturbations, many of which are due to human influence, including the extinction of species.
Knowing the response of ecosystems to large perturbations is of importance for preservation politics, but also for a deeper understanding of the stabilizing mechanisms in ecosystems or food webs. We investigate numerically the response of model food webs that are dynamically stable to the deletion of a species. We quantify the species deletion stability by counting how many species survive after one species has been removed. The data are evaluated in dependence of the trophic function and properties of the eliminated species in order to determine which species are significant for the persistence of the whole food web. Our food web models include nonlinear population dynamics equations with Holling type II functional response, intraspecific competition, and adaptive foraging. The metabolic rates of the species scale allometrically with body mass, and we investigate the influence of different body mass ratios between predator and prey on the stability of the food webs.

BP 7.5 Mon 17:15 P3 Coexistence of mass-selective predators feeding on a growing prey — LAURIN LENGERT, CHRISTIAN GUIL, and BARBARA DROSSL — TU Darmstadt, Institut für Festkörperphysik

The body mass of an organism affects many ecologically relevant quantities, such as maximal food ingestion and respiration rate, population growth rate, carrying capacity, and prey choice. We show by numerical simulations that in body masses of predator and prey are positively correlated and the attack rate has been revealed as being a hump shaped function of the body mass ratio between predator and prey.

In natural food webs, species ontogeny, especially growth in body mass, alters body mass ratios. When considering seasonal species, the correlation between predator and prey body mass leads to a variation of the food web structure.

We present for the first time a model that includes several predator species, together with a prey that grows in size, leading to time dependent attack rates.

We will focus on the question how prey growth affects the coexistence of predators.

BP 7.6 Mon 17:15 P3 Upstream swimming of a model micro-swimmer in a microchannel — ANDREAS ZÖTTL and HOLGER STARK — TU Berlin

Many microorganisms in the human body swim in confined environments like sperm cells in the Fallopian tube or E. coli bacteria in the colon. Also pathogens use narrow channels like the urethra to swim to their destinations. Micro-swimmers exhibit hydrodynamic interactions with bounding surfaces that change their swimming speeds and orientations. In particular, pushers and pullers show different behaviors. Pushers such as sperm cells or bacteria propel themselves with flagella attached at the back of the cell body and get attracted by a wall. Pullers like the algae Chlamydomonas typically have a propelling function, while the bacteria have a propelling tangential surface velocity, different for pushers and pullers. We model the hydrodynamics of squirmers including thermal noise using multi-particle collision dynamics. This method introduces ballistic and collision steps of effective particles in order to solve the Navier-Stokes equations. We systematically investigate the swimming behavior of both pushers and pullers in a cylindrical microchannel with an imposed Poiseuille flow. When the strength of the flow is sufficiently small, pushers swim upstream at the wall. Pullers can swim upstream between the walls when the channel width is small enough. Increasing the imposed flow strongly, pushers and pullers now swim downstream and tumble due to flow vorticity similar to passive particles.

BP 7.7 Mon 17:15 P3 A Switch Like Response of Photosynthetic Bacteria to Changing Redox and Light Conditions — DIETRICH FLÖCKERZI1, Marcus J. B. HAUSER2, and RONNY STRAUß3 — 1Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany — 2Institute of Experimental Physics, Otto-von-Guericke University, Magdeburg, Germany — 3Biophysics Group, Leipzig University, Germany

Facultative photosynthetic bacteria switch their energy generation mechanism from respiration to photosynthesis depending on oxygen tension and light. Part of this transition is mediated by the conserved transcriptional repressor PpsR which specifically represses components of the photosynthetic apparatus under aerobic conditions. In Rhodobacter sphaeroides the repressive action of PpsR is antagonized by the redox and blue light sensitive flavoprotein AppA. At intermediate oxygen levels the interaction between AppA and PpsR leads to the repression of photosynthesis genes under high light illumination which is believed to reduce the risk of photo-oxidative stress. To elucidate the underlying mechanism for this phenotype we developed a simple mathematical model. Investigations of the steady-state behavior show that high light repression can indeed occur at intermediate oxygen levels if PpsR is reduced on a faster time scale than AppA. The model further shows that if AppA copy numbers exceed those of PpsR the low to high light transition can occur via a bistable switch which might help the bacterium to cope with changing light conditions, especially at intermediate oxygen levels.

BP 7.8 Mon 17:15 P3 The influence of stochastic fluctuations on the cyclic dominance of pacific salmon — CHRISTIAN SCHMIDT, CHRISTIAN GUIL, and BARBARA DROSSL — Institut für Festkörperphysik, TU Darmstadt

The four-year oscillations of the number of spawning sockeye salmon that return from the ocean to their native lake within the Fraser River basin in Canada are a striking example of population oscillations. A recently introduced three-species model for these fish, their predators and their prey, was able to reproduce the four-year oscillation as a stable attractor of the dynamics. This model describes the population dynamics in the lake between spring and fall by coupled differential equations, while the survival of the adult salmon in the ocean and the resulting initial condition in the lake at the beginning of each season are modeled by a discrete map. Since the sockeye populations are subject to various types of fluctuations due to the many factors affecting the parasitic and survival, we investigate now the robustness of the model under several types of noise. In particular, we evaluate the frequency of phase shifts in the four-year oscillation, and the extent of synchronization between different sockeye populations.

BP 7.9 Mon 17:15 P3 Phase transitions in competitive foraging of bats — PIA BACKMANN and ALEXANDER K. HARTMANN — Universität Oldenburg

Foraging of animals is driven by competition, hence it can be seen as complex system of interacting individuals. Each animal has the aim to increase its profit by developing different foraging strategies.

We use an Individual Based Model to optimize the competitive foraging of bats feeding from nectar - a renewable resource - by improving the bats’ ability to perceive, if the individual profit of a flower is high or not.

It shows, that a higher notice of flower quality yields to applying different foraging strategies and thus to individually and globally better harvesting results.

We use the Kullback-Leibler-Divergence to show that the more foraging is optimized, the more do bats divide their habitat into territories, several of each bat, so the intersection in resources is lower and flower-visits more efficient.

We find a phase transition between a solvable and a not-solvable phase for finding a given target amount of nectar. By applying finite-size scaling we find the critical exponent υ = 1.9(3) describing the growing correlation when approaching the phase transition.

BP 7.10 Mon 17:15 P3 Age dependent branching in phylogenetic trees — STEPHANIE KELLER-SCHMIDT1, MURAT TUGRUL2,3, VICTOR M. EGUILUZ4, EMILIO HERNANDEZ-GARCIA5, and KONSTANTIN KLEIN1 — 1Dynamical Systems Group, Loughborough University, UK — 2ISC, Palma de Mallorca, Spain — 3IST Austria, Klosterneuburg, Austria

The evolutionary diversification of biological species is a branching process reconstructed as phylogenetic trees. According to analysis of large databases (TreeBase and PANDIT), these trees have a shape (systematic imbalance) not explained by a process of uncorrelated branching events. Here we introduce the age model where the branching probability of a node (species) is inversely proportional to the time since the node was last involved in speciation. We find that the scaling of the average number of ancestors (called depth d) with total number of species n scales as d ∼ ln(log n)2. This result is in agreement with the scaling observed by exhaustive analysis of the databases Treebase and Pandit. Compared with a previously suggested model [1], the age model yields larger likelihood values on the trees in the databases with up to 20 leaves (where exact likelihood computation is feasible).

The Influence of local Symmetries on the Properties of large Complex Systems — HELGE AUFDERHEIDE, LARS RUDOLF, and THILO GROSS — MPI-PKS, Dresden, Germany

The stability of large complex systems is a topic of intense scientific research. In this work, we investigated topological properties of their graph representations. In particular, we focused on local symmetries, called orbits, whose properties were connected to those of the whole network by applying results from graph theory. A powerful tool to study stability in this context is the generalized models approach, which can be used to study asymptotic stability properties of complex systems without being limited to the specific functional forms of a model. Combining graph theory arguments with generalized model, we investigated the example of trophic food webs. Thereby we were able to establish a link between the occurrence of local symmetries and stability on the global level.

Winning the marathon. Multiplayer games at the mutation-selection equilibrium — CHAITANYA GOKHALE and ANNE TRAULSEN — Research Group for Evolutionary Theory, Max-Planck-Institute for Evolutionary Biology, August-Thienemann-Str. 2, 24306 Plön, Germany

Evolutionary game theory is an abstract and simple, but very powerful way to model evolutionary dynamics. Even complex biological phenomena can sometimes be abstracted to simple two-player games. But often, the interaction between several parties determines evolutionary success. In these cases, one can resort to multiplayer games, which are inherently more complicated than two-player games, yet can yield simple results. Another important evolutionary force is mutational success. In these cases, one can resort to multiplayer games, multiple strategy system in the mutation-selection equilibrium. We obtain the average frequencies of the strategies at this equilibrium. The result is a simple expression which can be obtained by recursions using coalescence theory [3]. This approach can be modified to suit a variety of contexts, e.g. to find the equilibrial frequencies of a finite number of alleles in a polymorphism or the equilibrial frequencies of different strategies in a social dilemma in a cultural context.


Interaction Dynamics of Colloidal Particles in Scanning Line Optical Tweezers — BENJAMIN TRÄNKLE and ALEXANDER ROHRBACH — Lab for Bio- and Nano-Photonics, University of Freiburg, Germany

Inter-particle distances are of vital importance for the accomplishment of biological processes, e.g. the fusion of vesicles or drug delivery. Here, the vesicle motions are confined by compartments inherent to the cell structure and also determined by physical interactions, i.e. hydrodynamic and entropic forces. We mimic the biological system by observing the diffusive modes of silica spheres in an elongated potential, which is generated by an oscillating optical trap. The particle positions in 3D are obtained by back focal plane interferometry. Scanning frequencies up to 10 kHz and a spatial precision in the nanometer range are achieved. Our model system allows the particles to get in close contact to one another due to Brownian position fluctuations. Thus pair interactions and dynamics of microspheres can be investigated, e.g. by analyzing the particle trajectories in terms of correlated and anti-correlated motions. Here, the characteristic timescales, i.e. the interaction times are impaired by the shape and stiffness of the trapping potential. We use an acousto-optic deflector to control the laser intensity and hereby vary the trap properties in a broad range. This enables the study of different aspects of particle dynamics.

Evolution in Group-Structured Populations — JONAS CREMER, ANNA MELBINGER, and ERWIN FREY — Arnold Sommerfeld Center for Theoretical Physics, Department of Physics, Ludwig-Maximilians Universität München

Populations of microbial organisms show a very versatile evolutionary behavior. One very important factor co-determining the evolutionary dynamics is the structure of the population in a complex environment. In fact, the evolutionary outcome in highly structured populations can strongly alter from well-mixed ones; different sub-populations can evolve almost separately, only in weak contact to each other. Here, we study the evolution of cooperation in a population regularly forming new sub-colonies. While, due to their metabolic costs, cooperative traits have a selection disadvantage within each group, groups with a higher level of cooperation grow faster. As we show, there are two distinct evolutionary mechanism which allow for both, the evolution and maintenance of cooperation.

Supertree construction using superparamagnetic clustering — PASCAL FIRTH1,2, ALEXANDER K. HARTMANN1, and OLAF R.P. BININDA-EMONDS2 — 1Institute of Physics, University of Oldenburg 2Department of Biology and Environmental Sciences, University of Oldenburg

Superpamagnetic clustering [1] is a non-parametric clustering method for a set of data points using the Potts model with a suitable distance definition. In a numerical simulation [2] of the data points represented as spins in a thermodynamic system, regions of aligned spins, corresponding to clusters, are detected. Here, this method is used for supertree construction, a phylogenetic approach to merge phylogenetic trees only according to their tree topologies, so that overlapping rather than identical taxon sets are needed [3].

The corresponding distance definition is empirically optimized for the used method. Further the dependency of the quality of the reconstruction of a known tree on the size and number of the used source trees is analyzed.


Investigating intrinsic fluctuations in biochemical systems — JOSEPH CHALLENGER1, JUERGENV PAILLE2, ALAN MCKANE1, and PEDRO MENDES2 — 1School of Physics and Astronomy, The University of Manchester, Manchester, UK — 2School of Computer Science, The University of Manchester, Manchester, UK

Mathematical models of biochemical reaction systems are usually constructed from deterministic rate equations. However, this approach is not appropriate when the number of molecules involved is low. Here the underlying stochasticity present in the system becomes important.

The rate equations treat the molecular concentrations as smoothly varying functions. In this talk, a master equation approach is used, where the system is described by discrete states, namely the molecular populations of the chemical species involved. In the mean field limit the rate equations can be recovered. In addition to this, leading order corrections to the rate equations can be obtained by using the system-size expansion due to van Kampen.

We have incorporated these results into COPASI, a software package designed to simulate and study biochemical reaction systems. This allows the expansion procedure to be automated. Once the reaction system has been described, COPASI can calculate the covariance matrix associated with the fluctuations exhibited by the chemical species present in the system. We give examples of the application of the method to biologically relevant systems.

Carpets of chiral motors — MARIA STREMPPEL1,2, SEBASTIAN FÜRTHHAUER1,2, STEPHAN W. GILLI2, and FRANK JÜLICH1 — 1Max Planck Institute for the Physics of Complex Systems, Dresden — 2Max Planck Institute of Molecular Cell Biology and Genetics, Dresden

We study the flows and stresses emerging in a two-dimensional arrangement of chirally beating cilia close to a surface using a continuum theory for active polar fluids, including chiral terms. Our theory is generic, as it is based on conservation laws and the symmetries of the system. Considering the force and torque balance in the thin interfacial layer close to the surface, we identify a novel chiral friction term which is proportional to the cilia local rotation rate. This term is generic to the difference of the forward and the backward stroke of the tilted cilia. Our generic approach allows us to relate the vorticity of the emerging flow to the local rotation rate of the cilia. Furthermore we confirm that in an arrangement of tilted cilia, the chiral symme-
tory of the emerging flow is broken. Such symmetry breaking flows are observed in experiments on Kupfers vesicle in the zebrafish and the ventral node of mouse embryos and seem to play an important role in left-right symmetry breaking of the vertebrate body.

BP 7.18 Mon 17:15 P3
Active chiral fluids — Sebastian Fürthauer 1,2, Stephan W. Grill 1,2, and Frank Jülicher 1
1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Max Planck Institute of Molecular Cell Biology and Genetics

Dynamic cellular processes such as cell division and cell motility rely on the cytoskeleton, a meshwork of polymer elastic filaments. Motor proteins provide active crosslinking between these filaments and every internal force in the network as they consume a chemical fuel (ATP). We extend previous continuum descriptions of active gels in the hydrodynamic limit to take into account active chiral effects. Such chiral effects stem from the chirality of motor-filament interactions and are for example very prominent in the chiral beat of cilia. We derive generic constitutive equations for a chiral active fluid. Our theory can describe very prominent in the chiral beat of cilia. We derive generic constitutive equations for a chiral active fluid. Our theory can describe generic behaviors on large scales in active chiral systems ranging from chiral swimmers to the collective motion generated by cilia that beat on surfaces.

BP 7.19 Mon 17:15 P3
Evolution of increasingly complex molecules — Philipp Zimmer 1, Christian Lay 2, Eva Wollrab 3, Albrecht Ott 2, and Karsten Kruse 1—3
1Universität des Saarlandes, Theoretische Biologische Physik, Postfach 151150, 66041 Saarbrücken — 2Universität des Saarlandes, Biologische Experimentalphysik, Postfach 151150, 66041 Saarbrücken

Biological evolution started at the level of molecules. A long standing aim is to identify conditions under which molecules of increasing complexity can emerge. Such a process must necessarily be out of thermodynamical equilibrium. We consider a simple case, where the complexity of a molecule is given directly by its length. Starting from a fixed number of identical subunits, we consider two processes that can lead to molecules of increasing length: assisted and spontaneous catalysis. Assisted catalysis is achieved when the head-to-tail conformation of two molecules is stabilised by pairing these molecules with a third molecule. We find that below a critical rate of spontaneous catalyses, the system produces ‘islands’ of increasing complexity. We suggest that this situation can be realized experimentally using palindromic DNA sequences and ligases.

BP 7.20 Mon 17:15 P3
Protocells: From a Closed to an Open System — Hans Kubitschke and Claus Fütterer
1Institut für Experimentalphysik I, Universität Leipzig, Linnéstraße 5, 04009 Leipzig

Nutrition and energy management is crucial for preventing an early protocell to run into the thermodynamic equilibrium with lethal consequences. But cell membranes per se are impermeable to many required molecules and hence a controlled passage possibility for nutritive substances as amino acids or nucleotides has to be realized to escape starvation. How this is accomplished is not only an indispensable element of the development of the first cells but also a surprisingly simple but very sensitive (since amplification due to feed-back is involved) bioreactor suited for high throughput screening of the properties of all components: transcription apparatus, membrane pore, phospholipids, co-expressed other proteins. The system can be used to measure processing rates of enzymes, flux and effective diffusion coefficients membrane pores. Noireaux and Libchaber published experimental results in 2004 integrating a transcription apparatus into a vesicle expressing pores getting spontaneously inserted into the vesicle membrane. This work inspired our basic model describing the dynamics of pore proteins and the transcription dynamics, which we present here. The set of ordinary non-linear differential equations balance membrane pore generation due to gene expression, allowing to keep metabolism alive, against its degradation due to blockage or chemical destruction. Integration of other properties allows to extend the model conveniently to various other assays.

BP 7.21 Mon 17:15 P3
Tuning a gene oscillator — Ernesto M. Nicola 1, Saul Aires 2, and Luis G. Morelli 1,2
1IFISC (CSIC-UIB), Campus Universi-
tat Illes Balears, E-07122 Palma de Mallorca, Spain — 2Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 3Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

Self regulatory elements are a fundamental component of cellular control systems. These elements can regulate their own abundance through closed feedback loops. A pure negative feedback loop can result in oscillations on the levels of gene products, while a positive feedback may lead to multi-stability. Recent work has recognized that systems of gene switches combining both positive and negative feedback loops can be very robust oscillators, offering the possibility to tune the frequency of the oscillations without affecting their amplitude. In this contribution we propose a family of simple models that combine positive and negative feedback loops. We perform a detailed study to determine the conditions which ensure tunability. Our analysis of this generic models reveals general principles underlying the tunability of oscillations.

BP 7.22 Mon 17:15 P3
How is the timing of cell division influenced by variation in temperature? — D. Bertran-Vázquez 1, Abigail Klopfer 1, 2, Maria Begasse 2, and Stephan Grill 1,2
1Max Planck Institute for the Physics of Complex Systems — 2Max Planck Institute for Molecular Cell Biology and Genetics

Accurate timing of early embryogenesis is crucial for the development of an organism, and is subject to sensitive dependence on fluctuations in temperature. We investigate the correlation between timing and temperature using C. elegans as a model organism, which benefits from having early cell divisions and an inability to maintain a constant body temperature independent of ambient conditions. We propose a simple model which attributes an observed Arrhenius temperature dependence to the combined dependence of individual chemical reactions involved in the cell cycle. We question whether the experimental results are best explained by just one limiting chemical reaction, as suggested in previous studies, or by a more complex sequence of reactions that function in synchrony. We compare the temperature dependence of C. elegans and C. briggsae, two closely related organisms known to differ in their optimal temperature range.

BP 7.23 Mon 17:15 P3
Traveling Waves in Strong-Noise Reaction-Superdiffusion Systems — Marc Szoj 1, Oscar Hallatschek 2 — Biophysics & Evolutionary Dynamics Group, MPI for Dynamics and Self-Organization, Göttingen, Germany

Traveling waves resulting from reaction and diffusion of particles describe a wide range of phenomena like epidemic waves, range expansions of populations or the dispersal of a chemical concentration. In systems of discrete particles, number fluctuations are inevitable and significantly affect the velocity and shape of such traveling waves. Here we investigate the effect of anomalous diffusion on noisy traveling wave solutions of the Fisher-Kolmogorov equation. Instead of a regular random walk, particles perform scale free Lévy Flights leading to long-range migration. Latter concept has proven to successfully describe the dynamics of human travel [1] and can also be applied to expanding populations in the context of biological evolution. While this problem has already been studied in the regime where number fluctuations are small [2], we discuss here the case of strong noise. We analyze the dependence of the wave velocity on the Lévy exponent and noise strength. Our results show considerable differences to the weak noise regime. We confirm our analytical results with detailed simulations.


BP 7.24 Mon 17:15 P3
Microbial Stain Effect — Christopher J. Seedig 1, Oscar Hallatschek 2 — Biophysics & Evolutionary Dynamics Group, MPI for Dynamics and Self Organization, Göttingen, Germany

Droplets of colloidal suspensions leave annular patterns after drying on solid surfaces [1]. This phenomenon is commonly observed in coffee stains, therefore the underlying effect has been termed coffee stain effect. If the suspended colloids have two different sizes, the coffee stains therefore the underlying effect has been termed coffee stain effect. If the suspended colloids have two different sizes, the coffee stains can be very robust oscillators, offering the possibility to tune the frequency of the oscillations without affecting their amplitude. In this contribution we propose a family of simple models that combine positive and negative feedback loops. We perform a detailed study to determine the conditions which ensure tunability. Our analysis of this generic models reveals general principles underlying the tunability of oscillations.

tion of the final colony. We quantify this "selection advantage" as a function of important control parameters, such as cell size difference or cell density. We argue that the microbial stain effect may play an important role in molecular biology, as it occurs on a daily basis in most modern bio-labs.


BP 7.25 Mon 17:15 - P3
Construction of Phylogenetic Trees Using a Clustering Approach — •Johannes Josef Schneider1, Thomas Bukur2, and Antje Krause2 — 1Department of Physics, Mathematics, and Computer Science, Johannes Gutenberg University of Mainz, Staudinger Weg 7, 55099 Mainz, Germany — 2Fachhochschule Bingen – University of Applied Sciences, 55411 Bingen, Germany

Recently, we introduced an extension of the Traveling Salesman Problem which we coined Traveling Salesman Problem with Clustering [1]. In this extension, the constraint that nodes close to each other should be visited contiguously in the tour is added to the original problem, thus minimizing the overall tour length and generating clusters in parallel. In this talk, we demonstrate how this approach is adopted to the problem of constructing phylogenetic trees, defining the distances between various species with the overlap between them. 


BP 8: Posters: Protein Structure & Dynamics

Location: P3

BP 8.1 Mon 17:15 - P3
Conformational Adsorption Reaction of BSA on the Surfaces of Nanosilica and Nanodiamond — •Victor Wei-Kem Wu — Department of Chemical and Materials Engineering, National Kaohsiung University of Applied Sciences(KAUS), 80782 Kaohsiung City, Taiwan — Victor Basic Research Laboratory e. V.(VBR)

From the fluorescences (excitation at 280 nm) of BSA of 0-10000 mM in 7 mM PPBS at pH=4.70 before and after adsorption reactions on the surfaces of nanosilica(NS) and nanodiamond(ND) of diameter 100 nm as suspension solutions(50µg/20µL), the adsorption thresholds, reaction constants as well as coverages have been obtained. Adsorption thresholds were located at 150 nM for both systems. The adsorbed BSA were 420 mg for two particles in g; 28.0 and 7.64 mg, on unit surfaces of NS and ND, respectively. Adsorption constants 1.2x10^7 and 6.5x10^7 (nM)^-1 for systems BSA-NS and BSA-ND, respectively, have been obtained. Comparing with the respective constants 1.2x10^7 and 6.5x10^7 for systems lysozyme-NS and lysozyme-ND, the biomolecular conformations as well as behaviors are different. The spatial fitting between depression or hole on the nanosurface as carrier, and dimension of the protein with significant activity should also be considered, besides the charge-charge interactions between the surface and protein, and among the proteins. Financial aids by groups 510 and NB11 of IAMS, Taipei, and VBR, Bielefeld; support with Fluorescence Spectrophotometer F-4500 FL, Hitachi, Japan, by KUAS are acknowledged. Ref. V. W.-K. Wu and F. Kure, Chin. J. Chem. 28 (2010).

BP 8.2 Mon 17:15 - P3
L-edge X Ray Spectroscopy Revealing Structure and Dynamics of Metalloprotein Active Centers — •Kathrin Maria Lange1, Ronny Golnak1, Sebastien Bonhommeau2, and Emad Flear Aziz1,3 — 1Helmholtz-Zentrum Berlin für Materialien und Energie, Albert-Einstein-Str. 15, 12489 Berlin — 2Institut des Sciences Moléculaires, UMR 5255 CNRS, 351 cours de la Libération, 33405 Talence Cedex, France — 3Freie Universität Berlin, FB Physik, Arnimallee 14, D-14195 Berlin, Germany

Reactions catalyzed by metalloproteins occur at their active centre, accordingly determining its electronic structure allows drawing conclusions about the protein function. We revealed for the first time the electronic structure of metalloproteins in physiological media using L-edge X-ray absorption spectroscopy on the iron active centre.1 By comparing the electronic structure of haemoglobin and catalase, the origin of the high enzymatic activity of catalase could be revealed.2 Furthermore the preferential ligation of myoglobin was investigated recently.3 The electronic structure of its iron active centre upon binding to O2, CO, CN and NO were compared to the reduced form and the electronic structure of its iron active centre upon binding to O2, CO, CN and NO were compared to the reduced form and the oxidized form of low-spin hemoglobin.3 The presence of an inhibitor changes the Rigidity of such systems.


BP 8.3 Mon 17:15 - P3
Effect of thermostating and electrostatics on the wildtype LOV1 domain of phototropin and its mutants — •Emmanuel Peter, Bernhard Dick, and Stephan A. Barzinger — Fakultät für Chemie und Pharmazie, Universität Regensburg, 93040 Regensburg, Deutschland

Phototropins are blue-light photoreceptors in plants and algae, which consist of 2 LOV-(light oxygen voltage sensitive)-domains and 1 kinase domain. Each LOV-domain contains a noncovalently bound flavin-mononucleotide-(FMN)-chromophore, which after absorption of blue light at around 450 nm undergoes a photoreaction with a cysteine-residue attached to an apoprotein, inducing a signal in the organism via the kinase-domain. Both the signal transduction as well as the mechanism of the photoreaction of these domains are still only poorly understood. In this presentation we show results of molecular dynamics simulations, where we investigated the effect of electrostatics and thermostating on the solution structure and dynamics of signal transduction of the LOV1-domain. We compare the calculation results with various experimental data and demonstrate that these computational issues have an important influence on the equilibrium and time behavior of such systems.

BP 8.4 Mon 17:15 - P3
Anomalous diffusion of oligomerized transmembrane proteins — •Ulrich Schmidt1,2 and Matthias Weisz1,3 — 1Cellular Biophysics Group, German Cancer Research Center, c/o BIOQUANT, Im Neuenheimer Feld 267, 69120 Heidelberg — 2Laboratory for Computational Cell Biology, Department of Cell Biology, Harvard Medical School, Boston, USA — 3Experimental Physics I, University of Bayreuth, 95440 Bayreuth

Transmembrane proteins frequently form (transient) oligomers on biomembranes, e.g. while participating in protein sorting and signaling events. Using coarse-grained membrane simulations we show here that transmembrane proteins show a subdiffusive motion on short time scales when being part of a linear oligomer, i.e. a flexible polymer, embedded in a two-dimensional membrane. Our results are in agreement with previous experimental observations. They further indicate that polymers of transmembrane proteins are well described by predictions from Rouse theory in two dimensions even in the presence of hydrodynamic interactions.
extent to which the protein is able to move in these directions.

Investigation of self-assembled desmin filament networks by atomic force microscopy — Mareike Dieding1, Volker Walhorn1, Andreas Brodeh2, Hendrik Metzing2, and Dario Anselmetti1 — 1Experimentelle Biophysik und Angewandte Nanowissenschaften, Fakultät für Physik, Universität Bielefeld, Universitätsstr. 25, D-33615 Bielefeld — 2Hertz- & Diabeteszentrum NRW, E. & H. Klessmann-Institut fuer Kardiovaskuläre Forschung und Entwicklung, Georgi, 11, D-32254 Bad Oeynhausen.

Arrhythmogenic right ventricular cardiomyopathy (ARVC) is an inherited heart disease, primarily accompanied by sudden cardiac death and terminal heart failure. Various point mutations in the intermediate filament desmin are potential candidates for the trigger factor. Desmin serves as a mechanical integrator of neighboring Z-discs in the sarcomere and also as an important structural component of the intercalated disc by binding to desmosomal plaque proteins.

We investigated the self-assembled desmin filament network structure by means of atomic force microscopy (AFM) under ambient conditions in topographic experiments. We were able to reveal various mutation specific structural defects in the desmin network. Our in vitro results are supporting additional in vivo confocal laser scanning microscopy (CLSM) studies of desmin-transfected cells.

Winklæbbningselige Ramanspektroskopie an Photosystem-II-Kristallen — Georg Bens1, Katharina Broise1, Athina Zouni1 and Janina Maultzsch1 — 1Forschungszentrum Jülich, Institut für Physikalische und Theoretische Chemie, D-52425 Jülich, Germany.

The ability of DNA as a material for bottom-up approaches has been recognized for some time, but only a few scientific publications have been dedicated to this research field. The basic idea is to use Watson-Crick base pairing which is unstable upon heating. We developed a new method to synthesize thermostable 2D and 3D DNA nanostructures by connecting DNA building blocks, so called tiles. Most of these methods have some exceptions, the principle behind such DNA self-assemblies is the hybridization of complementary sequences through Watson-Crick base pairing which is unstable upon heating. We developed a new method to synthesize thermostable 2D and 3D DNA nanostructures by connecting DNA building blocks.
single-stranded DNA (ssDNA) parts via covalent bonds. In order to demonstrate this approach, we used a ssDNA circle that contained four different internal modifications on its poles. These circles were cross-linked via the formation of covalent bonds with a ssDNA molecule that includes a modification on its 3' and 5' ends. We performed experiments using a circle with four amine functionalities and alternatively a circle, that contained thiol and amine functionalities at its opposite poles to yield DNA nanotubes. The single-stranded approach makes those structures suitable to guide patterning of nanoparticles, proteins and transition metals. Furthermore, the stability upon heating gives an outstanding erase/rewrite functionality, providing the possibility of a controlled release of the attached nanomaterials.

Die räumliche Synthese und Kodierung der DNA-Doppelhelix — Norbert Sadler — 85540 Haar; Wasserburger Str. 25a


Information transfer and readout in complex DNA mixtures — Harsh Borkasam and Albrecht Ott — Institute for Biological Experimental Physics, University of Saarland, Saarbruecken, Germany

Project: Development of an enzyme based method for the copy of oligos with predetermined length form biological template, given knowledge of the therein contained oligonucleotide sequence.

In this project, we modify the conventional PCR technique by using single primers to generate linearly amplified copies of single stranded oligos. This way the timescale of temperature cycle, which determines the length of the transcribed sequence is easier to control.

Results & Discussion: We find that single stranded DNA oligos of length b/w 400bp-200bp can be generated using this method. In order to determine the accuracy of the method the ssDNA is hybridised on a DNA coated surface with complementary oligos. We have shown that the time course of the hybridisation is almost identical to an error free sequence. This suggests the fidelity of the transcription.

Conclusion: Our method has given very promising results so far. Currently we are performing experiments along two lines: 1) Validate our technique by transcribing single DNA sequences from a complex mixture. 2) Testing a different enzymes and polymerases for isothermal amplification and controlled extension of primers into short oligos. This will further improve the yield and also narrow the length distribution of the obtained products.

A Probabilistic Polymer Model for Mitotic Chromosomes — Yang Zhang and Dieter W. Heermann — Institute for Theoretical Physics, Heidelberg University, Heidelberg, Germany

Despite many years of extensive studies the structure of the mitotic chromosome still remains unclear. The present work introduces a new probabilistic polymer model for mitotic chromosomes. The key assumption of the model is the ability of the chromatin to associate to crosslink to itself due to the dynamic binding of proteins to the fiber. These protein-chromatin interactions were included by a probabilistic and dynamic mechanism. This is motivated by the observation of high repulsive forces between ring polymers. Computer simulations were performed to examine the validity of the model. Our results show that the presence of loops leads to a tight compaction and contributes significantly to the bending rigidity of chromosomes. Moreover, its qualitative prediction of the force elongation behaviour are close to experimental findings. The dynamic loop model indicates the crucial role of loops in mitotic chromosomes and a strong influence of their number and size on the mechanical properties. This shows that changes of these mechanical characteristics under different conditions can be explained by an altered loop structure.

Modelling the recruitment of DNA repair enzymes — Gregor Weiss, Daniel Löhr, and Barbara Drossel — Institut für Festkörperphysik, TU Darmstadt

We investigate the recruitment dynamics of repair enzymes during Base Excision Repair (BER) of DNA damage. Our focus lies on the possible competition of the enzyme loading platforms XRCC1 and PCNA in short patch BER. We also include Poly(ADP-ribose)polymerase-1 (PARP-1) in the model, which is indispensable for XRCC1 association with the DNA lesion.

We construct different possible models for the recruitment to DNA damage and dissociation of these three proteins, and perform numerical simulations of the models. In order to decide which models are more realistic, the simulation data are compared to empirical data obtained in living cells obtained using GFP-tagged proteins. Furthermore, these models are used to simulate the effect of protein inhibition, and to obtain more generally a relation between various model ingredients and signatures of the protein recruitment data curves.

Computer simulation of chromatin: Modeling the influence of nucleosome repositioning — Oliver Müller, René Stein, Robert Schöpplin, Ramona Etting, Nick Kepper, Karsten Rippe, and Gerhard Wedemann — University of Applied Sciences Stralsund, 18435 Stralsund, Germany and German Cancer Research Center & BioQuant, 69120 Heidelberg, Germany

The three-dimensional structure of chromatin is a key factor for controlling the DNA accessibility for protein factors, DNA replication and repair. However, it is still subject to extensive research since the interpretation of the experimental data is fraught with difficulties. Several structural models exist, many of which assume a strictly regular fiber. This irregularity implies a highly periodic positioning as well as equal distances the fiber geometry changes significantly. This serves as a tentative explanation for the different effects of repositioning on processes such as DNA transcription.

Dynamics of RNA based transcription control — Michael Faber and Stefan Klumpp — Max Planck Institut für Kolloid- und Grenzflächenforschung Potsdam

Initiation of transcription is the main step at which gene expression is regulated. Bacteria often use a control mechanism called transcription attenuation that is at work immediately after the initiation of transcription. A transcribed sequence between the promoter and the coding region for the gene allows two, mutually exclusive structures the RNA transcript can form. The decision on whether transcription continues or is terminated, is made by choosing one of these structures which are therefore referred to as terminator and antiterminator. In recent years much effort has been expended to characterise such sequences. We have developed a structure-based model for studying the dynamics of RNA secondary structures, in particular, the dynamics of folding and unfolding of such competing structures. To simulate this dynamics of RNA, we use a method with Metropolis rates, which are determined using the same parameters for the energy calculation as in models commonly used in RNA structure prediction like the individual nearest-neighbor model.
Recent genome-wide maps of nucleosome positions in different eukaryotes have revealed a common pattern around transcription start sites, involving a nucleosome-free region flanked by a pronounced periodic pattern in the average nucleosome density. For the yeast S. cerevisiae, a description of the periodic pattern has been established based on the statistical positioning mechanism of Kornberg and Stryer. This description derives from the physics of a dense one dimensional gas consisting of fixed-size particles. Here, we consider 12 Hensincomyotya yeast species, each of which displays a distinct nucleosome pattern. Since the chromatin constituents are highly conserved between species, and thus the mechanism underlying the formation of the patterns is expected to be related, we present a unified quantitative description. We extend the simple one-dimensional gas model account for transient unwrapping of short segments of nucleosomal DNA. Chromatin behavior in the majority of species is well described by this generalized gas model - only the average nucleosome density is a species-dependent variable. An exception is K. lactis, where we find an increased effective nucleosome width (potentially due to an increased use of linker histone H1 in this species). Together, our results provide a biochemically plausible role for nucleosome unwrapping in global chromatin behavior and establish a unified nucleosome gas model, providing a basis for quantitative analysis of chromatin effects on cis-regulatory transcription control.

BP 10: Posters: Tissue Dynamics & Developmental Processes

Time: Monday 17:15-20:00

BP 10.1 Mon 17:15  P3
Entwicklung eines Versuchsauflaufs zur räumlich aufgelösten in-vivo-Messung der viskoelastischen Eigenschaften der humanen Augenlinse — •STEPHAN RESS1, OLIVER STACHES2, RUDOLF GUTTRAU3, and HEINZ-DIETER STOLZ2
1Institut für Physik, Universität Rostock, Rostock — 2Medizinische Fakultät, Augenklinik, Universität Rostock, Rostock — 32055


BP 10.2 Mon 17:15  P3
Novel Magnetic Tweezer with first Applications to Cell and Tissue Stimulation and Rheology — •CLAUS FÖTTERER1, and •CARLO CALDERIRA2,3 — 1University of Leipzig, Faculty of Physics and Earth Science Institute for Experimental Physics I, Soft Matter Physics Division, Developmental Biophysics, Leipzig, Germany — 2Universidade de Lisboa, Faculdade de Ciencias, Departamento de Fisica, Lisabon, Portugal

Studying biological samples with laser tweezers releases cosiderable heat perturbing eventually the sample. AFM requires a cantilever to approach the tip to the object in question. Magnetic fields in contrast do not disturb biological samples at all and it is possible to apply forces directly between superparamagnetic micro and nanoparticles applied to the sample in question without the need of immobilization. These nano and microparticles have been extensively used to measure the visco-elastic properties on the cell membrane plus actin cortex. By switching perpendicular fields we found a new way to assemble those particles to a rich variety of macro-objects and to disassemble them again. 1. We discuss the objects which we found and explain the mechanism of stability. 2. We further discuss applications to study rheology of Hydra Vulgaris tissues in order to find out about the relation of visco-elastic properties and influence of mechanical stimulation onto the symmetry breaking transition during its development. This approach is well suited for high throughput assays in other applications.

BP 10.3 Mon 17:15  P3
Optimal morphogen profiles for combinatorial position determination in the Drosophila embryo — •TIAGO RAMALHO and ULRICH GERLAND — Arnold Sommerfeld Center, Dept. of Physics, Ludwig Maximilians Universität München, Theresienstr. 37 80333 München, Germany

Complex gene transcriptional networks control cell differentiation in the Drosophila embryo, however their behavior depends on the initial concentration profiles of a few morphogens. These morphogens convey positional information by regulating downstream target genes in a combinatorial way. Which combinations of profiles are best suited to accurately determine position anywhere within the embryo? We address this question using established thermodynamic models for combinatorial transcriptional regulation in combination with an optimization procedure based on a quantitative criterion for positional accuracy. We report the optimal profiles for different numbers of input morphogen profiles and discuss our results in the light of the experimentally known profiles for the anteroposterior axis of Drosophila embryos.

BP 10.4 Mon 17:15  P3
Two redundant negative feedback loops in the zebrafish segmentation clock — •Saul Ares1, Luis G. Morell2, Christian Schröter2, Korneli J. I. Hens3, Sebastian J. Maerkl1, Bart Deplancke3, Andrew C. Oates3 and Frank Jülicher4 — 1Max Planck Institute for the Physics of Complex Systems, Dresden — 2Max Planck Institute of Molecular Cell Biology and Genetics, Dresden — 3École Polytechnique Fédérale de Lausanne, Switzerland

Rhythmic processes are widespread in biology and organisms have evolved different mechanisms to control them. The segmentation clock is a transcriptional oscillator that operates during development and organizes the segmentation of the vertebrate body axis. The hes6 gene has recently been shown to control the clock's period. However, its interaction with other components of the clock, as the cyclic genes her1 and her7, is not known. To study the role of hes6 in the zebrafish segmentation clock, we propose a theory of the gene network controlling the expression of cyclic genes her1 and her7. This gene network is motivated by experimental evidence from genetics, yeast one-hybrid and in vitro assays. The theory comprises two distinct, redundant negative feedback loops. One of these loops relies on a Her7/Hes6 heterodimer, and the other on a Her1 homodimer. Intercellular communication is mediated by different Her6 heterodimers and a Her1 protein homodimer. An intriguing finding in our experiments is the rescue of the strong her7 mutant phenotype by further mutating hes6. The theory describes this rescue as an effect of restoring the balance in intercellular communication, which is perturbed in the her7 mutant.

BP 10.5 Mon 17:15  P3
In situ uv/vis spectroscopic imaging of retinal cell degeneration — •Julia Hollmач1, Julia Schweizer1, Gerald Steiner1, Richard H. W. Fuchs2, Lilla Knels2, and Edmund Koch2 — 1Dresden University of Technology, Faculty of Medicine, Clinical Sensing and Monitoring, Dresden, Germany — 2Dresden University of Technology, Faculty of Medicine, Anatomy, Dresden, Germany

In the western world retinal diseases like age-related macular degeneration have become an important cause of visual loss depending on increasing life expectancy and lifestyle habits. Since there is no sufficient treatment, early diagnosis and prevention are the only possibilities to preserve eyesight. The protein cytochrome c (cyt c) is a suitable marker for degeneration processes, because it is involved in the apoptosis pathway. In particular, the local distribution and oxidative state of cyt c are of clinical interest. Cyt c shows two overlapping absorption bands between 500 and 600 nm. Uv/vis spectroscopic
imaging was used to characterize the oxidation state and the distribution of the protein in a layer of retina cells. The major challenge was the separation of molecular information from the scattering signal. Extended Multiplicative Scatter Correction in combination with Principal Component Analysis was performed to separate the signals in order to study spectral variances. After that, multivariate data analysis, cyt c could be identified. The imaging exhibits domains and ‘hot spots’ of cell degeneration processes. The results demonstrate that spectroscopic imaging in conjunction with sophisticated multivariate methods is a suitable tool to characterize degeneration processes under in situ conditions.

BP 10.6 Mon 17:15 P3
An experimental study of basic correlations of human cardiorespiratory system variables — Heike Leuthäuser1, Thorsten Schäffer1, Christian Jeelazon2, Christian Wierand3, and Bernhard Hensel1 — 1Max Schädlich-Stiftungspark für Biomedizinische Technik, Universität Erlangen-Nürnberg — 2Anästhesiologische Klinik, Universitätssklumkinikum Erlangen — 3METEAN, Fraunhofer IIS, Erlangen

The human cardiorespiratory system adapts its regulation parameters continuously to variations of physiological demand. The simultaneous and continuous recording of system variables is a necessary basis for findings of any kind of correlation analysis and the understanding of the cardiorespiratory regulating system. In a experimental trial the most important non-invasively accessible physiological variables have been measured on 10 healthy volunteers during a dedicated exercise protocol. The recordings include ECG, SpO2, etcO2, respiratory mechanics and continuous non-invasive blood pressure. The test record includes the Stroop Test as psychological stress test and several physiological exercises, like paced respiration with breathing rates from 4 to 25 breaths per minute, an active orthostatism manoeuvre, a stress test with a bicycle ergometer and the Valsalva manoeuvre. The recorded data are subject to a variety of algorithms to reveal correlations of the underlying physiological parameters. First results of these investigations are presented. The ultimate goal of the projected work is to derive a cardiorespiratory state parameter that clearly reflects the state of health, respectively fitness, or the progression of disease.

BP 10.7 Mon 17:15 P3
Studying dynamical changes in lung parenchyma by using optical coherence tomography combined with confocal fluorescence microscopy — Maria Gaertner1, Peter Cimalla1, Lilla Knebel2, Sven Meissner1, Wolfgang M. Kuebler1, and Edmund Koch3 — 1TU Dresden, Faculty of Medicine Carl Gustav Carus, Clinical Sensing and Monitoring, Dresden, Germany — 2TU Dresden, Faculty of Medicine Carl Gustav Carus, Department of Anatomy, Dresden, Germany — 3Institute for Physiology, Charité Berlin, Germany and and Department of Surgery, University of Toronto, Ontario

Realistic lung dynamical investigations on the alveolar microscale are hardly obtainable with conventional techniques such as light microscopy of tissue sections, micro computer tomography or magnetic resonance imaging due to preparation artifacts and damages of the sample or insufficient spatial and temporal resolution, respectively. Optical coherence tomography (OCT) as well as intravital microscopy provide noninvasive, high-resolution (μm), real-time (in 2D) imaging, capable of application to in vivo situations. Furthermore, OCT even extends the morphological information to three dimensions by successive recording of real-time two-dimensional cross-sections within a few seconds. As a new approach, the combination of OCT and confocal fluorescence microscopy shall not only provide 3D data of lung tissue but also localization of elastic fibers embedded in the biological structure through visualization of specifically binding fluorophores. Dynamic studies in an ex vivo mouse model allow for an estimation of overall elasticity as well as investigation of fiber rearrangements.

BP 10.8 Mon 17:15 P3
Finite size corrections to scaling behavior in sorted cell aggregates — Gabigal Klopper1,2, Gabby Kirn3, Stephan Ghi1,2, and Carl-Philipp Heisenberg3 — 1Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, D-01187 Dresden, Germany — 2Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 118, D-04103, Leipzig, Germany — 3Institute of Science and Technology Austria, Am Campus 1, A-3400 Klosterneuburg, Austria

Cell sorting is a widespread phenomenon pivotal to the early development of multicellular organisms. In vitro cell sorting studies have been instrumental in revealing the cellular properties driving this process. However, these studies have as yet been limited to two-dimensional analysis of three-dimensional cell sorting events. Here we describe a method to record the sorting of primary zebrafish edctoderm and mesoderm germ layer progenitor cells in three dimensions over time, and quantitatively analyze their sorting behavior and vertex order parameter in relation to the dynamics of the phenotype. We investigate the cell population size distribution of sorted aggregates and find that the germ layer progenitor cells engooled in the final configuration display a relationship between total interfacial length and system size according to a simple geometrical argument, subject to a finite size effect.

BP 10.9 Mon 17:15 P3
Active fluid: cell-substrate adhesion and cell density cooperatively drive and regulate collective cell migration. — Kenechukwu David Nnetu, Melanie Knohr, Dan Streible, Thomas Ehr, Florian Huber, and Joseph Käs — Institut für Experimentelle Physik I, Universität Leipzig, Linnéstr. 5, 04109, Leipzig, Germany

The collective movement of cells is important for physiological processes such as embryogenesis, cancer metastasis and wound healing. Recent studies showed that marginal and sub-marginal cells drive sheet migration by generating traction forces transmitted through cell-cell contacts, while interfacial tension maintains cohesiveness. By studying the dynamics of sheet migration in 3 dimensions, we show for the first time that collectively, cells spread like a fluid with surface tension playing no role in maintaining dynamic collectivity. We observed further that, reductions in cell height and density led to a loss in cohesion. Moreover, in comparison to single-cell migration, neighboring cells add a random contribution to the collective spreading, driving the cells into a ballistic motion. These findings together suggest that on 2 dimensional substrates, cell-substrate adhesion drives sheet migration while cell density and intercellular signaling predominantly regulate collectivity as the monolayer spreads like a fluid.

BP 10.10 Mon 17:15 P3
Biochemical and Mechanical Regulation of Growth in Developing Epithelia — Peter Mucmu1, Ottfrid Waltz2, Marcos González-Gaitán3, and Frank Jülicher1 — 1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Department of Biochemistry and Department of Molecular Biology, Geneva University, Switzerland

Developing tissues possess intrinsic growth control mechanisms that determine the final size and shape. The basic principles of growth regulation are still poorly understood. However, there is a lot of evidence that certain morphogens act as growth factors and play a key role in this process. Morphogens are a special class of signaling molecules that are secreted from localized sources, spread throughout the tissue and form graded concentration profiles. We study growth regulation from a theoretical viewpoint using a two-dimensional vertex model that describes the organization of cells by a network of polymers, including the dynamics of morphogen distributions as additional variables. In this theoretical framework, we can study the consequences of specific growth rules according to which cells divide when subject to relative temporal changes of the cellular morphogen levels. We discuss a scenario that is consistent with experimentally observed growth curves obtained in the fruit fly Drosophila. We also discuss the role of mechanical stresses in this system, which can reduce spatial growth inhomogeneities and the rate of cell death.

BP 10.11 Mon 17:15 P3
Vertex model for planar cell polarity: emergence and reorientation of large scale polarity — Matthias Merkl, Douglas B. Staple, Reza Farhadifar1,2, Benoît Aigouy3, Andreas Sagner3, Suzanne Eaton3, and Frank Jülicher1 — 1Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Germany — 2FAS Center for Systems Biology, 7 Divinity Avenue, Cambridge MA 02138, USA — 3Max-Planck-Institut für molekulare Zellbiologie und Genetik, Pfotenhauerstr. 108, 01307 Dresden, Germany

Epithelia are two-dimensional sheets of cells, which often exhibit large scale patterns of planar cell polarity (PCP) in the tissue plane. Cell polarity is reflected in an anisotropic distribution of a class of proteins, which are referred to as PCP proteins. This work is motivated by results in the Drosophila wing, where during development, large scale reorientation of PCP can be observed. We develop a vertex model in which cells are polygons and the local organization of PCP proteins is described by
variables on all bonds. The PCP dynamics is modeled by an attractive interaction within cells and a repulsive interaction across cell borders. Furthermore, we introduce a coupling between PCP and cell shape. We demonstrate how large scale polarity can arise and we study the effect of pure and simple shear on the reorientation of PCP. We introduce instabilities to the system which are not present in phase descriptions, and were not described by genetic regulatory networks. We find that the amplitude effects of the amplitude of the oscillations in the segmentation clock. Not consider amplitude effects, gene regulatory networks are too complex to draw any general conclusion about them. Here we address the effects of the amplitude of the oscillations in the segmentation clock. We propose a model based on the Complex Ginsburg-Landau equa-
tion. This equation describes an oscillatory medium close to a super-critical Hopf bifurcation, in agreement with accepted gene regulatory network models of the segmentation clock. When the amplitude introduces instabilities to the system which are not present in phase descriptions, and were not described by genetic regulatory networks. These instabilities can lead to distinct regimes, including spatiotem-
poral chaos. Our theory suggests perturbations to developing embryos that could disrupt the behavior of the segmentation clock.

Moreover, we introduce a coupling between PCP and cell shape. We demonstrate how large scale polarity can arise and we study the effect of pure and simple shear on the reorientation of PCP. We introduce instabilities to the system which are not present in phase descriptions, and were not described by genetic regulatory networks. We find that the amplitude effects of the amplitude of the oscillations in the segmentation clock. Not consider amplitude effects, gene regulatory networks are too complex to draw any general conclusion about them. Here we address the effects of the amplitude of the oscillations in the segmentation clock. We propose a model based on the Complex Ginsburg-Landau equa-
tion. This equation describes an oscillatory medium close to a super-critical Hopf bifurcation, in agreement with accepted gene regulatory network models of the segmentation clock. When the amplitude introduces instabilities to the system which are not present in phase descriptions, and were not described by genetic regulatory networks. These instabilities can lead to distinct regimes, including spatiotem-
poral chaos. Our theory suggests perturbations to developing embryos that could disrupt the behavior of the segmentation clock.
We used SFM based SMFS [2] to measure interaction forces between mono- and multivalent coordination compounds of pyridine nanorods with different metal salts such as Zn(NO₃)₂ and CuSO₄ in aqueous solutions. Force-distance measurements were performed over a broad range of loading rates to estimate associated binding properties according to the Bell-Evans model [3]. In combination with computational calculations of the bond dissociation under force we propose different rupture mechanisms of the divalent complexes with Copper and Zinc. Our model system can be extended to various geometries and therefore provides essential knowledge about geometrical factors influencing multivalency.


BP 11.5 Mon 17:15 P3
High-Resolution Scanning Near-Field Optical Microscopy of Dye Labelled Single Tobacco Mosaic Viruses — ALEXANDER HARDEN1, SVEN DEGENHARD2, FABIAN EBER2, FANIA GEIGER3, JOACHIM SPATZ4, HOLGER JESKE5, CHRISTINA WERCK5, and DARIO ANSIELMETTI6 — 1Experimental Biophysics & Applied Nanoscience, Bielefeld University, Germany — 2Molecular Biology and Virology of Plant, Stuttgart University, Germany — 3Max Planck Institute for Metals Research, Stuttgart, Germany — Technische Universitaet Muenchen, Physik Department, Garching, Germany

Scanning near-field optical microscopy (SNOM) is a fluorescence microscopy technique achieving optical resolution of better than 20 nm by means of strongly confined non-propagating electromagnetic fields. We investigated dye-labelled single Tobacco mosaic viruses (TMV) with apertureless SNOM by using standard Si-AFM tips illuminating their apex with a focused laser beam. Our home-built SNOM device system additionally allows simultaneous atomic force microscopy (AFM) tapping topographic measurements [1]. In the future concurrent high structural and optical resolution will allow the investigation of virus orientation as well as site-specific immobilization that is prerequisite for possible bioengineering applications of TMV based channels.

BP 11.6 Mon 17:15 P3
Friction dynamics of peptides at polar and non-polar surfaces — AVYKT ERBAS, DOMINIK HORNIEK, and ROLAND R. NETZ — Technische Universitaet Muenchen, Physik Department, Garching, Germany

The friction forces and mobilities for the c₄₈ spider silk and various peptides on polar and non-polar surfaces are investigated using molecular dynamics simulations. For both surfaces, the velocity dependence of the monomer mobility is determined and interpreted with non-linear analytical models. The obtained diffusion coefficients are in good agreement with experiments. It is concluded that the reason for the high friction forces on polar surfaces is hydrogen bonding. It is further shown that each hydrogen bond contributes equally to the total friction force, independent of the concentration of surface-polar groups or the type of amino acid.

BP 11.7 Mon 17:15 P3
Single-Molecule Force Spectroscopy Binding Studies of DNA Recognition by Transcription Factor Epitopes — ADIELINE BIEKER1, VOLKER WALKHORN1, GEZA NIEMANN2, MARKUS RITZFELD2, NORBERT SELWALD2, and DARIO ANSIELMETTI3 — 1Experimental Biophysics and Applied Nanoscience, Universitaet Bielefeld, Deutschland — 2Organic and Bioorganic Chemistry, Universitaet Bielefeld, Deutschland

Interactions between proteins and DNA are essential for the regulation of cellular processes in all living organisms. In this context, it is of special interest to investigate and quantify the sequence-specific molecular recognition between peptidic transcription factors and their cognate DNA sequences [1].

We investigated protein epitopes and peptides originating from the DNA-binding domain (DBD) of the Escherichia coli transcription factor PhoA. The base-stabiliised single molecule Force Spectroscopy (SMFS) we investigated the specific binding forces and molecular elasticities to elucidate the DNA-protein complex stability. Based on the Bell-Evans Model [2] we estimated the thermal dissociation rate constants \( k_{off} \) and the molecular interaction length \( x_{ij} \), that allowed a structure related interpretation of the physical binding mechanisms involved.

BP 11.8 Mon 17:15 P3
Permeation through nanochannels: Revealing fast kinetics


BP 11.9 Mon 17:15 P3
Stochastic reconstruction of interactions within protein complexes from single-molecule force spectroscopy — MAGNUS SCHWÖREN and ULRICH GERLAND — Arnold Sommerfeld Center for Theoretical Physics, LMU München, Munich, Germany

Dynamic Force Spectroscopy is a well-established technique where a pulling force is applied with a certain rate of loading to probe the (un)folding of biomolecules or the interaction between two biomolecules. The technique typically permits to extract information such as the barrier height and distance to the transition state, and ideally even the entire free energy landscape along the reaction coordinate of this process. Here, we explore theoretically which information could be obtained when this technique is applied to macromolecular complexes. Specifically, we consider the subsequent application of dynamic force spectroscopy to all pairs of constituents within such a complex, and test to which extent the interactions between the constituents can be reconstructed. Our analysis is based on a simple toy model.

BP 11.10 Mon 17:15 P3
Stochastic enzymatic reactions with spatially arranged enzymes — FABIENNA ARENDT, ALEXANDER BUCHNER, and ULRICH GERLAND — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München

To efficiently catalyze multi-step biochemical reaction pathways, cells have optimized the synergistic action of a multitude of enzymes. Not only do they carefully control the concentrations and activities of enzymes as a function of the external conditions, but in many known cases cells also coordinate the enzymes that catalyze different steps in the same biochemical reaction pathway by arranging them in self-organized multi-enzyme complexes. In these complexes the enzymes of several types are localized on well-defined spots. So far, the theoretical study of these systems has focused on the deterministic level. Here, we investigate the behaviour of spatially arranged enzymes in different configurations including stochastic effects.

BP 11.11 Mon 17:15 P3
Coronavirus nsp7-nsp8 complex formation investigated by single-molecule methods — HEINRICH SHIDEL1, YIBEI XIAO2, ROLF HILGENFELD3, and CHRISTIAN G. HUBNER1 — 1Institute of Physics, Ratzeburger Allee 160, 23562 Lübeck, Germany — 2Institute of Biochemistry, Ratzeburger Allee 160, 23562 Lübeck, Germany

The self-organized structure building capabilities of proteins are fascinating biophysicists since decades. With the advent of single-molecule methods, namely fluorescence correlation spectroscopy (FCS) and fluorescence resonance energy transfer (FRET), the process of complex formation is becoming accessible to direct observation.

Coronaviruses are enveloped positive-stranded RNA viruses. For SARS-CoV, it was shown that coronaviruses encode a RNA-dependent RNA-polymerase (RdRp) build from non-structural protein 7 (nsp7) and non-structural protein 8 (nsp8). This hexadecameric nsp7-nsp8 complex is a hollow, cylinder-like structure assembled from eight copies of nsp7 and held together by eight nsp7 molecules. We are aiming at understanding the assembly process and conformational changes of the complex for the related Feline Coronavirus. The structural and functional examination of the nsp7-nsp8 complex formation should help in...
understanding the replication and transcription mechanisms of Fe-CoV and other coronaviruses like SARS-CoV.

**BP 11.12** Mon 17:15 P3
Hydrodynamic Interaction destabilizes soft bonds. — **Suman Das**, Dimitri Peschla, Mithun Biswas, and Anirban Saha.

**BP 11.13** Mon 17:15 P3
A theoretical description of the 3D orientation determination of dipoles near interfaces — Richard Börner and Christian G. Hübner.

**BP 12.1** Mon 17:15 P3

**BP 12.2** Mon 17:15 P3
Biocompatibility of single crystalline Fe70Pd30 ferromagnetic shape memory films for cell activation — Mareike Zink, Yanhong Ma, and Stefan Mavlyanov.

**BP 12.3** Mon 17:15 P3
Photobleaching higher Order - ein eng mit intrazellulärer Ablation verbundener Low-Density Plasma Prozess — Stefan Kalies, Kai Kühtemeier, and Alexander Heisterkamp.

The strong excitonic coupling is not an important factor in the fast excitation energy transfer in phycocyanin of A.marina. — Albert Collins, Ngaoue Assongkeng.

The Cyanobacterium Acaryochloris Marina (A.marina) is unique in nature because it contains Chl d instead of Chl a as major pigment. In addition to the Chl containing light harvesting antennas A.marina has also a Phycobiliprotein (PBP) antenna as a light harvesting complex that shows a more simple structure than phycobilisomes of other typical cyanobacteria. This PBP-antenna is a rod shaped complex consisting of three homologous Ppcys Phycocyanin and a hetero-hexameric containing PC and Allophycoerythrin absorbing in the spectral range between 560 nm and 630 nm, where the absorption of the chlorophylls is low. In order to get another insight in the fundamental processes of excitation energy transfer (EET) in this antenna system we performed time resolved absorption studies as well as measurements of the transient anisotropy. The maximum value of 0.37 that is close to theoretical limit for weak interaction of 0.4 indicates that strong excitonic coupling is not an important factor in the fast EET in PC of A.marina.

The fluorescence originating from immobilized beads containing a low fluorescence and imaged by a CCD camera. A line illumination of the sample leads to a pseudo-image with one coordinate corresponding to the spatial dimension and the other coordinate to the emission wavelength. To image the whole field of view, the excitation line has to be scanned across the sample. The beads present within the illuminated line are automatically identified and their spectrum compared with a set of reference spectra. We present a simple technique for the detection and identification of fluorescent probes at low concentration.

The beads present within an extended structure, for example, the internal bonds in a folded protein or a DNA/RNA loop. They also act as linkers between two structures, for example, a protein grafted in a cell membrane or a protein linking the cell membranes of two neighboring cells. Typically, the breakage of a bond depends on the strength of the binding potential and viscosity of the medium. But when extended structures couple to the bond, as in the above examples, the dynamics of the structure also has to be considered in order to understand the bond breakage phenomenon. Here we consider a generic model, a stretched polymer an extended structure tethered to a soft bond and study how the dynamics of the polymer, in addition to thermal noise, influences bond breakage. We also explore how the hydrodynamic interaction due to the fluid, which couples the distant parts of the polymer, change the bond breakage rate. We find that breakage rate is enhanced and also the motion becomes more coherent.

We investigate both theoretically and experimentally the limits of the ability to correctly identify the spectrum, depending on the spectral overlap and the noise level. The possibility of resolving beads with many different concentration ratios, and the effects of the interference of the bead autofluorescence, are being explored.

Technische Universität Dresden, Tatzberg 47/49, 01307 Dresden, Germany.

The fluorescence originating from immobilized beads containing a low fluorescence and imaged by a CCD camera. A line illumination of the sample leads to a pseudo-image with one coordinate corresponding to the spatial dimension and the other coordinate to the emission wavelength. To image the whole field of view, the excitation line has to be scanned across the sample. The beads present within the illuminated line are automatically identified and their spectrum compared with a set of reference spectra. We present a simple technique for the detection and identification of fluorescent probes at low concentration.

The fluorescence originating from immobilized beads containing a low fluorescence and imaged by a CCD camera. A line illumination of the sample leads to a pseudo-image with one coordinate corresponding to the spatial dimension and the other coordinate to the emission wavelength. To image the whole field of view, the excitation line has to be scanned across the sample. The beads present within the illuminated line are automatically identified and their spectrum compared with a set of reference spectra. We present a simple technique for the detection and identification of fluorescent probes at low concentration.
Combining Optical Trapping and Confocal Microscopy — • Constantine Spille, Florian Revefeld, and Christoph F. Schmidt — Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany

Mechano-sensing and force transduction play an essential role in many cellular processes but the sensitivity limits have not been understood. Acto-myosin stress fibers are key players in the physical response to the mechanical micro-environment. Optical trapping allows us to accurately measure forces exerted by the cell on trapped silica beads with pN accuracy and high time resolution. However, the cellular processes responsible for the forces cannot be resolved with a normal epifluorescence microscope due to the spherical shape of the cells when suspended in solution. We therefore built a dual optical trap into a commercial confocal microscope to be able to combine confocal scanning with optical trapping. We here discuss basic design considerations and show proof-of-principle data.

Using an ultrastable AFM to measure pN-forward forces of a growing neuronal Growth Cone — • Thomas Fuchs and Josef A. Käs — Universität Leipzig, Soft matter physics, Leipzig, Germany

We have already shown how to use an AFM to measure forward pushing protrusion forces of fast moving fish keratocytes on glass substrates at room temperature. But when trying this technique to measure slow moving neuronal growth cones at 37°C, one can no longer assume a drift-free system because of thermally induced artifacts. Therefore we incorporated an optical trap into our AFM-setup to measure, and correct for, the substrate’s drift. Yet the scan head of the AFM does not allow us to measure the forward scattered signal of the optical trap. To get position information nonetheless we use the backscattered light of our marker bead. With this we can still reduce the drift of the AFM scan head with respect to the substrate to less than 50 nm/h in all 3 dimensions. Using this stabilization we can realize the necessary observation times of 1h and even longer, while still being sensitive in the pN force range.
tinct structures of the hydrogen bonding network: While in the polar acetonitrile environment, a shared solvation leads to string-like structures, the less polar chloroform solvent facilitates an immediate phase separation, and a clustering of the water molecules. At the interface to two spatial shifted overlapping confocal volumes. Following these results, we present a novel, called three-focus FCS, which enables for the determination of the direction of directed motion of molecules by shifting three or more detection volumes relatively to one excitation spot. We will present a theoretical description of 3FCS. Moreover, extensive simulations allow for the evaluation of the capabilities of this method. The simulations are compared with the first experimental results. The study of protein-protein interactions in vivo is often hindered by the limited acquisition speed of typical instrumentation used, for instance, for lifetime imaging microscopy. Anisotropy polarization is altered by the occurrence of Forster Resonance Energy Transfer (FRET) and anisotropy imaging was shown to be comparatively fast and simple to implement. Here, we present the adaptation of a spinning disc confocal microscope for fluorescence anisotropy imaging that allowed to achieve in vivo imaging at high spatial and temporal resolution. We demonstrate the capabilities of this system and in-house developed analysis software by imaging living Caenorhabditis elegans expressing constitutive dimeric and monomeric proteins that were tagged with GF.
very simple to implement and offers the attractive possibility to de-
termine the positions of many particles in parallel, real-time tracking
rates have so far been limited to several tens of frames per second due
to the high computational effort of the employed software routines.
Here we demonstrate 3 dimensional real-time tracking at 5,000 frames
per second with sub-nanometer accuracy using a fast CMOS camera
for image acquisition and employing GPU based computing. Compu-
tationally demanding parts of the tracking algorithm are carried out in
the GPU that is specialized for highly parallelized execution. Track-
ing of the lateral particle positions is obtained by cross-correlating the
image with its mirror image. The axial position is obtained from the
radial intensity profile of the particles diffraction pattern when imaged
in focus. High tracking rates are crucial to overcome the shot-noise
limitations of camera-based detection at the second time scale and to
resolve fast, dynamic processes.

BP 12.18 Mon 17:15 P3

Analytic solution for image analysis in localization mi-
scopy with full accuracy — Frederick Grull, Manfred
Kirchgesner, and Udo Kebschull — Kirchhoff Institute for
Physics, Heidelberg University, Germany

In localization microscopy the resolution limit is improved by calculat-
ing the centroid of the image of each fluorescent point-like object. Cur-
rent algorithms obtain the center by fitting a Normal distribution and
optimize the maximum likelihood or least squares iteratively. Faster
analytical approaches exist, but come with a reduced precision in noisy
environments. We propose an algorithm that is based on maximum
likelihood, but solves the problem analytically. Results show that we
maintain full accuracy also for noisy images with a speedup of more
than 100 compared to numerical fits, and provide an accurate error
estimation for each localization. As a consequence image analysis for
localization microscopy becomes real-time capable on standard com-
puter hardware.

BP 13.1 Mon 17:15 P3

Physical description of endosome dynamics — Jonathan
Edward Dawson1, Lionel Foerst2, Roberto Villasen3, Yann-
alis Kalaidzidou3, Lutz Brusch1, Andreas Deutsch4, Marino
Zerial1, and Yannis Kalaidzidis2 — 1Max Planck Institute for
the Physics of Complex Systems, Dresden, Germany — 2Ecole Normale
Superieure, LPS, Paris, France — 3Max Planck Institute of Molecular
Cell Biology and Genetics, Dresden, Germany — 4ZIH-TUD, Dresden
, Germany

We present a theoretical study describing the collective dynamics of
a endosomal population in a cell. Endosomes are vesicular structures
that sort and transport cargo molecules internalized into the cell by en-
docytosis. Dynamics of endosomal trafficking and sorting involves large
number of individual endosomes which exchange material by fusion and
fission thereby establish a network. In particular, using fluorescence
microscopy with image analysis we quantify cargo distributions in a
specific endosomal network and present a general theory that presents
a quantitative understanding of experimental data. The steady state
distribution of total fluorescence intensity of cargo molecules in en-
dosomes strikingly display a broad power law, which is robust. Our
terms of the lateral particle positions is obtained by cross-correlating the
image with its mirror image. The axial position is obtained from the
radial intensity profile of the particles diffraction pattern when imaged
in focus. High tracking rates are crucial to overcome the shot-noise
limitations of camera-based detection at the second time scale and to
resolve fast, dynamic processes.

BP 13.2 Mon 17:15 P3

Physical description of endosome dynamics — Jonathan Ed-
ward Dawson1, Lionel Foerst2, Claudio Collinet3, Roberto
Villasen3, Yannis Kalaidzidou3, Lutz Brusch1, Andreas
Deutsch4, Marino Zerial1, and Frank Jülicher2 — 1Max Planck
Institute for the Physics of Complex Systems, Dresden, Germany —
2Ecole Normale Superieure, LPS, Paris, France — 3Max Planck
Institute of Molecular Cell Biology and Genetics, Dresden, Germany —
4ZIH-TUD, Dresden, Germany

We present a theoretical study describing the collective dynamics of
an endosomal population in a cell. Endosomes are vesicular structures
that sort and transport cargo molecules that are internalized into the
cell by endocytosis. Dynamics of endosomal trafficking and sorting in-
volves a large number of individual endosomes which exchange material
by fusion and fission thereby establish a dynamic network. Using fluo-
rescence microscopy and automated image analysis we quantify cargo
distributions in a specific endosomal network and present a general
theory that provides a quantitative description of cargo trafficking in
the network. The steady state distribution of total fluorescence in-
tensity of cargo molecules in endosomes display a power law. Our
terms of the lateral particle positions is obtained by cross-correlating the
image with its mirror image. The axial position is obtained from the
radial intensity profile of the particles diffraction pattern when imaged
in focus. High tracking rates are crucial to overcome the shot-noise
limitations of camera-based detection at the second time scale and to
resolve fast, dynamic processes.

BP 13.3 Mon 17:15 P3

Shape and fluctuations of a membrane pinned to a patterned
substrate — Daniel Schmidt1, Udo Seifert1, and Ana-Suncana

Smith2 — 1II. Institut für Theoretische Physik, Universität Stuttgart
— 2Institut für Theoretische Physik und Excellence Cluster: Engineer-
ing of Advanced Materials, Universität Erlangen-Nürnberg

We study the interplay between tension and nonspecific adhesion of a
fluctuating phospholipid bilayer by pinning the membrane on a square-

Patterned substrate. The membrane itself is described by the Helfrich
Hamiltonian. The membrane-substrate nonspecific interaction, which
is in our model approximated by a harmonic potential, has a mini-
mum at a finite distances from the substrate and thus induces mem-
brane deformations. By minimizing the total free energy and using the
equipartition theorem, we determine the shape and the roughness of
the membrane, and follow the behavior of the membrane over the
whole range of tension.

By applying the theoretical results to the data acquired in experi-
ments on an analogous in-vitro system, we can unambiguously deter-
mine the strength of the potential and the tension in the measurements.

BP 13.4 Mon 17:15 P3

Dynamics of specific adhesion — Timo Bihr1, Ana-Suncana

Smith2, and Udo Seifert1 — II. Institut für Theoretische Physik,
Uni Stuttgart — 2Institut für Theoretische Physik und Excellence
Cluster: Engineering of Advanced Materials, Universität Erlangen-
Nürnberg

We perform dynamic Langevin simulations of a membrane specifically
adhering to the substrate. The membrane is modeled by a Hamiltonian
that apart from the Helfrich term contains a harmonic contribution ac-
counting for the nonspecific membrane-substrate potential and a term
associated with the formation of ligand-receptor bonds. During the
simulation the receptors are immobilized on the substrate, whereas the
ligands diffuse freely through the membrane. Ligand-receptor binding
and unbinding is modeled by time-dependent rate constants that sat-
ify detailed balance.

We find that when the correlations between the bonds are weak,
sparse arrangement of bonds are observed and the increase of the num-
ber of bonds in time is associated with a squeezed exponential. When
the correlations between the bonds are strong, a domain grows rad-
ially out of a nucleation center. In the reaction limited regime, this
behavior is analytically modeled and the results compare well to those
arising from several experimental studies.

BP 13.5 Mon 17:15 P3

Pore-spanning lipid bilayers on microchips — Theresa
Kaufeld and Christoph F. Schmidt — Drittes Physikalisches
Institut, Georg-August-Universität Göttingen

Pore-spanning lipid bilayers (nano- or micro-black lipid membranes
(BLM)) are useful for reconstituting and studying ion channels. These
bilayers combine the stability of solid-supported membranes and the
accessibility to both sides of the bilayer of classical BLMs. Due to
defects in the bilayers it is, however, difficult to create fully electrically
equally out of a nucleation center. In the reaction limited regime, this
behavior is analytically modeled and the results compare well to those
arising from several experimental studies.

We have therefore designed microchips for simultaneous electrical

Rossetti and coworkers demonstrated the functionalization of two-dimensional, bio-bilayers. The substrates and lipid bilayers were visualized by fluorescence microscopy, atomic force microscopy, and ion channel recordings. The substrates were further functionalized by depositing a titanium/gold layer on the microporous arrays. A self-assembled layer was produced using standard clean-room techniques. Aper-recording and fluorescence microscopy to study ion channels. The substrates and lipid bilayers were visualized by fluorescence microscopy and atomic force microscopy.

Characterization of polymer-supported lipid membranes by confocal Raman microscopy — Fernanda F Rossetti, Emanuel Schneck, Cristina Deichmann, Almut Köhler, Doris Wiedlich, and Motomi Tanaka.

Characterization of polymer-supported lipid membranes by X-ray and neutron reflectivity — Fernando F Rossetti, Emanuel Schneck, Giovanna Fragnetto, Oleg Konvalina, and Motomi Tanaka.

Characterization of polymer-supported lipid membranes by X-ray and neutron reflectivity — Fernando F Rossetti, Emanuel Schneck, Giovanna Fragnetto, Oleg Konvalina, and Motomi Tanaka.

Self Organized Criticality and Fractal characteristics in Ion Channels: studies on Voltage Dependent Anion Channel — Subhendu Ghosh, Jytisimov Bankeriev, Smarajit Mann, Ivan Chizhic, Roelf-Peter Baumann, Daniel Frank Noll, and Frank Hönig.

Self Organized Criticality (SOC) is a phenomenon which is highly talked about in various fields. We discuss the existence of SOC in the electrical behavior of the artificial and cell membranes, specifically in ion channels. We have measured the single-channel and multi-channel currents (with noise) through Voltage Dependent Anion Channel (VDAC) isolated from rat brain mitochondria, reconstituted into Bilayer Lipid Membrane (BLM) under various applied voltages. Power Spectrum analysis of Open Channel current time series data indicates power-law noise of 1/f nature. We argue that the origin of 1/f noise in open ion channels is self-organized-criticality as evident from waiting time statistics of big events. In addition we demonstrate that the experimental time series data of gating of VDAC at selected membrane potentials have Fractal behavior. On the other hand, we demonstrate that the multi-channel VDAC current (open) shows Multi-fractal properties. We conclude that Self-Organized-Criticality and Fractals are the realities of Ion Channels.


Purple membranes (PM) from Halobacterium salinarum comprise bacteriorhodopsin (BR) and lipids only and form a 2-D crystalline lattice inside the cell membrane. The combination of the chlororhodopsin BR variant D87T we have observed a tuneable tendency to form crystalline domains, which depends on pH-value and chloride ion concentration. We have combined small-angle X-ray scattering, atomic force microscopy and electrical conductivity measurements. The measured thickness of the hydrated cellulose films.

Crystallinity of purple membranes comprising the chloride-pumping bacteriorhodopsin — Halina Zhurov, Ivan Chizhik, Roelf-Peter Baumann, Frank Noll, and Norbert Hamp.

Crystallinity of purple membranes comprising the chloride-pumping bacteriorhodopsin — Halina Zhurov, Ivan Chizhik, Roelf-Peter Baumann, Frank Noll, and Norbert Hamp.

Crystallinity of purple membranes comprising the chloride-pumping bacteriorhodopsin — Halina Zhurov, Ivan Chizhik, Roelf-Peter Baumann, Frank Noll, and Norbert Hamp.

Crystallinity of purple membranes comprising the chloride-pumping bacteriorhodopsin — Halina Zhurov, Ivan Chizhik, Roelf-Peter Baumann, Frank Noll, and Norbert Hamp.
microscopy and freeze-fracture electron microscopy to analyze structural transitions within PM-D8ST statistically as well as on the single membrane level. PM-D8ST is a model system to study membrane protein association upon substrate binding in a native environment.

**BP 13.12 Mon 17:15** P3

**Atomic Simulations of Hydration Forces between Biological Surfaces — •Emanuel Schneck, Felix Sedlemeyer, and Roland Netz — Technical University of Munich**

Biological surfaces interact via a complex interplay of various forces, some of which still elude a quantitative theoretical description. For instance, the experimentally observed repulsion between hydrophobic surfaces at short distances, known as hydration repulsion, is not yet fully understood, despite its crucial role in controlling the equilibrium distance between biomembranes. In this study we use atomistic molecular dynamics simulations to quantify the water-mediated repulsion between extended hydrophobic surfaces as a function of their distance. By using a novel method, based on the determination of the pressure-dependent chemical potential of water between the surfaces, we obtain pressure-distance relationships with very high accuracy. For rigid surfaces we find oscillations in the repulsion strength, originating from the discrete nature of water molecules. For soft surfaces we find a monotonic increase in the repulsion strength with decreasing water layer thickness. The latter case resembles the interaction of soft, hydrophilic biomembrane surfaces. Here, our results show quantitative agreement with experiments over the whole data range.

**BP 13.13 Mon 17:15** P3

**Membrane Adhesion via Homophilic Saccharide–Saccharide Interactions Investigated by Neutron Scattering — •Emanuel Schneck1, Bruno Denti2, Christian Gehrke1,3, and Motomu Tanaka4,5 — University of Heidelberg — 2Intitut Laue-Langevin, Grenoble — 3University of Konstanz — 4Karlsruhe Institute of Technology**

Solid-supported membrane multilayers doped with membrane-anchored oligosaccharides bearing the LewisX motif (LeX lipid) were utilized as a model system of membrane adhesion mediated via homophilic carbohydrate–carbohydrate interactions. Specular and off-specular neutron scattering in bulk aqueous electrolytes allowed us to study multilayer structure and membrane mechanics at full hydration at various Ca2+ concentrations, indicating that membrane-anchored LeX cross-links the adjacent membranes. In order to estimate forces and energies required for cross-linking, we theoretically modeled the interactions between phospholipid membranes and compared this model with our experimental results on membranes doped with LeX lipids. We demonstrated that the bending rigidity, extracted from the off-specular scattering signals, is not significantly influenced by the molar fraction of LeX lipids, while the vertical compression modulus and thus the inter-membrane confinement increases with the molar fraction of LeX lipids.

**BP 13.14 Mon 17:15** P3

**Electroformation of super-giant unilamellar vesicles containing cationic lipids — •Christoph Herold, Petra Schmilde, and Eugene P. Petrov — Biophysics, BIOTEC, TU Dresden, Tatzberg 47/49, 01307 Dresden, Germany**

Super-giant unilamellar vesicles (SGUVs) of sizes > 100 μm are a convenient model system for freestanding lipid bilayers with a negligible curvature at a scale of tens of microns. This facilitates the investigation of dynamics and conformation of molecules/polymer interactions with the non-supported membrane by means of single molecule tracking [1].

Electroformation of inorganic tin-oxide (ITO) coated glass slides is a standard method to produce GUVs [2]. When applied to lipid mixtures containing cationic lipids (e.g. DOTAP, EDOPC, etc.) the standard electroformation method frequently produces GUVs with sizes not exceeding 10-20 μm, which are additionally surrounded by a dense network of lipid tubules. We demonstrate that annealing of the ITO slides at t ∼ 150 °C before the electroformation procedure allows one to reliably produce samples containing cationic SGUVs with diameters of 100 to 300 μm not contaminated by lipid tubular structures.


In vertebrate eyes, images are projected onto an inverted retina where photons must pass most of the retinal layers before they are captured by the light-sensitive cells. Scattering in the retinal layers the light passes should obstruct clear vision yet our eye displays splendid visual abilities. This contradiction can be resolved by the function of radial glial (Müller) cells as effective light-guiding fibers in the living retina. For light that hits a Müller cell endfoot, intraretinal light scatter is minimized, and the beam diameter is conserved suppressing divergence such that the photon intensity arriving at the photoreceptors is high. Thus, an optimized signal-to-noise ratio overrides the visual obstacle of retinal layers light has to pass through and increases visual sensitivity and contrast. Moreover, by quantitative evaluation we show that the ratio between Müller cells and cone photoreceptors - responsible for acute vision - is roughly one. This suggests that high spatiotemporal resolution may be achieved by each cone receiving part of its image via its 'individual' Müller cell-light guide.

Noise reduction in systems of coupled hair bundles — Kai Dierkes, Benjamin Lindner, and Frank Jülicher — Max Planck Institute for the Physics of Complex Systems, Dresden
Auditory signal detection relies on amplification to boost sound-induced vibrations within the inner ear. Active motility of sensory hair-cell bundles has been suggested to constitute a decoupling component of this amplifier. The responsiveness of a single hair bundle to periodic stimulation, however, is limited by intrinsic fluctuations. In vivo, hair bundles are often attached to overlying membranes. Such elastic coupling can synchronize hair-bundle motions and lead to an effective noise reduction, thus enhancing a hair bundle’s sensitivity and frequency selectivity (Dierkes et al. (PNAS, 2008), Barral et al. (PNAS, 2010)). Here, we discuss the mechanism underlying this coupling-induced noise reduction within the framework of a mean-field type argument. In particular, we show that for strong coupling, fluctuations limiting a hair bundle’s responsiveness are effectively reduced in proportion to the number of coupled hair bundles.

Measurements from neuronal networks cultured on multi-electrode arrays (MEAs) yield noisy time series of the extracellular potential. As each electrode records signals from multiple neurons a principled component analysis followed by a cluster finding analysis is performed to be able to assign spikes to neurons [1]. Although this procedure can be formulated by means of the basic linear algebraic subroutines (BLAS) library the large amount of raw data requires to investigate non-standard hardware like GPUs to achieve best performance. Due to the inherent hardware-dependence of most BLAS libraries programming effort can only be minimized by abstracting the algorithm employed from BLAS and hence hardware specifics. We show how to resolve this dependency by designing a C++-based domain-specific embedded language [2] so that algorithms can be stated in a hardware independent, compact vectorized form. We discuss the performance of the algorithm proposed in [1] on different kinds of hardware architectures for a particular example (10000 spikes emitted by several hundred neurons).

Harvard University, Cambridge, MA, USA

Our recently developed novel multiscale approach which concurrently couples a mesoscopic fluid solvent with molecular motion has been efficiently applied to the problem of biopolymer translocation through narrow and wide pores. Our results of up to 10^8-48 biopolymers provide valuable insight into the cooperation of the biopolymer and lipid bilayer interaction. For wide pores, capable of hosting multiple polymer strands, there is clear evidence of folding quantization, leading to a deviation from the single-exponent power-law characterizing the single-file translocation through narrow pores. The translocation proceeds through multi-folded configurations, characterized by a well-defined integer number of folds. In this case, the translocation time acquires a dependence on the average protein-lipid bilayer interaction, leading to a deviation from the single-exponent power-law characterizing the single-file translocation through narrow pores. We discuss some recent results when electrokinetic effects are also considered.

BP 15.4 Tue 11:15 ZEU 250
Magnetic Torque Tweezers: Probing the torsional properties of DNA, RNA, and DNA filaments — JAN LIPPERT, GARY SKINNER, MATTHEW WIGGIN, JACOB KERSEMANNERS, and NYNKE DECKER — Department of Bionanoscience, Delft University of Technology, The Netherlands

The double-stranded nature of DNA links cellular processes such as replication, transcription, and repair to rotational motion and torsional strains. Here we present a novel implementation of magnetic tweezers, magnetic torque tweezers (MTT), that enables the direct measurement of torque [1]. The MTT torque measurement is based on a tracking protocol that monitors x, y, z, and angle and on a redesigned magnet configuration. We have applied the MTT to DNA, RNA, and RecA-DNA heteroduplex filaments. We find the effective torsional stiffness of dsDNA to be significant force-dependent, reconciling previous partially conflicting measurements. Torque measurements on RecA-DNA heteroduplex filaments reveal an initial torsional stiffness about two-fold higher than that of dsDNA. However, at relatively moderate torques further build-up of torsional strain is prevented by structural transitions in the filament. Preliminary results on the torsional properties of fully double-stranded RNA indicate static properties overall similar to dsDNA, but significantly different dynamics of supercoil formation. Finally, we present a related magnetic tweezers approach that allows straightforward measurements of free rotation, termed freely-orbiting magnetic tweezers [2]. [1] Lippert, et al. Nature Methods (2010) [2] Lippert, Wiggins, et al. Nature Methods, under review

15 min. break.

BP 15.5 Tue 11:45 ZEU 250
Single-molecule spectroscopy on pigment proteins and biobionano hybrids — MARC BRECHT1, ROBERT BITTL2, JANA NIEKER2, and MARTIN HUSSELE2 — Universität Tübingen Institut für Physikalische Chemie, Universität Tübingen, 72076 Tübingen — 2FU Berlin Fachbereich Physik Arnimallee 14 14195 Berlin

I will present low temperature single-molecule fluorescence experiments on photosystem I (PSI) and PSI coupled to nano structures. The spectra show even at low temperature changes of the fluorescence emission during time like time hopping, anti-correlated intensity fluctuation or line broadening. Those changes are due to small conformational changes within the binding site of the pigments [1]. The influence of metal-nanostuctures on the fluorescence properties of photosystem I, serving as an example for a multi-chromophore FRET-coupled system, will be shown [2]. Beside fluorescence-enhancement significant changes of the characteristic fluorescence emission from PSI were observed. These changes indicate altered energy transfer within the multi-chromophore assembly affecting the functionality of this protein complex. The observed spectral changes are discussed in a general framework of plasmonic interaction with multi-chromophore systems.


BP 15.6 Tue 12:00 ZEU 250
Scanning evanescent fields in TIRF microscopy using a single-point-like light source and a DNA worm drive — HERMANN DUTZER, FRIEDRICH W. SCHWARZ, and RALF SIEDEL — Biotechnologisches Zentrum, TU Dresden, Tatzberg 47/49, 01307 Dresden

Total internal reflection fluorescence (TIRF) microscopy is an elegant technique that limits the dimension of the excitation volume along the z-direction to the hundred nanometer-scale. The method makes use of the evanescent field arising when light is totally internally reflected at the boundary to a medium of lower refractive index. Often the penetration depth of this exponentially decaying field is left undetermined limiting the reproducibility in different experiments. We directly measure this quantity by using a quantum dot as a point-like light source and a Holloway junction as a drive to move the fluorescent probe with nanometer precision along the z-direction. The junction serves as a worm drive, which couples rotation into translational motion within the DNA pitch serves as an intrinsic ruler. The junction is forced to migrate by adding negative turns to the DNA stretched perpendicular to the surface using magnetic tweezers. This causes the quantum dot, which is attached upstream of the junction, to decrease its height above the surface by 3.4 nm per turn. Thus it can be moved continuously through the excitation field while monitoring its height-dependent fluorescence signal. Since the quantum dot is a point-like light source, the intensity decay of the evanescent field can be obtained by dividing the signal recorded in TIRF illumination by the one recorded in conventional epi-illumination without further corrections.

BP 15.7 Tue 12:15 ZEU 250
Weak kinesin-8 steps and slips on Microtubules — ANITA JANNASCH1, MARKO STORCH2, JONATHON HOWARD3, and ERIK SCHÄFFER4 — 1Nanomechanics Group, Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany — 2Max Planck Institute of Molecular Cell Biology and Genetics, Pflotenauerstr. 108, 01307 Dresden, Germany

The budding yeast kinesin-8 motor, Kip3p, is a very processive plus-end directed motor protein. In addition, Kip3p is a microtubule length-dependent depolymerase. Here, we studied the operation of Kip3p under load using optical tweezers as a force and position sensitive tool. We expressed and purified the recombinant Kip3p-GFP fusion protein and attached it to a microsphere surface via a polyethylene glycol linker preserving its full functionality. Our studies show that single Kip3p can carry cargo with a stall force of 1.2 pN while moving with 8 nm steps along the microtubule. The velocity of the motor strongly depended on the load force. Furthermore, the motor started to slip under load. Compared to conventional kinesin, Kip3p is a slow and weak motor, which might be a trade-off for its high processivity.

BP 15.8 Tue 12:30 ZEU 250
CXCR4-SDF1 mediated chemotaxis on the single molecule level — SUSANNE FENZ1, CASSANDRA VERHEUL1, EWA SNAAR-JAGALSKA2, and THOMAS SCHMIDT1 — 1Leiden Institute of Physics, Leiden University, The Netherlands — 2Leiden Institute of Biology, Leiden University, The Netherlands

Directed cell movement in a chemical gradient, chemotaxis, is not only a prerequisite for many vital processes like the immune response, but also the basis for cancer spreading in metastasis. Chemotaxis is governed by extracellular gradients of small molecules, the chemokines. The receptor CXCR4 and its chemokine SDF1 play a crucial role in directing migration of tumor cells to neighbouring tissue as well as in metastasis to distant sites in the body. Two potential ordering parameters, the receptor mobility and cytoskeleton-induced membrane domains, were investigated on a molecular level in living fibroblasts and endothelial cells. We applied single-molecule fluorescence microscopy to characterize the diffusion behaviour of CXCR4-eYFP in resting cells and upon stimulation with SDF1. Particle Image Correlation Spectroscopy (PICS) reveals two populations of receptors on resting cells: stimulation half of the receptors are immobile while the other half exhibits free diffusion with D = 0.3 mum2/s on short timescales (up to 100 ms). At longer timescales the receptors show confined diffusion within micrometer domains. Global stimulation with SDF1 switches a subset of the receptors from the immobile to the mobile fraction. We hypothesize that the impact of a gradient of SDF-1 might lead to asymmetric receptor diffusion and subsequently polarized cell behavior.

BP 15.9 Tue 12:45 ZEU 250
Tracking single FoF1-ATP synthases in a living E. coli cell — MARC RENZ, TORSTEN RENDLER, ANDREA ZAPPE, JÖRG WACHTRUP, and MICHAEL BÖRSCHE — 3Physikalisches Institut, Universität Stuttgart, Pfaffenwaldstr. 57, 70569 Stuttgart, Germany

We measured the diffusion of single fluorescence-marked FoF1-ATP synthases in the plasma membrane of living E. coli bacteria. The biophysical questions of temporary clustering and interactions with other
membrane proteins are investigated. We have built a total internal reflection fluorescence microscope for imaging single molecules in living cells. The membrane protein FoF1-ATP synthase has been fluorescently labeled by two different approaches using small fusion proteins. Because of the size (2000 nm x 500 nm) and the shape of the bacterial membranes data analysis of the diffusing proteins is complicated. The algorithm used to extract the Mean Square Displacement (MSD) from the processed raw data will be discussed which allows to calculate a diffusion coefficient. The influence of the finite size of the observation area on the statistics of the measured MSD will be discussed and compared to Monte Carlo simulations.

**Invited Talk**

**BP 16.1 Tue 10:15 ZEU 260**

The dynamic organization in the membrane of a G-protein-coupled receptor is related to its functional state — **Laurence Salome** — IPBS, Toulouse, France

The analysis of membrane diffusion is the most promising approach to investigate the compartmentalization of G-protein-coupled receptors, particularly as relevant to receptor signalling processes. We developed two complementary techniques: the fluorescence recovery after photobleaching (FRAP) performed at variable spot radius and the single particle tracking (SPT). We report the results of our study of a G-protein-coupled receptor involved in pain treatment, the human mu-opiod receptor (hMOR), using these techniques. We will survey the effects of the presence of distinct agonist ligands, antagonist ligand or opioid receptor (hMOR), using these techniques. We will survey the effects of the presence of distinct agonist ligands, antagonist ligand or the activation of other receptors on the diffusional behaviour of the receptor. Our observations suggest that the functional state of a receptor is correlated to its dynamic organisation in the plasma membrane.

**BP 16.2 Tue 10:45 ZEU 260**

**Dynamic structure formation of membrane proteins** — **Germain Guigas**, **Diana Morozova**, and **Matthias Weiss** — Experimental Physics I, University of Bayreuth — Cellular Biophysics Group, German Cancer Research Center, Heidelberg

Cellular membranes are not mere passive envelopes but act as a reaction space for a multitude of vital cellular processes. While it is generally anticipated that biomembranes are highly dynamic and self-organizing entities, molecular mechanisms that underlie structure formation on lipid bilayers are still far from being fully understood. Here, we show by means of coarse-grained membrane simulations that proteins can form higher-order structures due to membrane-mediated interactions. Structure formation originates from characteristic protein-induced bilayer perturbations that particularly affect the coupling between membrane leaflets. Examining transmembrane proteins as well as peripheral membrane proteins, we observe the formation of protein oligomers and templates, even between proteins residing in different membrane leaflets. Also raft-like cross-leaflet associations of proteins and lipid patches are observed. Key parameter of this structure formation is the protein geometry. Apart from their potential influence on the organization of biomembranes, these effects may also support the formation of templates for signaling processes, the assembly of transport intermediates, or protein sorting events.

**BP 16.3 Tue 11:00 ZEU 260**

**Spatio-temporal modeling of MARCKS protein binding at biological membranes** — **Sergio Alonso** and **Markus Bär** — Physikalisch-Technische Bundesanstalt

Proteins inside the cell strongly interact with biological membranes. Depending on the lipid composition of the membrane and the interaction with other proteins, they can spontaneously bind by an electrostatic interaction with acidic phospholipids. We consider a simple model of membrane organization into domains based on a cyclic binding and unbinding of the unfolded MARCKS protein at membranes composed by acidic lipids known as myristo-electrostatic (ME) switch. The function of such proteins is the protection of the phospholipids from hydrolysis by enzymes. Membrane-bound MARCKS may be phosphorylated by Protein kinase C (PKC), which produces the unbinding of the protein. This process is activated by Calcium. Finally, phosphatases dephosphorylate the MARCKS proteins in the cytoplasm, which may bind again at the membrane. The model describes the formation of membrane domains under nonequilibrium conditions, because the ME switch consumes ATP and leads to non-vanishing currents of proteins. Two main mechanisms of domain formation are obtained: a long-wave instability and a mechanism based on the bistability of two spatially homogeneous steady-states. Finally, we compare the predictions of our model with experiments in living cells obtained from the literature and with experimental measurements obtained in vitro.

Break (10 min)

Invited Talk  
**BP 17.3 Tue 11:40 HSZ 201**  
**Plant movements and biomimetic actuators — Peter Fratzl, Sebastien Turcaud, John Dunlop, Matt Harrington, and Ingo Burgert** — Max Planck Institute of Colloids and Interfaces, Potsdam, Germany  
The secondary plant cell wall is a composite of cellulose nano-fibrils and a water-swelling matrix containing hemicelluloses and lignin. Recent experiments showed that this swelling capacity helps generating growth stresses, e.g., in conifer branches or in the stem when subjected to loads. A similar mechanism also provides motility to wheat seeds. A simple mechanical model for the cell wall predicts that - depending on the detailed architecture of the cellulose fibrils - swelling may lead either to significant compressive or tensile stresses or to large movements at low stresses. The model reproduces most of the experimental observations in the wood cells and in the awns of wheat seeds. The general principle is based on the modification of the isotropic swelling of a gel by embedded oriented fibres, or on a non-symmetric distribution of swelling elements and non-polar body. More generally, actuation systems in plants provide guidelines for designing material architectures suitable to convert isotropic swelling into complex movements and forces of various kinds and directions.

---

**BP 18.1 Tue 14:00 ZEU 250**  
**Amyloid at the nanoscale: single molecule and ensemble studies of amyloid-lipid interactions — Vinod Subramaniam** — Nanobiophysics, MESA+/MIRA, University of Twente, Enschede, The Netherlands  
Misfolding and aggregation of proteins into nanometer-scale fibrillar assemblies is a hallmark of many neurodegenerative diseases. Despite decades of research, the underlying biology remains a mystery. A particularly interesting and relevant question is the role of early aggregates in modulating the dynamics of protein nucleation and aggregation, and the mechanism of interactions of these species with lipid membranes. The transient nature, inherent heterogeneity, and low numbers of early stage aggregates necessitate single molecule spectroscopy approaches and other methods that can detect distributions of structures in ensembles. We have worked extensively on the conformational dynamics and self-assembly of the human intrinsically disordered protein alpha-synuclein, involved in the etiology of Parkinson’s disease. In this talk, I will summarize recent work using a broad repertoire of quantitative single molecule and ensemble biophysical techniques to characterize, at nanometer length scales, conformational and morphological details of alpha-synuclein amyloid nanostructures, and their interactions with lipid membranes.

**BP 18.2 Tue 14:30 ZEU 250**  
**Magnetic force driven dissociation kinetics in case-mixed protein interaction assays — Asha Jacob, Leo J. van IJzendoorn, Arthur M. de Jong, and Menno W.J. Prins** — Eindhoven University of Technology, The Netherlands  
We quantify dissociation kinetics in assays with mixed specific and non-specific protein interactions. Ligand coupled superparamagnetic particles are incubated on surfaces coated with a mixture of specific receptors and non-specifically interacting proteins. Consequently, a case-mixed population of surface bound particles is formed with different binding strengths. Magnetic field gradients were used to apply translational forces on the bound complexes, either constant or increasing in time (applying a loading rate). Using a multi-component dissociation analysis, we observe case-dependent dissociation mechanisms of the particles. The classical Bell and Evans model successfully describes bond dissociation from the deep potential well of a specific bond. Bond characteristics in terms of rate constants, energy barriers and minima’s in the dissociation pathway are revealed for the anti-biotin/biotin and streptavidin/biotin bond; and are in good agreement with values from SPR, other force clamp techniques, and molecular dynamics calculations. The particles bind non-specifically via interactions that show a force induced dissociation mechanism distinctly different from that of the specifically bound particles. The ability to rapidly differentiate and characterize specific and non-specific protein interactions in parallel, and affinity-rank different protein-ligand interactions on the basis of their binding pocket characteristics, will find various applications.

**BP 18.3 Tue 14:45 ZEU 250**  
**Friction dynamics of peptides at polar and non-polar surfaces — Aykut Erbas, Dominik Horinek, and Roland R. Netz** — Technische Universitaet Muenchen, Physik Department, Garching, Germany  
The friction forces and mobilities for the C16 spider silk and various peptides on polar and non-polar surfaces are investigated using molecular dynamics simulations. For both surfaces, the velocity dependence of the monomer mobility is determined and interpreted with non-linear analytical models. The obtained diffusion coefficients are in good agreement with experiments. It is concluded that the reason for the high friction forces on polar surfaces is hydrogen bonding. It is further shown that each hydrogen bond contributes equally to the total friction force, independent of the concentration of surface-polar groups or the type of amino acid.

**BP 18.4 Tue 15:00 ZEU 250**  
**Getting closer to the nature of specific bonds: Dynamic force spectroscopy on the binding of monoclonal antibodies and tau peptides — Wagner Carolin1, Singer David2, Hoffmann Ralf2, and Kremer Friedrich1** — 1Leipzig University, Department of Molecular Physics, Leipzig, Germany — 2Leipzig University, Center for Biotechnology and Biomedicine, Leipzig, Germany  
Optical tweezers-assisted dynamic force spectroscopy (DFS) is employed to investigate specific receptor/ligand-bonds on a single contact level. Here, the specific binding of two monoclonal antibodies (mAbs), HPT-110 and HPT-104, to synthetic tau-peptides with different phosphorylation pattern is analyzed. The specificity of HPT-110 to the tau-peptide containing a phosphorylation at Ser235 and of HPT-104 to the tau-peptide containing a phosphorylation at Thr231 is confirmed. Additionally, our approach allows for a detailed characterization of the unspecific interactions that are observed between HPT-104 and the peptide phosphorylated only at Ser235 and between HPT-110 and the peptide phosphorylated only at Thr231. By analyzing the measured rupture-force distributions it is possible to separate unspecific from specific interactions. Thereby for the latter characteristic parameters like the lifetime of the bond without force 0, the characteristic length xts and the free energy of activation DG are determined. The results are in accordance with conventional ELISA tests but offer a much more refined insight.
Biological Physics Division (BP) Tuesday

BP 19.2 Tue 14:15 ZEU 260
Lipid bilayers interacting with polymer chains — ∙MARCO WERNER1,2 and JENS-UWE SOMMER1,2 — Leibniz-Institut für Polymerforschung Dresden, Germany — 2Technische Universität Dresden - Institut für Theoretische Physik
We apply the bond fluctuation model [L. Carmesin and K. Kremer, Macromol. 21, 2819 (1988)], a lattice-based Monte Carlo method, to study amphiphile bilayers and their interactions with polymers. Hydrophobic interactions are induced by explicit solvent. This allows us to simulate self-assembling planar bilayers, vesicles and hydrophobic polymers avoiding artificial freezing effects. We focus on the spectrum of effects which arise when bringing together fluctuating bilayers and flexible polymers of various compositions and hydrophobic interactions. Particular effects like translocation of polymers through membranes [T. Goda, Y. Goto and K. Ishihara, Biomaterials 31, 2380 (2010)] and changes in membrane-permeability [A.L. Lynch, R. Chen, P.J. Dominkovsz, E.Y. Shalaev, R.J. Yancey Jr. and N.K.H. Slater, Biomaterials 31, 2380 (2010)] have been observed experimentally and might become relevant for drug delivery and cell reprogramming. In our simulations we look for local permeability of the membrane as a measure for the perturbation due to interacting polymers. We found that homopolymers with moderate hydrophobicity get weakly adsorbed hence inducing larger fluctuations. This enhances the permeability for solvent locally. On the other hand, strongly hydrophobic chains are trapped in the hydrophobic layer where they act as stoppers for permeating solvent.

BP 19.3 Tue 14:30 ZEU 260
Surface viscosity and intermonolayer friction in a soft, solvent-free model of lipid bilayers — ∙MARTIN HÖMBERG and MARCUS MÜLLER — Institut für Theoretische Physik, Georg-August-Universität, 37077 Göttingen, Germany
In coarse-grained models of lipid bilayers one integrates out several microscopic degrees of freedom so that the study of membranes comprising thousands of lipids becomes feasible in computer simulations. Thermodynamical, structural, and mechanical properties of biophysical bilayers can be accurately reproduced in these models. However, the coarse-graining also eliminates degrees of freedom that should appear in the coarse-grained dynamics as dissipation and thermal noise. Hence, the coarse-grained and the actual dynamics may differ severely. Here we employ a solvent-free, coarse-grained model to analyze two dynamical quantities: the surface viscosity and the intermonolayer friction. We compare the surface viscosity obtained within a Green-Kubo approach with the one obtained from reverse NEMD simulations. The measurement of the intermonolayer friction differs from experiments and simulations with an explicit solvent, therefore we are using a modified version of the SL-theory of the dynamics of bilayer undulations and another Green-Kubo approach for obtaining it.

Finally, we discuss how to map our bead-spring model onto a two-dimensional model of coupled monolayers where the lipids are represented by point particles. The interactions and the thermostat are tuned so that it reproduces the RDF and the structure factor, but more importantly also the surface viscosity and the intermonolayer friction.

BP 19.4 Tue 14:45 ZEU 260
Chemical oscillations in cell membranes — ∙CHRIS HÄNDEL1, UNDINE DIETRICH2, SERGIO ALONSO3, MARCUS BARK4, and JOSEF KAS5 — 1Division of Soft Matter Physics, University of Leipzig, Germany — 2Division of Soft Matter Physics, University of Leipzig, Germany — 3Physikalisch-Technische Bundesanstalt, Berlin, Germany — 4Physikalisch-Technische Bundesanstalt, Berlin, Germany — 5Division of Soft Matter Physics, University of Leipzig, Germany
The MARCKS protein is an actin filament cross-linking protein which has relevant functions in different organisms. It is located at the plasma membrane and interacts via electrostatic forces with PIP2 containing cell membranes. In a model membrane, designed by a mixed DPPC/PIP2- monolayer, the binding of MARCKS peptide to the membrane increases the lateral pressure. The unbinding dynamics modulated by PKC generates a reaction-diffusion system. This leads to oscillations of the lateral pressure which can be attributed to changes in the liquid condensed domain size. An adequate and sensitive tool for monitoring these oscillations is the Langmuir trough technique combined with a film balance. The present work confirms the theoretical calculations of this reaction-diffusion system by using model membranes. These calculations describe the dynamic distribution of acidic lipids in response to cytosolic proteins and regulating enzymes. We obtained oscillations in lateral pressure and analyzed the images of the domains depending on the lateral pressure. Furthermore, our results indicate that the oscillations correlate with changes in shape and size of the domains.

BP 19.5 Tue 15:00 ZEU 260
Minimalistic model for bilayer membranes: hydrophobic inclu- sions: application to membrane fusion — GIOVANNI MARELLI1, JELGER RISSELADA2, and MARCUS MUELLER3 — 1Institut für theoretische Physik Friedrich Hund Platz 1 37077 Göttingen — 2Max Planck Institute for Biophysical Chemistry, Fassberg 11 37077 Göttingen
We develop a coarse-grained solvent free model to study the interactions of a hydrophobic inclusion with a lipid membrane. For different sets of system's parameters we have calculated the mechanical properties of the self-assembled structures (e.g., bending rigidity and line tension of a pore) as well as the phase behavior (lamellar vs inverted hexagonal morphology). We propose two alternative methods to describe a hydrophobic inclusion: a rigid cylinder or a collection of tightly coupled particles and place it in the hydrophobic shell of the membrane. The inclusion induces in the membrane a local ordering of the lipids (e.g. packing effects) and a long-range distortion of the membrane thickness. The surface tension induced by the protein induce pore formation at a certain distance away from its center and the superposition of many proteins result in a stable pore and we present the local pressure profile. This is a first step towards studying the role of the proteins in the fusion process and to understand how their radius and surface tension can select different fusion pathways.
Invited Talk

**Quantitative universality and non-local interactions in neuronal pattern formation**

**Biological Physics Division (BP) Wednesday**

**BP 20.1 Wed 10:15 ZEU 250**

Invited Talk


The occurrence of universal quantitative laws in a strongly interacting multi-component system indicates that its behavior can be elucidated through the identification of general mathematical principles rather than by the detailed characterization of its individual components. In this talk I show that universal quantitative laws govern the spatial layout of orientation selective neurons in the visual cortex in three mammalian species separated in evolution by more than 65 million years. Most suggestive of a mathematical structure underlying this universality, the average number of pinwheel centers per orientation hyper-column in all three species is statistically indistinguishable from the constant π. Mathematical models of neural pattern formation can reproduce all observed laws if non-local interactions are dominant, indicating that non-local interactions are constitutive in visual cortical development. The spatial layout adheres to these laws even if visual cortical organization exhibits marked overall inhomogeneities and when neuronal response properties are experimentally altered. These results demonstrate that mathematical principles can shape the organization of the brain as powerfully as an organism’s genetic make-up.

**BP 20.2 Wed 10:45 ZEU 250**


Transflecting neurons to express the light-gated ion channel Channelrhodopsin2 (ChR2) makes it possible to influence their activity non-invasively, by means of photostimulation [1]. We have implemented a feedback control system using optical stimulation at a frequency between 400 and 1800 Hz which can be used to regulate the firing rate of neural networks cultured on multielectrode arrays. Our system allows closed loop feedback on timescales comparable to those of synaptic response (1–5 ms). We present an experimental setup for adjusting the average firing rate of neurons by means of feedback controlled photostimulation, thus devising a way of optically clamping an ensemble of cells. [1] Boyd et al., Nat Neurosci 8, 1263-1268, doi:10.1038/n4152

**BP 20.3 Wed 11:00 ZEU 250**

A nonlinear oscillator underlies flight control in flies — Jan Bartussek, Kadir Mutlu, Martin Zappotocky, and Steven N. Fire

— Institut für Neuroinformatik, Uni/EHT Zürich, Schweiz
— Akademie der Wissenschaften der Tschechischen Republik, Prag Tschechien
— FB Biologikum, Hochschule Rhein-Waal, Deutschland

Flies serve as model organisms for research on neuromotor control since decades. Despite huge efforts, it is still unclear how such complex and robust behavior emerges from a relatively small number of motorneurons. Especially, theoretical control principles that relate to the known neuromotor feedback circuits remain largely elusive. In our approach we consider the stretch activated thorax-power muscle system as a nonlinear oscillator (NLO) and the steering muscles as an external forcing, whose magnitude depends on the perceived mechanosensory feedback. We developed an experimental setup, in which a piezoelectric actuator can control the angle of the fly's head to stimulate its mechanoreceptors. A laser Doppler vibrometer was used to measure the stimulation amplitude and phase relative to the wingbeat, while simultaneously recording the induced response of the fly. We determined regions of synchronization within the amplitude-frequency parameter space, the so-called Arnold tongues. As expected for NLOs, synchronization occurred at various ratios n/m of wingbeat frequency n and stimulation frequency m. Moreover, we show that flies display adaptive entrainment consisting of phase and frequency locking. The results emphasize the importance of the inherent nonlinearity of the musculoskeletal dynamics for understanding flight control in flies.

**BP 20.4 Wed 11:15 ZEU 250**

Spatio-temporal encoding of sound in the inferior colliculus — Aneta Weigenand, Thomas Martinetz, and Jens Christian Claussen

— Bernstein Focus for Neurobiology of Audition, Bernstein Center for Computational Neuroscience, Berlin, Germany
— Neuro- und Bioinformatik, Univ. zu Lübeck, Neurosystem Neural systems exhibit complex dynamics on several time scales that can be significantly longer that that of single neuron spikes. The cortical slow oscillation is such an example where awake-like bursts (Up-states) are interrupted by Down states: low activity and absence of bursts. Up-Down state transitions are the dominant dynamical phenomenon manifesting mammalian slow wave sleep, and occur as macroscopic oscillations over the whole cortex. To model their minimal constituting dynamical mechanism still remains a challenge. An important means of model testing is to investigate perturbations of the model which correspond to an electrical stimulation in the experiment. A paradigmatic recent experiment [1] investigated the on- and off switching of bursting activity in ferret brain slices. We use a conductance-based model [2] following the approach of [3] to reproduce the spike-burst dynamics and the triggering of up states as observed in [1]. We also investigate the phase diagram of the qualitatively different network states depending on the coupling strength and network noise intensity [4]. While designed for the cortical up- down switching, it could be seen as a generic model of a driven fast-slow dynamical system.


**BP 20.5 Wed 11:45 ZEU 250**

Up-Down state stimulation of a cortical model for slow waves in sleep — Arne Weigenand, Thomas Martinetz, and Jens Christian Claussen

— Neuro- und Bioinformatik, Univ. zu Lübeck, Neurosystem Neural systems exhibit complex dynamics on several time scales that can be significantly longer that that of single neuron spikes. The cortical slow oscillation is such an example where awake-like bursts (Up-states) are interrupted by Down states: low activity and absence of bursts. Up-Down state transitions are the dominant dynamical phenomenon manifesting mammalian slow wave sleep, and occur as macroscopic oscillations over the whole cortex. To model their minimal constituting dynamical mechanism still remains a challenge. An important means of model testing is to investigate perturbations of the model which correspond to an electrical stimulation in the experiment. A paradigmatic recent experiment [1] investigated the on- and off switching of bursting activity in ferret brain slices. We use a conductance-based model [2] following the approach of [3] to reproduce the spike-burst dynamics and the triggering of up states as observed in [1]. We also investigate the phase diagram of the qualitatively different network states depending on the coupling strength and network noise intensity [4]. While designed for the cortical up- down switching, it could be seen as a generic model of a driven fast-slow dynamical system.


**BP 20.6 Wed 12:00 ZEU 250**

How stochastic adaptation currents shape interspike interval statistics - theory vs experiment — Thomas Martinetz, Jan Benda, and Benjamin Lindner

— Bernstein Focus for Neurobiology of Audition, Bernstein Center for Computational Neuroscience, Berlin, Germany
— Biocentrum der LMU, Department Biologie II, Planegg-Martinsried, Germany

Trial-to-trial variability and irregular spiking is an ubiquitous phenomenon throughout the nervous system. In many cases, the origin of this neural noise is not known and difficult to access experimentally. Here, we explore the possibility to distinguish between two kinds of intrinsic noise solely from the interspike interval (ISI) statistics of a neuron. For this end, we use a paradigmatic model with spike-frequency adaptation in which fluctuations (channel noise) are either associated with fast ionic currents or with slow adaptation currents. We show by means of analytical techniques that the shape of the ISI histograms and the ISI correlations are markedly different in
both cases: for a deterministic adaptation current, ISIs are distributed according to an inverse Gaussian density and the ISI correlations are negative. In contrast, for stochastic adaptation currents, the ISI density is more peaked than an inverse Gaussian density and the serial correlations are positive. We applied these measures to intracellular recordings of locust auditory receptor cells in vivo. By varying the stimulus intensity, we observed intriguingly similar statistics corresponding to both cases of the model. The results suggest that stochasticity of slow adaptation currents may contribute to neural variability in sensory neurons. Ref.: Schwager T, Fisch K, Bend J, Lindner B, PLoS Comp Biol 2010

BP 20.7 Wed 12:15 ZEU 250

Interspike Interval Statistics of Neurons Driven by Stochastic Oscillations: Theory vs. Experiment — Christoph Bauermeister1, Tilø Schwager1, Alexander Neiman1,2, and Benjamin Lindner1 — 1Max-Planck-Institut für Physik komplexer Systeme, Dresden, Germany — 2Department of Physics and Astronomy, Ohio University, Athens, Ohio 45701, USA

Stochastic oscillations are a ubiquitous phenomenon in neuronal systems. We study the role of these oscillations in an analytically tractable model, the stochastic perfect integrate-and-fire neuron with narrow-band (harmonic) noise. The latter represents stochastic oscillations. We obtain approximations for the firing statistics including interspike interval density, serial correlations and power spectrum of the spike train. We apply our formulas to experimental data of electro-sensory receptors in the paddlefish and show how to infer intrinsic parameters of this system from its firing statistics.

BP 20.8 Wed 12:30 ZEU 250

Sensitivity dependence on single spike perturbations in the dynamics of cortical circuits — Michael Monteforte1,2,3 and Fred Wolf1,2,3 — 1Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — 2Bernstein Center for Computational Neuroscience, Göttingen, Germany — 3Georg-August-University, Göttingen, Germany

The experiments with actin bundles in confinement show that the persistence length of actin bundles \( \ell_p \) increases proportionally with the number of filaments present in a bundle \( n \) as: \( \ell_p \approx n^{1.3} \). In the next step, we try to form more complex networks using cross-linking proteins such as \( \alpha \)-actinin, filamin, HMW and use FRET microscopy to analyze it.

BP 21: Biopolymers and Biomaterials II (with CPP)

BP 21.1 Wed 10:15 ZEU 260

Stretching Proteins out of equilibrium: how extracellular matrix proteins serve as mechano-transducers — Viola Vogel — Department of Materials, ETH Zürich, Switzerland

While physical factors and material properties regulate many cell functions, the underpinning mechanisms how cells and tissues sense mechanical stimuli and convert them into biochemical signals are not well understood. As cells explore their environments, they pull on extracellular matrix and thereby stretch those proteins that physically connect the cells to their microenvironment with the contractile cytoskeleton. Detailed mechanisms will be discussed how the stretching of proteins can switch their functional display. Deciphering how proteins can serve as mechano-chemical signaling switches is not only essential to learn how cells probe and respond to their environments, but it has also far reaching implications in tissue engineering, systems biology and medicine.

BP 21.2 Wed 10:45 ZEU 260

Formation and Confinement of Actin Networks in Microchambers — Siddharth Deshpande1, Dagmar Steinhauser2, and Thomas Piom1,2 — 1Chemistry Department, University of Basel, Switzerland — 2Max Planck Institute for Dynamics and Self Organization, Göttingen, Germany

Our aim is to study the spatiotemporal evolution of biopolymer networks (e.g. actin, collagen, fibrin) with the aid of microfluidics and using a bottom-up approach. We have designed microfluidic devices consisting of microchambers of different shapes and sizes connected to the main channel by narrow connecting channels. High flow conditions can be achieved in the main channel to control the concentration and composition of the aqueous solution while the transport of molecules into the microchambers is governed by diffusion.

Rhodamine labeled actin monomers are used for the experiments and visualized by fluorescence microscopy. Once polymerized, the actin filaments formed inside the chamber are confined and form an entangled actin network, which can be analyzed for various network properties such as connectivity distribution of nodes, length distribution of links, node fluctuations, link fluctuations and fluctuations in the mesh size.

The experiments with actin bundles in confinement show that the persistence length of actin bundles \( \ell_p \) increases proportionally with the number of filaments present in a bundle \( n \) as: \( \ell_p \approx n^{1.3} \). In the next step, we try to form more complex networks using cross-linking proteins such as \( \alpha \)-actinin, filamin, HMW and use FRET microscopy to analyze it.

BP 21.3 Wed 11:00 ZEU 260

Mechanics and Dynamics of Individual Intermediate Filaments — Bernd Nöding, Susanne Bauch, and Sarah Köster — Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany

The mechanical rigidity of a polymer is characterized by its persistence length \( \ell_p \). In the case of the intermediate filament (IF) protein vimentin, \( \ell_p \) is found to be on the order of one micrometer using static measurement methods. In contrast, we perform dynamic measurements on fluorescently labeled IFs confined in microchannels, thereby realizing the Odijk confinement regime. Since IFs can be classified as semiflexible polymers \( (L \approx \ell_p) \) we assume the worm-like chain model for our fluctuation analysis. The channel walls are included as a parabolic potential in our calculations. Interaction of the filament and the confining microchannel gives rise to an additional length scale, the deflection length \( \lambda \). We combine IF data with literature data for actin. Thereby we can access both the channel dimension \( d \) and \( \ell_p \), and define the scaling laws \( \ell_p \sim d \lambda \). The scaling law is fully confirmed by our experiments. Additionally our dynamic measurements yield \( \ell_p \) on the order of one micrometer for vimentin filaments.

BP 21.4 Wed 11:15 ZEU 260

A constitutive law for cross-linked actin networks by ho-
mogenization techniques — Denis Calleire1, ⋆Karin John2, Chaoqi Misbah2, Philippe Feyla2, and Annie Raoult2 — 1L3S-R, BP 53 - 38041 Grenoble Cedex 9, France — 2LSP, UJF Grenoble & CNRS, BP 87 - 38492 Saint-Martin-d’Hères, France — 3LMAPS, Université Paris Descartes, 45 rue des Saints Pères, 75270 Paris Cedex 06, France.

Inspired by experiments on the actin driven propulsion of micrometer sized beads we develop and study a minimal mechanical model of a two-dimensional network of stiff elastic filaments grown from the surface of a solid circle. Starting out from a discrete model of the network structure and of its microscopic mechanical behavior we derive a macroscopic constitutive law by homogenization techniques. We calculate the axisymmetric equilibrium state and study its linear stability depending on the microscopic mechanical properties. We find that thin networks are linearly stable, whereas thick networks are unstable. The critical thickness for the change in stability depends on the microscopic elastic constants. The instability is induced by the increase in the compressive load on the inner network layers as the thickness of the network increases. The here employed homogenization approach combined with more elaborate microscopic models can serve as a basis to study the evolution of polymerizing actin networks and the mechanism of actin driven motion.

15 min. break

BP 21.5 Wed 11:45 ZEU 260 Dynamics and mechanics of formin mediated actin bundles — Florian Rückerl, Timo Betz, and Cécile Sykes — UMR168, Institut Curie, Paris

In our experiments actin filaments and actin bundles are produced by polymerization by the formin mDia1(FH1FH2). To probe their dynamics and mechanics, we use a state of the art optical tweezers setup and create multiple traps (2 to 5) with acousto-optical deflectors (AODs). Digitally controlled AODs in time sharing mode allow to position and move several traps simultaneously. Employing a four quadrant diode as a position detector results in high temporal and spatial resolution, 10μm and <1μm, respectively. This allows to investigate the polymerizing dynamics of mDia1 by directly observing the deflection of formin coated beads inside the optical trap. Preliminary results indicate single monomer addition events at infrequent intervals.

By attaching several beads to individual bundles we can create picoliter Newton forces in arbitrary directions. The mechanical properties of the bundle are then probed by bending, pushing and pulling on the bundle. We find that pulling on a bundle leads to its elongation, presumably by relative sliding of the bundle filaments to each other.

Furthermore, the setup can be used for the direct manipulation of the bundles without beads attached to it, allowing for an in situ non invasive measurement. Correlating the local fluctuations at several positions on the bundle yields its persistence length and gives an estimate of the number of filaments in the bundle.

BP 21.6 Wed 12:00 ZEU 260 Network Formation of Cytoskeletal Proteins — Christian Dammann, Bernd Nöding, Susanne Bauch, and Sarah Köster — Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany

The structure and function of biological systems is determined by their bio-environment. Therefore, a drop-based microfluidic device is tailored to probe context-sensitivity of biological systems. In this device a series of monodisperse aqueous drops is created and used as picoliter bio-compartments. The composition of the drops is varied from drop to drop. Thus, the biological system is encapsulated in drops with tunable chemical content. These drops are then stored in the device for long-time observations. The content composition of each individual drop can be reconstructed. Possible applications of this tool are manifold. The device proves to be suitable for in vitro studies on cytoskeletal proteins. We focus on the assembly and network formation of vimentin intermediate filament. The assembly of vimentin depends on the ionic strength. We are able to directly image the networks of the fluorescently tagged protein and show that divalent ions induce compaction of these networks.

BP 21.7 Wed 12:15 ZEU 260 Functionalized lipid bilayers for rapid cell attachment — Samira Heintrich, Martin Huth, and Bert Nickel — Ludwig-Maximilians-Universität, Department für Physik and CeNS, Geschwister-Scholl-Platz 1, 80539 München

The behavior of cells in contact to interfaces varies significantly depending on the surface properties. Bioadhesive coatings can act as an interlayer between cells and anorganic interface, tuning the interaction of cells with the surface. Here, a multilayer system consisting of a supported lipid bilayer and two protein layers is used to produce a surface favoring neural stem cell attachment. Biotin and streptavidin act as a layer of linkers in between the lipid bilayer and the cell adhesive polypeptide AK-cyclo(RGDfC).

The trilayer system was characterised by x-ray reflectometry (D4, HASYLAB) and neutron reflectometry (N-REX, FRM2) measurements, which allowed for the determination of the layers thicknesses and the hydration of both lipids and proteins. Cell attachment to the coated surface was verified via fluorescence microscopy [1]. Microscopy confirms rapid attachment of stem cells while reflectometry indicated a dense on edge configuration of the AK-cyclo(RGDfC) thus maximizing the number of exposed RGD groups. Experiments have been performed in collaboration with E. Mardarasz and G. Menzo from the Hungarian Academy of Science (HAS).


BP 21.8 Wed 12:30 ZEU 260 Two-component Polymer Scaffolds for Controlled Three-dimensional Cell Culture — Benjamin Richter1,2, Franziska Klein1, Thomas Striebel1, Clemens Franz2, Georg von Freymann2, Martin Wegener2, and Martin Bastmeyer1,2 — Zoologisches Institut, Karlsruher Institut für Technologie, 76131 Karlsruhe — 2Angewandte Physik, Karlsruher Institut für Technologie, 76131 Karlsruhe — 3AG Optische Technologien und Photonik, Technische Universität Kaiserslautern, 67663 Kaiserslautern

Fibrous collagen or matrigel matrices are commonly used to study three-dimensional (3D) cell behaviour, but these matrices have a random pore size and are structurally and chemically ill defined. We and others have recently shown that direct laser writing (DLW) is a versatile technique to fabricate tailored 3D cell-culture scaffolds in the micrometer to nanometer range. By using an adequate photore sist, elastic 3D scaffolds for cell-force measurements have also been realized. These DLW scaffolds have been homogeneously coated with ECM molecules. Ideally, they should rather have an adjustable distribution of cell-substrate contact sites to manipulate cell adhesion and cell shape in all three dimensions. By sequential DLW of two different photoresists, composite-polymer scaffolds with distinct protein-binding properties are fabricated and selectively bio-functionalised thereafter. Cells cultured in these scaffolds selectively form cell-adhesion sites with the functionalised parts, allowing for controlling cell adhesion and cell shape in 3D - forming the basis for future designer tissue-culture scaffolds.

BP 21.9 Wed 12:45 ZEU 260 Characterizing bacterial adhesion: The role of van der Waals forces — Nicolas Thewes, Peter Loskill, Sebastian Hümmer, and Karin Jacobs — Department of Experimental Physics, Saarland University, 66041 Saarbrücken, Germany

Bacterial adhesion to surfaces is a complicated process that not only depends on the type of bacterium and the type of surface, but also on substrance composition, as we have shown in a recent study. To probe the adhesion of s. carnosus, various surfaces have been prepared, ranging from hydrophilic to hydrophobic, from smooth to rough surfaces. To probe the effect of substrate composition on the adhesion strength, Si wafers with different Si oxide layer thicknesses have been used. Clearly, the adhesion is stronger on wafers with thin Si oxide layer, irrespective if the wafer was hydrophobized by a monolayer of silanes or not, which is a clear evidence that long-range van der Waals forces play a crucial role for bacterial adhesion. It moreover shows that subsurface composition must be taken as characteristics of a sample, forces play a crucial role for bacterial adhesion. It moreover shows that subsurface composition must be taken as characteristics of a sample, forces play a crucial role for bacterial adhesion.
A common mechanism connects diverse reaction-diffusion morphology, spatio-temporal actin dynamics and membrane tension, with mathematical modeling to explain how global shape and speed of the lamellipodium emerge from the underlying assembly and disassembly dynamics of the actin network within an inextensible membrane bag.

A central challenge in cell motility research is to quantitatively understand how numerous molecular building blocks self-organize to achieve the necessary conditions to generate cell polarity. In particular, we find that positions and sizes of organelles show fairly large variations in an ensemble of cells despite a common geometry and symmetry-dependent correlations between features of different organelles.

In the lamellipodium of migrating animal cells, the growth of the actin cytoskeleton is driven by a treadmilling actin network. We combine detailed measurements of lamellipodial morphology, spatio-temporal actin dynamics and membrane tension, with mathematical modeling to explain how global shape and speed of the lamellipodium emerge from the underlying assembly and disassembly dynamics of the actin network within an inextensible membrane bag.

We study a minimal mathematical model for polarization in mass-conserved systems. We find that the symmetry-breaking mechanism leading to cell polarization is similar to a Turing instability and typically divides the system in two regions as observed in experiments. We also find that the topology of the bifurcations present in the parameter-space of our minimal model is equivalent to the parameter-spaces of a number of more realistic mass-conserved reaction-diffusion models proposed in the literature. This equivalence suggests that the conservation of mass, a rapid cytoplasmic diffusion and bistability are sufficient and necessary conditions to generate cell polarity.

Influence of cell shape on organelle organization — Nina Malchus and Matthias Weiß — DFKZ e/O BIOQUANT, Heidelberg, Germany. Cells within a tissue often display a well-defined geometry in contrast to culture cells that adopt a wide variety of phenotypes. Using patterned substrates, we have forced cells into distinct geometries and examined the subcellular organization of organelles. To this end, we quantified the positions and shapes of organelles like the nucleus and the Golgi apparatus and determined correlations of these features within an ensemble of cells and in single cells as a function of time.

In particular, we find that positions and sizes of organelles show fairly large variations in an ensemble of cells despite a common geometry and symmetry-dependent correlations between features of different organelles.

Single cell motility in flow: how parasites invade tissue — Sivavanti Uppaluri, Niko Heddergott, Eric Stellmanns, Stephan Herminghaus, Markus Engstler, and Thomas Pfohl — Max Planck Institute for Dynamics and Self Organization, Göttingen, Germany. Foreign cells in the mammalian blood stream have to navigate through a dense and rapid stream of red blood cells to invade host tissue. Trypanosomes, parasites responsible for devastating disease in Africa, are found in the mammalian bloodstream and penetrate the central nervous system during late stages of African Sleeping Sickness. Using microfluidics as a tool to mimic blood vessels, we investigate single cell trypanosome motility. In flow, trypanosomes experience a velocity dependent lift force away from vessel walls and migrate to the centre of the vessel. Purely hydrodynamic effects arising from the trypanosome’s shape and density are distinguished from effects of cell motility by comparing with immobilised trypanosome behaviour. While immobilised trypanosomes are aligned parallel to the vessel walls in flow, self-propelling cells orient themselves perpendicular to the wall. Typical blood vessels have a cell free layer near the channel walls due to the migration of red blood cells towards the centre of the vessel. We confirm that in high flow velocities active trypanosomes are found in the depletion layer near the . Our studies show that despite relatively high flow velocities both hydrodynamic interactions and cell motility play a strong role in the overall swimming behaviour of parasites.

Influence of cell shape on organelle organization — Nina Malchus and Matthias Weiß — DFKZ e/O BIOQUANT, Heidelberg, Germany. Cells within a tissue often display a well-defined geometry in contrast to culture cells that adopt a wide variety of phenotypes. Using patterned substrates, we have forced cells into distinct geometries and examined the subcellular organization of organelles. To this end, we quantified the positions and shapes of organelles like the nucleus and the Golgi apparatus and determined correlations of these features within an ensemble of cells and in single cells as a function of time.

In particular, we find that positions and sizes of organelles show fairly large variations in an ensemble of cells despite a common geometry and symmetry-dependent correlations between features of different organelles.

Single cell motility in flow: how parasites invade tissue — Sivavanti Uppaluri, Niko Heddergott, Eric Stellmanns, Stephan Herminghaus, Markus Engstler, and Thomas Pfohl — Max Planck Institute for Dynamics and Self Organization, Göttingen, Germany. Foreign cells in the mammalian blood stream have to navigate through a dense and rapid stream of red blood cells to invade host tissue. Trypanosomes, parasites responsible for devastating disease in Africa, are found in the mammalian bloodstream and penetrate the central nervous system during late stages of African Sleeping Sickness. Using microfluidics as a tool to mimic blood vessels, we investigate single cell trypanosome motility. In flow, trypanosomes experience a velocity dependent lift force away from vessel walls and migrate to the centre of the vessel. Purely hydrodynamic effects arising from the trypanosome’s shape and density are distinguished from effects of cell motility by comparing with immobilised trypanosome behaviour. While immobilised trypanosomes are aligned parallel to the vessel walls in flow, self-propelling cells orient themselves perpendicular to the wall. Typical blood vessels have a cell free layer near the channel walls due to the migration of red blood cells towards the centre of the vessel. We confirm that in high flow velocities active trypanosomes are found in the depletion layer near the . Our studies show that despite relatively high flow velocities both hydrodynamic interactions and cell motility play a strong role in the overall swimming behaviour of parasites.

Actin network growth in the tail of small propelled particles — Julian Weichsel and Ulrich S. Schwarzb — ITP and Bioquant, University of Heidelberg.

In the lamellipodium of migrating animal cells, the growth of the actin network against the plasma membrane generates the work required to push the cell envelope forward. The same mechanism is exploited by...
patterns explain experimentally observed anomalies in growing actin networks. The steady state structure of the growing actin network in the lamellipodium can dramatically differ from what simulations and a rate equation theory predict. Fact even plastic beads, vesicles or oil droplets can be propelled in this way.

In pathogens like the Listeria bacterium and the Vaccinia virus as they move through the cytoplasm of the infected host cell, this propulsion mechanism can be observed experimentally. Even small ensembles are often difficult to detect by optical microscopy. ECIS can serve as a biosensor for detection of spatiotemporal changes on the nanometer scale such as shape, size, junctional resistance, or cell-substrate separation.

However, it is unclear how this ~500 gene machine works. Which molecular machines work at which forces on which time scales? What are the energetic of this apparatus and how do they change during external disturbances? We try to answer these questions by optically trapping the whole bacterium in a light tube, which consists of a high speed scanning line optical trap. Although propelling and kinking, the bacterium remains in the focal plane and can thereby be observed with video microscopy. In addition, trapping light scattered at the slopes of the helix gives precise 3D information about its dynamics, which is analyzed and modelled with Fourier-techniques. We show experimental results, including energies and forces involved in its motility, and compare them to simulation data. Further, we present a first model of how this minimal machine could work and which amount of power it needs for self-propulsion.

Biophysical Chemistry, University of Heidelberg, Heidelberg, Germany — Max-Planck Institute for Metals Research, Stuttgart, Germany — Biochemical Physics, University of Heidelberg, Heidelberg, Germany

Filamentous actin is one of the most investigated components of the cytoskeleton in cells. The polymerization process forming the filaments from their globular actin subunits is well known to play a crucial role in cell protrusion, such as the formation of filopodia and lamellipodia. Recent theoretical predictions suggested that the process of bundle formation of the newly polymerized actin filaments may also contribute to the forces pushing the cell membrane ahead in such protrusions. Rheology experiments reported during the last two decades on in-vitro actin gels have provided indirect information on the interactions with or without various crosslinker agents present.

We have measured the forces acting between two actin filaments using holographic optical tweezers during the bundling process in the presence of divalent cations (5mM (2+), 25-200 mM) or polyethylene glycol (PEG) polymer as depletion agents. The results indicate forces up to about 0.1 - 0.2 pN in a saturation manner, independent of the concentration of the magnesium ions above 50 mM. The magnitude of these forces is comparable to the forces produced by the polymerization ratchet, providing a direct hint that the bundling forces may contribute to the formation of cellular protrusions significantly.
solvent molecules are replaced by random thermal kicks and an effective friction acting on the particles of interest. For Brownian Dynamics the friction has to be so strong that the particles' velocities are damped much faster than the duration of an integration timestep. Here we show that this conceptual limit can be dropped with an analytic interpretation of the equations of motion. In the resulting Langevin integration scheme our recently proposed approximate form of the hydrodynamic interactions between the particles [1] can be incorporated conveniently, leading to a fast multi-particle propagation scheme, which captures more of the short-time and short-range solvent effects than standard BD. Comparing the dynamics of a bead-spring model of a short peptide, we recommend to run simulations of biological molecules and polymers with the Langevin type finite damping and to include the hydrodynamic interactions [2].


Transport of a semiflexible filament in a network — ● TERESA BAUER1, FELIX HÖFLING1, ERWIN FREY2, and THOMAS FRANOSCH3 — 1Arnold Sommerfeld Center (ASC) for Theoretical Physics and Center for NanoScience (CeNS), Fakultät für Physik, Ludwig-Maximilians-Universität München, Germany — 2Max-Planck-Institut für Metallforschung, Stuttgart and Institut für Theoretische und Angewandte Physik, Universität Stuttgart, Germany — 3Institut für Theoretische Physik, Universität Erlangen-Nürnberg, Germany

The cytoskeleton of a cell is comprised of a network of various biopolymers. A prominent example is the filamentous actin, a semiflexible polymer studied extensively also in vitro. The transport of a single semiflexible filament in a strongly entangled network is highly directed along the confining tube formed by the surrounding network.

We have investigated the dynamics of a semiflexible filament in a plane in the presence of immobilized obstacles mimicking the constraints of the crosslinked network. The inextensibility constraints are encoded via a bead-rod-algorithm extended by a suitable collision rule and extensive simulations are performed. In particular we quantify the translational and rotational diffusion investigated for a broad density range and visualize the dynamics using representative animations. Furthermore we discuss issues of numerical stability.

15 min. break

Interplay of conformational degrees of freedom and crosslink binding in filamentous biopolymer bundles — ● CLAUS HEUSINGER — Institute for Theoretical Physics, University of Goettingen, Germany

Crosslinked F-Actin bundles constitute principal components of a multitude of cytoskeletal processes and play key roles in many cellular functions. Much of the special properties of crosslinked biopolymer bundles derives from the entanglement of bundled and degrees of freedom with the internal binding status of the crosslinking agent. Depending on probing time- and length-scales this interplay can lead to interesting dynamical effects as well as non-trivial elasto-plastic phase-behavior. By employing theoretical considerations combined with Monte-Carlo simulations, we will discuss some aspects of the internal dynamics of the cross-linker whose binding affinity serves to stabilize the bundle. We show how an imposed bundle deformation modifies the equilibrium binding constant and even allows for the coexistence of different bundle states.

Thermophoresis quantifies the Conformation and Stability of Biomolecules — ● CHRISTOPH JENS WIENKEN, PHILIPP BAASKE, STEFAN DUHR, and DIETER BRAUN — Systems Biophysics, LMU, München, Germany

Thermophoresis is the directed movement of molecules in a temperature gradient. It depends on surface characteristics of the molecule, such as size, charge and hydrophobicity [1]. Its sensitivity for small changes in above parameters was recently shown by analyzing the binding reactions of DNA aptamers and a variety of proteins [2,3].


Liquid-liquid phase separation in protein solutions induced by multivalent counter ions — ● MARCELL WOLF, FAJUN ZHANG, FELIX ROOSEN-RUNGE, ANDREA SAUTER, and FRANK SCHREIBER — Institut für Angewandte Physik, University of Erlangen, Germany

The liquid-liquid phase separation (LLPS) in concentrated protein solutions can be induced by multivalent counter ions such as the sickle cell anemia protein, HbS, or Yttrium Chloride (YCl3). The phase diagram of proteins with YCl3 in the c12 concentration) - c3 (salt concentration) plane is determined. The protein solution undergoes a phase-separation upon adding salt up to a critical value c*. Further, beyond c* the system is thermodynamically equivalent to the phase behavior

(AWI). Furthermore, we showed that the role of membranes in amyloidogenesis has been previously underestimated; in an in vitro-like situation (with no AWI), anionic liposomes (containing dioleoylphosphatidylglycerol) enhanced islet amyloid polypeptide (IAPP) fibrilogenesis far more than described previously in conventional assay conditions (in the presence of an AWI). These findings have implications for the protein misfolding field and in assay design to target toxic protein aggregation.


Keratin homogeneity in the tail feathers of peacocks — • Silvia Parischi1,2, Stephan Puchegger1, Ingrid M. Weiss3, Helmut O. Kirchmair1, and Herwig Peterlik1 — 1University of Vienna, Faculty of Physics, Vienna, Austria — 2Institute for Materials Chemistry, University of Technology, Institute for Materials Chemistry, Vienna, Austria — 3INM-Leibniz Institute for New Materials, Saarbrücken, Germany

X-ray diffraction studies successfully clarified the structure of avian feathers: Each filament has a helical structure with four repeating units per turn.[1] The structure of avian feathers is very stable though their relative density is low. The keratin structure in the cortex of peacock's feathers is studied by X-ray diffraction along the feather, from the calamus to the tip. It changes considerably over the first 5 cm close to the calamus and remains constant for about 1 m along the length of the feather. We attribute the X-ray patterns to a shrinkage of a cylindrical arrangement of beta-sheets, which is not fully formed initially. In the final structure, the crystalline beta-cores are fixed by the rest of the keratin molecule. The hydrophobic residues of the beta coiled into a zip-like arrangement. Tensile and compression tests are additionally performed in-situ to follow the structural change as consequence of varying load.

of a hard sphere with short range interactions, which exhibits a sta-
ble gas-solid transition and a metastable LLPS. The phase boundary
is determined by UV and X-ray absorption. The effective protein-
protein interactions in solutions upon LLPS are investigated by SLS
and SAXS. The resulting interaction potential has been compared and
discussed based on the thermodynamic criteria. [1] J.D. Gunton, A.
Shiryayev, D. L. Pagan, Protein Condensation, 2007, Cambridge Uni-

BP 24: Physics of Cells II

Time: Thursday 10:15–13:00
Location: ZEU 250

BP 24.1 Thu 10:15 ZEU 250
Anomalous reaction kinetics in crowded fluids — Marcel Hellmann1,2, Dieter W. Herrmann2, and Matthias Reiss1,3
1 Cellular Biophysics Group, German Cancer Research Center, D-69120 Heidelberg, Germany — Institut für Theoretische Physik, Uni-
versität Heidelberg, D-69120 Heidelberg, Germany — Experimental Physics I, University of Bayreuth, D-95440 Bayreuth, Germany

Anomalous diffusion in crowded fluids, e.g. in the cytoplasm or on
membranes of living cells, is a frequent phenomenon. The experi-
mentally observed subdiffusive characteristics is most consistent with
fractional Brownian motion, i.e. the motion of particles in a viscoelas-
tic medium. Here, we show that biochemical reactions, e.g. (mul-
tiple) phosphorylation events, are massively influenced by the reac-
tants’ (sub)diffusion characteristics. In virtually all studied cases an
anomalous kinetics was observed, i.e. a time-dependent rate coefficient
emerged along with a segregation of reactants. As a consequence, mul-
tiple phosphorylation events, e.g. in intracellular signaling cascades,
may occur with a higher probability as compared to reactions in purely
viscous (water-like) environments that are fueled by a normal diffusion.

BP 24.2 Thu 10:30 ZEU 250
Thermal Measurements in Single Cells — Simona Hecht1, Miriam Giesguth2, Genter Reiss3, and Karl-Josef Dietz2
1 Fakultät für Physik, Universität Bielefeld — 2 Fakultät für Biologie, Universität Bielefeld

Thermocouples based on the Seebeck effect are commonly used as
thermal sensors for a wide range of applications. Since the voltage
measured at the reference points only depends on the temperature dif-
ference between the overlap of the two metals and the reference points
and not on the size of the system, thermo couples can also be manu-
factured on chip or even onto a glass capillary.

Ni and NiCr (Seebeck coefficient = 40 μV/K) was placed on the op-
opposite sites of a glass capillary, which can be manipulated with a
micromanipulator system. In this way, it is possible to place the cap-
illary in a plant leaf and to measure the temperature increase during
illumination. Due to the fine control of the micromanipulator, the mi-
crocapillary can also be inserted into a single cell, like a trichome of
Arabidopsis italiana.

BP 24.3 Thu 10:45 ZEU 250
High resolution imaging of the surface of single bacterial cells — Dominik Greif, Daniel Wesner, Jan Rectmeyer, and Dario Anselmetti
Experimental Biophysics & Applied Nanoscience, Bielefeld University, Universitätsstr. 25, 33615 Bielefeld, Germany

Native surface structures of living bacteria are difficult to analyse by
imaging with traditional scanning electron microscopy (SEM) because
of possible artefacts that stem from the often necessary sample prepa-
ration procedures.

We systematically investigated the origin of surface morphology ob-
served on Sinorhizobium meliloti bacterial cells by comparing results of
the complementary techniques atomic force microscopy (AFM) and
SEM. Those were applied from living bacteria in physiological environ-
ment to fixed bacteria in high vacuum. Stepwise, we applied different
micromanipulator system. In this way, it is possible to place the cap-
illary in a plant leaf for proper chromosome segregation. In an early
pathway (PW), the older of the two spindle pole bodies (oSPB) is
moved towards the mother-bud neck by astral microtubules (aMT). Duri-
ing a late pathway, the aMTs grow inside the bud and get captured by
the dynein anchor Num1 located in the bud cell cortex. Dynein trans-
lates the oSPB through the neck by pulling on the aMTs.

Fast live cell imaging, quantitative image analysis and mathematical
modeling is applied. Wild-type (WT) cells and cells lacking the early
PW nearly all finished translocation of the spindle within 30 minutes
from the onset of mitosis (spindle L ≥2μm), only 80% of the cells
lacking the late PW were able to do so. The spindle movement often
shows pulling events (PE), i.e. rapid jumps of the spindle. In WT

cells, these PE more often occur after the oSPB entered the bud. Cells
lacking the late PW show much less PE and cells without the early PW
show hardly any PE before the spindle entering. Thus, the efficiency
of the delivery of the oSPB to the daughter cell depends mainly on the
late PW, whereas the early PW is required to orient the spindle.

15 min. break

BP 24.6 Thu 11:45 ZEU 250
Using novel microscopy methods to correlate pluripotent stem cell state with subcellular structure — Kevin Chalut, Markus Hoepfler, Andrew Ekpenyong, and Jochen Guck
Max Planck-Institute for Cell Biology and Genetics, Dresden

The function of pluripotent stem cells (PSCs) is to commit to all types of
tissue cells needed for an organism while self-renewing and main-
aining their pluripotency until all lineages are established. PSC state — pluripotent, pre-committed, or committed — has primarily been probed by investigating biochemical properties, but the mystery of how bio-
chemical diversity is established while maintaining pluripotency remains
unsolved. In an effort to solve this mystery, we probed PSC state by
evaluating their physical properties. These physical properties include their internal structure, particularly changes in chromatin structure. To visualise the relationship between chromatin structure and PSC state, we used a fluorescent label for heterochromatin proteins, and then imaged using confocal microscopy and STED. Furthermore, we used digital holographic microscopy, a live-cell and label-free technique, to visualise chromatin structure and correlate it with PSC state. We saw in all techniques that, prior to differentiation, the chromatin structure opens up considerably, diffusing throughout the nucleus. This opening up of chromatin correlates with greater transcriptional accessibility.

### Anomalous diffusion of intracellular lipid granules

**Christine Selhuber-Unkel,1,2,3 Pernille Yde,2,3 Jae-Hyung Jeo3, Vincent Tejedor3, Kirstine Berg-Sorensen4, Ralf Metzler5, and Lene B. Oddershede6 — 1University of Copenhagen, Niels Bohr-Institute — 2Technical University Munich, Physik-Department — 3Technical University of Denmark, Department of Physics, Kgs. Lyngby**

The intracellular motion of cellular compartments plays an essential role for directed and undirected intracellular transport processes. We used live cell imaging and optical tweezers to track single endogenous, intracellular particles with high temporal and spatial resolution in order to investigate the diffusion properties of the granules in the different phases of the cell cycle. We found that the majority of the lipid granules underwent subdiffusive motion during all stages of the cell cycle. Interestingly, our results indicate that the cytoplasm is more elastic during interphase than during cell division and that its elasticity is relatively constant during the stages of cell division. In interphase, a comparison of our data with complementary analytical results has shown evidence for anomalous diffusion and ageing. We demonstrate that in the millisecond regime the granules follow subdiffusive motion according to the laws of continuous time random walk theory. At longer times granule motion is consistent with fractional Brownian motion.

### Physical description of centrosome assembly and disassembly

**David Zwicker1, Markus Decker2, Steffen Jaensch2, Anthony A Hyman3, and Frank Jülicher1 — 1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany**

The size of many cell organelles is strongly correlated with cell size. Achieving this requires a robust mechanism for scaling subcellular structures. Here, we propose a theoretical description of the growth phase of the centrosome, an organelle involved in mitosis. We identify a possible mechanism by which the centrosome volume may be controlled. Not only can our theory explain the growth dynamics for all cell sizes down to the sixteen cell stage of the C. elegans embryo, but it does also account for data acquired in experiments with aberrant numbers of centrosomes or altered cell volumes. Additionally, the model can describe the dissolution phase occurring during cell division and centrosomes of unequal size observed in cells with disturbed centrosomes.

### Spatial organization of the cell cytoplasm: Protein gradients and liquid-liquid phase separation in the C. elegans embryo

**Chu Fan Lee1, Clifford P. Brangwynne2, Zdeněk Petrášek3, Jörn Gehrakhani1, Anthony A. Hyman2, and Frank Jülicher1 — 1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — 3Biotechnologisches Zentrum der TU Dresden, Dresden, Germany**

During the asymmetric division of the one-cell stage embryo of the nematode C. elegans, germ line granules (P-granules) segregate and localize in the posterior half of the cell in order to be unequally distributed to the two daughter cells. Segregation occurs via a spatial gradient of supersaturation of P-granule components which nucleate in droplets on in the posterior side and dissolve in the anterior side. This supersaturation gradient is generated by convection–diffusion of the protein Mex-5. Using a combined experimental and theoretical approach, we show that the Mex-5 gradient is established by modulation of the diffusivity of Mex-5 via reactions that occur at the cell cortex and within the cytoplasm. We propose that Mex-5 may control P-granule phase separation via its competitive RNA binding activity, by which the local Mex-5 concentration influences the saturation point of the phase transition that triggers P-granule formation.
that the evolution of the network strongly depends on the efficiency of the protoplasmic transport in the arteries.


A Thermal Trap for DNA Replication

Christoph B. MAST and Dieter BRAUN — Systems Biophysics, Physics Department, Center for Nanoscience, Ludwig Maximilians Universität München, Amalienstr. 54, 80799 München, Germany

The hallmark of living matter is the replication of genetic molecules and their active storage against diffusion. We implement both in the simple non-equilibrium environment of a temperature gradient. Convective flow both drives the DNA replicating polymerase chain reaction (PCR) while concurrent thermophoresis accumulates the replicated 143 base pair DNA in bulk solution. The time constant for accumulation is 92 s while DNA is doubled every 50 s. The length of the amplified DNA is checked with thermophoresis. Finite element simulations confirm the findings. The experiments explore conditions in pores of hydrothermal rock which can serve as a model environment for the origin of life.

Negative design in protein folding: The role of correlations

Jonas Mtsning1, Ugo Bastolla2, and Markus Porto3

1 Institut für Festkörperphysik, Technische Universität Darmstadt, Germany — 2Centro di Biologia Molecolare ‘Severo Ochoa’, Madrid, Spain — 3Institut für Theoretische Physik, Universität zu Köln, Germany

Assessing the stability of a protein sequence folded into its native structure is a crucial aspect of protein design and of understanding protein evolution. Folding stability has two sides: (i) stability against the unfolded ensemble, which is usually achieved by evolution providing the native state with native contacts that are attractive enough to compensate for the loss of conformational entropy (positive design), and (ii) stability against incorrectly folded (misfolded) structures with low free energy, which is achieved through negative design.

A simple approximation based on the Random Energy Model (REM) and hence on the neglect of correlations predicts that negative design can be achieved by reducing the variance of the contact interaction energies of all possible residue-residue contacts. We verify that this approximation provides a good fit of the minimum free energy of misfolded structures. Nevertheless, our results suggest that negative design in protein evolution follows actually a completely different strategy, namely utilizing structural correlations between pairs of positions in the misfolded ensemble, which are neglected in the REM approach. We discuss how a REM approach might be generalized to include these correlations.

15 min. break

Assessing the asymptotic fitness distribution of beneficial mutations from incomplete data sets

Ivan Szendro1, Martin Evans1, and Joachim Krug2

1 Bernstein Center for Computational Neuroscience Göttingen, Germany — 2Network Dynamics Group, Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Migration between different habitats is ubiquitous among biological populations. Here we discuss a simple model for evolution of sexual organisms in two different habitats coupled by one-way migration as well as mutations. This gives rise to clusters of closely related genotypes (quasispecies). The habitats are assumed to have different fitness landscapes, i.e., organisms which are well-adapted in the primary habitat are likely to be maladapted in the secondary habitat. The model undergoes a dynamical phase transition: at a critical value of the migration rate, the time to reach the steady state diverges. Above the transition, the population is dominated by immigrants from the primary habitat. Below the transition, the genetic composition of the population is highly non-trivial, with multiple coexisting quasispecies which are not native to either habitat. Using results from localization theory, I will show that the critical migration rate may be very small — demonstrating that evolutionary outcomes can be very sensitive to even a small amount of migration.

The role of population size in the evolution of microbial populations

Joachim Krug1, Kavita Jain2, and Su-Chan Park3

1 Institut für Theoretische Physik, Universität zu Köln, Cologne, Germany — 2Theoretical Sciences Unit and Evolutionary and Organisal Biology Unit, Jawaharlal Nehru Centre, Bangalore, India — 3Department of Physics, The Catholic University of Korea, Bucheon, Korea

The speed of adaptation of a population placed into a new environment is generally expected to increase with increasing population size, for at least two reasons: The supply of beneficial mutations is proportional to population size, and the probability of fixation of deleterious
mutations is negligible in large populations. Contrary to this expectation, recent experiments on microbial populations have shown that small populations evolving in a complex nutrient medium may achieve a higher fitness than large ones due to the increased heterogeneity of adaptive trajectories. We introduce a class of haploid three-locus fitness landscapes that allows to investigate this scenario in a precise and quantitative way. Our main result derived analytically shows how the probability of choosing the path of largest initial fitness increase grows with the population size. This makes large populations more likely to get trapped at local fitness peaks and implies an advantage of small populations at intermediate time scales. Additional studies using ensembles of random fitness landscapes show that the results achieved for a particular choice of three-locus landscape parameters are robust and also persist as the number of loci increases.

**BP 26: Biophysics II: Mechanics and Flow in Biological Systems (joint AG jDPG, BP)**

**Invited Talk**

**BP 26.1** Thu 10:30 HSZ 201

**The Hydrodynamics of Microswimmers** — [Gerhard Gompper](https://www.istp.uni-leipzig.de/en/) — Institut für Festkörperforschung and Institute of Advanced Simulations, Forschungszentrum Jülich, Jülich, Germany

Both in soft matter and in biology, there are numerous examples of swimmers and self-propelled particles. With a typical size in the range of a several micro-meters, both low-Reynolds-number hydrodynamics and thermal fluctuations are essential to determine their dynamics [1,2]. Prominent examples are sperm cells which are propelled by a snake-like motion of their tail, bacteria like *E. coli* which move forward by a rotational motion of their spiral-shaped flagella, and synthetic bimetallic nanorods. We have studied the behavior of sperm cell and self-propelled rods by performing multi-particle collision dynamics (MPC) simulations, a particle-based mesoscale hydrodynamics technique which captures the hydrodynamic behavior of a wide range of complex fluids very well [3,4]. We focus here on the cooperative behavior of swimming sperm [5], and on the dynamic properties of individual sperm cells and nanorods near surfaces [6,7]. Both sperm cells and self-propelled rods display a strong surface excess in confined geometries. For rods, scaling laws for the dependence of the surface excess on the rod length and the propulsive force are derived [6].

---


---

**Invited Talk**

**BP 26.2** Thu 11:00 HSZ 201

**What sperm head wiggling can tell us about flagellar hydrodynamics** — [B.M. Friedrich](https://www.tu-berlin.de/en/) — I.H. Riedel-Kruse, J. Howard, and F. Julicher — Weizmann Institute of Science - Department of Materials and Interfaces, Rehovot, Israel — [Max-Planck-Institute for the Physics of Complex Systems, Dresden, Germany] — Stanford University, Stanford, USA — [Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany]

Sperm cells propel themselves in a liquid by generating regular bending waves of their whip-like flagellum. At the relevant length and time scales of sperm swimming, inertia is negligible and self-propulsion is achieved purely by viscous forces. The shape of the flagellar beat determines the path along which a sperm cell swims. To test a simple hydrodynamic theory of flagellar propulsion known as resistive force theory, we conducted high-precision measurements of the head and flagellum motions during circular swimming of bull spermatozoa near a surface. On short time-scales, the sperm head “wiggled” around an averaged path with the frequency of the flagellar beat. We found that the fine-structure of sperm swimming represented by this rapid wiggling is, to high accuracy, accounted for by resistive force theory and results from balancing forces and torques generated by the beating flagellum. By comparing experiment and theory, we could determine the hydrodynamic friction coefficients of the flagellum.

On time-scales longer than the flagellar beat cycle, sperm cells followed circular paths of non-zero curvature due to an asymmetry of their flagellar bending waves, in agreement with quantitative predictions of resistive force theory.

Finally, I will discuss how sperm cells can actively regulate the non-zero curvature of their swimming paths and address the relation to sperm navigation in a concentration gradient of a chemoattractant.

References


---

**BP 27: Physics of Cells III**

**Invited Talk**

**BP 27.1** Thu 14:00 ZEU 250

**Inelastic Mechanics of Biopolymer Networks** — [Klaus Kroy](https://www.uni-leipzig.de/) — Institut für Theoretische Physik, Universität Leipzig

Live cells have ambiguous mechanical properties. They were often described as either elastic solids or viscoelastic fluids and have recently been classified as soft glassy materials characterized by weak power-law rheology. Nonlinear rheological measurements have moreover revealed a pronounced inelastic response indicative of a competition between viscoelastic stiffening and inelastic fluidization. It is an intriguing question whether these observations can be explained from the material properties of much simpler in-vitro reconstituted networks of cytoskeletal biopolymers. I will summarize some recent theoretical advances in this direction.

---

**BP 27.2** Thu 14:30 ZEU 250

**Buckling instability of motor driven rotating bacterial flagella** — [Reinhard Vogel](https://www.tu-berlin.de/) and Holger Stark — TU Berlin

Many types of bacteria, such as *E. coli* and *Salmonella*, swim by rotating a bundle of helical filaments also called flagella. Each filament is driven by a rotary motor. When its sense of rotation is reversed, the flagellum leaves the bundle and undergoes a sequence of configurations characterized by their pitch, radius, and helicity (polymorphism).

Finally the flagellum assumes its original form and returns into the bundle.

The bacterial flagellum consists of three parts; the rotary motor embedded in the cell membrane, a short proximal hook that couples the motor to the third part, the long helical filament. The helical shape of the filament converts rotational motion into a thrust force that pushes the bacteria forward.

In our contribution, we demonstrate how the hook, which transfers the motor torque to the filament, can be modeled. We then investigate how the flexible filament reacts on the applied motor torque. For small torques and a resulting thrust force pushing the bacterium forward, the helical axis is approximately parallel to the motor torque and the filament is only slightly compressed. However, when the torque is increased, the straight helical form becomes unstable and we observe a buckling instability or Hopf bifurcation when the compression becomes too strong. We analyze how the mobility of the cell body and thermal noise influence the instability and discuss its biological implications, in particular, for the formation of the bundle.

---

**BP 27.3** Thu 14:45 ZEU 250

**Novel micro-analytical techniques for diagnostics of malaria infected red blood cells** — [Jakob Mauritz](https://www.tu-berlin.de/), Clemens Kaminiski, Teresa Tiffert, and Virgilio Lew — Universitàt Cambridge,
Vereinigtes Königreich

We report on the application of advanced microanalytical techniques for the study of Plasmodium falciparum infected red blood cells. Using confocal microscopy, volume and shape changes of living red blood cells can be measured at femtolitre resolution throughout the intraerythrocytic infection cycle of the parasite. The cytomechanical properties are studied using a novel optical stretcher device constructed by the authors, which enables individual infected cells to be trapped and manipulated optomechanically in microfluidic channels. Finally, novel results of X-ray microanalysis and fluorescence lifetime imaging for the quantification of haemoglobin and ion content and concentrations are reported on. In their combination, these methods offer unique insight into the homeostasis and volume regulation during the infection cycle of the red blood cell.

BP 27.4 Thu 15:00 ZEU 250
Friction Modulated Traction Force in Cell Adhesion — Tilo Pompe, Stepan Glö rowski, Stephanie Johnne, Maria Kasimir, Martin Kaufmann, Lars Renner, Manfred Bobeth, Wolfgang Pompe, and Carsten Werner.

The force balance between the extracellular microenvironment and the intracellular cytoskeleton controls cell fate decisions. We report a new mechanism of receptor force control in cell adhesion originating from friction between cell adhesion ligands and the supporting matrix. Myosin motor activity in conjunction with assembly of fibronectin ligands non-covalently coupled to polymer surfaces of graded physics-chemistry is shown to result in modulated traction forces of adherent cells. By using a diffusion process for the description of ligand reorganization with the growing fibronectin fibrils acting as local sinks, the determined ligand mobility is correlated to traction force measurements. We conclude that the modulation of the ligand-support anchorage allows to tune cellular traction forces at adhesion receptors in the pN range by a frictional mechanism. Hence, adhesion-ligands friction has to be considered to be highly relevant in studying mechanotransduction and cell development of adherent cells.

BP 27.5 Thu 15:15 ZEU 250
Elastic interactions with the substrate can guide spatial re-organization during myofilibrin assembly — Benjamin M. Friedrich, Amin Buchoz, Dennis E. Discher, and Samuel A. Safran.

Myofilibrin bundles can dynamically assemble and disassemble on the cell-substrate interface. In the presented study cells, artificially suspended by trypsin, were investigated to elucidate the influence of calcium signals on the mechanical properties of the same cell by applying oscillatory forces. Here, we present results on cell contractility of 3T3 fibroblasts and use biochemical perturbations (e.g. blebbistatin, a potent non muscle myosin II inhibitor) to elucidate the contributions of different cytoskeletal elements to the active and passive mechanical properties of a cell.

BP 27.6 Thu 15:30 ZEU 250
Contractile network models for adherent cells — Philip Guthardt Torres, Ilka B. Bischof, and ULRICH S. Schlessinger.

Cells communicate with their environment biochemically, but also through mechanical interactions. Cells can generate contractile forces through their acto-myosin network and use these forces to actively probe the mechanical response of their surroundings. This results in cellular reactions, a process called mechanosensing.

Our dual optical-trap setup allows us to perform high-resolution measurements of the forces a cell generates between two fibroinectin-coated beads by analyzing the fluctuations of the beads at high spatial and temporal resolution. Simultaneously, we actively probe the visco-elastic properties of the same cell by applying oscillatory forces.

Under physiological conditions many cells must react to mechanical stimuli. This raises interesting questions regarding the mechanisms by which cells register and respond to applied forces. For adherent cells focal adhesions seem to play an important role in mechano-tranduction. Also calcium, one of the most important second messengers, is involved in a number of known mechano-activated cell responses.

In the presented study cells, artificially suspended by trypsin, were investigated to elucidate the influence of calcium signals on the mechanical properties of cells independent of focal adhesions. To this end techniques to visualize, quench, and artificially induce calcium signals were combined with the Optical Stretcher, a tool to probe global mechanical behavior of single cells in suspension. In the Optical Stretcher, cells are trapped by two anti-parallel laser beams. By increasing the laser power, the momentum transferred to the cell surface causes visible deformations. Different cells such as fibroblasts, epithelial cells, myotubes and a TRPV1 transfected kidney cell line were investigated by a combination of Optical Stretching and fluorescence calcium imaging in the Laser Scanning Microscope.

BP 27.7 Thu 16:00 ZEU 250
High-Resolution Cell Mechanics with a Dual Optical Trap — Florian Schlosser, Christoph F. Schmidt, and Florian Rehfeldt.

High-Resolution Cell Mechanics with a Dual Optical Trap — Florian Schlosser, Christoph F. Schmidt, and Florian Rehfeldt.

The crawling of eukaryotic cells on substrates is driven by the cytoskeleton and its contraction due to myosin II motor activity. In contrast to Hookean and passive cable networks, here shape and force distribution are determined by local rather than global determinants and thus are suited to endow the cell with a robust sense of its environment. We compare our numerical results with analytical approaches and discuss an extension of this approach which considers adaptive linker mechanics.

15 min. break

BP 27.8 Thu 16:15 ZEU 250
Influence of Calcium Signaling on Biomechanics of Single Suspended Cells in the Optical Stretcher — Markus Gyger and Josef A. Käs.

The crawling of eukaryotic cells on substrates is driven by the cytoskeleton. How the cytoskeleton is organized and how it responds to external stimuli during this process is still poorly understood. Spontaneous polymerization waves have been suggested to provide a means for cytoskeletal organization. We theoretically investigate the response of such waves to applied forces and to local modifications of the polymerization activity. We identify conditions under which a wave is reflected and when it is captured by an obstacle. Our results suggest a possible mechanism for responses of cells encountering another cell. It might be relevant for T cells that need to decide quickly whether to kill a cell they encountered or to crawl away and search other cells.

BP 27.9 Thu 16:30 ZEU 250
Responses of cytoskeletal waves to stimuli and possible implications for cell behaviour — Alexander Drehner, Konstantin Dubroviskii, and Karsten Kruse.

The crawling of eukaryotic cells on substrates is driven by the cytoskeleton. How the cytoskeleton is organized and how it responds to external stimuli during this process is still poorly understood. Spontaneous polymerization waves have been suggested to provide a means for cytoskeletal organization. We theoretically investigate the response of such waves to applied forces and to local modifications of the polymerization activity. We identify conditions under which a wave is reflected and when it is captured by an obstacle. Our results suggest a possible mechanism for responses of cells encountering another cell. It might be relevant for T cells that need to decide quickly whether to kill a cell they encountered or to crawl away and search other cells.

BP 27.10 Thu 16:45 ZEU 250
The contribution of cytoskeleton networks to stretch is strain dependent. — KEHENCHUKU DAVID NYETU, TOBIAS KRIESSLING, ROLAND STANGE, and JOSEF KAS — Institut für Experimentelle Physik I, Universität Leipzig, Linnéstr 5, 04103, Leipzig Germany

The interaction between the cytoskeleton filaments in a cell provides it with mechanical stability and enables it to remodel its shape. The rheological response of cells has been characterized either as viscoelastic or soft-glassy which neglects the molecular origin of cell response. In this work, by using a large amount of cells (> 10,000) exceeding previous statistics by a decade, we link observed cell response to its molecular origin by showing that actin and microtubule networks maintain the mechanical integrity of cells in a strain dependent manner. While the actin network solely regulates cell deformation at small strain, the microtubule network was responsible for cell relaxation. At large strain, actin and microtubule networks dominated cell response with microtubules having a biphasic effect on cells upon stabilization. This effect explains the relapse of some cancer after chemotherapy treatment using Taxol thus providing a bridge between soft condense matter physics and systems biology.

BP 28: Statistical Physics in Biological Systems IV (joint DY, BP)

Time: Thursday 14:00–16:45

BP 28.1 Thu 14:00 ZEU 260

Evolution of complex chemical mixtures: a problem linked to the origin of life — EVA WOLLRAH1, SABRINA SCHEERR1, CHRISTIAN LIV1, MANUEL WOST3, PHILIPP ZIMMERM, KARSTEN KRUSE2, and ALBRECHT OTT1 — 1Universität des Saarlandes, Biologische Experimentalfysik, 66123 Saarbrücken; 2Universität des Saarlandes, Theoretische Biologische Physik, 66123 Saarbrücken

How self-reproducing structures can form in a chemical mixture and how a steady increase in biochemical complexity of these cycles may occur is still unknown. We approach this question experimentally from two different directions.

In the first class of experiments highly reactive, primitive compounds are mixed. We track the temporal development of the mixture using mass spectrometry for analysis. Tools from bioinformatics help us to develop ideas about the underlying chemical network.

The second class of experiments employs DNA. The DNA is designed to form autocatalytic reaction pathways. These experiments are designed to inductively find new conditions for self-reproducing chemical cycles. We suggest that this situation can be simulated in silico by autocatalytic reactions that exhibit fluctuations of the reaction pathways.

BP 28.2 Thu 14:15 ZEU 260

Complexity-stability relations in generalized food-web models with realistic parameters — SEBASTIAN PLITZEG, CHRISTIAN GULL, and BARBARA DROSSEL — Institut für Festkörperphysik, TU Darmstadt, Hochschulstraße 6, 64289 Darmstadt, Germany

We investigate conditions for positive complexity-stability relations in the niche model for food webs by evaluating the local stability of the fixed points of the system. We use a generalized method, where the fixed points are normalized to 1, which allows for an efficient numerical evaluation. We find that positive relations between local stability and complexity can be obtained if prey is not scarce, biomass loss due to predation is low and density-dependent mortality effects dominate over other contributions to mortality. Since these conditions are expressed in terms of the generalized parameters, we then determine the range of values of these parameters within locally stable niche model food webs with explicit dynamical equations. These equations include allometric scaling and parameter values that are realistic. We find that the values of the generalized parameters obtained from this explicit dynamical model depend on the trophic level. The range of these parameters is such that positive complexity-stability relations can be obtained.

BP 28.3 Thu 14:30 ZEU 260

Statistical topography of fitness landscapes — JASPER FRANK1, ALEXANDER KLOZEN1, J. ARIAN G. M. DE VISSER2, and JOACHIM KRUC1 — 1Cologne University, Cologne, Germany; 2Wageningen University, Wageningen, Netherlands

The adaptive evolution of a population under the influence of mutations and selection is governed by the structure of the underlying fitness landscape. Previous theoretical studies of topographical quantities on fitness landscapes have mostly focused on local properties such as local maxima.

Here we investigate the global property of accessible paths traversing the complete genome configuration space towards the global optimum. Numerical and analytical studies and comparison to empirical data suggest a surprising universality across almost all established theoretical models, indicating high accessibility of the globally optimal configuration in the biologically relevant limit of very long genome sequences.

BP 28.4 Thu 14:45 ZEU 260

Speed of Evolution in Spatially Extended Populations — JASPER A. MARTHA and OSCAR HAALSTRA — Group for Biophysics and Evolutionary Dynamics, Max Planck Institute for Dynamics and Self-Organization, 37075 Göttingen, Germany

How fast do species adapt to a given environment? This is one of the most fundamental questions in evolutionary biology. Many theoretical models are restricted to the case of well-mixed populations. To characterize the speed of evolution in spatially extended populations, it is necessary to consider the wave-like spread of evolutionary novelties. The presence of such wave-like sweeps reduces the speed of evolution for two reasons. First, the waves are slower than the exponential spread of beneficial mutations known from well-mixed populations. Second, because these sweeps are slower, spatially extended populations are more prone to be in a state where multiple beneficial mutations sweep simultaneously. This problem of clonal interference has been demonstrated in microbial experiments and has recently gained scientific interest. We simulate the spread of mutations in spatial dimensions using computer simulations, where we include effects of recombination and long-range migration. We find that 1) the adaptation rate obeys robust power laws, which 2) are independent of the particular choice of selective fitness distributions ("universality"), 3) that spatial populations experience clonal interference over a broader range of parameters, and 4) that the effects of clonal interference can be mitigated by recombination and long-range migration. We therefore speculate that both processes are selectively favorable.

BP 28.5 Thu 15:00 ZEU 260

Predators, parasites and food web stability — LARS RUDOLP1, NEO MARTINEZ2, and THILO GROSS1 — 1Max-Planck-Institut für Physik komplexer Systeme, Dresden — 2Pacific Ecoinformatics and Computational Ecology Lab, Berkley, USA

Predator-prey interactions and their influence on food web stability are a major topic of ecological research. The investigation of parasitic interactions, which are another fundamental part of the most ecological communities, has been less intensive. To close that gap, we used generalized modeling and studied several million replicates of food webs with different proportions of parasitic species. In this way we determine the impact of parasitism on different food web properties and how these properties affect food web stability. Specifically, we show that a moderate proportion of parasitic species enhances food web stability.

15 min. break

BP 28.6 Thu 15:30 ZEU 260

Dynamics of mutants in a stochastic compartment approach of hematopoiesis — BENJAMIN WERNER and ARNE TRAULSEN — Research Group for Evolutionary Theory, Max Planck Institute for Evolutionary Biology, 24306 Plön

Cancer is typically caused by at most a handful of mutations that increase the reproductive fitness of a single cell. The probability of such a mutation, the dynamics of the resulting clone of cancer cells, and thus the effect to an organism is under intense investigation. First we present an established stochastic compartment model of hematopoiesis [1,2], CML as well as other blood disorders [3,4] can be embedded and analyzed in this framework. We show that there
is a closed deterministic solution to the dynamics of mutants in this model that fits the averages of the stochastic process. This solution enables us to connect different model parameters directly to observed cell dynamics and thus gives in principle yet unknown information about disease progression and the impact of drug treatment. 

References:

Stochastic slowdown in evolutionary processes

We examine birth-death processes with state dependent transition probabilities and at least one absorbing boundary. In evolution, this describes selection acting on two different types in a finite population where reproductive events occur successively. If the two types have equal fitness the system performs a random walk. If one type has a fitness advantage it is favored by selection, which introduces a bias (asymmetry) in the transition probabilities. How long does it take until advantageous mutants have invaded and taken over? Surprisingly, we find that the average time of such a process can increase, even if the mutant type always has a fitness advantage. We discuss this finding for the Moran process and develop a simplified model which allows for a more intuitive understanding. We show that this effect can occur for weak but non-vanishing bias (selection) in the state dependent transition rates and infer the scaling with system size. We also address the Wright-Fisher model commonly used in population genetics, which shows that this stochastic slowdown is not restricted to birth-death processes.

Evolutionary Game Theory in Growing Populations

Existing theoretical models of evolution focus on the relative fitness advantages of different mutants in a population while the dynamic behavior of the population size is mostly left unconsidered. We present a generic stochastic model which combines the growth dynamics of the population and its internal evolution. Our model thereby accounts for the fact that both evolutionary and growth dynamics are based on individual reproduction events and hence are highly coupled and stochastic in nature. We exemplify our approach by studying the dilemma of cooperation in growing populations and show that genuinely stochastic events can ease the dilemma by leading to a transient but robust increase in cooperation.

A Non-Equilibrium Phase Transition in Expanding Populations

Recently, expanding bacterial populations found much attention in both experimental and theoretical work [1]. These “range expansions” have interesting statistical properties, as constant genetic re-sampling from a small population at the expanding front induces strong fluctuations. The influence of non-neutral mutations on the dynamics is less well studied. Here, we introduce an extension of the Eden model [2], including mutations. Using Monte Carlo simulations, we analyze the interplay of kinetic surface roughening, mutations and selection at the front. While beneficial mutations always take over the front eventually, for detrimental mutations one finds two generic cases: if rare, mutant sectors are independent and wild types prevail. If mutants spawn more frequently, sectors coalesce and wild types are soon lost in the bulk. Between these regimes one finds self-affine patterns, and we identify a non-equilibrium phase transition. We measure critical exponents near this transition, and find universal scaling behavior for this model of evolution in expanding populations.

Combining microfluidics and SAXS to access intermediate filament form of the processes in the generalized model our results hold for a whole class of stoichiometric producer-grazer systems. To understand the differences and commonalities between specific stoichiometric models we map the specific bifurcation diagrams into the generalized parameter space. On the one hand, these combined bifurcation diagrams show how the generic results of the generalized analysis are represented in the specific model. On the other hand, it becomes clear that some model features like the sequence of bifurcations observed during enrichment scenarios can be tied to specific modelling assumptions and are hence not structurally stable.
Effect of bias voltage on wear particle size distribution of DLC coatings in artificial hip joints — **Ying Ren**¹, Ingo Erdmann³, Friederike Deuerler³, Berrin Küzün³, and Volker Buck² — ¹Faculty D-Department of Mechanical Engineering, University of Wuppertal, 21199, Wuppertal, Germany — ²Thin Film Technology Group, Faculty of Physics, University Duisburg-Essen and CeNIDE, 47057, Duisburg, Germany

Due to the biocompatibility, Diamond-like carbon (DLC) is an inert and impervious material with properties suitable for use in tribological implants such as hip joint replacements. Currently the lifetime of such joints is just about 15 years. It is an urgent need to extend the life expectancy especially for younger patients under 50 years old. Wear particles causing bone resorption which may lead to aseptic implant loosening have been identified as the main factor limiting the lifetime of the implants. To date, the study of the amount of wear particles has attracted more and more researchers. However, reports about wear particle size distributions are rare to see. In this study, we deposited DLC coatings on P2000 steel substrates by vacuum arc adjustable from anodic to cathodic operation mode, and investigated the relation between the deposition parameters and wear particle size distribution. In order to improve the adhesion of DLC coatings on P2000 steel substrates, titanium metallic interface layers are deposited first by cathodic vacuum arc evaporation. It is shown that the wear particle size distributions are influenced by the deposition parameters.

**Effect of bias voltage on wear particle size distribution of DLC coatings in artificial hip joints**

**Ying Ren**¹, Ingo Erdmann³, Friederike Deuerler³, Berrin Küzün³, and Volker Buck²

¹Faculty D-Department of Mechanical Engineering, University of Wuppertal, 21199, Wuppertal, Germany — ²Thin Film Technology Group, Faculty of Physics, University Duisburg-Essen and CeNIDE, 47057, Duisburg, Germany

Due to the biocompatibility, Diamond-like carbon (DLC) is an inert and impervious material with properties suitable for use in tribological implants such as hip joint replacements. Currently the lifetime of such joints is just about 15 years. It is an urgent need to extend the life expectancy especially for younger patients under 50 years old. Wear particles causing bone resorption which may lead to aseptic implant loosening have been identified as the main factor limiting the lifetime of the implants. To date, the study of the amount of wear particles has attracted more and more researchers. However, reports about wear particle size distributions are rare to see. In this study, we deposited DLC coatings on P2000 steel substrates by vacuum arc adjustable from anodic to cathodic operation mode, and investigated the relation between the deposition parameters and wear particle size distribution. In order to improve the adhesion of DLC coatings on P2000 steel substrates, titanium metallic interface layers are deposited first by cathodic vacuum arc evaporation. It is shown that the wear particle size distributions are influenced by the deposition parameters.
The interpretation of SFM data is supported by results obtained with confocal laser scanning Raman spectroscopy and environmental scanning electron microscopy with energy dispersive x-ray spectroscopy.

Enhancing mechanical properties of calcite by Mg substitution: A quantum-mechanical study — Pavlina Elstnerova, Martin Friak, Tilmann Hickel, Helge Otto Fabritius, Dirk Raabe, Andreas Ziegler, Sabine Hildebrandt, and Joerg Neugebauer

Nearly 90 percent of all animal species in nature protect themselves by a cuticle that represents a hierarchical biocomposite often containing calcite as a mineral stiffening component. Calcite crystals rarely occur in their stoichiometric state and contain impurities. Common impurities in these systems are Mg or P, their role however is still the topic of intense debates. We present results of a parameterfree quantummechanical study of thermodynamic, structural, and elastic properties of calcite single crystals containing Mg atoms. Density functional theory calculations were performed employing 30atomic supercells within the generalized gradient approximation (GGA). Based on the calculated thermodynamical results, the site preference of Mg atoms was determined. Experimental structural properties and the behavior of the carbonate group is shown to be nearly independent on either the volume or concentration of Mg atoms. Based on the computed elastic values, the Mg atoms are predicted to stiffen the calcite crystals, specifically to increase the bulk modulus, also the Mg concentration along the filaments which can be used to monitor the local strain differences.

Cooperative dynamics of microtubule ensembles under force — Björn Zelinski, Jan Kierfeld, and Andreas Ziegler

We investigate the cooperative dynamics of an ensemble of microtubules growing against an external linear force. Stochastic simulations show that the interplay between force sharing and dynamic instability gives rise to a complex dynamics with synchronous growth, interrupted by cooperative switching into a shrinking state and cooperative rescue back to synchronous growth. We quantify the dynamic behaviour by a mean-field theory, which allows us to estimate the average number of cooperatively pushing microtubules and to calculate the generated ensemble polymerization force and its dependence on microtubule number. We also investigate the dependence on switching rates of the dynamic instability, which can be involved in cellular regulation mechanisms.

Microehorology of composite networks of microtubules and F-actin — Marcel Bremerich, Frederick C. MacKintosh, and Christoph F. Schmidt

Understanding the material properties of living cells remains challenging. The mechanics are determined by the viscoelastic properties of the cytoskeleton, which is composed of various biopolymer filaments together with associated proteins and vary over large spatial and temporal scales. In optical trapping-based microrheology micron-sized probe particles are used to investigate the local mechanical response of reconstituted networks of biopolymers with high bandwidth and high spatial resolution.

We have performed one- and two-particle microrheology in composite networks of microtubules and F-actin as model systems for the cytoskeleton. We used a combination of active and passive measurements to quantify the material properties over a wide frequency range of up to 100 kHz. We obtained complex shear moduli and compared the results to theoretical descriptions of composite networks as well as to the properties of similar networks consisting only of microtubules or F-actin respectively.

Length Dynamics of Active Polar Filaments — Christoph Erkenkämper and Karsten Kruse

F-actin and microtubules are linear polymers with distinct chemical properties at both ends. Assembly and disassembly of these polar filaments are active processes as they depend on the hydrolysis of energy rich ATP or GTP, respectively. Together, the polarity and the activity of the filaments can lead to treadmilling, where one end of the filament grows on average while the other shrinks. We theoretically study the length dynamics of active polar filaments and find that the steady-state length distribution peaks at a typical value. We show that the intrinsic length regulation is intimately linked to treadmilling as both depend on the formation of a gradient in the local ATP or GTP concentration along the filaments. We present approximate expressions for the typical filament lengths and treadmilling velocities.
In addition to the irreversible supercontraction, a reversible (cyclic) relaxation-contraction response to wetting and drying has been found. By contrast, similar supercontraction has so far not yet been observed in natural Bombyx mori silk, but occurred in regenerated silk when a special spinning regime was applied.

The exploration of a coordinated, two dimensional microtubule network and temporal scale in living cells as a response to a variety of external stimuli. Most of the highly complex intracellular processes like cell motility, and the cyclic contraction mechanisms.

BP 29.15 Thu 17:15 P3
Rule of mixing in composite cytoskeletal networks — •C. HEUSINGER1, E.M. HUISMAN2, C. STORM3, and G.T. BARKEMA4,4 — 1Institute for Theoretical Physics, University of Goettingen, Germany — 2Instituut Lorentz, Universiteit Leiden, The Netherlands — 3Department of Applied Physics and Institute for Complex Molecular Systems, Eindhoven University of Technology, The Netherlands — 4Institute for Theoretical Physics, Universiteit Utrecht, The Netherlands

The basic design of most structural biological materials is that of a composite meshwork of different semiflexible protein polymers. The cell cytoskeleton, built up from microtubules, actin filaments and intermediate filaments, is just one striking example of such a filamentous composite. Here we study the mechanical properties of a model two-component system that consists of two types of filaments with different bending stiffnesses. Combining theory with network MC-simulations we can reveal a non-trivial relationship between the mechanical behavior of the network, the stiffness contrast between the filaments and the relative fraction of stiff polymer: when there are few stiff polymers, non-percolated stiff "inclusions" are protected from large deformations by an encompassing floppy matrix, while at higher fractions of stiff material the stiff network is independently percolated and dominates the mechanical response.

BP 29.16 Thu 17:15 P3
Instabilities of active gels confined by a fluid membrane — •DOMINIC JOURDAIN and KARSTEN KRUSE — Theoretische Physik, Universitat des Saarlandes, Postfach 151150, 66041 Saarbrücken, Germany

From a physical point of view, the cytoskeleton can be viewed as an active gel. Various theoretical analysis have shown that such a material can display instabilities, provided that the activity exceeds a critical threshold. Cellular systems are usually confined by lipid membranes. We want to first the influence of such membranes on the dynamics of the cytoskeleton. As a simple example, we analyse the stability of an active gel inside a membrane tube. To this end, we use a multicomponent hydrodynamic description that captures the behaviour of active gels on macroscopic length and time scales. We find that the active stresses in the gel can induce a pearling-like instability of the tube and determine the dependence of the activity threshold on parameters characterising the membrane.

BP 29.17 Thu 17:15 P3
Artificial biopolymer networks with optically trapped anchor points — •MATTHIAS KOCH, DOMINIC RUH, and AXANDER ROHRBACH — University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

Microtubules are biopolymers which self-organize over a large spatial and temporal scale in living cells as a response to a variety of external stimuli. Most of the highly complex intracellular processes like cell division or mechanotransduction are based on microtubule networks. The mechanical properties of single microtubules as well as their composite filaments have already been studied in a wide context. However, the exploration of a coordinated, two dimensional microtubule network has not been studied so far.

Optical tweezers allow generating an array of anchor points for artificial polymer networks consisting of fluoroscen labelled microtubules trapped separately or simultaneously on a trap fiber at a time. The aim is to build up such networks using time-multiplexed optical traps for both 3D force generation and measurements. Thereby, the trapping laser focus, steered by an acousto-optic deflector, is displaced in the focal plane of a photonic force microscope at a rate of up to 50 kHz in order to create multiple (up to 40) time shared optical traps. The positions of the trapped particles can be evaluated using back focal plane interferometry, allowing resolving momentum propagation through the microtubule network. This configuration will allow probing the viscoelastic properties of biopolymers and obtain deeper insights in their complex interaction as part of the cytoskeleton.

BP 29.18 Thu 17:15 P3
Van der Waals forces and their influence on the structure of adsorbed protein layers — •WILLIAM K. HERRMANN, CASPER D. VAN RENEN, and KARIN JACOBS2 — 1Department of Experimental Physics, Saarland University, D-66041 Saarbrücken, Germany — 2Faculty of Physics/DELTA, TU Dortmund, D-44221 Dortmund, Germany

The adsorption of proteins from aqueous solution to surfaces is an omnipresent phenomenon. Common examples for which adhesion control is of utmost importance are biomedical applications such as implants or artificial tissues. The adsorption process itself, however, is still not fully understood. In our study, we concentrate on the interactions present between proteins and substrate.

In former studies, it could already been shown that a variation of subsurface composition of the substrate may lead to altered adsorption kinetics [1]. Here, we present X-ray studies that reveal the in situ structure of the adsorbed protein layers. By a judicious choice of substrates, we could separate the influence of surface and underlying material on the adsorbing proteins. Additionally, proteins with different isoelectric points and conformational stability as well as different buffer solutions were used in order to separate the influence of the various interactions involved. The strong difference of protein film structure on hydrophobic and hydrophilic substrates—as expected from literature—could clearly be seen. Yet, even differences in subsurface composition altered the properties of the adsorbates demonstrating the influence of the van der Waals interactions.


BP 29.19 Thu 17:15 P3
Investigation of the nanomechanical properties of in vitro assembled Keratin 8/18 networks — •ANKE LEITNER1, TOBIAS PAU1, KRISTEN DAMMERTZ1, HARALD HERRMANN2, MICHAEL BELL2, and OTHEMAR MARTI2 — 1Institute of Experimental Physics, Ulm University, Ulm, Germany — 2Division of Molecular Genetics, German Cancer Research Center, Heidelberg, Germany — 3Department of Internal Medicine I, Ulm University, Ulm, Germany

The mechanical properties of epithelial cells are mainly determined by the cytoskeleton. The cytoskeleton consists of three different protein networks: Microtubules, the transport pathways of the cell, actin filaments, responsible for the cell motility, and intermediate filaments that provide the stiffness and response to mechanical stimuli. In pancreatic cancer cells especially the keratin cytoskeleton plays a major role. In order to find out more about its mechanical properties it is useful to have a look on in vitro assembled keratin filaments. In the work presented here we investigate the mechanical properties of in vitro assembled keratin 8/18 networks in different polymerisation conditions. For this purpose we use micro rheology measurements with embedded tracer beads. Observing the beads motion with a CCD-High-Speed-Camera then leads to the dynamic shear moduli. From electron microscopy images we calculated the meshsize and connectivity of the different network structures and link these results to the mechanical properties of the different networks.

BP 29.20 Thu 17:15 P3
Mechanically Tunable Hydrogels as Biomimetic Matrices — •CHRISTINA JAYACHANDRAN1 and FLORIAN REHFELDT2 — 1Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany — 2Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany

Cells face various micro-environments in vivo that differ significantly both in physical and biochemical properties and the extra cellular matrix (ECM) is essential to provide these cues. Mimicking the diverse environments in vitro is necessary to understand the fundamental processes that govern cell matrix interactions but also of great importance for medical applications such as regenerative medicine.

Polyacrylamide (PA) gels with varying elasticity are routinely used to study how cells respond to matrix stiffness. Our strategy is based on hyaluronic acid (HA), one of the major polysaccharides in the ECM that is FDA approved for various medical applications. Chemically modified HA is cross-linked to form a hydrogel and the stiffness of...
these gels can be finely tuned over the whole physiologically relevant range. Combining these mechanically tunable hydrogels with different ECM proteins we can mimic distinct in vivo niches and study the response of cells on the physical and biochemical cues.
tion. One of the obstacles for fundamental studies is the preparation of suitable HAP samples, which exhibit usually a rough and porous surface that is hard to prepare in a reproducible manner. These types of samples are moreover unsuitable for many surface science analysis methods such as X-ray photoelectron spectroscopy (XPS) or atomic force microscopy (AFM). We therefore have developed a preparation procedure that allows the fabrication of locally smooth (RMS roughness < 1 nm) and dense HAP surfaces (without open porosity).

**BP 30: Posters: Physics of Cells**

**Time:** Thursday 17:15–20:00

**Location:** P3

**BP 30.1 Thu 17:15 P3**

*Platelets on Micropatterned Surfaces — Rabea Sandmann, Sarah Henriques G. Schwartz, and Sarah Köster — Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany*

Stress fiber formation - the process of force generation in cells - depends on the substrate: Blood platelets on glass (50-90 GPa) show distinct stress fibers, which is not the case for soft polyacrylamid substrates (19 kPa). Platelets are essential for blood clotting and wound healing. Malfunctional platelets are the origin of many diseases like atherosclerosis. Despite of their important function in mammals, the composition of platelets is simple as they lack a nucleus. This renders them a convenient model system to study mechanosensing and mechanotransduction of cells. During the activation process (part of blood clotting) the platelets’ contractile cytoskeleton exerts forces upon the environment. However, the mechanisms of force generation are still unclear. In order to investigate the influence of substrate topology and chemistry on stress fiber generation in platelets, we structure polydimethylsiloxane substrates with patterns ranging from 0.5 μm to 2.5 μm both topologically and chemically and stain both stress fibers and focal adhesions at certain time points of activation.

**BP 30.2 Thu 17:15 P3**

*Influence of Confinement on Keratin Bundles in Live Cells — Jannick Langfahl-Klabes, Britta Weinhausen, Jens Nolting, and Sarah Köster — Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany*

The major components of the eukaryotic cytoskeleton are actin filaments, microtubules and intermediate filaments (IFs). An abundant representative of the IF family is keratin, which can be found in large quantities in epithelial cells and is believed to play a key role in cell mechanics by maintaining cell shape and providing mechanical strength and stability against external forces. We carry out buckling experiments on cytoplasmic keratin bundles to investigate their mechanical properties and draw conclusions about the internal structure. The surrounding cytoskeletal (actin) network has a major influence on the bundles’ buckling behavior via lateral reinforcement. Constraints imposed by the embedding network are also found in further analyses of time-lapse live cell imaging experiments. Our studies show that keratin bundles are strongly confined and perform restricted fluctuations inside a tube-like space. We use the results to estimate the internal structure of the keratin bundles and the influence of the surrounding network on the buckling behavior.

**BP 30.3 Thu 17:15 P3**

*Microfluidic shear on keratin networks in live cells — Jens-Friedrich Nolting, Jannick Langfahl-Klabes, and Sarah Köster — Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany*

Intermediate filaments are a major component of the eukaryotic cytoskeleton along with microtubules and microfilaments. They play a key role in cell mechanics, providing cells with compliance to small deformations and reinforcing them when large stresses are applied. Here, we present a study of fluorescent keratin intermediate filament networks in live cells with respect to their behavior in the presence of external forces. We expose the cells to specified shear forces applied by microfluidic methods and investigate the response of the keratin network in situ. We accomplish a description of the full shear stress distribution acting on the cell using finite element method simulations of the flow conditions. This investigation shows that the shear flow does not lead to a noticeable deformation of the cells but apparently interacts with the cells’ interior in an indirect way by inducing changes of internal processes. We find a considerable stiffening of the keratin bundle motion with the establishment and further increase of the shear flow. The dynamics change from a free and relatively independent "wobble"-motion to a restricted one, reminiscent of rigid rods.

**BP 30.4 Thu 17:15 P3**


Division of Vascular Surgery, University of Utah, USA — Transfusion Department, University Clinic of Göttingen, Germany

Contraction at the cellular level is vital for living organisms. A most prominent type of contractile cells are heart muscle cells, a less well known example are blood platelets. Blood platelets are responsible for clot formation in mammals. They activate at damaged blood vessel sites by changing their shape, interlinking with each other and contracting to build a compact blood clot. Apart from being of great medical importance, blood platelets represent an ideal model system for studies of cellular contraction for two main reasons: They are simple being anucleate and their activation, which occurs within minutes, can be triggered and synchronized by the addition of thrombin. In our experiments we look at force generation at the level of single cells during platelet contraction. To this end, we use traction force imaging which enables time-resolved measurements of force fields generated by isolated cells. Furthermore, we fix cells at different activation stages and stain both vinculin and actin in order to map focal adhesion sites and describe cytoskeletal reorganization steps. In combining both traction force microscopy and fluorescence imaging we can resolve traction force maps for single cells and simultaneously access information about force generating mechanisms in the cytoskeleton. Finally, we gather our experimental findings into a mechanical model for cellular contraction.

**BP 30.5 Thu 17:15 P3**

*Cells on different substrates. An investigation with AFM and optical microscopy. — Daniele Martinis, Michael Beil, Thomas Schimmel, and Othmar Marti — 1 Department of Experimental Physics, Ulm University — 2 Department of Internal Medicine, Ulm University Hospital — Forschungszentrum Karlsruhe — Karlsruhe University*

In this poster we discuss the influence of the substrate nanostructure on mechanical properties and motility of the cells.

The chemical and physical properties of the substrate can influence the cell motility and the mechanics and arrangement of the cytoskeleton. Nanopatterns of adhesion islands can be produced with lithography: in this way the mechanisms governing the determination of cell shape in response to external adhesive conditions can be analyzed. Changes in these characteristics can be observed measuring the stiffness of the cells with the AFM, making an indentation of a few hundred nanometers. We estimate the stiffness applying the Hertz model to the obtained Force-Distance curve. Moreover, cell motility is also modulated by the substrate. In particular, we observed that cells cultivated on gold moves twice as fast as those on PS. Cells on aluminum move three times faster then those on PS.

**BP 30.6 Thu 17:15 P3**

*The network of the RNA-binding protein AtGRP7, a component of a molecular slave oscillator in A. thaliana — Christoph Schmal, Dorothee Staiger, and Peter Reimann*

1 Theorie der Kondensierten Materie, Fakultät für Physik, Universität Bielefeld — 2 Molekülare Zellphysiologie, Fakultät für Biologie, Universität Bielefeld — 3 Bioinformatics of Signaling Networks, Center for Biotechnology, Universität Bielefeld

The AtGRP7 autoregulatory circuit is the first identified molecular "slave" oscillator that is coupled to the circadian ("master") oscillator of Arabidopsis thaliana. The AtGRP7 protein regulates the accumulation of its own mRNA at the posttranscriptional level via alternative splicing. It was recently shown that there is also a cross regulation with the AtGRP8 autoregulatory circuit. We model the system composed

**BP 30.7 Thu 17:15 P3**

*The network of the RNA-binding protein AtGRP7, a component of a molecular slave oscillator in A. thaliana — Christoph Schmal, Dorothee Staiger, and Peter Reimann*

1 Theorie der Kondensierten Materie, Fakultät für Physik, Universität Bielefeld — 2 Molekülare Zellphysiologie, Fakultät für Biologie, Universität Bielefeld — 3 Bioinformatics of Signaling Networks, Center for Biotechnology, Universität Bielefeld

The AtGRP7 autoregulatory circuit is the first identified molecular "slave" oscillator that is coupled to the circadian ("master") oscillator of Arabidopsis thaliana. The AtGRP7 protein regulates the accumulation of its own mRNA at the posttranscriptional level via alternative splicing. It was recently shown that there is also a cross regulation with the AtGRP8 autoregulatory circuit. We model the system composed
of these autoregulatory circuits interconnected with the "master" oscillator via an ordinary differential equation approach. As for many biological systems the parameters of these equations are barely known. We define a cost function that quantifies the overlap between our model and key experimental features. A search in parameter space evaluates if our proposed model fits with the given experimental data.

**BP 30.7 Thu 17:15 P3**

**Manipulation of magnetic particles in living cells — ●Haleh Eshraghian — Bielefeld University, Thin Films and Physics of Nanostructures, Bielefeld, Germany**

In recent years, the so called Lab-on-the-chip system was developed and miniaturized for hand held applications. This system can also be extended for the analysis of heat stress or signaling pathways by the manipulation of magnetic particles in living cells. For the manipulation of particles inside cells, three different steps are required:

1. Moving of particles by magnetic forces outside of cells. The manipulation had been done by magnetic forces which was generated by conducting lines applying 1.2 V.
2. Injection of particles into cells 1 μm diameter magnetic particles were injected into living cells of a fungus (\textit{Mucor mucedo}) a protoplast of Cress (\textit{Arabidopsis thaliana}), and an epidermis protoplast of barley (\textit{Hordeum vulgare}).
3. Positioning of cells by special trapping design in a micro-fluidic channel.

The aim of this work is the penetration and movement of single magnetic particles into the cells on Lab-on-the-chip system.

**BP 30.8 Thu 17:15 P3**

**Nanosized vesicle transport in quasi 1D prepatterned Huvec Channel.**

of Cress (\textit{Arabidopsis thaliana}), and a epidermis protoplast of barley (\textit{Hordeum vulgare}).

Directed transport processes. This suggests, that the 1D projection is a motility of cells. Our aim is to measure the growth dynamics and thickness of these structures using total internal reflection fluorescence (TIRF) microscopy. Upon sending a laser beam on a cover slip with an angle above the critical angle of total reflection an evanescent intensity field appears in the plane on the surface of the glass. The penetration depth is in the range of 50 to 1000 nm, which is also the expected thickness of lamellipodia. When one linearly increases the laser angle the fluorescence intensity of excited fluorophores behind the cover slip decreases exponentially. Fitting the intensity as a function of penetration depth gives the size of the fluorescent object. This procedure works well with dried latex beads with a diameter of 100 to 500 nm. In the next step we will produce fluorescent layers with a defined variable thickness. The intention is to get a scale for measuring dyed lamellipodia as well as to optimize the theoretical background for fitting the intensity result.

**BP 30.9 Thu 17:15 P3**

**Mechanical Characteristics of Primary Cilia — ●Christopher Battle and Christoph F. Schmidt — Drittes Physikalisches Institut, Georg-August-Universität, Göttingen, Germany**

Recent studies have shown that the primary cilium, long thought to be a vestigial cellular appendage with no function, has remarkable sensory abilities. One system of interest, from both a biophysical and medical standpoint, is the primary cilium of kidney epithelial cells, which has been demonstrated to act as a flow sensor. The mechanics of this structure is expected to influence the mechano-electrochemical response that characterizes biological ciliary function. We have developed cell cultures that allow us to visualize and manipulate primary cilia. We explore the mechanical properties of cilia using optical trapping and fluorescence microscopy.

**BP 30.10 Thu 17:15 P3**

**Cell stretching with a vertical optical trap — ●Kai Bodensiek\(^1\), Schanila Nawaz\(^2\), Michael Simons\(^2\), and Iwan A. T. Schiap\(^1\) — 1Max Planck Institute of Experimental Medicine, Göttingen, Germany, 2Göttingen-Planck Center for Nanoscale Science, Göttingen, Germany**

Multiple methods are available to measure cell mechanics. Since most of them operate in the nano-Newton range or higher, they will not only measure but also affect the properties of the cell. Here we describe a method, based on an optical trap to measure the cell response at forces below 20 pN. In contrast to conventional optical trapping which is in which the bead is moved in the horizontal plane, we have built an instrument in which the bead motion can be manipulated and detected in the vertical direction (perpendicular to the microscope coverslip). Thus a surface bound cell can be compressed or stretched between a single optically trapped bead and the surface; we will present first results obtained on 3T3 fibroblasts. In addition we will present routines to detect contact between the bead and the cell, and methods to minimize the effects of Fabry-Pérot interference between the bead and the surface that is caused by the coherent nature of the laser light.

**BP 30.11 Thu 17:15 P3**

**Quantitative TIRF Microscopy of Fluorescent Layers — ●Hauken Greve and Hans-Günter Döbereiner — Institut für Biophysik, Universität Bremen, Germany**

Lamellipodia play an important role for the motility of cells. Our aim is to measure the growth dynamics and thickness of these structures using total internal reflection fluorescence (TIRF) microscopy. Upon sending a laser beam on a cover slip with an angle above the critical angle of total reflection an evanescent intensity field appears in the plane on the surface of the glass. The penetration depth is in the range of 50 to 1000 nm, which is also the expected thickness of lamellipodia. When one linearly increases the laser angle the fluorescence intensity of excited fluorophores behind the cover slip decreases exponentially. Fitting the intensity as a function of penetration depth gives the size of the fluorescent object. This procedure works well with dried latex beads with a diameter of 100 to 500 nm. In the next step we will produce fluorescent layers with a defined variable thickness. The intention is to get a scale for measuring dyed lamellipodia as well as to optimize the theoretical background for fitting the intensity result.

**BP 30.12 Thu 17:15 P3**

**Growth dynamics of \textit{Physarum polycephalum} on different length scales — ●Christina Oettmeier, Erik Bernitt, and Hans-Günter Döbereiner — Institut für Biophysik, Universität Bremen, Germany**

The amoeboid slime mold \textit{Physarum polycephalum} is a single-celled organism with several hundred or thousands of nuclei. It can reach sizes of 10 to 100 cm or larger. \textit{Physarum} exhibits a wide range of movement patterns, ranging from amoeboid crawling to oscillations with different amplitudes and periods. The most prominent example is the so-called shuttle streaming, the contraction and relaxation of the organism's veins. This rhythmic pattern of contraction and relaxation serves to transport cytoplasm throughout the network and is caused by the contraction of acto-myosin structures.

Microplasmodia, a special growth form characterized by its sphericity which was used for pattern forming experiments. High-resolution movies were taken under a bright-field microscope and provide insights into the spatio-temporal dynamics. Pronounced oscillations could be observed and analysed quantitatively: A fast oscillation with a period of 1 to 2 minutes as well as a superimposed slow oscillation with a period of about 20 minutes were found. Lateral contraction waves running along the periphery with a speed of about 10 μm/s could also be observed. Additionally, the morphology of the microplasmodia was investigated by transmission electron microscopy (TEM) and scanning electron microscopy (SEM) pictures. Pores with a diameter of about 2 μm were located together with a system of corresponding channels.

**BP 30.13 Thu 17:15 P3**

**Establishment of Cell Polarity in Yeast Saccharomyces cerevisiae — ●Ben Klünder, Tina Freisinger, Jared L. Johnson, Roland Wiedlich-Soldner, and Erwin Frey — 1Department of Chemistry, Am Klopferspitz 18, D-82152 Martinsried, Germany, 2Max Planck Institute of Biochemistry, Ithaca, New York 14853, Germany**

Cell polarization is a prerequisite for processes such as cell motility, proliferation, and stem cell differentiation. The yeast Saccharomyces cerevisiae contains a ability to polarize spontaneously in the absence of spatial cues and without help of cytoskeletal structures. The emergence of polarity instead was found to rely on a network of regulatory proteins of the central polarity GTPase Cdc42. However, the fundamental mecha-
nisms for polarity establishment still remain to be identified. Based on new experimental findings we propose a minimal model of cell polarization which uses local self-amplification of activation and recruitment of Cdc42 to establish a stable cap of Cdc42 on the plasma membrane. Using a combination of analytical and numerical methods we study the effect of mutations in Cdc42 regulators, which lead to either loss of polarization or characteristic changes of experimentally accessible observables. Our results are consistent with measurements from in vivo studies and indicate that cell polarization of yeast depends on self-enhanced recruitment of Cdc42 coupled to rapid cycling of GTPase activity.

BP 30.14 Thu 17:15 P3 Interplay Between Compartmentalization of Cells and Tumor Spreading — ∙STEVE LAWLER, ANATOL FRITSCH, MARIEKE ZINK, and JOSEPH A. KAS — Institute for Experimental Physics I, Soft Matter Physics Division, University of Leipzig, Germany

The formation of cellular compartments is a universal and essential process during embryonic development. It generates well-defined boundaries and barriers for various differentiated cell types. Cells of the same type adhere better to each other, whereas mixtures of different migrating cell types segregate. Studies in the field of developmental biology show that the interplay between single cell biomechanics, cell adhesion, and cell migration contributes to the formation of cellular compartments by causing a surface tension at the compartment boundaries. In this context, we investigate to which extend the physical principles described above affect tumor growth and spreading between compartments. It has been observed that metastasis and tumor aggressiveness are associated with a loss of epithelial cell characteristics and the acquisition of a migratory phenotype. Due to this behavior, tumor cells are able to overcome compartment boundaries. Further studies indicate that surface tension plays a crucial role for tumor progression, but this has not been systematically investigated so far. We apply a variety of techniques such as “Optical Stretching”, scanning force microscopy, and droplet cultures to study the cellular mechanical properties and interactions of healthy and malignant cells.

BP 30.15 Thu 17:15 P3 Granule motion in pathogenic amoebae studied with particle-tracking methods — ∙JULIA RÖVERREY1, MATTHIAS LIEBPE, and CHRISTINE SELHUBER-UHLMANN1 — 1Institute for Materials Science, Bio compatible Nanomaterials, Christian-Albrechts-University, Kaiserstr. 2, 24143 Kiel, Germany — 2Zoological Institute, Zoophysiology, Christian-Albrechts-University, Am Botanischen Garten 1-9, 24118 Kiel, Germany

Entamoeba histolytica and Acanthamoeba are parasitic amoebae which can cause severe diseases, such as human amoebiasis, amoebic encephalitis and keratitis, respectively. They destroy target cells by an extracellular killing mechanism that is preceded by the formation of a close contact between amoeba and target cell. Subsequently, granules that contain membrane-active proteins are transported to the contact site between amoeba and target cell. Therefore, the intra-amoebic motion of granules plays an essential role for the pathogenicity of the amoeba. For a deeper understanding of this amoebic killing mechanism, we record sequences of granule movement with phase-contrast microscopy in combination with a high-speed camera under physiological conditions. The motion of the granules within the amoeba is evaluated using particle tracking algorithms. In our final analysis, we particularly focus on distinguishing between passive diffusion and active transport of the granules.

BP 30.16 Thu 17:15 P3 Setup and improvements of dual trap optical tweezers for analyzing the cytoskeleton of epithelial cancer — ∙THOMAS FRÖHLICH1, THOMAS PAU1, MICHAEL BEIL2, and OTHMAR MARTI1 — 1Institute of Experimental Physics, Ulm University — 2Department of Internal Medicine I, Ulm University

Optical trapping of dielectric particles is a powerful tool to manipulate and measure biological objects such as cells. Based on acousto-optic deflectors (AODs), quadrant photo diode detection, high speed camera and piezo electric sample positioning, we have built an optical tweezers device for a specially constructed optical microscope. This instrument has two permanent traps. Due to the two axes of the AOD scanning system, one trap can oscillate freely in the image plane and since there are no moving masses, we gain access to a high frequency range. The second trap is adjusted manually with a mirror and is used as a static measure point to gain information about the mechanical properties of the space between the two traps. Because of the high performance of the AOD system, it is also possible to get additional traps by time sharing for more complex measurements. To stabilize the system and to minimize the adjustment time, a rail system for the optical components is used.

With this instrument we can manipulate and measure mechanical properties of biological samples in a wide frequency range. The efficiency of this setup was demonstrated with measurements of the dynamic shear modules of the intermediate filament cytoskeleton of pancreatic carcinoma cells.

BP 30.17 Thu 17:15 P3 Collective dynamics during the early stage of biofilm formation — ∙MATTHIAS THERVES and CARSTEN BETA — Biologische Physik, Universität Potsdam

Biofilms are communities of sessile bacteria, embedded in an extracellular polymeric structure (EPS), which form at solid-liquid or liquid-air interfaces. First, we use biocompatible microfluidic channels together with time-lapse microscopy to study the recruitment of planktonic Pseudomonas putida to a glass surface as well as the subsequent development from attached colonies leading to the mature biofilm. The results serve as a starting point for comparable experiments with Bacillus subtilis, a model organism for biofilm formation capable of ‘swarming motility’, a state of rapid, flagella-driven colony expansion across surfaces. We finally develop a high-speed setup for digital in-line holography (DIIH) to investigate the full three-dimensional picture of the collective motion of both swimming and surface attached bacteria that initiates biofilm formation. In future experiments microfluidic tools will help us to understand the initial interactions and manipulate environmental cues which trigger the biofilm development.

BP 30.18 Thu 17:15 P3 Correlative Microscopy: On the position of extracted pancreatic carcinoma cells — ∙Tobias Paust1, Thomas Förlich1, Samuel Vollmer1, Tobias Pusch2, Paul Walther2, Michael Beil3, and Othmar Marti — 1Institute of Experimental Physics, Ulm University — 2Central Electron Microscopy Unit, Ulm University — 3Department of Internal Medicine I, Ulm University

Microrheology measurements of particles which are embedded in the cytoskeleton of extracted carcinoma cells show the mechanical properties of the network. The network stiffness then can be calculated dependent on the position of the bead.

To ensure that a measurement of a cells shows up correct values for storage and loss modulus the same cell should be checked in the Electron Microscope. Therefore we developed a sample chamber which makes it possible to find the position of the microrheological measurement in the Electron Microscope. So only particles in a proper position can be used for calculations.

On this poster we want to show how to find cells and also take a look on the statistics on the amount of lost cells during the preparation process for the Electron Microscope.

BP 30.19 Thu 17:15 P3 Microrheology: A new algorithm for the conversion of mean squared displacement to dynamic shear moduli — ∙Tobias Paust1, Anne Leitner1, Michael Beil2, and Othmar Marti1 — 1Institute of Experimental Physics, Ulm University — 2Department of Internal Medicine I, Ulm University

For describing the mechanical properties of a viscoelastic medium a possible way is to measure the thermal motion of a particle embedded in the material and compute the shear transform.

The conversion of the mean squared displacement to the dynamic shear moduli is in the focus of interested in this work. We provide a new method for calculating the Laplace transform and therefore gather information about the mechanical properties of the sample. A superposition of well-defined analytical functions which are fitted to the measured data leads to the thermal motion and compute the shear transform.

To the two we can describe the viscoelastic behavior of the system in the needed frequency range without any approximation.

We show examples of mean squared displacements and the calculations of the elastic and diffusive part of different systems.

BP 30.20 Thu 17:15 P3 Changes of Min-protein patterns in growing Escherichia coli — ∙Mike Bonny1, Elisabeth Fischer-Friedrich1, and Karsten Kruse2 — 1Theoretische Physik, Universität des Saarlandes, 66041
Regulation of Dynamic Cell Response with Laterally Confined Domains Embedded in Supported Membranes

The ability of cells for self-determined motility plays a crucial role in many biological processes, like food gathering of single amoeba or tissue invasion of whole cell ensembles during angiogenesis. In order to migrate, cells require advanced control over their cytoskeleton, in principle consisting of the actin cortex and microtubules. While many studies examine the influence of perturbations of the actin cortex in restricted to flat substrates, although many cellular functions in a tissue context are known to be closely related to the three-dimensionality of the natural environment. We have recently shown that direct laser writing is a versatile technique to fabricate tailored 3D-scaffolds that are sufficiently elastic such that they can be deformed by muscle cells [1]. Here, we demonstrate that also softer scaffolds can be produced that are deformed by weaker tissue cells such as fibroblasts. In order to evaluate scaffold deformation in a comprehensive manner, we apply finite element modeling both to the synthetic scaffolds and for cellular environments we are able to analyze cellular motility in a comprehensive manner, we apply finite element modeling both to the synthetic scaffolds and for implementing a novel biophysical model for cell contractility.

1. Xiong et al., BMC Sys. Biol. 4, 33
2. Arcizet et al., PRL 101, 248103

Flexible three-dimensional scaffolds for cell adhesion studies

Flexible three-dimensional scaffolds for cell adhesion studies

Thomas Striebel1,2, Franziska Kleins1, Denis Danilov1, Thomas Boehlke2, Martin Wegener1, Martin Bastei1, and Ulrich S. Schwarz2
1 Karlsruhe Institute of Technology (KIT) — 2 ITP, University of Heidelberg

Tools from materials science such as microcontact printing of adhesive patterns or preparation of flexible polymer substrates are widely used for cell culture experiments. However, most of these studies are restricted to flat substrates, although many cellular functions in a tissue context are known to be closely related to the three-dimensionality of the natural environment. We have recently shown that direct laser writing is a versatile technique to fabricate tailored 3D-scaffolds that are sufficiently elastic such that they can be deformed by muscle cells [1]. Here, we demonstrate that also softer scaffolds can be produced that are deformed by weaker tissue cells such as fibroblasts. In order to evaluate scaffold deformation in a comprehensive manner, we apply finite element modeling both to the synthetic scaffolds and for implementing a novel biophysical model for cell contractility.


Flow-Alignment Coupling in the Cortex of C. elegans Embryo

Flow-Alignment Coupling in the Cortex of C. elegans Embryo

Thomas Pfohl1,2, Tobias Kirsseling1, Roland Stange1, Joseph Kästere,3 and Matthias Engstler3
1 Department of Chemical Physics, Weizmann Institute of Science, Rehovot 76100 Israel
2 Department of Physics, University of Heidelberg, Germany — 3 Department of Physics, University of Cambridge, UK

The mechanical properties of cells are largely governed by the cytoskeleton, an internal hybrid polymer network, and its connection to the cell nucleus. We have used an optical stretcher to investigate the microscopic origin of the rheological properties of various cells in suspension, which differ characteristically from attached cells. Suspended cells are more amenable to polymer theoretical comparison because their cytoskeleton is rather isotropic and not confined by stiff fibers. Also the function of molecular motors is contrary to that of attached cells, and leads to a viscous softening in suspension. Finally, cell rheological properties will be discussed in the context of stem cell plurioty, epigenetic chromatin condensation, correspond- changes during differentiation and in laminopathies.


Regulation of Dynamic Cell Response with Laterally Confined Domains Embedded in Supported Membranes

The position of the division site in the rod-like bacterium E. coli is precisely be controlled by the length of fluorocarbon chains. The fluorinated lipids form mono-dispersed domains whose domain size and inter-domain correlation can be precisely be controlled by the length of fluorocarbon chains. The fluorinated lipid domains were modified with carbohydrates or an apoptosis-inducing protein ligand (CD95L) which could successfully activate the specific cell response of macrophages and cancer cells. The dynamic spreading of murine macrophage and apoptosis of pancreatic cancer cells were analyzed by a combination of confocal microscopy and reflection interference contrast microscopy (RICM). The lateral confinement of ligand molecules revealed a significant effect on the adhesion behavior of cells.


Flexible three-dimensional scaffolds for cell adhesion studies

The Role of Microtubules in Cell Motility

The platform of free movement of ligand molecules revealed a significant effect on the adhesion behavior of cells. The laterally confined ligand molecules could be regulated by the length of fluorocarbon chains. The fluorinated lipid domains could be modified with carbohydrates or an apoptosis-inducing protein ligand (CD95L) which could successfully activate the specific cell response of macrophages and cancer cells. The dynamic spreading of murine macrophage and apoptosis of pancreatic cancer cells were analyzed by a combination of confocal microscopy and reflection interference contrast microscopy (RICM). The lateral confinement of ligand molecules revealed a significant effect on the adhesion behavior of cells.

1. Xiao et al., BMC Sys. Biol. 4, 33
2. Arcizet et al., PRL 101, 248103

Flexible three-dimensional scaffolds for cell adhesion studies

The mechanical properties of cells are largely governed by the cytoskeleton, an internal hybrid polymer network, and its connection to the cell nucleus. We have used an optical stretcher to investigate the microscopic origin of the rheological properties of various cells in suspension, which differ characteristically from attached cells. Suspended cells are more amenable to polymer theoretical comparison because their cytoskeleton is rather isotropic and not confined by stiff fibers. Also the function of molecular motors is contrary to that of attached cells, and leads to a viscous softening in suspension. Finally, cell rheological properties will be discussed in the context of stem cell pluripotency, epigenetic chromatin condensation, correspond- changes during differentiation and in laminopathies.

In the nematode C. elegans embryo, anteroposterior polarization is ensured by a cortical flow powered by myosin activity (Mayer&AI, Nature, 2010). Here we investigate the consequence of this flow on the alignment of actin filaments in the cortex. A generic hydrodynamic theory of the actin cortex predicts the formation of an actin ring at the boundary between the anterior and posterior region and the formation of an ingression which may explain the apparition of a pseudocleavage furrow. The alignment can be characterized with a nematic order that we measure on embryos carrying a Lifeact probe allowing to visualize the actin cortex. Strikingly, we have been able to observe this ring and furrow. The alignment can be characterized with a nematic order parameter at different stages of the polarization flow. Such coupling may be a generic feature in biological systems involving actin networks.

BP 30.28 Thu 17:15 P3

Exploring the microtubule role in nuclear centering of S. pombe —**DAMEN RAMUNNO-JOHNSON, NICOLA MAGHERLI, VLADIMIR KRSTIC, NENAD PAVIN, ALEXANDER KRULL, FRANK JÜLICHER** — 1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Max Planck Institute for Molecular Cell Biology and Genetics, Dresden, Germany

During embryonic development, precursor germ cells contain aggregates of proteins and RNA known as germ granules ("P-granules"), which are important in the specification of a functioning germ line. In the first cell division of the fertilized egg of the worm, C. elegans, P-granules segregate towards the posterior side of the cell; upon cell division, they are found only in the posterior daughter cell. This segregation occurs through preferential growth of the P-granules on the posterior side of the cell. This preferential growth is maintained by a gradient in the concentration of the protein MEX-5 along the anterior-posterior axis of the cell. MEX-5 appears to decrease the saturation point for a phase transition into the condensed granule phase along this axis, thereby allowing a spatially asymmetric nucleation and growth. We use a simulation based on the Lifshitz-Slyozov model for droplet growth to study this system, where the model is expanded to include a spatial supersaturation gradient. We find that P-granules preferentially stay at the posterior side due to two effects: i) the lower saturation point allows for greater P-granule growth, and ii) larger P-granules diffuse more slowly.

BP 30.32 Thu 17:15 P3

Search strategy for a lost kinetochore based on random angular movement of the microtubule —**NENAD PAVIN, IANA KALININA, AMITABHA NANDI, ALEXANDER KRULL, BENJAMIN LINDNER, and IVA TOLIĆ-NÖRRELYKKE** — 1Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 2Faculty of Science, Zagreb, Croatia — 3Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

In living cells, proper segregation of genetic material between the two daughter cells requires all chromosomes to be connected to the spindle microtubules. Linkers between chromosomes and MTs are kinetochores (KCs), protein complexes on the chromosome. In fission yeast, KCs are clustered at the spindle pole body (SPB), which facilitates their interaction with MTs that grow from the SPB. If the spindle is compromised, it is able to recover including capturing KCs that have been lost in the nuclear lam. It is, however, unknown how MTs find lost KCs. We found that lost KCs can be captured by random angular movement of the microtubule. By using live cell imaging, we observed that astral MTs pivot around the SPB, in cell with and without lost KCs. By studying relationship between the MT angular diffusion and MT lengths, we found that this movement is most likely driven by thermal fluctuations. In addition, we found that KCs and astral MTs by performing random movement explore comparable fraction of space. Finally, by introducing a theoretical model, we show that the process of KC capture can be explained by the observed random movement of astral MTs and of the KC.
Kinesin-3 (UNC-104) can act as a dimeric motor during axonal transport. C. elegans neurons in vivo. — Volker Christoph Henschel1, Alessandra Esposito2, Christoph Friedrich Schmidt1, Fred Sylvester Wouters3, and Dieter Robert Klopfenstein1 — 1Drittes Physikalisches Institut, Biophysics, Georg-August-University Göttingen, Göttingen, Germany — 2MRC Cancer Cell Unit, Hutchison/MRC Research Centre, Cambridge, UK — 3Laboratory of Cellular and Molecular Systems, Department of Neuro- and Sensory Physiology, Georg-August-University Göttingen, Göttingen Germany

Monomeric Kinesin-3 (UNC-104) is responsible for the transport of presynaptic vesicles to synaptic termini in C. elegans. To investigate the role of the endogenous coiled-coils, we introduced point mutations in the motors coiled-coil region in the neck promoting either dimer formation of Kinesin-3 or reducing the likelihood of dimerization. We verify dimerization by cross-linking of purified truncated motors in vitro. We show by live in vivo imaging, that reducing dimerization of Kinesin-3 leads to decreased vesicle transport velocities and affects the control of muscle contraction. C. elegans with reduced dimerization properties exhibit a 45% reduction in anterograde velocity. Additionally, severe motility and a significant egg laying defect are observed. To assess dimer formation in vivo we combine Förster Resonance Energy Transfer (FRET) and anisotropy imaging with spinning-disc laser confocal microscopy. Our data suggest a direct link between dimerization status and transport velocities.

Tug-of-war of small ensembles of myosin II motors — Philipp Albert, Thorsten Erdmann, and Ulrich S. Schwarz — Institute of Theoretical Physics, University of Heidelberg

Myosin II motors are non-processive and therefore have to work together in ensembles in order to generate appreciable levels of force. In the actin cytoskeleton of cells these ensembles are usually small and stochastic effects are therefore expected to be pronounced. The parallel cluster model (PCM) recently developed for small ensembles of myosin II motors takes advantage of the separation of time scales present in the myosin II hydrolysis cycle. The PCM reduces the complex network of stochastic transitions occurring in an ensemble consisting of several myosin II motors to a one-step master equation. We extend the PCM to a bipolar myosin II minifilament, resulting in a model for the stochastic tug-of-war between two non-processive motor ensembles. Stochastic simulations reveal that the movement of the bipolar minifilament can be described by a diffusive process, with a diffusion constant that depends on the size of the minifilament. In order to investigate mechanosensitivity of molecular motors, springs are added to the system as an external elastic element. For sufficiently large ensembles, increasing the stiffness results in a transition from a state with frequent detachment to an attached state.

BP 31: Posters: Biological Machines & Motor Proteins

Time: Thursday 17:15–20:00

BP 31.1 Thu 17:15 P3
Neck-linker-length dependence of processive Kinesin-5 motility — André Desselber, Christina Thieme, Stefan Kramer, Christoph F. Schmidt, and Stefan Lakämper — Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany

To explore the basic motor activity of the mitotic Kinesin-5, we previously constructed a stable dimeric Kinesin-5 head/Kinesin-1 stalk chimera (Eg5Kin), which contains the motor domain and 14 amino acids of the neck linker of Xenopus leavis Eg5 fused to the neck coiled-coil of Drosophila melanogaster Kinesin-1. We have here investigated the effect of varying neck-linker length on the motile properties of Eg5Kin. We generated six Eg5Kin constructs comprising of 13 to up to the 18 amino acids of the native Eg5 neck linker, possibly providing a physiological context.

Using single-molecule fluorescence, we found that all six constructs are active motor molecules capable of processive motility. In a first set of experiments, we found that the neck-linker length influences the run length, but not the velocity of the motor. We thus confirm the findings of Shastry and Hancock (2010, Curr. Biol. 20:939) with a different motor. In addition we used optical-trap assays to investigate the change in the average force the motor constructs generated and found only a small variation. Our data thus suggest that the neck-linker length of Eg5 is at least not the sole determinant for speed and force generation.

BP 31.2 Thu 17:15 P3
Tug-of-war of small ensembles of myosin II motors — Philipp Albert, Thorsten Erdmann, and Ulrich S. Schwarz — Institute of Theoretical Physics, University of Heidelberg

Myosin II motors are non-processive and therefore have to work together in ensembles in order to generate appreciable levels of force. In the actin cytoskeleton of cells these ensembles are usually small and stochastic effects are therefore expected to be pronounced. The parallel cluster model (PCM) recently developed for small ensembles of myosin II motors takes advantage of the separation of time scales present in the myosin II hydrolysis cycle. The PCM reduces the complex network of stochastic transitions occurring in an ensemble consisting of several myosin II motors to a one-step master equation. We extend the PCM to a bipolar myosin II minifilament, resulting in a model for the stochastic tug-of-war between two non-processive motor ensembles. Stochastic simulations reveal that the movement of the bipolar minifilament can be described by a diffusive process, with a diffusion constant that depends on the size of the minifilament. In order to investigate mechanosensitivity of molecular motors, springs are added to the system as an external elastic element. For sufficiently large ensembles, increasing the stiffness results in a transition from a state with frequent detachment to an attached state.

BP 31.3 Thu 17:15 P3
Kinesin-3 (UNC-104) can act as a dimeric motor during axonal transport. C. elegans neurons in vivo. — Volker Christoph Henschel1, Alessandra Esposito2, Christoph Friedrich Schmidt1, Fred Sylvester Wouters3, and Dieter Robert Klopfenstein1 — 1Drittes Physikalisches Institut, Biophysics, Georg-August-University Göttingen, Göttingen, Germany — 2MRC Cancer Cell Unit, Hutchison/MRC Research Centre, Cambridge, UK — 3Laboratory of Cellular and Molecular Systems, Department of Neuro- and Sensory Physiology, Georg-August-University Göttingen, Göttingen Germany

Monomeric Kinesin-3 (UNC-104) is responsible for the transport of presynaptic vesicles to synaptic termini in C. elegans. To investigate the role of the endogenous coiled-coils, we introduced point mutations in the motors coiled-coil region in the neck promoting either dimer formation of Kinesin-3 or reducing the likelihood of dimerization. We verify dimerization by cross-linking of purified truncated motors in vitro. We show by live in vivo imaging, that reducing dimerization of Kinesin-3 leads to decreased vesicle transport velocities and affects the control of muscle contraction. C. elegans with reduced dimerization properties exhibit a 45% reduction in anterograde velocity. Additionally, severe motility and a significant egg laying defect are observed. To assess dimer formation in vivo we combine Förster Resonance Energy Transfer (FRET) and anisotropy imaging with spinning-disc laser confocal microscopy. Our data suggest a direct link between dimerization status and transport velocities.

BP 32: Posters: Other Topics in Biological Physics

Time: Thursday 17:15–20:00

BP 32.1 Thu 17:15 P3
The Nanowizard® The Most Flexible, High Resolution AFM With True Optical Integration — Gerhard Bräuchle — JPK Instruments, Berlin, Deutschland

The NanoWizard® represents the latest in AFM technology. The new Vortis controller series uses the latest FPGA architecture to guarantee highest digital performance. Fast signal acquisition and control, advanced feedback and analysis are key components of a modular and ultra flexible controller. The high-speed data acquisition makes the controller perfect for time resolved force spectroscopy, higher harmonics imaging or high frequency cantilever use. Cantilever calibration by thermal noise method up to 3.25 MHz is unique. HyperDrive is a soft sample imaging technique in liquid which provides sub-nanometer lateral resolution with minimal tip-sample interactions and works with off-the-shelf cantilevers. This is made possible by the new optics and electronics of the NanoWizard® AFM head, which gives the lowest noise levels in the cantilever deflection detection system available commercially. The NanoWizard® maximizes stability, performance and ease of handling for samples in fluid and for full integration with optical microscopy. This enables the simultaneous acquisition of high quality AFM images with optical imaging, under physiological conditions. The unique DirectOverlay software for the JPK NanoWizard systems uses the tip location to calibrate accurately the optical images and integrate them into the AFM software for direct AFM navigation. In addition, exact, quantitative correlation of AFM and optical features is possible.

BP 32.2 Thu 17:15 P3
Time resolved optical Measurements of Dye-Functionalized Quantum-Dots with Polymer-Coating: A step towards Mult...
The effect of glycerol and DMSO on the phase behavior of lysozyme — •CHRISTOPH GÖGELEIN1, GERHARD NAGEL2, DANA WAGNER3, FREDERIC CARDINAUX1,2, and STEPHAN U. EGELEHAAR3 —
1Max-Planck-Institut für Dynamik und Selbstorganisation, BunsenStraße 10, 37077 Göttingen, Germany
2Forschungszentrum Jülich, 52425 Jülich, Germany
3Heinrich-Heine-Universität Düsseldorf, Universitätsstr. 1, 40225 Düsseldorf

Additives such as salt, glycerol and dimethyl sulfoxide (DMSO) are widely used to modify the stability of protein solutions [1]. In this work, we study the effect of these additives on the second virial coefficient and the phase behavior of lysozyme. We show that glycerol reduces the attractive interaction of lysozyme, whereas the addition of sodium chloride increases the attraction between the lysozyme molecules. Adding DMSO amplifies the strength of the interaction potential so that the influence of the temperature on the second virial coefficient becomes more pronounced. We compare our experimental findings with theoretical predictions based on the Derjaguin-Landau-Verwey-Overbeek (DLVO) effective pair potential for the protein interaction. Moreover, we compute the crystallization and gas-liquid coexistence curves using thermodynamic perturbation theory (TPT). It is shown that the DLVO-type description predicts qualitatively the influence of salt and glycerol. However, the DLVO model fails to describe the effect of DMSO.


Under-filling trapping objectives optimizes the use of available laser power in optical tweezers — •MOHAMMED MAHMAD2, CITALI FÉREZ CAMPOS1, and ERIK SCHAFFER3 —
1Nanomechanics Group, Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany — 2Max Planck Institute of Molecular Cell Biology and Genetics, Pfenchnerstraße 108, 01307 Dresden, Germany

For optical tweezers, especially when used in biological studies, optimizing the trapping efficiency reduces photo damage or enables the generation of larger trapping forces. One important parameter that affects the efficiency is the filling ratio — the laser beam width relative to the numerical aperture (NA) diameter that accords with Abbe’s sine condition. Here, we measured the optimal filling ratio for 0.5–2μm diameter microspheres and compared the results to Mie theory calculations. We show that slightly under-filling a 1.3 NA objective with a filling ratio of 0.95 using 0.85μm diameter microspheres resulted in the highest overall trapping efficiency. Under these conditions, the maximum trap stiffness is 30% higher compared to a filling ratio of 1.3. The optimal filling ratio varied with microsphere size in the lateral but not in the axial direction. Our findings suggest that apart from the choice of optimal microsphere size, under-filling the objective is key for optimal performance of an optical trap.

A simple three-point-force model for Chlamydomonas Reinhardt — •RUUD BOESTEN1,2, HOLGER STARK3, and IGNACIO PAGONABARRAGA3 — 1TU Berlin, Germany — 2TU Eindhoven, Netherlands — 3University of Barcelona, Spain

There is an abundance of swimming organisms on the micrometer scale. From unicellular algae in the oceans, to pathogenic bacteria in human blood vessels. The motility of these microorganisms affects macroscopic properties. For suspensions of Bacillus subtilis, the viscosity has been measured with respect to the viscosity of the suspending medium [1]. In contrast, for suspensions of Chlamydomonas Reinhardtii (CR) an increase was measured [2]. Very recently, on the millisecond time and micrometer length scale the flow field of several micro-swimmers has been measured [3]. The understanding of these phenomena on all length and time scales could give us information about the behaviour and role of micro swimming in a broad range of environments.

Inertial forces are small compared to viscous forces on the size of a microorganism. We investigated a simple 3-point-force model for CR. The resulting flow field is the superposition of the 3 induced stokeslets. This model can explain both the flow field within a beat cycle on the length scale of several body lengths, as well as the effective viscosity of a suspension of CRs on large time scales.

[1] Sokolov et al., PRL, 103, 148101 (2009)

Sequential gene-regulatory logic: Design schemes and quantitative characteristics — •PATRICK HILLENBRAND, GEOFF FRITZ, and ULRICH GERLAND — Department of Physics and CeNS, LMU München

Epigenetic memory plays a pivotal biological role in bacteria and eukaryotes alike, and permits the transient storage of information. In digital electronics, logic elements that involve the processing of internal memory states are referred to as sequential logic circuits. The basic elements of sequential logic are addressable one-bit memory elements (so-called latches). Here, we study a genetic equivalent of the most versatile such element, the genetic J-K latch. The J-K latch is able to stably hold both states, and to perform the logical operation of ‘set’ and ‘reset’. Our analysis indicates that designs based on protein-protein interaction and protein-DNA binding, are in principle sufficient to implement the desired functionality. We show that stable oscillations are necessary for the circuit to faithfully switch its state upon the toggle command. These oscillations are generated by a time delay in the system caused by overlapping protein binding sites on the DNA. Finally, we also discuss an extension of the genetic J-K latch to a master-slave latch, which switches its state upon a toggle signal without displaying oscillatory behavior. The master-slave latch exhibits a particularly robust functionality, is a useful element for synthetic biology, and may be employed also in natural regulatory circuits.

Measuring the non-harmonic potential of an optical trap — •MARCUS JAHNEL1,2, MARTIN BEHRNDT1,2, ANITA JANNASCH1,2, ERIK SCHAFFER1, and STEPHAN W. GRILL1,2 — 1Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — 2Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — 3Biotechnology Center, TU Dresden, Germany

Using optical traps to measure or apply forces on the molecular level requires a precise knowledge of the trapping potential. Close to the trap center, this potential is usually approximated as harmonic. However, applications demanding high forces at low laser intensities can probe the light-bead interaction beyond the linear regime. Here we measure the full non-linear force and displacement response of an optical trap in two dimensions using a dual-beam optical trap setup. We observe a stiffening of the trap beyond the linear regime that depends on bead size, in agreement with Mie theory calculations. We also find that the linear range for inferring forces from a back-focal-plane voltage detector signal is much larger than for inferring bead displacements from the same signal. Our approach thus allows for a complete two-dimensional characterization of the force response of an optical trap.

Grating-based X-ray phase contrast tomography of human proliferating — •GEORG SCHAUL1, TIMM WEITKAMP2, IRENE ZANETTE3, FRANZ PFIEFFER4, CHRISTIAN DAVID5, ELENA REZNKINOVA6, and BEHT MÜLLER1 — 1BMC, University of Basel, Switzerland — 2Synchrotron Soleil, Gif sur Yvette, France — 3ESRF,
A Riemanian geometric approach to human arm dynamics, movement optimization and invariance — Armin Briss1, 

Tamar Flash2, and Dario G. Liebermann3 — 1Max-Planck-Institute for Dynamics and Self-Organization, 37073 Göttingen, Germany — 2Department of Applied Mathematics and Computer Science, The Weizmann Institute of Science, Rehovot 76100, Israel — 3Physical Therapy Department, Sackler Faculty of Medicine, Tel Aviv University, Ramat Aviv 69978, Israel

In modeling human arm movements optimization principles have been used to describe mathematically the kinematics and dynamics of point-to-point arm movements. Most models have assumed an underlying Euclidean structure of space in the formulation of the cost functions that determine the model predictions. We present a generally covariant formulation of human arm dynamics and optimization principles in Riemannian configuration space. We extend the one-parameter family of mean squared-derivative (MSD) cost-functionals, previously considered in human motor control, from Euclidean to Riemannian space. Solutions of the one-parameter family of MSD variational problems in Riemannian space are given by (re-parametrized) geodesic paths, which correspond to arm movements with least muscular effort. Finally, movement invariants are derived from symmetries of the Riemannian manifold. We argue that the geometrical structure of the arm's configuration space may provide insights into the emerging properties of the movements generated by the human motor system.
the a-subunit and one c-subunit with two different fluorophores and measuring steps by single-molecule Förster resonance energy transfer (FRET). For ATP synthesis activity the protein must be reconstituted in an artificial membrane, or for longer observation times, has to be immobilized on a Ni-NTA-surface. Here we show rotary motion of the c-ring by FRET using an duty-cycle optimized alternating laser excitation scheme (DCO-ALEX).

15 min. break

BP 33.5 Fri 11:45 ZEU 250
Towards in vitro reconstitution of motor-driven nuclear oscillations — ∙Manuel Neitz1, Stefan Direk1,2, and Iva Tolic-Norrelykke1 — ∙Max Planck Institute of Molecular Cell Biology and Genetics, Dresden — ∙B CUBE, Dresden
Molecular motors are necessary for fundamental cell functions such as cell division and intracellular transport. These vital processes rely on the interplay of a multitude of motors exerting force on microtubules, which leads to concerted movements in the cell. The one dimensional nuclear oscillations in the fission yeast Schizosaccharomyces pombe represent an easily accessible model process to study intracellular movements driven by molecular motors and microtubules. Similar oscillations have been observed in other organisms during mitosis. For the oscillations in S. pombe the minus-end directed motor protein dynein is necessary, which generates pulling forces by binding to microtubules and the cell cortex [Yam 06]. In S. pombe microtubules grow on the interplay of a multitude of motors exerting force on microtubules, which leads to concerted movements in the cell. The one dimensional nuclear oscillations in the fission yeast Schizosaccharomyces pombe represent an easily accessible model process to study intracellular movements driven by molecular motors and microtubules. Similar oscillations have been observed in other organisms during mitosis. For the oscillations in S. pombe the minus-end directed motor protein dynein is necessary, which generates pulling forces by binding to microtubules and the cell cortex [Yam 06]. In S. pombe microtubules grow opposite directions from the spindle pole body, and the movement of dynein all along the microtubules gives rise to antagonistic pulling forces [Vog 09]. We investigated the resulting dynamics by studying the gliding of cross-linked anti-parallel microtubules in vitro. Currently we are working with stabilized microtubules and the plus-end directed motor protein kinesin [Led 10]. We will extend the approach to anti-parallel dynamic microtubules gliding on yeast dynein. [Yam 06] Yamamoto et al., J. Cell Biol., 145 (1999); [Vog 09] Vogel et al., PLoS Biology, 7 (2009); [Led 10] Leduc et al., PRL, 105 (2010);

BP 33.6 Fri 12:00 ZEU 250
Actin filaments undergo local structural transitions at random sites — ∙Thomas Niederhaver1, Antoine Jégou1, Emmanuelle Helpérin2, Guillaume Romet-Lemonn2, Marie-Franck Carlier2, and Reinhard Lipowsky1 — ∙Abteilung Theorie und Bio-Systeme, Max-Planck-Institut für Kolloid- und Grenzflächenforschung, 14424 Potsdam, Germany — ∙Laboratoire d’Enzymologie et Biochimie Structurales, CNRS, 91918 Gif-sur-Yvette, France
After the polymerization of actin monomers into filaments, the actin-bound ATP is hydrolyzed into ADP, a process that is believed to decrease the filament stability. Recent experiments suggest the opposite behavior, however, namely that actin filaments become increasingly stable with time. Several mechanisms for this unexpected behavior have been proposed, ranging from structural transitions of the whole filament helix to pure artifacts arising, e.g., from the capping or surface attachment of the filament ends. We performed novel fluorescence microscopy experiments on single filaments to clarify this controversial issue. We find that filaments do indeed cease to depolymerize in an abrupt manner, and that this transition happens on relatively long time scales that exceed those of both ATP cleavage and phosphate release. We also developed a theory that allows us to distinguish the different possible transition mechanisms. A detailed comparison of theory and experiment implies that the sudden truncation of the shrinkage process does neither arise from artifacts nor from a collective transition of the whole filament. Instead, our results provide strong evidence for a local transition process occurring at random sites within the filament.

BP 33.7 Fri 12:15 ZEU 250
Kinesin-3 (UNC-104) can act as a dimeric motor during axonal transport C. elegans neurons in vivo — ∙Volker Christoph Henschel1, Alessandro Esposito2, Christoph Friedrich Schmidt3, Fred Sylvester Wouters3, and Dieter Robert Klopfenstein1 — ∙Drittes Physikalisches Institut, Biophysik, Georg-August-University Göttingen, Göttingen, Germany — ∙2MRC Cancer Cell Unit, Hutchison/MRC Research Centre, Cambridge, UK — ∙3Laboratory of Cellular and Molecular Systems, Department of Neuro- and Sensory Physiology, Georg-August-University Göttingen, Göttingen Germany
Monomeric Kinesin-3 (UNC-104) is responsible for the transport of presynaptic vesicles to synaptic termini in C. elegans. To investigate the role of the endogenous coiled-coils, we introduced point mutations in the motors coiled-coil region in the neck promoting either dimer formation of Kinesin-3 or reducing the likelihood of dimerization. We verify dimerization by cross-linking of purified truncated motors in vitro. We show by live in vivo imaging, that reducing dimerization of Kinesin-3 leads to decreased vesicle transport velocities and affects the control of muscle contraction. C. elegans with reduced dimerization properties exhibit a 45% reduction in anterograde velocity. Additionally, severe motility and a significant egg laying defect are observed. To assess dimer formation in vivo we combine Förster Resonance Energy Transfer (FRET) and anisotropy imaging with spinning-disc laser confocal microscopy. Our data suggest a direct link between dimerization status and transport velocities.

BP 33.8 Fri 12:30 ZEU 250
Computational/Genetic approach characterizes the construction of the Drosophila ear — ∙Björn Nadorowski1,2, Thomas Effertz2, and Martin Göpfert2 — ∙Theoretische Physik, Universität des Saarlandes, Campus E2.6, 66123 Saarbrücken — ∙Abt. Zelluläre Neurobiologie, Universität Göttingen, MPI für Experimentelle Medizin, Hermann-Rein-Str. 3, 37075 Göttingen
Hearing relies on dedicated mechano-electrical transduction (MET) channels that convert stimulus forces into electrical signals. We present a physical model that quantitatively links ion channel mechanics and movements of molecular adaptation motors to the dynamics of the entire ear. We fit the model parameters to data obtained from both wild-type and mutant flies. We show that the experimental data obtained in the absence of NompC (a candidate MET gene), can be interpreted as the absence of a transduction channel in a transducer system that consists of two parallelly arranged channel populations, one of them constituted by NompC. We further show evidence that NompC might be specifically needed to detect low stimulus amplitudes (i.e. sound stimuli), whereas the other channel population might serve for the detection of wind and/or gravity.

BP 33.9 Fri 12:45 ZEU 250
The molecular basis of filopodial retraction analyzed with photonic force based microscopy — ∙Felix Kohler1,2 and Alexander Rohrbach1,2 — ∙Bio and Nano-photons, IMTEK, University of Freiburg, Germany — ∙BIOS Centre for Biological Signalling Studies, Freiburg, Germany
Filopodia are needle-like protrusions of the cell surface. These actin rich protrusions are highly dynamic structures that extend and retract over the timescale of a few seconds. Besides actin polymerization and depolymerization, coordinated transport of molecular motors seems to control filopodial mechanics. Apart from sensing the environment and anchorage of cells to a substratum filopodia are also involved in phagocytosis. We use photonic force microscopy to investigate the mechanical concepts of the filopodial retraction during phagocytosis. The motion of an optically trapped bead is attached to tip of a filopodium and tracked interferometrically in 3D with nanometer precision at a microsecond timescale. The measurement of e.g. the beads mean displacement allows determining the retraction forces of filopodia at various retraction speeds. We have measured F-actin dependent steps by single-molecule Förster Resonance Energy Transfer (FRET) and anisotropy imaging with spinning-disc laser confocal microscopy. Our data suggest a direct link between dimerization status and transport velocities.

**Invited Talk BP 34.1 Fri 10:15 ZEU 260**

Super-resolution fluorescence imaging of cellular structure and dynamics — ●MARCUS SÄUER, SEBASTIAN VAN DE LINDE, TERESA KLEIN, ANNA LÖSCHBERGER, THORGE HOLM, and SVEN PROPPER — Biotechnology and Biophysics, Julius-Maximilians-University Würzburg, Germany

We introduce direct stochastic optical reconstruction microscopy (dSTORM), a new general approach for multicolor super-resolution fluorescence imaging based on reversible photointeraction of standard small organic fluorophores. Photoswitching of organic rhodamine and oxazine fluorophores, i.e. the reversible transition from a fluorescent to a non-fluorescent state in aqueous buffers exploits the formation of long-lived radical anions through reaction with thiol compounds and repopulation of the singlet ground state by reaction with molecular oxygen. We unravel the underlying switching mechanism, investigate the importance of labeling strategies and densities, and demonstrate super-resolution imaging with different commercially available organic fluorophores with high spatial and temporal resolution. Finally, we demonstrate that dSTORM in combination with suited chemical tags can be advantageously used for dynamic live cell imaging at resolutions ~20 nm.

**BP 34.2 Fri 10:45 ZEU 260**

Nanoscale Localisation of Adhesion Receptors and Binding Domains of Matrix Proteins Using Electric Field Microscopy — ●CHRISTINA MÖLLER1, DIMITR STANOV1, CARSTEN WEHNER1,2, and TILO FOMPY3 — 1Leibniz Institute of Polymer Research Dresden, 01069 Dresden, Germany; 2Center for Regenerative Therapies Dresden, 01307 Dresden, Germany

Biomaterial interfaces constitute the intersection of living tissues and artificial scaffolds. In order to reveal exogenous cues in guiding cell behaviour a precise localisation of adhesion receptors and their ligands at the extracellular matrix (ECM) at biomaterial interfaces is needed. Although several techniques allow for the determination of spatial protein distributions, most of them require special conditions (electron microscopy) or lack high resolution (optical microscopy). We applied scanning force microscopy to provide at the same time nanoscale resolution and easy access to biological samples at material interfaces. Using electric force microscopy and immunogold labelling we revealed the localisation of cell adhesion receptors, i.e. integrins, at ECM reorganised by adherent cells. The modulated anchorage of the adhesion ligands by the polymer support lead to different reorganisation patterns of fibronectin fibrils at the adhesion sites together with differences in the distribution and density of integrins. By probing specific domains at fibronectin fibrils, we additionally found them in a stretched state caused by the involved receptor forces. The versatility and straightforward implementation suggests the used method to further characterise different sets of ECM structures and corresponding receptors.

**BP 34.3 Fri 11:00 ZEU 260**

Distance measurements in the nanomter range by in-cell EPR — ●MALTE DRESCHER — Emmy-Noether-Gruppe Physikalische Chemie Universität Konstanz, 78457 Konstanz

In the past years, electron paramagnetic resonance (EPR) spectroscopy has witnessed tremendous methodological and instrumental developments. These new methods have strong impact on biotechnological research. Diamagnetic material such as most biomacromolecules (DNA, proteins, etc.)can be investigated by site-directed spin-labeling. Of particular interest are Double Electron Electron Resonance (DEER) techniques giving access to inter- and intramolecular distance distributions in the nanometer range. EPR dynamics can be monitored on a scale from picoseconds to microseconds. The utilization of pulsed EPR methods is especially useful for addressing structural features in complex systems. In particular, our current effort to go beyond in-vitro approaches and to in-cell EPR will be introduced. Distance measurements by in-cell EPR using a spin-labeled DNA model system will be demonstrated.


**BP 34.4 Fri 11:15 ZEU 260**

Optical manipulation of neuronal networks bursting dynamics — ●GAZALEH AFSHAR1,2,3, AHMED EL-HADAY2,3, THEO GEISEL1,2,4, WALTER STUBER1,2,4, and FRED WOLF1,2,4 — 1Max Planck Institute for Dynamics and Self Organisation, Göttin- gen, Germany; 2Max Planck Institute of Experimental Medicine, Göttingen, Germany; 3Bernstein Center for Computational Neuroscience, Göttingen, Germany; 4Facility of Physics, Georg August University, Göttingen, Germany

Cultures of channelrhodopsin-2 transfected hippocampal neurons allow simultaneous optical stimulation and electrical recording from neuronal networks. As has been previously reported, after maturation, these networks develop an electrical activity that is characterized by synchronized bursts. In this work, we study the influence of whole field blue light illumination on burst dynamics of these cultures. During stimulation the mean firing rate is significantly different than before and after stimulation. Moreover, the mean spike rate during burst is significantly higher during stimulation. After turning off the stimu- lus, a silent period follows and then the network gradually switches into an ongoing state of bursting activity with even higher mean spike rate during stimulation. In fact, the mean duration of burst decreases during and after stimulation compared to non-perturbed spontaneous activity. We conclude that light stimulation can be used to persistently influence bursting dynamics in biological neuronal networks.

15 min. break

**BP 34.5 Fri 11:45 ZEU 260**

Dip-Pen Nanolithography and Polymer-Pen Lithography for Bio-Medical Applications — ●FALKO BRINKMANN1,2,3,4, SYLVIA SEKULA1, MICHAEL HITZ2, and HARALD FUCHS1,2,3,4 — 1Institut für Nanotechnologie, Karlsruher Institut für Technologie, 76128 Karlsruhe, Germany; 2Physikalisches Institut, Westfälisches Wilhelms-Universität Münster, 48149 Münster; 3Center for Nanotechnology (CeN Tec), 48149 Münster; 4Institut für Tumorbiologie, Universitätsklinikum Hamburg-Eppendorf, 20246 Hamburg

Dip-Pen Nanolithography (DPN) is a versatile tool for the fabrication of arbitrary patterns on a wide range of surfaces. It uses the tip of an atomic force microscope (AFM) as a miniature quill-pen which is dipped into inks like silanes or phospholipids. Its capability to pattern different functional materials on the same surface with 1D or 2D tip arrays simultaneously (multiplexing) leads to wide interest in biology and medicine. Feature sizes range from less than 100 nm to the several micrometers.

Polymer-Pen Lithography (PPL) is based on a polydimethylsiloxane (PDMS) stamp with millions of tips. Compared to silicon tip arrays, polymer pens are inexpensive and are able to deposit inks with higher throughput. Multiplexed dot-arrays can be accomplished in nanometer resolution over many square centimeters within a few minutes.

Both DPN and PPL can be used to fabricate functional nano- and micropatterns for bio-medical studies like protein-binding, virus-detection and cell-adhesion with potential application in biosensors and medical lab-on-chip devices.

**BP 34.6 Fri 12:00 ZEU 260**

Combined 3D structural and molecular imaging using optical coherence tomography and laser scanning microscopy — ●MARIA G A R T H N E R1, PETER C I M A L L A2, LILLY K N E L S2, SVEN MEISSNER1, WOLFGANG M. K U H R L1, and EDMUND KOCH1 — 1TU Dresden, Faculty of Medicine Carl Gustav Carus, Clinical Sensing and Monitoring, Dresden, Germany; 2TU Dresden, Faculty of Medicine Carl Gustav Carus, Department of Anatomy, Dresden, Germany; 3Institute for Physiology, Charité Berlin, Germany and Department of Surgery, University of Toronto, Ontario

Since the early 1990s, optical coherence tomography (OCT) has an emergent impact on biomedical and biophysical research. As a non-invasive optical technique, it provides three-dimensional, contactless, high-resolution (μm) imaging of tissue substances with penetration depths of up to several millimeter. Exploiting its abilities, in vivo histological studies become feasible without extraction of biological tissue. The sample’s morphology can easily be obtained within a few
milliseconds. Apart from all its benefits, the lack of molecular specific interactions limits this method to a mere coarse investigation of tissue architecture. Utilizing laser scanning microscopy, the detailed molecular structure of biological samples can be obtained via specifically binding dyes to the substance of interest. In this study, we present a combined setup for simultaneous OCT and confocal fluorescence microscopy, allowing fast three-dimensional imaging of lung morphology and detection of elastic fiber distributions arising from the biomolecule elastin within lung tissue.

**BP 34.7** Fri 12:15 ZEU 260
Enhancing the penetration depth in biological matter using Microscopy with Self-Reconstructing Beams — CHRISTIAN Gohn-Kreuz and ALEXANDER Rohrbach — University of Freiburg, Laboratory for Bio- and Nano-Photonics, 79110 Freiburg, Germany

Microscopy with Self-Reconstructing Beams (MISERB) is an imaging technique derived from the concept of light-sheet based microscopy. In this technique optical sectioning, i.e. the avoidance of out-of-focus light, is achieved by creating a thin sheet of light within a fluorescently labeled sample, while detecting the emitted light in a direction perpendicular to the illumination axis. In contrast to regular light sheet based microscopy, where the light sheet is either created by a cylindrical lens or a laterally scanned Gaussian beam, the light sheet in MISERB is created by a laterally scanned Bessel beam [1]. This beam belongs to the class of self-reconstructing beams. It recovers its beam profile a short distance behind a scattering object. Due to this fact Bessel beams can provide a higher penetration depth than Gaussian beams in dense biological media like e.g. human skin. The penetration depth and image quality deep inside an object however is still limited by scattering artifacts. These artifacts result from the fact that the original beam profile gets distorted while propagating through thick scattering media. In this work we will investigate the controlled reduction of scattering artifacts by individually matching the illumination beam to the sample under consideration, thus enhancing the penetration depth in thick scattering media. [1] F. O. Fahrbach, P. Simon, and A. Rohrbach, Nature Photonics 4, 780-785 (2010)

**BP 34.8** Fri 12:30 ZEU 260
NanoFocus Endstation of MiNaXS Beamline @ PETRA III — CHRISTINA Krzywka 1, STEPHAN Roth 2, RALPH DöHRMANN 2, and MARTIN Müller 2 — Christian-Albrechts-Universität zu Kiel, Institute of Optical and Atomic Physics, Leibniz Institute of Solid State Research, 24098 Kiel, Germany — 1 Technical University of Denmark, Denmark — 2 Helmholtz-Zentrum Geesthacht, Max-Planck-Straße 1, 21502 Geesthacht

Experiments can be performed in both wide-angle and small-angle x-ray scattering geometry (WAXS and SAXS) and this combined with the targeted spatial resolution being so far unique. The planned future extensions.

**BP 35.3** SYBE: Statistical Physics and Biological Evolution

**Invited Talk**
**BP 35.1** Fri 10:30 TRE Ma
Microbial evolution in spatially-structured environments — ARIAN DE VISSER — Laboratory of Genomics, Wageningen University, The Netherlands

The theory of evolution is increasingly powerful in explaining the diversity of life by looking back, but is still largely unable to predict the future course of evolution. One problem with the development of a predictive theory of evolution is the lack of direct experimental tests of evolutionary models, which are constrained by the slow pace of evolution. Microbial experimental evolution offers a promising tool in this respect. Microbes, such as bacteria and fungi, allow relatively rapid evolutionary changes under controlled conditions that can be replicated. Moreover, they can be temporarily stored in non-evolving state in the freeze and molecular tools allow the manipulation of their genotypes and identification of evolved genetic changes. One limitation of these studies so far has been the use of unstructured well-mixed environments, while natural environments are spatially structured. Spatial environmental structure has several consequences for the process of evolution, including (i) increased environmental heterogeneity allowing more diverse adaptive opportunities, (ii) fragmentation of populations into small semi-isolated subpopulations with a greater role of genetic drift, and (iii) decreased access to nutrients due to slow diffusion leading to inefficient local resource competition among clone mates. I will introduce the approach of experimental evolution, and present examples of studies addressing various consequences of spatial variation and evolution.

PETRA III, located on the site of DESY (Hamburg) is the world’s most brilliant synchrotron radiation source. The nanofocus endstation of its MiNaXS-Beamline (Micro- and NanoFocus X-ray Scattering) is currently on the verge of entering into user-dedicated mode.

MiNaXS was designed to provide a high flux, low divergence monochromatic x-ray beam (8-23 keV) and it’s nanofocus endstation is targeting to deliver a nanofocused beam with a focal spot size in the order of 100nm * 100nm and a high coherence option dedicated for diffraction experiments at both biological and synthetic materials.

Experiments can be performed in both wide-angle and small-angle x-ray scattering geometry (WAXS and SAXS) and this combined with the targeted spatial resolution being so far unique.

The very first commissioning experiments were successfully performed in November and December 2010 at the nanofocus endstation, rendering the MiNaXS beamline operational at both of it’s endstations. This contribution presents the current status of the nanofocus endstation, the results of the commissioning experiments as well as the planned future extensions.

**BP 34.9** Fri 12:45 ZEU 260
Evolutionary algorithms used to study fluorescence decay curves of photosystem II core complexes from Thermosynechococcus elongatus — JOACHIM BÖRNER 1, FRANZ-JOSEF SCHMITT 2, ATTHINA ZOUN 3, HANS JOACHIM EICHEL 1, and GERNOT RENGER 1 — 1 Institute of Optics and Atomic Physics, Berlin Institute of Technology — 2 Max-Valmer-Laboratory of Biophysical Chemistry, Berlin Institute of Technology

The character of kinetic limitation of the exciton trapping in Photosystem II (PS II) is not yet clarified. It is a matter of discussion whether the exciton trapping energy transfer (ETT) from core antennas to the reaction center or the succeeding electron transfer (ET) is the rate limiting step of the overall process. In order to address this problem we investigated complex core structures from Thermosynechococcus elongatus by using the technique of time correlated single photon counting with picosecond resolution. The obtained fluorescence decay curves were analyzed assuming a framework of a structure based model with a set of coupled differential equations. Self-designed evolutionary algorithms were used to achieve a satisfying fit of the experimental data by simulated decay curves. The algorithm allows the determination of transition rates of EET and ET processes in PS II and the stability and variance of these rates by random modifications of an initial set. Our results revealed that the ETT from the core antennas to the reaction center is most likely limiting the overall exciton trapping with typical transfer time constants in the order of some tens of picoseconds whereas the charge separation (electron transfer) is accomplished within a few ps only.

**BP 35.2** Fri 11:00 TRE Ma
Correlated mutations: Facts or artifacts? — AMNON HOROVITZ — Weizmann Institute, Rehovot, Israel

Mutations that affect protein function by structural perturbation at one site are often compensated for by mutations at other sites. Such correlated mutations are thought to occur since there is greater selective pressure to conserve protein structure and function than sequence. Correlated mutation analyses have indicated that distant sites in proteins are often coupled to each other. It has not been clear, however, whether such correlations between distant positions reflect real long-range interactions or common ancestry. In order to address this question, lattice models of proteins were subjected to mutation and selection for greater stability and long-range correlations that arose as a result were characterized. Our results show that long-range correlations with non-zero coupling energies do exist in lattice models [1] and that they are more common when the stability of the native state is achieved by negative design, i.e. by destabilizing non-native contacts [2]. The implications of these findings for real proteins will be discussed.

Invited Talk

Macroscopic laws in bacterial genome evolution — Erik van Nimwegen — Biozentrum, Universität Basel, Switzerland

Over the last century an enormous effort has been invested into the modeling of evolutionary dynamics, but validation of these models with real data have been limited for several reasons: Until the 1950s it was simply not known what the substrate of natural selection was and until recently data was limited to small fractions of the genomes of a small number of organisms. In addition, none of the existing evolutionary models capture all the complexities of evolution in the real world, so that it is generally unclear which predictions of evolutionary models one would expect to observe in real world data.

However, recently the number of publicly available complete genome sequences has grown from one (in 1995) to currently almost 1500. This has offered researchers, for the first time, a chance to identify ‘laws’ of genome evolution not from general theoretical considerations, but directly by analysis of the available genome data. Indeed such studies have recently uncovered several remarkable macroscopic laws in genome structure and evolution. These quantitative laws concern features such as the distribution of evolutionary rates and gene family sizes, the distribution of genes across different functional categories, and large-scale properties of regulatory networks. In this talk I will discuss some of these laws and their implications for our understanding of genome evolution in prokaryotes.

Invited Talk

The role of horizontal gene transfer in the evolution of bacterial genomes — Paul Higgs — McMaster University, Hamilton, Ontario, Canada

For a set of related genomes, the core is the set of genes found in every genome, and the pan-genome is the set found in at least one genome. The pan-genome is usually much larger than the core. Genes can be lost by deletion and they can be gained by duplication, by de novo evolution of a new sequence, or by horizontal gene transfer (HGT) from another organism. We analyze clusters of related genes from a large number of complete genomes in order to estimate the relative rates of these processes. If the rate of HGT is very high, the traditional tree-like picture of evolution breaks down. It has been argued that the HGT rate was so high in the earliest cells that there were no separate lineages of organisms. Only when the HGT rate began to fall would lineages begin to emerge with their own distinct sets of genes. This phenomenon has been called the Darwinian Threshold. We study a model for genome evolution that incorporates both beneficial and detrimental effects of HGT and show that the model predicts the occurrence of a Darwinian Threshold.