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Fachverband Biologische Physik (BP)

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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 Ellenberg
BP 2.1	Mon	10:15–10:45	ZEU 260	**Protein Structure and Dynamics from Low-Resolution Data** — •Gunnar F. Schröder
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 Salomé
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 21.1	Wed	10:15–10:45	ZEU 260	**Stretching Proteins out of equilibrium: how extracellular matrix proteins serve as mechanotransducers** — •Viola Vogel
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 33.1	Fri	10:15–10:45	ZEU 250	**Clamping DNA Strands Together: The Mechanics of Single-strand Annealing** — •Erik Schäffer
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 14.1–14.3	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 26.1–26.2	Thu	10:30–11:30	HSZ 201	**Biophysics II: Mechanics and Flow in Biological Systems (joint AG jDPG, 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)

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

Invited Talk BP 1.1 Mon 10:15 ZEU 250

High throughput microscopy for systems biology: from genome-wide profiling to the analysis of protein complexes — •Jan Ellenberg — 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 genes 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 genome-wide 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 — Knut Drescher[1], •Jörn Dunkel[1], Luis Cisneros[2], Sujoy Ganguly[1], and Raymond Goldstein[1] — [1]DAMTP, University of Cambridge, Wilberforce Road, Cambridge CB3 0WA, UK — [2]Department 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, assemblages 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[3], Viktor Sourjik[3], and Yuhai Tu[1] — [1]IBM T. J. Watson Research Center, Yorktown Heights, NY 10598, USA — [2]Max Planck Institute for the Physics of Complex Systems, Dresden 01187, Germany — [3]Zentrum fur Molekulare Biologie der Universitat 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.

BP 1.4 Mon 11:15 ZEU 250

Looped Star Polymers: Lessons for Bacterial Chromosome Packaging — •Dieter Heermann, Miriam Fritsche, and Pascal Reiss — Institute für Theoretische Physik, Universität Heidelberg

Inspired by the topological organization of the circular Escherichia coli chromosome, which is compacted by separate domains, we study a polymer architecture consisting of a central ring to which either looped or linear arms are attached. A transition from a spherical to a toroidal shape takes place as soon as the inner ring becomes large enough for the attached arms to fit within its circumference. Building up a torus, the system flattens depending on the effective bending stiffness of the chain induced by entropic repulsion of the attached loops and, to a lesser extend, linear arms. We propose that the natural formation of a toroidal structure induced by a specific chromosome topology could be one driving force, among others, that nature exploits to ensure proper packaging of the genetic material within a rod-shaped nucleoid.

15 min. break

BP 1.5 Mon 11:45 ZEU 250

Heterogeneous timing of gene induction as a regulation strategy — •Noreen Walker[1,2], Georg Fritz[1,2], Sonja Westermayer[2], Judith Megerle[2], Joachim Raedler[2], and Ulrich Gerland[1,2] — [1]Arnold Sommerfeld Center for Theoretical Physics — [2]Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

Heterogeneity within a genetically homogeneous population is a common phenomenon in nature. While it has long been known that noise in gene expression leads to heterogeneity in protein levels, recent studies also demonstrated heterogeneity in the timing of gene induction. When a colony of E. coli cells is suddenly exposed to a new sugar, the onset time for expression of the specific sugar utilization system is broadly distributed, if the sugar concentration is low [1]. Whereas the underlying mechanism has been characterized [1], it is currently unclear whether this heterogeneous timing is a side effect or a genuine strategy to optimize growth and survival. Here, we first present further experimental evidence for heterogeneous timing. We then perform a theoretical analysis of the cost and benefit of different regulation strategies for gene induction within a coarse-grained growth model. We find that at low sugar concentrations, heterogeneous timing can indeed be an optimal regulation strategy, while a homogeneous response is favorable at high sugar concentrations.

[1] J. Megerle et al., Biophys. J. **95**, 2103-2115 (2008)

BP 1.6 Mon 12:00 ZEU 250

Resolution of gene regulatory conflicts caused by combinations of antibiotics — •Tobias Bollenbach[1,2] and Roy Kishony[1] — [1]Harvard Medical School, Boston, MA, USA — [2]IST Austria, Klosterneuburg, Austria

Regulatory conflicts occur when two signals, which individually trigger opposite cellular responses, are present simultaneously. Here, we investigate how such gene regulation conflicts are resolved in the bacterial response to antibiotic combinations. We use an *Escherichia coli* promoter-GFP reporter library to study the genome-wide transcriptional response to either additive or antagonistic drug pairs at fine two-dimensional resolution of drug concentration. Using principal component analysis (PCA), we find that this complete dataset can be almost fully characterized as a surprisingly simple linear sum of only two components. The first component, accounting for over 70% of the variance in the data set, represents the response to the net effectiveness of the drug combination in inhibiting growth. The second component describes how regulatory conflicts are resolved for genes that respond differently to each of the individual drugs. We find that for the non-

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 Baresel and Rudolf Friedrich — Insitute 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 translation or rotation 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 — •Pawel Romanczuk[1], Vishwesha Guttal[2], Lutz Schimansky-Geier[1], and Iain D. Couzin[2] — [1]Department of Physics, Humboldt Universität zu Berlin, Germany — [2]Department 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 generelized 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.

[1] S. J. Simpson *et. al.*, Proc. Natl. Acad. Sci. USA, 103, 4152 (2006)
[2] P. Romanczuk *et. al.*, Phys. Rev. Lett., 102, 010602 (2009)
[3] S. Bazazi *et. al.*, Proc. Roy. Soc. B, doi 10.1098/rspb.2010.1447

BP 1.9 Mon 12:45 ZEU 250

Spontaneous spiking in presence of an autaptic feedback loop — Yunyun Li[1], •Gerhard Schmid[1], Peter Hänggi[1], and Lutz Schimansky-Geier[2] — [1]Universität Augsburg, Germany — [2]Humboldt 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.

[1] Y. Li, G. Schmid, P. Hänggi, L. Schimansky-Geier, Phys. Rev. E, in press (arXiv:1009.5198)

BP 2: Protein Structure & Dynamics

Time: Monday 10:15–13:00 Location: ZEU 260

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 (> 4Å) data, which are not sufficient to fully determine atomistic 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-Jα-photosensor from Avena sativa — •Emanuel K. Peter, Bernhard Dick, and Stephan A. Baeurle — Fakultaet für Chemie und Pharmazie, Universitaet Regensburg, 93040 Regensburg, Deutschland

Fusion proteins containing light-activable 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-activable LOV2-Jα-protein domain from phototropin1 of Avena sativa (AsLOV2-Jα) 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-Jα-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].

[1] E. Peter, B. Dick and S. A. Baeurle, Nature Communications 1 : 122 (2010); doi: 10.1038/ncomms1121 (2010)

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 inter convert the respective enzyme species between a high and a low catalytic activity form. Here, I show that the concurrent action of such 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. *PNAS* **78**, 6840 (1981). [2] N. I. Markevich, J. B. Hoek and B. N. Kholodenko *J. Cell Biol.* **164** 353 (2004).

BP 2.4 Mon 11:15 ZEU 260

Lateral Diffusion and Correlation of Membrane Anchored Proteins — •Wasim Abuillan[1], Andreas Hartel[2], Nicola Jones[2], Markus Engstler[2], and Motomu Tanaka[1] — [1]Institute for Physical Chemistry, Heidelberg University, Germany — [2]Department of Cell and Developmental Biology, Würzburg University, Germany

Many Glycosylphosphatidylinositol (GPI) - anchored proteins are found on the plasma membrane.e.g. ~ 0.5 % of cellular proteins in eukaryotes are GPI-anchored. 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 is essential for them to maintain 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 detect 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 Lauck[1,2] and •Tihamer Geyer[1] — [1]Center for Bioinformatics, Saarland University, Saarbrücken — [2]Dep. 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 Wolff[1], Michele Vendruscolo[2], and Markus Porto[3] — [1]Institute for Condensed Matter and Complex Systems, University of Edinburgh, UK — [2]Department of Chemistry, University of Cambridge, UK — [3]Institut 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 much 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. 1dv0), for which we find an essentially symmetric free energy landscape [2].
[1] H. Lei *et al.*, Proc. Natl. Acad. Sci. USA **104**, 4925 (2007)
[2] K. Wolff *et al.*, *submitted*

BP 2.7 Mon 12:15 ZEU 260

Impact of compatible solutes on the local water structure and the structural organization of lipid monolayers — •Jens Smiatek[1], Rakesh Kumar Harishchandra[2], Oliver Rubner[1], Hans-Joachim Galla[2], and Andreas Heuer[1] — [1]Institut für Physikalische Chemie, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany — [2]Institut 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 the characteristics of the local ordering of 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 comaptible 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 Leibfarth[1], Felix Roosen-Runge[1], Fajun Zhang[1], Nina Fischer[2], Oliver Kohlbacher[2], Sophie Weggler[3], Michael Ziller[1], Andreas Hildebrandt[3], Elena Jordan[1], and Frank Schreiber[1] — [1]Institut für Angewandte Physik, Universität Tübingen — [2]Zentrum für Bioinformatik, Universität Tübingen — [3]Zentrum für Bioinformatik, Universität des Saarlandes

Experiments indicate that the effective charge of proteins in solution can be inverted by binding trivalent metal ions [1]. In addition, X-ray diffraction data show that metal ions bind to negatively charged carboxylic 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 Y^{3+}. Firstly, a classical protonation titration approach was adopted to trivalent ion binding [1, 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 Schmitt[1], Jörg Pieper[2], Christoph Theiss[1], Inga Trostmann[3], Harald Paulsen[3], Thomas Renger[4], Hans Joachim Eichler[1], Thomas Friedrich[1], and Gernot Renger[1] — [1]Berlin Institute of Technology, Germany — [2]University of Tartu, Estonia — [3]Johannes Gutenberg University Mainz, Germany — [4]Johannes Kepler University Linz, Austria

Spectroscopic studies on pigment-pigment and pigment-protein interactions of Chl a and b bound to the recombinant class IIa WSCP from cauliflower are presented. Two Chls form a strongly excitonically 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 dioxygen 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 functionalizing 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.

BP 3: Biopolymers and Biomaterials I (with CPP)

Time: Monday 10:30–13:00 Location: ZEU 222

Topical Talk BP 3.1 Mon 10:30 ZEU 222

Crayfish combine amorphous and crystalline mineral to build a functional tooth structure — •Barbara Aichmayer[1], Shmuel Bentov[2,3], Ali Al-Sawalmih[1], Admir Masic[1], Paul Zaslansky[1], Peter Fratzl[1], Amir Sagi[3,4], and Amir Berman[2,4] — [1]Department of Biomaterials, Max Planck Institute of Colloids and Interfaces, 14424 Potsdam, Germany — [2]Department of Biotechnology Engineering, Ben-Gurion University of the Negev, 84105, Israel — [3]Department 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, measured by 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 Ene[1], Periklis Papadopoulos[2], and Friedrich Kremer[1] — [1]Institüt für Experimentelle Physik I, Leipzig, Germany — [2]Max-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 Schmied[1,4], Wolfgang Fischer[2,4], Ulrich Hirn[2,4], Robert Schennach[3,4], and Christian Teichert[1,4] — [1]Institute of Physics, University of Leoben, 8700 Leoben, Austria — [2]Institute for Paper, Pulp and Fiber Technology, Graz University of Technology, 8010 Graz, Austria — [3]Institute of Solid State Physics, Graz University of Technology, 8010 Graz, Austria — [4]CD-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 than 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 — •Ezzeldin Metwalli[1], Alexander Diethert[1], Joseph Adelsberger[1], Robert Cubitt[2], Ulrich Kulozik[3], and Peter Müller-Buschbaum[1] — [1]TU München, Physik Department, LS Funkt. Mat., James-Franck-Str. 1, 85748 Garching, Germany — [2]ILL, 6 rue Jules Horowitz, b.p. 156, 38042 Grenoble, France — [3]TU München, Chair for Food Proc. Eng. and Dairy Tech., 85354 Weihnstephan, Germany

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 D_2O 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. Metwalli 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 Baeurle[1], Michael G Kiselev[2], Elena S Makarova[2], and Evgenij A Nogovitsin[2] — [1]Department of Chemistry and Pharmacy, Institute of Physical and Theoretical Chemistry, University of Regensburg, Universitätsstr. 31, D-93053 Regensburg, Germany — [2]Institute 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 behavior on the molecular level has been hindered due to the lack 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 Kreuzer[1], Markus Strobl[2], Matthias Reinhardt[2], Reiner Dahint[1], and Roland Steitz[2] — [1]Universität Heidelberg, Physikalisch 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 and BioRef neutron reflectometer at the Helmholtz-Zentrum Berlin, in excess D2O verified, that a oligolamellar DMPC lipid bilayer coating remains stable on a silicon substrate at 21°C in its ordered state (Lβ)

with a d-spacing of 66Å, but detaches almost completely at 38°C in its chain-disordered Lα 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 Günther[1], Ralf Seidel[2], and Michael Mertig[1] — [1]Technische Universität Dresden, Institut für Physikalische Chemie, Mess- und Sensortechnik, 01069 Dresden, Germany — [2]Technische Universität Dresden, Biotechnology Center, Tatzberg 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 untwisting 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 Hellweg[1], Laura Rodriguez-Arriaga Rodriguez-Arriaga[2], Ivan Lopez-Montero[2], Bela Farago[3], and Francisco Monroy[2] — [1]Universität Bielefeld, PC III, Universitätsstr. 25 33615 Bielefeld, Germany — [2]Universidad Complutense, 28040 Madrid, Spain — [3]ILL, 6 rue Jules Horowitz, BP 156, F-38042 Grenoble Cedex 9, France

In the present contribution the center of mass diffusion and shape fluctuations 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 different 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 κ of the bilayer. A stiffening effect monitored as an increase of κ 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 κ or of substances like e.g. Gramicidine.

[1] Rodriguez Arriaga, L., I. Lopez-Montero, F. Monroy, G. Orts Gil, B. Farago und T. Hellweg: Biophys. J., **96**, 3629–3637, 2009.
[2] Arriaga, L. R., R. Rodriguez-Garcia, I. Lopez-Montero, B. Farago, Th. Hellweg, und F. Monroy: Euro. Phys. J. E, **31**, 105–113, 2010.

BP 3.9 Mon 12:45 ZEU 222

Investigation of L-Cysteine in aqueous solution using the RIXS-map approach — •Frank Meyer[1], Lothar Weinhardt[1], Monika Blum[2], Marcus Bär[3], Regan Wilks[3], Wanli Yang[4], Clemens Heske[2], and Friedrich Reinert[1] — [1]Exp. Physik VII, Universität Würzburg — [2]Department of Chemistry, University of Nevada Las Vegas, USA — [3]Solar Energy Research, Helmholtz-Zentrum Berlin für Materialien und Energie GmbH — [4]Advanced 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 liquids 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 thin films and of related molecules.

BP 4: DNA & DNA Enzymes

Time: Monday 14:00–17:00 Location: ZEU 260

Invited Talk BP 4.1 Mon 14:00 ZEU 260

Single-molecule detection of DNA repair in real-time — •Terence Strick[1], Kevin Howan[1], Nigel Savery[2], Seth Darst[3], and MM2M FP7 Consortium[4] — [1]CNRS Institut Jacques Monod Paris, France — [2]University of Bristol, UK — [3]Rockefeller Institute, NY, USA — [4]Erasmus 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 Klumpp[1], Marco Mauri[1], and Terence Hwa[2] — [1]Max Planck Institute of Colloids and Interfaces, Potsdam — [2]University of California, San Diego

How frequently a gene is transcribed depends not only on its regulation, but also on the availability of the necessary molecular machinery, RNA polymerases (RNAPs) and their associated factors. The concentration 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 functional 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 overexpression. 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.

[1] S. Klumpp and T. Hwa, Proc Natl Acad Sci USA 105, 10245 (2008).

BP 4.3 Mon 14:45 ZEU 260

A model for the degradation of messenger RNA in bacteria — •Carlus Deneke, Angelo Valleriani, and Reinhard Lipowsky — Max-Planck-Institut für Kolloid- und Grenzflächenforschung, Department 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 initiated 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 life time 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.

BP 4.4 Mon 15:00 ZEU 260

A Stochastic Model of DNA Replication Dynamics — •Daniel Löb and Barbara Drossel — 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.

An important ingredient of the model is the structuring of DNA into zones of euchromatin and heterochromatin, which have different rates of replication initiation. The sizes of these zones affect the time course of replication of the two chromatin types.

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.

BP 4.5 Mon 15:15 ZEU 260

Unfolding mechanisms and the free energy landscape of the DNA i-motif — •Jens Smiatek and Andreas Heuer — Institut für Physikalische Chemie, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany

Since the discovery of the DNA i-motif, the formation and function of this specific structure has attracted broad interest. Actually the pH-dependent reversible folding/unfolding mechanism has been nowadays used in technological applications like in the construction of nanocontainers. We investigate the unfolding mechanism in high temperature unfolding simulations and characterized it in terms of its eigenvectors. Furthermore we present the results of Molecular Dynamics simulations for the free energy landscape for different reaction coordinates which has been computed by a generalized version of the metadynamics approach. Our results indicate that at room temperature the planar hairpin structure is more stable than the totally stretched chain.

15 min. break.

BP 4.6 Mon 15:45 ZEU 260

Development of an inter-nucleotide potential for DNA based on Density Functional theory — •Maria Fyta[1,2], Greg Lakatos[1], Pierfrancesco Rosini[3], Amanda Peters[1], Simone Melchionna[1,4], and Efthimios Kaxiras[1] — [1]Department of Physics and School of Engineering and Applied Sciences, Harvard University, Cambridge, MA, USA — [2]Physics Department, Technical University of Munich, 85748 Garching, Germany — [3]Laboratory for Multiscale Modeling of Materials, EPFL, Lausanne, Switzerland — [4]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 physiologic conditions. The generated potential model will be capable to investigate the behavior of dsDNA in interesting biophysical processes.

BP 4.7 Mon 16:00 ZEU 260

Type III restriction enzymes use 1D diffusion to communicate the relative orientation of their distant target sites — •Friedrich W. Schwarz[1], Julia Tóth[2], Kara van Aelst[2], Mark D. Szczelkun[2], and Ralf Seidel[1] — [1]BIOTEC TU-Dresden — [2]University of Bristol, UK

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 domains. 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 fast 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.

BP 4.8 Mon 16:15 ZEU 260

Probing the elasticity of DNA on short length scales by modeling supercoiled DNA under tension — •Robert Schöpflin[1], Hergen Brutzer[2], Oliver Müller[1], Ralf Seidel[2], and Gero Wedemann[1] — [1]University of Applied Sciences Stralsund, 18435 Stralsund, Germany — [2]Biotechnology Center Dresden, University of Technology Dresden, 01062 Dresden, Germany

The worm-like-chain (WLC) is the most commonly used theoretical framework for modeling the flexibility 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 supercoiling experiments of DNA under tension [2] using high-resolution Monte Carlo simulations. DNA supercoiling under tension is accompanied by an abrupt buckling at the transition from the stretched to the superhelical, i.e. plectonemic, state. This transition is due to the extreme bending of the DNA in the end loop of the plectoneme and serves therefore as a sensitive benchmark for model evaluations. While simulations that employ regular WLC bending energetics quantitatively reproduce the buckling transition, the buckling almost disappears for SEC models. Thus, DNA bending is best described by a harmonic model down to bending radii of 3 nm.

[1] Wiggins, P., et al. Nat Nanotechnol. 1(2):137-41 (2006)
[2] Brutzer, H., et al. Biophys J. 98(7):1267-76 (2010)

BP 4.9 Mon 16:30 ZEU 260

Optical Tweezers Force Spectroscopy of a Single DNA-bound Protein during Nanopore Translocation — •Andy Sischka[1], Andre Spiering[1], Sebastian Getfert[2], Peter Reimann[2], Janine König[3], Karl-Josef Dietz[3], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanoscience, Bielefeld University, Germany — [2]Condensed Matter Theory, Bielefeld University , Germany — [3]Biochemistry and Plant Physiology, Bielefeld University, Germany

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 nanopore potential compares very well with the measured force curves and explains a linear voltage dependency and a small hysteresis during back and forth translocation cycles. Translocation dynamics reflects the stochastic nature of the thermally activated hopping between two adjacent states in the nanopore [2]. This opens new and fascinating applications for label-free localization and discrimination of DNA-binding ligands, where positional and structural binding phenomena can be investigated in real-time at the single molecule level.

[1] A. Sischka et al.: J. Phys - Condens. Matt. 22: 454121 (2010)
[2] A. Spiering et al.: submitted (2010)

BP 4.10 Mon 16:45 ZEU 260

The interplay of mutations and electronic properties in disease-associated genes — Chi-Tin Shih[1,2], Stephen A Wells[3], Ching-Lin Hsu[4], Yun-Yin Cheng[1], and •Rudolf A Römer[3] — [1]Department of Physics, Tunghai University, 40704 Taichung, Taiwan — [2]The National Center for Theoretical Sciences, 30013 Hsinchu, Taiwan — [3]Dept. of Physics and Ctr for Scientific Computing,University of Warwick, Gibbet Hill Road, Coventry, CV4 7AL, UK — [4]Department of Physics, Chung-Yuan Christian University, Chung-Li, Taiwan

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) 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 a decade of intense efforts. Here we show, by analysing 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 conductance of the double helix, that is significant.

BP 5: Tissue Dynamics & Developmental Processes

Time: Monday 14:00–16:45 Location: ZEU 250

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 Zink, Anatol Fritsch, Tobias Kiessling, K. David Nnetu, Steve Pawlizak, Franziska Wetzel, and Josef Käs — 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 functional, materials 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 strain 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 — •Dmitry Fedosov, Julia Fornleitner, and Gerhard Gompper — 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. Staple[1], Reza Farhadifar[1], Benoît Aigouy[2], Andreas Sagner[2], Jens-Christian Röper[2], Suzanne Eaton[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max 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 Ranft[1,2], Markus Basan[1], Jens Elgeti[1], Jean-François Joanny[1], Jacques Prost[3], and Frank Jülicher[2] — [1]Institut Curie, 26 rue d'Ulm, 75005 Paris, France — [2]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Str. 38, 01187 Dresden, Germany — [3]ESPCI, 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.

[1] Ranft et al., PNAS, 2010 Nov 15. (Epub ahead of print)

BP 5.5 Mon 15:15 ZEU 250

Pattern formation in active fluids — •Justin Bois[1,2], Frank Jülicher[1], and Stephan Grill[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany

We discuss pattern formation in active fluids in which active stress is regulated by diffusing molecular components. Nonhomogeneous active stress profiles create patterns of flow which transport stress regulators by advection. Our work is motivated by the dynamics of the

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 Zumsande[1], Dirk Stiefs[1], Stefan Siegmund[2], and Thilo Gross[1] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany. — [2]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 analyse 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 properties 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 Plachta[1], •Tobias Bollenbach[2,3], Shirley Pease[1], Scott E. Fraser[1], and Periklis Pantazis[1] — [1]California Institute of Technology, Pasadena, CA, USA — [2]Harvard Medical School, Boston, MA, USA — [3]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 outwards signs of lineage patterning. By tracing the lineages of the cells in these two distinct sub-populations, we find that Oct4 kinetics predicts 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. Plachta et al., Nature Cell Biology, accepted.

BP 5.8 Mon 16:15 ZEU 250

Mechanotaxis in the brain — •Kristian Franze[1,2], Hanno Svoboda[2], Pouria Moshayedi[1,3], Andreas Christ[1], James Fawcett[3], Christine Holt[2], and Jochen Guck[1] — [1]Department of Physics — [2]Department of Physiology, Development and Neuroscience — [3]Brain Repair Centre, University of Cambridge, 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 nerve tissue along which neurons grow *in vivo*. 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 asexual reproduction in planarians — Bryan Lincoln, Sofia Quinodoz, and •Eva-Maria Schoetz — 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)

Time: Monday 14:00–17:00 Location: HÜL 186

Topical Talk BP 6.1 Mon 14:00 HÜL 186

Collective dynamics in the cytoskeleton and swimming bacteria — •Falko Ziebert[1,2], Sumanth Swaminathan[3], Shawn Ryan[4,5], Leonid Berlyand[4], and Igor Aranson[5] — [1]PCT - UMR CNRS Gulliver 7083, ESPCI, Paris, France — [2]Physikalisches Institut, Universität Freiburg — [3]Engineering Sciences and Applied Mathematics, Northwestern University, Evanston, U.S. — [4]Department of Mathematics, Pennsylvania State University, U.S. — [5]Materials 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 bacteria 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.

BP 6.2 Mon 14:30 HÜL 186

Stochastic amplification in an epidemic model with seasonal forcing — •Andrew Black and Alan McKane — Theoretical Physics Group, University of Manchester, UK

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 pattens 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'Asta[1], Fabio Caccioli[2], and Deborah Beghè[3] — [1]ICTP, Trieste, Italy — [2]Santa Fe Institute, Santa Fe, NM — [3]Università di Parma, Parma, Italy

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 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 spatial correlations (strong- noise regime).

BP 6.4 Mon 15:00 HÜL 186

Active colloidal suspensions exhibit orientational order under gravity — •Mihaela Enculescu und 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 orientational 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 — •Ines-Kristin Weber and Ludger Santen — Department of Theoretical Physics, Saarland University, 66041 Saarbrücken

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 — •Sujin Babu and Holger Stark — 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 net of vertices connected 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 conformations 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 — •Ronny 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 impact on the output of a signaling pathway and the inverse of the average MFPT can be used as the diffusion-limited association rate between the molecule and the target site. We have recently shown that in two dimensions the MFPT can be expressed in terms of an associated Neumann function [1] whose regular part can significantly contribute to the average MFPT. Here, I provide simple expressions for the average MFPT in different membrane patch geometries [2] including a square-shaped domain, a cylindrical domain and the surface of a sphere. I also discuss the impact of the presence of multiple target sites on the MFPT. These results can be used to estimate the average MFPT, the foward rate constant or the time scale of receptor clustering for biological membranes of various shapes.

[1] D. Coombs, R. Straube, M. J. Ward, *SIAM J. Appl. Math.* **70**, 302–332 (2009). [2] F. Wei, D. Yang, R. Straube, J. Shuai, submitted to *Phys. Rev. E*

BP 6.8 Mon 16:00 HÜL 186

Perturbation analysis of a reduced model for collective motion: Effects of the initial condition — •Chiu Fan Lee — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

In a system of noisy self-propelled particles with interactions that favor directional alignment, collective motion will appear if the density of particles increases beyond a certain threshold. We argue here that such a threshold may depend also on the profiles of the initial perturbation in the particle directions. Specifically, we perform mean-field, linear stability, perturbative and numerical analyses on an approximated form of the Fokker-Planck equation describing the system. We find that if an angular perturbation to an initially homogeneous system is large in magnitude, it will be amplified even if the density of the system is below the threshold density obtained from mean-field approximation.

Reference: C.F. Lee. Fluctuation-induced collective motion: A single-particle density analysis. Physical Review E **81**, 031125 (2010).

BP 6.9 Mon 16:15 HÜL 186

Active Transport and Cluster Formation on Filament Networks — •Maren Westkott[1], Philip Greulich[2], and Ludger Santen[1] — [1]Department of Theoretical Physics, Saarland University, 66041 Saarbrücken, Germany — [2]Department of Physics & Astronomy, University of Edinburgh, Edinburgh EH9 3JZ, UK

We introduce a model for active transport on inhomogeneous networks embedded in a diffusive environment which is motivated by vesicular transport on actin filaments. In the presence of a hard-core interaction, particle clusters are observed that exhibit an algebraically decaying distribution in a large parameter regime, indicating the existence of clusters on all scales. The scale-free behavior can be understood by a mechanism promoting preferential attachment of particles to large

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 adjusting 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.

[1] P. Greulich and L. Santen, Eur. Phys. J. E 32, 191-208 (2010)

BP 6.10 Mon 16:30 HÜL 186

Modelling the adsorption of biofilms — •Olaf Leidinger and Ludger Santen — Department of Theoretical Physics, Saarland University, 66041 Saarbrücken, Germany

The very first step of the formation of a biofilm at a surface, the adsorption of proteins, is investigated. Therefore a colloidal 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 was 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 experimentally 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.

[1] Y. Schmitt et al 2010 Biomicrofluidics 4, 032201
[2] A. Quinn et al 2008 EPL 81 56003

BP 6.11 Mon 16:45 HÜL 186

Thermally activated fragmentation of a homopolymer chain — •Simon Fugmann and Igor M. Sokolov — Humboldt-Universität zu Berlin, Department of Physics, Newtonstrasse 15, 12489 Berlin

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 ends. 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.

BP 7: Posters: Statistical Physics in Biological Systems

Time: Monday 17:15–20:00 Location: P3

BP 7.1 Mon 17:15 P3

Boundary-induced polarity of random intra-cellular filament networks and vesicle agglomerations — •Philip Greulich[1] and Ludger Santen[2] — [1]University of Edinburgh, Edinburgh, UK — [2]Universität des Saarlandes, Saarbrücken

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.

BP 7.2 Mon 17:15 P3

Quorum sensing by yeast cells — •André Weber[1], Yury Prokazov[2], Thomas Mair[1], Werner Zuschratter[2], and Marcus Hauser[1] — [1]Abteilung Biophysik, Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany — [2]Leibniz-Institut für Neurobiologie, Speziallabor Elektronen- und Laserscanmikroskopie, Brenneckestr. 6, 39118 Magdeburg, Germany

Glycolysis is a central pathway in the energy metabolism of cells, and it may display temporal and spatiotemporal self-organization, which can be observed in cell colonies of the yeast Saccharomyces carlsbergensis. The dynamics of the cell population dependens on the cell density: At high cell densities all cells of the population show synchronous and coherent oscillations, which can be detected as global oscillations in a population of yeast cells. The collective behaviour ceases at a critical, low cell density. This phenomenon is called 'quorum sensing'.

So far, little is known about the behaviour of the individual cells at concentrations below the quorum. Using highly sensitive single photon counting fluorescence microscopy, we study the dynamics of individual, immobilized yeast cells at low cell densities. Our focus lies in elucidating the mechanism of the transition between individual and collective dynamics. At very low cell densities, the individual cells perform metabolic oscillations, the frequencies of which show a very broad distribution. As the cell density approaches the quorum, we observe that the frequency distribution narrows and synchronized collective behaviour sets in.

BP 7.3 Mon 17:15 P3

Universal clustering properties in bacteria — •Fernando Peruani[1], Joern Starruss[2], Vladimir Jakovljevic[3], Lotte Sogaard-Andersen[3], Marks Baer[4], and Andreas Deutsch[3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Center for Information Services and High Performance Computing - Technische Universität Dresden, Dresden, Germany — [3]Max Planck Institute for Terrestrial Microbiology, Marburg, Germany — [4]Physikalisch-Technische Bundesanstalt, Berlin, Germany

Collective behaviour of individual cells marks the onset 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.

BP 7.4 Mon 17:15 P3

Species deletion stability of model food webs that include allometric scaling and adaptive foraging — •Lotta Heckmann[1], Christian Guill[2], and Barbara Drossel[1] — [1]Institut für Festkörperphysik, TU Darmstadt, Germany — [2]Systemic Conservation Biology, J.F. Blumenbach Institute of Zoology and Anthropology, Georg-August-University Göttingen, Germany

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 Guill, and Barbara Drossel — 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.

Many empirical studies confirm that the 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 prey and predator 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 behavior. 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 apparatus in the front and are reflected by a wall.

As a simple model microorganism we use the so-called *squirmer*. It has a spherical shape with a prescribed axisymmetric 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 — •Rakesh Pandey[1], Dietrich Flockerzi[1], Marcus J. B. Hauser[2], and Ronny Straube[1] — [1]Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany — [2]Institute of Experimental Physics, Otto-von-Guericke University, Magdeburg, 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 — •Christoph Schmitt, Christian Guill, and Barbara Drossel — 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 their growth and survival, we investigate now the behaviour of this 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 for 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 $\nu = 1.9(3)$ describing the growing correlation when approaching the phase transition.

BP 7.10 Mon 17:15 P3

Age dependent branching in phylogenetic trees — •Stephanie Keller-Schmidt[1], Murat Tugrul[2,3], Victor M. Eguiluz[2], Emilio Hernandez-Garcia[2], and Konstantin Klemm[1] — [1]Bioinformatics Group, Leipzig University, Germany — [2]IFISC, Palma de Mallorca, Spain — [3]IST 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 $d \sim (\log n)^2$. 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).

[1] M.G. Blum and O. François, Syst. Biol. 55, 685-691 (2006).

BP 7.11 Mon 17:15 P3

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 modeling 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.

BP 7.12 Mon 17:15 P3

Winning the marathon. Multiplayer games at the mutation-selection equilibrium — •Chaitanya Gokhale and Arne 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 mutations, which has only recently yielded to analytical methods [1,2]. We derive the composition of a multiplayer, 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.

References: [1] T. Antal *et al.* Proc. Natl. Acad. Sci. USA, 106, 2009. [2] T. Antal, A. *et al.* J. Theor. Biol., 258, 2009. [3] J. Wakeley. Coalescent theory: an introduction. Roberts and Company Publishers, 2008.

BP 7.13 Mon 17:15 P3

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.

BP 7.14 Mon 17:15 P3

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.

BP 7.15 Mon 17:15 P3

Supertree construction using superparamagnetic clustering — •Pascal Fieth[1], Alexander K. Hartmann[1], and Olaf R.P. Bininda-Emonds[2] — [1]Institute of Physics, University of Oldenburg — [2]Department of Biology and Environmental Sciences, University of Oldenburg

Superparamagnetic 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.

[1] M. Blatt, S. Wiseman and E. Domany, *Superparamagnetic Clustering of Data*, (Physical Review E, 1998)
[2] A.K. Hartmann, *Practical Guide to Computer Simulations*, (World Scientific, 2009)
[3] O.R.P. Bininda-Emonds *The evolution of supertrees*, (TRENDS in Ecology and Evolution, 2004)

BP 7.16 Mon 17:15 P3

Investigating intrinsic fluctuations in biochemical systems — •Joseph Challenger[1], Juergen Pahle[2], Alan McKane[1], and Pedro Mendes[2] — [1]School of Physics and Astronomy, The University of Manchester, Manchester, UK — [2]School of Computer Science, The University of Manchester, Manchester, UK

Mathematical models of biochemical reaction systems are usually constructed from determinstic 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.

BP 7.17 Mon 17:15 P3

Carpets of chiral motors — •Maria Strempel[1,2], Sebastian Fürthauer[1,2], Stephan W. Grill[1,2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden

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 cilias local rotation rate. This term is related 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-

try 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] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Intitute of Molecular Cell Biology and Genetics

Dynamic cellcular processes such as cell division and cell motility rely on the cytoskeleton, a meshwork of polar elastic filaments. Motor molecules provide active crosslinking between these filaments and exert internal forces in the network as they consume a chemical fuel (ATP). We extend previous continuum descriptions of active gels in the hydrodynamnic 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 constituve 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[2], Albrecht Ott[2], and Karsten Kruse[1] — [1]Universität des Saarlandes, Theoretische Biologische Physik, Postfach 151150, 66041 Saarbrücken — [2]Universität 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 catenation. Assisted catenation 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 catenations, 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 Opened System — •Hans Kubitschke and Claus Fütterer — Institut 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 genetic oscillator — Ernesto M. Nicola[1], Saul Ares[2], and •Luis G. Morelli[3,2] — [1]IFISC (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Max 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 network motifs 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? — •Federico Vazquez[1], Abigail Klopper[1,2], Maria Begasse[2], and Stephan Grill[1,2] — [1]Max Planck Institute for the Physics of Complex Systems — [2]Max 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 rapid 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 Szabo and Oskar Hallatschek — 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.

[1] D.Brockmann, L.Hufnagel, T. Geisel, Nature 439, 462-465 (2006).
[2] D.Brockmann and L.Hufnagel, Phys. Rev. Lett. 98 178301 (2007).

BP 7.24 Mon 17:15 P3

Microbial Stain Effect — •Christopher J. Seedig and Oskar Hallatschek — 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 consist of separate rings: smaller beads end up further away from the droplet centre [2]. Here, we study the coffee stain effect using droplets of yeast suspensions on agar plates. These suspensions are mixtures of large and small cells, which can be distinguished by their fluorescent color. We find that, due to the initial positional head start, the small cells enjoy a significant advantage during the colony formation. As a consequence, the small cells occupy a disproportionally large frac-

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.

[1] Deegan et al., Nature (London), 389, 827-29 (1997)

[2] Byung Mook Weon, Jung Ho Je, Phys Rev E, 82, 015305(R) (2010)

BP 7.25 Mon 17:15 P3

Construction of Phylogenetic Trees Using a Clustering Approach — •Johannes Josef Schneider[1], Thomas Bukur[2], and Antje Krause[2] — [1]Department of Physics, Mathematics, and Computer Science, Johannes Gutenberg University of Mainz, Staudinger Weg 7, 55099 Mainz, Germany — [2]Fachhochschule 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.

[1] Johannes J. Schneider, Thomas Bukur, and Antje Krause, Traveling Salesman Problem with Clustering, J. Stat. Phys. 141, 767-784, 2010.

BP 8: Posters: Protein Structure & Dynamics

Time: Monday 17:15–20:00 Location: P3

BP 8.1 Mon 17:15 P3

Conformational Adsorption Reaction of BSA on the Surfaces of Nanosilica and Nanodiamond — •Victor Wei-Keh Wu — Department of Chemical and Materials Engineering, National Kaohsiung University of Applied Sciences(KUAS), 80782 Kaohsiung City, Taiwan — Victor Basic Research Laboratory e. V.(VBR) Gadderbaumer-Str. 22, D-33602 Bielefeld, Germany

From the fluorescences (excitation at 280 nm) of BSA of 0-10000 nM 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($50\mu g/20\mu L$), 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 partices in g; 28.0 and 7.64 mg, on unit surface in m^2 of NS and ND, respectively. Adsorption constants $1.2x10^8$ and $3.7x10^7$ $(nM)^{-1}$ 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 Lange[1], Ronny Golnak[1], Sebastien Bonhommeau[2], and Emad Flear Aziz[1,3] — [1]Helmholtz-Zentrum Berlin für Materialien und Energie, Albert-Einstein-Str. 15, 12489 Berlin — [2]Institut des Sciences Moléculaires, UMR 5255 CNRS, 351 cours de la Libération, 33405 Talence Cedex, France — [3]Freie 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 metmyoglobin. For the interpretation of the data muliplet calculations were used.

1 E F Aziz et al., Phys. Rev. Let. 102, 68103 (2009)

2 N Bergmann et al., Phys. Chem. Chem. Phys. Vol. 12, 18, 4827-4832 (2010)

3 K M Lange et al., in preparation (2010)

BP 8.3 Mon 17:15 P3

Effect of thermostating and electrostatics on the wildtype LOV1 domain of phototropin and its mutants — •Emanuel Peter, Bernhard Dick, and Stephan A. Baeurle — 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 Schmidt[1,2] and Matthias Weiss[1,3] — [1]Cellular Biophysics Group, German Cancer Research Center, c/o BIOQUANT, Im Neuenheimer Feld 267, 69120 Heidelberg — [2]Laboratory for Computational Cell Biology, Department of Cell Biology, Harvard Medical School, Boston, USA — [3]Experimental 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

BP 8.5 Mon 17:15 P3

Rigidity analysis of HIV-1 protease — Jack Heal, Stephen Wells, Emilio Jimenez-Roldan, and •Rudolf Roemer — Department of Physics and Centre for Scientific Computing, University of Warwick, Coventry, CV4 7AL, United Kingdom

We show the effect of different inhibitors on the rigidity profile of HIV-1 protease as it unfolds. A rigidity analysis of 40 protein crystal structures from the protein data bank is made using the software FIRST. The results are compared with and without inhibitors present. This study builds on a recent comparative study of protein structures using FIRST. In a simulated rigidity dilution, the unfolding pattern of the protein can be observed. The presence of an inhibitor slows the rigidity loss, in particular around the active site of the enzyme. FIRST is not computationally demanding and its results can be calculated on a timescale of CPU-minutes. We study protein mobility along low-frequency normal modes of motion using the FRODA software and the elastic network model. The presence of an inhibitor changes the

extent to which the protein is able to move in these directions.

BP 8.6 Mon 17:15 P3

Investigation of self-assembled desmin filament networks by atomic force microscopy — •Mareike Dieding[1], Volker Walhorn[1], Andreas Brodehl[2], Hendrik Milting[2], and Dario Anselmetti[1] — [1]Experimentelle Biophysik und Angewandte Nanowissenschaften, Fakultaet für Physik, Universitaet Bielefeld, Universitaetsstr. 25, D-33615 Bielefeld — [2]Herz- & Diabeteszentrum NRW, E. & H. Klessmann-Institut fuer Kardiovaskulaere Forschung und Entwicklung, Georgstr. 11, D-32545 Bad Oeynhausen

Arrythmogenic right ventricular cardiomyopathy (ARVC) is an inherited heart muscle disease, frequently accompanied by sudden cardiac death and terminal heart failure.

Various point mutations of the intermediate filament desmin are potential candidates for the trigger factor [1]. 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 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.

[1] B. Klauke et al., De novo desmin-mutation N116S is associated with arrhythmogenic right ventricular cardiomyopathy, Hum. Mol. Genet. 19 (23), 2010

BP 8.7 Mon 17:15 P3

Winkelabhängige Ramanspektroskopie an Photosystem-II-Kristallen — •Georg Bens[1], Katharina Brose[1], Athina Zouni[2] und Janina Maultzsch[1] — [1]Institut für Festkörperphysik, Technische Universität Berlin, Hardenbergstr. 36, 10623 Berlin, Germany — [2]Institut für Chemie, Technische Universität Berlin, Straße des 17. Juni 135, 10623 Berlin, Germany

Das Photosystem II ist als Ort der Wasseraufspaltung ein elementarer Bestandteil der Photosynthese. Im Reaktionszentrum des Photosystems II befinden sich drei β-Carotinmoleküle, deren Funktion bisher ungeklärt ist. Es wurde vorhergesagt, dass das Carotin CarD2 aus dem Reaktionszentrum am Elektronentransport nach der Wasserspaltung beteiligt ist [1] . Begründet wird dies durch das Vorhandensein eines Carotinkations im belichteten Reaktionszentrum. Da die Carotinmoleküle im Reaktionszentrum unterschiedliche Orientierungen aufweisen, versuchen wir mittels polarisationsabhängiger, resonanter Ramanspektroskopie und der winkelabhängigenen Signalcharakteristik zu bestimmen, welches der verschieden orientierten Carotinmoleküle ionisiert wird. Da das Carotinkation eine andere Resonanzfrequenz und ein anderes Ramanspektrum als neutrales β-Carotin hat, kann man es gut von den anderen Carotinmolekülen des Photosystems unterscheiden. Auf diese Weise soll identifi*ziert werden, welches der Carotine ionisiert wird.

[1] Schenderlein, M.: Elektronentransferprozesse in den Photosystemen I & II, Dissertation TU Berlin, 2010
http://opus.kobv.de/tuberlin/volltexte/2010/2586/

BP 8.8 Mon 17:15 P3

Tip-Enhanced Raman Spectroscopy on Membrane Proteins — •Elmar Hassan Hubrich, Kenichi Ataka, and Joachim Heberle — Free University of Berlin, Department of Physics, Exp. Molecular Biophysics, Arnimallee 14, 14195 Berlin, Germany

Tip-enhanced Raman spectroscopy (TERS) combines high spatial resolution of atomic force microscopy (AFM) with structural sensitivity of surface-enhanced Raman spectroscopy (SERS). Using a gold-coated AFM tip, it is possible to measure Raman signals with high spatial resolution ($\sim$30 nm).

The AFM allows imaging, measuring (e.g.: single-molecule force microscopy), and manipulating matter at the nanoscale. The information is gathered by "feeling" the surface with a mechanical probe.

Raman spectroscopy provides information about the molecular structure of proteins. In order to detect monolayer we use surface-enhanced Raman spectroscopy (SERS). The SERS signal is enhanced in the vicinity of (usually) silver- or gold-coated surfaces (up to a factor of 10^{9-12} compared to conventional Raman).

Up to now, this novel technique is mainly applied to surfaces modified with inorganic samples. However, TERS is a promising tool in investigation of membrane proteins since single molecules could be studied at atomic level by Raman spectroscopy under native biological conditions.

Here, we introduce the experimental setup and discuss the application of TERS to the investigation of membrane proteins.

BP 8.9 Mon 17:15 P3

Molecular docking study of histone deacetylases 1 and 3 in interaction with the benzamide histone deacetylase inhibitor MS-275 — •Davoud Pouladsaz[1], Azadeh Ebrahimi[2], and Michael Schreiber[1] — [1]Institut für Physik, Technische Universität Chemnitz — [2]Institut für Hirnforschung, Eberhard Karls Universität Tübingen

Numerous studies have shown that abnormal HDAC activity is associated with oncogenesis. On the other hand, HDAC inhibition has been reported in several studies to induce tumor cell differentiation, apoptosis, and cell cycle arrest. In this scheme, HDACs are considered potential targets for cancer therapy. One of the novel HDAC inhibitors is MS-275, a benzamide derivative with *in vivo* antitumor activity and selectivity against HDAC1 and HDAC3. However, the precise molecular and cellular mechanisms by which MS-275 acts to modulate HDAC activity have yet to be determined. In this work, we use molecular docking techniques to identify the active sites of HDAC1 and HDAC3 in interaction with MS-275. The results provide template structures for further drug experiments.

BP 9: Posters: DNA & DNA Enzymes

Time: Monday 17:15–20:00 Location: P3

BP 9.1 Mon 17:15 P3

Formation of DNA Tubes and Attachment of Nanoparticles — Matthew Wiens, Awadesh Dwivedi, Nora Haufe, •Anja Henning, and Michael Mertig — Professur für Physikalische Chemie, Mess- und Sensortechnik, TU Dresden, 01062 Dresden

Synthesizing cylindrical nanostructures is an important goal in supramolecular chemistry, material science and nanotechnology. DNA is one of the most promising materials for such structures since its sequence can be designed to self-assemble into tubular structures through complementary base pairing. Different approaches have been reported showing DNA tube generation from either single stranded DNA or DNA building blocks, so called tiles [1]. Most of these methods have the drawback that side products such as 2D lattices are formed and the length of the structures periodically extend over tens of micrometers.

We used two-dimentional DNA origami procedure similar to Douglas *et al.* in order to create a six helix bundle with a well defined geometry [2, 3]. The design provides binding sites in periodic distances for functionalized nanoparticles. This is a promising feature for possible applications of future nanoelectronic and -photonic devices or a template for the investigation of biomolecules.

[1] Sharma et al., Science 323, 112-116 (2009) [2] Rothemund, Nature 440, 297-302 (2006) [3] Douglas et al., PNAS 104, 6644-6648 (2007)

BP 9.2 Mon 17:15 P3

Synthesis of covalently linked DNA structures — •Anja Henning[1,2], Ofer I. Wilner[2], Bella Shlyahovsky[2], Michael Mertig[1], and Itamar Willner[2] — [1]Professur für Physikalische Chemie, Mess- und Sensortechnik, TU Dresden, 01062 Dresden, Germany — [2]Institute of Chemistry and The Center for Nanoscience and Nanotechnology, The Hebrew University of Jerusalem, Jerusalem 91904, Israel

The ability of DNA as a material for bottom-up approaches has been shown already in an enormous number of experiments. Apart from 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

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.

BP 9.3 Mon 17:15 P3

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

Es kann gezeigt werden, dass die räumliche DNA-Synthese sowie die Kodierung und Speicherrung der Erbinformation durch eine räumliche Gruppen-Transformation der Basen- Tripletts und der assoziierten Aminosäure nach der harm. Streckenteilung erfogt. Die Transformation erfolgt über Drehspiegelung und Translation zwischen einem Ikosaeder und dem dualen Dodekaeder mittels lokaler Potentialfelder. Die Gruppe der 20 Basen-Triplette wird dabei aus den 60 Triplett-Kanten des 20-dreieckfläch. Ikosaeders gebildet, wobei die codierte Aminosäure mit dem zentralen C-Atom auf einem der 20 Ecken-Potentiale des Dodekaeders lokalisiert ist. Triplett und C-Atom bilden ein Tranfer-tRNA Potential. Aufgrund der Pentagonstruktur erfolgt die Translation nach dem "Goldenen Schnitt"; Phi= 1,618. Am B-Typ der DNA kann dies bewiesen werden: Phi=(3,5nm;1Hel.Wind.+2,2nm;RNA-Abst.)/(3,5nm;1Hel.Wind.) Die Erbinformation und die Basensequenz kann in Form einer räumlichen Informationsspur auf und zwischen dem Dodekaeder und Ikosaeder, Computer unterstützt, zur Identifizierung der Primär-und Sekundärstruktur lokalisiert werden.

BP 9.4 Mon 17:15 P3

Information transfer and readout in complex DNA mixtures — •Harish Bokkasam 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 40bp-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 sequence. 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 multiple 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.

BP 9.5 Mon 17:15 P3

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 fibre to crosslink to itself due to the dyanmic 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.

BP 9.6 Mon 17:15 P3

Modelling the recruitment of DNA repair enzymes — •Gregor Weiss, Daniel Löb, 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.

BP 9.7 Mon 17:15 P3

Computer simulation of chromatin: Modeling the influence of nucleosome repositioning — •Oliver Müller[1], René Stehr[1], Robert Schöpflin[1], Ramona Ettig[2], Nick Kepper[2], Karsten Rippe[2], and Gero Wedemann[1] — [1]University of Applied Sciences Stralsund, 18435 Stralsund, Germany — [2]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 regularity implies a highly periodical positioning as well as equal occupancy of the fiber nucleosomes, which is unlikely for *in vivo* chromatin. Recent studies indicate that only a small subset of nucleosomes seems to be strongly positioned whereas the majority of nucleosomes adhere to a statistical positioning mechanism. Other important factors, such as chromatin remodelers and transcription factors are also implicated in nucleosome repositioning and occupancy. Here, we carry out Monte Carlo simulations with a coarse-grained chromatin model incorporating elastic fiber properties as well as a detailed description of the electrostatic and internucleosomal interactions to investigate the effects of nucleosome repositioning. Depending on the extent of the displacements the fiber geometry changes significantly. This serves as a tentative explanation for the effects of different remodeling complexes on processes such as DNA transcription.

BP 9.8 Mon 17:15 P3

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 whcih 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 efford 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, we use a Monte Carlo 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.

BP 9.9 Mon 17:15 P3

A unified model for statistical nucleosome positioning — •Brendan Osberg, Wolfram Moebius, and Ulrich Gerland — Ludwig Maximilians Universitaet, Munich, Germany

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 Hemiascomycota 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 Location: P3

BP 10.1 Mon 17:15 P3

Entwicklung eines Versuchsaufbaus zur räumlich aufgelösten in-vivo-Messung der viskoelastischen Eigenschaften der humanen Augenlinse — •Stephan Reiss[1], Oliver Stachs[2], Rudolf Guthoff[2] und Heinrich Stolz[1] — [1]Institut für Physik, Universität Rostock, D-18055 Rostock — [2]Medizinische Fakultät, Augenklinik, Universität Rostock, D-18055 Rostock

Die Alterssichtigkeit steht in enger Verbindung mit dem Verlust der Akkommodationsfähigkeit und den viskoelastischen Eigenschaften der Augenlinse. Eine in-vivo-Bestimmung dieser mechanischen Eigenschaften würde ein besseres Verständnis des natürlichen Alterungsprozesses der Linse ermöglichen. Mit den bisher zur Verfügung stehenden Messtechniken ist eine derartige Messung nicht möglich [1]. Wir berichten über ein neues Messverfahren zur ortsaufgelösten in-vivo-Messung der rheologischen Eigenschaften der Augenlinse auf Grundlage der spektroskopischen Auswertung spontaner Brillouin-Streuung mittels eines hochauflösenden "Virtually Imaged Phased Array" [2], welches eine bis zu 20 mal größere Winkeldispersion als ein optisches Gitter besitzt [3], wobei durch die Verwendung eines Multipass-Aufbaus die Auflösung soweit verbessert wurde, dass Messungen an elastisch intensiv streuendem biologischen Gewebe möglich sind. Außerdem präsentieren wir erste ortsaufgelöste Messergebnisse an entnommenen tierischen Augen und Linsen, sowie erste in-vivo-Messungen an einem Kaninchenauge. [1] J. F. Greenlaf, M. Fatemi, and M. Insana, Ann. Rev. Biomed. Eng. 5, 57-78 (2003); [2] M. Shirasaki, Opt. Lett. 21, 366-368 (1996); [3] A. Vega,A. Weiner, and C. Lin, Appl. Opt. 42, No. 20, 4152-4155, (2003)

BP 10.2 Mon 17:15 P3

Novel Magnetic Tweezer with first Applications to Cell and Tissue Stimulation and Rheology — Claus Fütterer[1] and •Rui Caldeira[1,2] — [1]University of Leipzig, Faculty of Physics and Earth Science Institute for Experimental Physics I, Soft Matter Physics Division, Developmental Biophysics, Leipzig, Germany — [2]Universidade de Lisboa, Faculdade de Ciencias, Departamento de Fisica, Lissabon, 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. Those 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 Ares[1], Luis G. Morelli[2], Christian Schröter[2], Korneel J. I. Hens[3], Sebastian J. Maerkl[3], Bart Deplancke[3], Andrew C. Oates[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden — [3]École 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 two different Hes6 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 retina cell degeneration — •Julia Hollmach[1], Julia Schweizer[1], Gerald Steiner[1], Richard H. W. Funk[2], Lilla Knels[2], and Edmund Koch[1] — [1]Dresden University of Technology, Faculty of Medicine, Clinical Sensoring and Monitoring, Dresden, Germany — [2]Dresden 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 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 Leutheuser[1,3], Thorsten Schaffer[1,3], Christian Jeleazcov[2,3], Christian Weigand[3], and Bernhard Hensel[1] — [1]Max Schaldach-Stiftungsprofessur für Biomedizinische Technik, Universität Erlangen-Nürnberg — [2]Anästhesiologische Klinik, Universitätsklinikum Erlangen — [3]METEAN, 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 a thorough mathematical analysis of the underlying parameters 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, SpO_2, $etCO_2$, 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 subjected 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 Gaertner[1], Peter Cimalla[1], Lilla Knels[2], Sven Meissner[1], Wolfgang M. Kuebler[3], and Edmund Koch[1] — [1]TU Dresden, Faculty of Medicine Carl Gustav Carus, Clinical Sensoring and Monitoring, Dresden, Germany — [2]TU Dresden, Faculty of Medicine Carl Gustav Carus, Department of Anatomy, Dresden, Germany — [3]Institute 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 — •Abigail Klopper[1,2], Gabby Krens[3], Stephan Grill[1,2], and Carl-Philipp Heisenberg[3] — [1]Max Planck Institute for the Physics of Complex Systems, Nöthnitzer Straße 38, D-01187 Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, D-01307 Dresden, Germany — [3]Institute 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 ectoderm and mesoderm germ layer progenitor cells in three dimensions over time, and quantitatively analyze their sorting behavior using an order parameter related to heterotypic interface length. We investigate the cell population size dependence of sorted aggregates and find that the germ layer progenitor cells engulfed 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 Knorr, Dan Strehle, Thomas Fuhs, Florian Huber, and Josef Käs — Institut für Experimentelle Physik I, University of Leipzig, Linnéstr 5, 04103, 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 migrations by generating traction forces transmitted through cell-cell coupling 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 in sheet migration ratify the randomness in single-cell migration 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 — •Peer Mumcu[1], Ortrud Wartlick[2], Marcos González-Gaitán[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Department 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 polygons, 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 Merkel[1], Douglas B. Staple[1], Reza Farhadifar[1,2], Benoît Aigouy[3], Andreas Sagner[3], Suzanne Eaton[3], and Frank Jülicher[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden, Germany — [2]FAS Center for Systems Biology, 7 Divinity Avenue, Cambridge MA 02138, USA — [3]Max-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, called 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.

[1] B. Aigouy, R. Farhadifar, D.B. Staple, A. Sagner, J.-C. Röper, F. Jülicher, and S. Eaton. *Cell* **142**(5), 773-786 (2010).

BP 10.12 Mon 17:15 P3

Amplitude equation description of vertebrate segmentation — •Adrian Jacobo[1], Damià Gomila[2], Manuel Matías[2], Saul Ares[1], Luis Morelli[1], Andrew Oates[3], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden — [2]Institute for Cross-Disciplinary Physics and Complex Systems (IFISC), Palma de Mallorca, Spain — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden

The segmentation of the vertebrate body axis is a rhythmic and sequential process controlled by a multicellular clock. This clock has been described either by models of regulatory networks or by simpler descriptions in terms of phase oscillators. While phase oscillators do 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 Ginzburg-Landau equation. This equation describes an oscillatory medium close to a supercritical Hopf bifurcation, in agreement with accepted gene regulatory network models of the segmentation clock. We find that 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 spatiotemporal chaos. Our theory suggests perturbations to developing embryos that could disrupt the behavior of the segmentation clock.

BP 10.13 Mon 17:15 P3

Mechanics and Morphology of the Dorsal-Ventral compartment boundary in the developing wing of the fly — •Maryam Aliee[1], Constanze Teichman[2], Katharina Landsberg[2], Jens Röper[2], Christian Dahmann[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden, Germany

During the development of tissues cells organize into distinct compartments of different cell lineages. The interfaces between these compartments, called compartment boundaries, maintain straight and sharp morphologies. An important model system to study the morphology of compartment boundaries during development is the wing disc of the fruit fly Drosophila where two such boundaries exist: the anterior-posterior boundary and the dorsal-ventral (DV) boundary.

Here, we discuss general physical mechanisms by which compartment boundaries are shaped during the growth phase. Using a vertex model to describe cell mechanics in a growing tissue, we show that the roughness of the compartment boundary can be controlled by increased cell bond tension along the boundary. In addition a locally reduced cell division rate near the boundary leads to an effective interfacial tension and thereby reduced boundary roughness. We compare our results with the shape and mechanics of the DV boundary at different times during the fly wing development. We analyze the role of increased cell bond tension in the morphology of DV boundary and we speculate about the role of localized reduction in cell proliferation.

BP 11: Posters: Single-Molecule Biophysics

Time: Monday 17:15–20:00 Location: P3

BP 11.1 Mon 17:15 P3

High Resolution Optical Tweezers for Single-Molecule Studies of Eukaryotic Transcription — •Korbinian Paul, Adam Muschielok, Noemi Maria Porcellato, and Jens Michaelis — Department für Chemie LMU München, Butenandstr. 5-13

Investigating mechanical aspects of single RNA polymerases will further our understanding of the molecular mechanism of transcription elongation. For these single-molecule experiments we establish a high resolution optical tweezers setup in the dual trap design, where one trap is moveable by a piezo-driven mirror. Experiments with 5 kbp DNA tethers attached to trapped beads have shown that our current resolution is about 0.5 nm for forces measured around 15 pN at a time resolution of approximately 0.1s. This is sufficient to study single base pair steps of RNA Polymerase II on DNA. In further experiments we will investigate the behavior of RNA Polymerases I and II from a mechanical perspective. In addition, we will study transcription regulation by performing experiments in presence of different transcription factors such as TFIIS and TFIIF.

BP 11.2 Mon 17:15 P3

Dynamics of a Single DNA-bound Protein Translocating through a Nanopore — •Andre Spiering, Andy Sischka, Katja Toensing, Karsten Rott, Sebastian Getfert, Peter Reimann, and Dario Anselmetti — Faculty of Physics, Bielefeld University, 33615 Bielefeld, Germany

In order to investigate the physical behaviour of DNA-bound ligands translocating through a nanopore, we threaded single DNA-protein complexes into a solid-state nanopore while simultaneously measuring the electrostatic forces and ionic currents through the pore. This controlled translocation was examined with pN force sensitivity, ms time resolution and pA ionic current sensitivity by a high precision 3D optical tweezers setup with backscattered light detection. We found that each ligand (RecA, EcoRI or 2-Cysteine-Peroxiredoxin-A) causes a reproducible and individual change of both the electrostatic force and the ionic current while dynamically threading and unthreading the complex [1]. Detailed studies of these charge-dependent translocation processes revealed a hopping between two states in the nanopore potential and a small hysteresis between threading and unthreading cycles. All experimental force response curves and the corresponding effects can be theoretically modelled and verified within a framework of thermally activated transitions in a time-dependent nanopore potential (Kramers theory) and reflect the stochastic nature of such nanopore translocation events [2].

[1] A. Sischka et al.: J. Phys.: Condens. Matter 22, 454121 (2010)
[2] A. Spiering et al.: submitted (2010)

BP 11.3 Mon 17:15 P3

Nano-Mechanics of Homologous Recombination — •Marcel Ander and Erik Schäffer — Biotec TU Dresden, Tatzberg 47-51, Dresden

Homologous recombination is the key biological process for exchanging DNA segments between two DNA molecules. It serves to repair DNA double strand breaks, re-launch stalled replication forks, and maintains genetic diversity by mediating horizontal gene transfer mechanisms such as conjugation and meiotic recombination. In all of these processes, a segment of DNA is stably integrated into the recipient DNA. Utilizing optical tweezers we analyzed the DNA single-strand annealing mechanism of homologous recombination studying the phage lambda protein Redβ. Redβ is the key actor in a technique termed recombineering ensuring efficiency of the recombination process. We discovered that Redβ can actually block annealing of complementary DNA strands, and is active towards the 3' end of a single-stranded DNA. If sufficient complementarity is given, Redβ holds complementary DNA strands together. This sheds light onto the mechanism of DNA single-strand annealing and highlights force as a crucial item in molecular genetics.

BP 11.4 Mon 17:15 P3

Analysis of multivalent effects using single molecule force spectroscopy (SMFS) on pyridine coordination compounds — •Manuel Gensler[1], Artur Galstyan[2], Ernst-Walter Knapp[2], and Jürgen P. Rabe[1] — [1]Institut für Physik, Humboldt-Universität zu Berlin, Newtonstr. 15, 12489 Berlin — [2]Institut für Chemie und Biochemie, Freie Universität Berlin, Fabeckstr. 36a, 14195 Berlin

Multivalent interactions are of great importance in chemistry, nanotechnology and biochemistry. They strongly increase binding free energies and association kinetics between partners of appropriate geometry [1]. Thus it is important to obtain a deeper understanding of the basic factors influencing multivalent interactions.

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 $Zn(NO_3)_2$ and $CuSO_4$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.

[1] M. Mammen et al. *Angew. Chem. Int. Ed.* **1998**, 37, 20, 2754-2794. [2] M.I. Gianotti et al. *ChemPhysChem* **2007**, 8, 2290-2307. [3] S. Guo et al. *Biophys. J.* **2008**, 95, 3964-3976.

BP 11.5 Mon 17:15 P3

High-Resolution Scanning Near-Field Optical Microscopy of Dye Labelled Single Tobacco Mosaic Viruses — •Alexander Harder[1], Sven Degenhard[2], Fabian Eber[2], Fania Geiger[3], Joachim Spatz[2], Holger Jeske[2], Christina Wege[2], and Dario Anselmetti[1] — [1]Experimental Biophysics & Applied Nanoscience, Bielefeld University, Germany — [2]Molecular Biology and Virology of Plant, Stuttgart University, Germany — [3]Max Planck Institute for Metals Research, Stuttgart, 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 — •Aykut Erbas, Dominik Horinek, and Roland R. Netz — Technische Universitaet Muenchen, Physik Department, Garcing, Germany

The friction forces and mobilities for the C_{16} 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 — •Adeline Bieker[1], Volker Walhorn[1], Gesa Niemann[2], Markus Ritzefeld[2], Norbert Sewald[2], and Dario Anselmetti[1] — [1]Experimental Biophysics and Applied Nanoscience, Universität Bielefeld, Deutschland — [2]Organic and Bioorganic Chemistry, Universität 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 PhoB. By means of AFM-based 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}) an the molecular interaction length (x_β), 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 — Kozhinjampara R. Mahendran, Pratik Raj Singh, Ulrich Kleinekathöfer, and •Mathias Winterhalter — Jacobs University Bremen, Campusring 1, D-28759 Bremen

The permeation of water soluble molecules across cell membranes is controlled by channel forming proteins and particularly the channel surface determines the selectivity. An adequate method to study properties of these channels is electrophysiology and in particular analysing the ion current fluctuation in the presence of permeating solutes provides information on possible interactions with the channel surface. Due to the limited time resolution, fast permeation events are not visible. Here we demonstrate that miniaturization of the lipid bilayer, varying the temperature or changing the solvent may enhance the resolution. Although electrophysiology is considered as a single molecule technique, it does not provide atomic resolution. Molecular details of solute permeation can be revealed by combining experiments and computer modelling.

K.R. Mahendran et al. J Phys. Condensed Matter 22 (2010) 454131; E. Hajjar et al. Biochemistry 49 (2010) 6928-35; I. Biro et al. Biophys J 98 (2010) 1830-9.

BP 11.9 Mon 17:15 P3

Stochastic reconstruction of interactions within protein complexes from single-molecule force spectroscopy — •Magnus Schwörer 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 sequential 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 Arends, 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-assembled multi-enzyme complexes. In these complexes, single 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 — •Henning Seidel[1], Yibei Xiao[2], Rolf Hilgenfeld[2], and Christian G. Hübner[1] — [1]Institute of Physics, Ratzeburger Allee 160, 23562 Lübeck, Germany — [2]Institute 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 nsp8 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[1], Dimitri Pescia[1], Mithun Biswas[1], and •Anirban Sain[1,2] — [1]Physics Department, IIT Bombay. Powai, Mumbai 400076, India. — [2]MPI-PKS, Nothnitzer Str. 38, 01187, Dresden.

Weak bonds are ubiquitous in biological structures. They often act as adhesive contacts 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.

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 — Insitute of Physics, University of Lübeck, Ratzeburger Allee 160, 23562 Lübeck, Germany

One of the unique features of single molecule absorption/emission is their anisotropy due to the well-defined transition dipoles for both processes allowing the determination of the molecules 3d orientation. Therefore, several techniques have been proposed in order to determine the full three-dimensional orientation of dipole emitters on a single molecule level. One of these techniques proposed by Hohlbein and Hübner in 2005 combines emission distribution and polarization detection. The theoretical background of this approach assumes an optical homogenous surrounding. In order to overcome this limitation we want to indicate an extension of the theory for dipole emitters near optical interfaces e.g. glass/water. Moreover, we implement the dipole excitation probability. In conclusion, we present extensive simulations, which allow for the evaluation of the capabilities of this extended method.

BP 11.14 Mon 17:15 P3

The strong excitonic coupling is not an important factor in the fast excitation energy transfer in phycocyanin of A.marina. — •albert collins nganou assonkeng — Institute of Optics and Max-Volmer-Laboratory for Biophysical Chemistry, Technical University Berlin, Str. 17 Juni 135, 10623 Berlin, Germany

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 homo-hexamers containing Phycocyanin (PC) and one hetero-hexamer containing PC and Allophycocyanin (APC) absorbing in the spectral range between 560 nm and 630 nm, where the absorption of the chlorophylls is low. In order to get a better 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 anisotropy 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.

BP 12: Posters: New Technologies

Time: Monday 17:15–20:00 Location: P3

BP 12.1 Mon 17:15 P3

Spectrally-resolved identification of fluorescent probes at low concentration — •Jens Wiedemann, Zdeněk Petrášek, and Petra Schwille — Biophysics group, Biotechnologisches Zentrum, Technische Universität Dresden, Tatzberg 47/49, 01307 Dresden, Germany

We present a simple technique for the detection and identification of a large number of spectrally distinct fluorescent probes at low concentration, based on the differences in their emission spectrum shape. The fluorescence originating from immobilized beads containing a low number (100s or less) of fluorescent molecules is dispersed by a prism 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 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 spectral signatures created by a combination of different fluorophores, including different concentration ratios, and the effects of the interference of the bead autofluorescence, are being explored.

BP 12.2 Mon 17:15 P3

Biocompatibility of single crystalline $Fe_{70}Pd_{30}$ ferromagnetic shape memory films for cell actuation — •Mareike Zink[1], Yanhong Ma[2], and S. G. Mayr[2] — [1]Abteilung Physik der weichen Materie, Fakultät für Physik und Geowissenschaften, Universität Leipzig, Leipzig, Germany — [2]Leibniz-Institut für Oberflächenmodifizierung e.V., Translationszentrum für Regenerative Medizin, Fakultät für Physik und Geowissenschaften, Universität Leipzig, Germany

Ferromagnetic shape memory alloys (FSMAs) have received great attention as an exciting class of smart functional materials. They exhibit large reversible strains at moderate stresses with external controllability at constant temperatures which make them excellent candidates for biomedical actuation devices. FSMAs bear the significant potential for miniaturized devices for single cell actuation which is capable of yielding magnetically controllable shear strains and/or volume dilations. However, the biocompatibility of this material must first be well confirmed as it has not been done yet. Thus, our work focuses on the interaction of fibroblast cells with single crystalline $Fe_{70}Pd_{30}$ FSMA films on MgO substrates. Additionally, corrosion resistance of the films was obtained employing simulated body fluid (SBF) tests. Calcium-phosphate aggregates with granular microstructure were detected on the film surface after soaking in SBF. Cell viability and biocompatibility tests with NIH 3T3 cells revealed that the cells adhered and proliferated on the FSMA surface, whereas cells were smaller compared to cells on culture dish surfaces. Biocompatible polymer coatings on the $Fe_{70}Pd_{30}$ film can be employed to improve cell-substrate interactions.

BP 12.3 Mon 17:15 P3

Photobleichung höherer Ordnung - ein eng mit intrazellulärer Ablation verbundener Low-Density Plasma Prozess — •Stefan Kalies, Kai Kuetemeyer und Alexander Heisterkamp — Laser Zentrum Hannover e.V., Hollerithallee 8, D-30419 Hannover

Photobleichung bei nichtlinearer Anregung, wie in der Multiphotonenmikroskopie, ist im Gegensatz zur Photobleichung bei linearer Anregung kaum charakterisiert. In diesem Fall spielen Prozesse mit teilweise höherer Ordnung als der Anregungsordnung eine Rolle. Wir untersuchten diese Photobleichung höherer Ordnung per Multiphotonenmikroskopie in lebenden Zellen in vitro. Verwendet wurde das in den Zellen exprimierte, mobile "Enhanced Green Fluorescent Protein" (EGFP) sowie das immobile, extrinsische Fluorophor Hoechst. Die Abhängigkeit der Photobleichungsrate von der Leistung war für das Fluorophor EGFP kubischer und ab einer bestimmten Grenzwellenlänge biquadratischer Ordnung, während für Hoechst eine quadratische in eine kubische Ordnung überging. Es zeigte sich, dass die Bleichung mit der Bildung reaktiver Sauerstoffspezies korreliert. Aus den durchgeführten Untersuchungen lässt sich schließen, dass neben der sequentiellen Anregung in höhere ionische Zustände eine Multiphotonenionisation zur Photobleichung höherer Ordnung führen kann. Im Gegensatz zur linea-

ren Photobleichung spielen Triplett-Zustände und molekularer Sauerstoff eine vernachlässigbare Rolle. Die Photobleichung höherer Ordnung zeigt starke Parallelen zur intrazellulären Ablation, die durch die Erzeugung eines Plasmas geringer Elektronendichte ("Low-Density Plasma") und reaktive Sauerstoffspezies erreicht werden kann.

BP 12.4 Mon 17:15 P3

Characterization and compensation of fs-Laser pulse broadening in a photonic crystal fiber for multi-photon endomicroscopy — •Tobias Ehmke, Sabine Donner, Alexander Krueger, and Alexander Heisterkamp — Laser Zentrum Hannover e.V., Hollerithallee 8, D-30419 Hannover

Multi-photon excitation microscopy is a fluorescence imaging technique which allows deep tissue imaging with short pulse infrared laser light. The optics of conventional multiphoton microscopes is too bulky for endo-microscopy and the rigid setup is unfavourable for many in-vivo applications. In order to gain flexibility and reduce size a fiber based probe for multiphoton endomicroscopy is under development. As a first step towards the endomicroscope problems associated with the propagation of short pulses in the optical fibers have to be addressed. Therefore, a setup consisting of a Ti:Sa laser emitting 140fs pulses, a prechirp unit, a double clad photonic crystal fiber and focussing optics are used. The dispersion and nonlinear effects in the fiber are studied with an autocorrelator and a spectrometer. The coupling efficiency of the fiber is determined to be over 60%. Without the prechirp unit pulse broadening into the ps-regime and a reduction of the spectral width is observed. The dispersion could be compensated by a grating compressor, generating a negative chirp for the pulse and is designed to put the pulse length back into the fs-regime behind the fiber. This is an important step towards the utilization of a fiber based multi-photon microscope for in-vivo applications.

BP 12.5 Mon 17:15 P3

Interdigitated micro-electrode arrays used as biosensors — •alireza mousavi[1,2], patriza lamberti[2], vincenzo tucci[2], and veit wagner[1] — [1]Jacobs University Bremen, Campus Ring 1, D-28759, Bremen, Germany — [2]University of Salerno, Dept. of Electrical and Information Engineering, 84084, Fisciano,Salerno, Italy

Detection of bio-molecules and pathogens by a rapid, sensitive and cost-effective method is of great importance in healthcare, food industry, water/environmental monitoring and for elimination of biosecurity threats. In this contribution various interdigitated microelectrode array designs are tested for their functionality as biosensors. Such electrode arrays have the advantage of low cost, low power consumption and miniaturized structure size. Test devices are fabricated either on silicon wafers or on low cost PET-foils. The adsorbates to be sensed are detected in two ways, i) by their specific dielectric signature via impedance measurements at different frequencies, and ii) by measuring the conductivity change in an additionally deposited, semiconducting surface layer patterned on top of the electrodes (field-effect transistor design). Both concepts allow label-free detection of adsorbed bio-molecules or cells. The experimental finding of the dependence on the geometry parameters of the interdigitated micro-electrode array and the electrical operation conditions are compared with predictions based on electrostatic and electroquasistatic theoretical finite-element analysis.

BP 12.6 Mon 17:15 P3

Microwave high-K based sensors for the analysis of liquids and molecules — •Eugen Hollmann, Roger Wördenweber, Thomas Grellmann, Kyrylo Greben, and Rolf Kutzner — Institute of Bio- and Nanosystems (IBN), Forschungszentrum Juelich, 52425

The aim of this work is the developement of microwave devises suitable for detection and alalysis of the properties of organic and biological solutions via microwave technology. Dielectric spectroscopy of liquids and molecules in liquid environment provides information about the mobility of molecules by probing its complex dielectric properties. The design of sensors is based on a number of thin film stripline topologies on different microwave suitable substrates (e.g., sapphire, LaAlO3)using high-k material for improvement of the devise sensitivity. Test measurements in a frequency regime up to 20GHz reveal the high resolution of this technology. Finally, it is demonstrated that the relaxation properties of water and aqueous solutions, alcohols and mixtures of alcohols with dipolar and non-polar solvents can be analyzed via these devices.

BP 12.7 Mon 17:15 P3

Combining Optical Trapping and Confocal Microscopy — •Constantin Spille, Florian Rehfeldt, 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 microscopic mechanisms are not yet 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.

BP 12.8 Mon 17:15 P3

Using an ultrastable AFM to measure pN-forward forces of a growing neuronal Growth Cone — •Thomas Fuhs 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 using 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.

BP 12.9 Mon 17:15 P3

The FIRST project: Fragmentation cross sections for hadron therapy — •Christoph Schuy — GSI, on behalf of the FIRST collaboration

Motivation: The possibility to treat highly radio-resistant tumors while sparing OAR (organs-at-risk) has led to an increasing importance of hadron therapy. To further optimize treatment planning and benchmark Monte Carlo codes, a detailed characterization of the interaction of carbon ions in biological tissue and other relevant materials is necessary. The FIRST (Fragmentation of Ions Relevant for Space and Therapy) experiment, performed by an international collaboration (France, Germany, Italy, Spain), aims at studying nuclear fragmentation processes for therapy and space relevant ion beams and measure double-differential cross sections for high energy fragmentation reactions.

Methods: A complex detector array will be used to measure charge, mass, angular distribution and energy of all fragments plus high-energy neutrons in forward direction. The experimental setup consists of Aladin detectors (Aladin magnet, TP-MUSIC IV, ToF wall) and LAND (Large Area Neutron Detector) as well as newly designed detectors in the interaction region.

Outlook: The first experiment with 200MeV/u and 400MeV/u carbon beams on a carbon target is scheduled for late summer 2011 and will be performed in cave C at the GSI Helmholtz Centre for Heavy Ion Research in Darmstadt, Germany.

BP 12.10 Mon 17:15 P3

The Nature of Water at Material Interfaces — •Kai F. Hodeck[1], Kathrin M. Lange[1], Ulrich Schade[1], Andrei P. Sommer[2], Dan Zhu[2], Alexander Kothe[1], and Emad F. Aziz[1,3] — [1]Helmholtz-Zentrum Berlin für Materialien und Energie — [2]Universität Ulm — [3]Freie Universität Berlin

We studied the hydrogen bonding of water at the interface to sample materials of different polarity using soft X-ray absorption (XA) and Fourier transform infrared (FT-IR) spectroscopy. We show that the electronic structure of isolated water molecules in liquid solvents is neither like in the gas phase nor like in the bulk liquid phase, but rather like in ice [1]. Increasing the concentration gives rise to a solvent-specific clustering of the water molecules and the formation of dis-

tinct structures of the hydrogen bonding network: While in the polar acetonitrile environment, a shared solvation leads to string-like water structures, the less polar chloroform solvent facilitates an immediate phase separation, and a clustering of the water molecules. At the interface to the non-polar benzene solvent, a preferential orientation of the water molecules is found, which we interpret in terms of a formation of cage-like structures [1]. Upon going to the layering structure of water at extended hydrophobic interfaces we provide evidence for a strong, direct interaction with visible light as it is unknown for the bulk liquid [2, 3]. [1] K. Lange et al.: The Nature of the Hydrogen Bond of Water in Solvents of Different Polarities, The Journal of Physical Chemistry B; in print, DOI: 10.1021/jp109790z [2] A. Sommer et al.: Tuning Nanoscopic Water Layers with Laser Light. Langmuir, 24, 635

BP 12.11 Mon 17:15 P3

Electrical characterization of single nanopores in 30 nm thick silicon membranes — •Vedran Bandalo[1], Yael Liebes[2], Nurit Ashkenasy[2], and Marc Tornow[1] — [1]Institut für Halbleitertechnik, TU Braunschweig, Germany — [2]Ben-Gurion University of the Negev, Beer Sheva, Israel

We present the fabrication of silicon nanopore devices and their electrical characterization for DNA translocation measurements. The devices are based on Silicon-On-Insulator (SOI) substrates, where a 30-50 nm thick Si membrane is released using highly anisotropic reactive ion etching, followed by direct pore drilling using a novel FEBIE (focused electron beam induced etching) process. We measured the ionic conductance through individual pores in 100 mM KCl electrolyte solution at a typical noise level of about 3,7 pA RMS and 37 pA p-p, at 100 mV bias. The observed, approximately linear current-voltage characteristics with resistances in the range of 140 to 160 MΩ correspond to pore diameters of about 20 nm, according to a simple cylindrical shape model for the pore and in good agreement with the diameter measured by SEM. Furthermore, first results of the translocation of lambda-DNA through the Si nanopores, as well as novel concepts for integrating an Ag/AgCl electrode on-chip, in a closed cavity-like nanopore device, will be presented.

BP 12.12 Mon 17:15 P3

Interferometric nanoparticle tracking with few photons — •Dennis Müller and Rainer G. Ulbrich — IV. Physikalisches Institut, Georg-August-Universität Göttingen, Germany

We report interferometric tracking of nanoparticles with subwavelength accuracy in the limit of low light intensities. With only few photons contributing to the far-field interferogram the ultimate accuracy of a position measurement which can be achieved from phase reconstruction is limited by shot noise of the detected photons. By means of Monte Carlo simulations we have studied the precision of interferometric tracking as a function of the number of contributing photons and compared it with other tracking methods. The results were experimentally confirmed by tracking a single gold nanosphere, which was immobilized and moved in a controlled way by a piezo actuator.

BP 12.13 Mon 17:15 P3

Electron cryo-microscopy of biological specimens on ultrathin graphene-like conductive carbon nanomembranes — •Daniel Rhinow[1], Matthias Büenfeld[2], Nils-Eike Weber[2], André Beyer[2], Janet Vonck[1], Michael Schranz[3], Armin Gölzhäuser[2], Werner Kühlbrandt[1], Norbert Hampp[3], and Andrey Turchanin[2] — [1]Max-Planck-Institut für Biophysik, Max-von-Laue-Str. 3, 60438 Frankfurt — [2]Universität Bielefeld, Fakultät für Physik, 33615 Bielefeld — [3]Universität Marburg, Fachbereich Chemie, Hans-Meerwein-Str., 35032 Marburg

We have tested ultrathin carbon nanomembranes (CNM) comprising cross-linked biphenyl precursors as support films for transmission electron microscopy of biological specimens. Due to their low thickness of 1 nm CNM add virtually no phase contrast to the transmission pattern thus allowing background-free structural analysis of biological samples, which comprise mainly light elements. Furthermore, we have tested conductive carbon nanomembranes (cCNM) comprising nanocrystalline graphene, obtained by thermal treatment of CNM, as supports for cryoEM of frozen-hydrated biological samples. cCNM are graphene-like substrates, which ideally match all requirements for cryoEM of electrically insulating biological specimens. To analyze the performance of cCNM support films we used purple membranes from Halobacterium salinarum and tobacco mosaic virus as test specimens.

BP 12.14 Mon 17:15 P3

Three-Focus-Fluorescence-Correlation-Spectroscopy (3fFCS) — •Lars Kreutzburg, Richard Börner, and Christian G. Hübner — Insitute of Physics, University of Lübeck, Ratzeburger Allee 160, 23562 Lübeck, Germany

Intracellular transport is achieved by the combination of diffusive and directed motion. FCS and its variants are well suited for the study of such processes. One of these variants presented by Dittrich and Schwille is the spatial-two-photon FCCS for one-dimensional flow measurements by shifting two detection volumes spatially in the precences of one large excitation volume. The later development of two-focus FCS (2fFCS) by Dertinger et al. allows for the determination of exact diffusion coefficients by splitting the optical pathways of two orthogonally polarized excitation beams via a DIC prism, which leads to two spatial shifted overlapping confocal volumes. Following these approaches, we propose a new variant, 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 3fFCS. Moreover, extensive simulations allow for the evaluation of the capabilities of this method. The simulations are compared with the first experimental results.

BP 12.15 Mon 17:15 P3

Detection of conformational states of proteins in *C. elegans in vivo* by confocal fluorescence anisotropy — •Volker Christoph Henschel[1], Alessandro Esposito[2], Eugenia Butekevich[1], Christoph Friedrich Schmidt[1], Fred Sylvester Wouters[3], and Dieter Robert Klopfenstein[1] — [1]Drittes Physikalisches Institut, Biophysics, Georg-August-University Göttingen, Göttingen, Germany — [2]MRC Cancer Cell Unit, Hutchison/MRC Research Centre, Cambridge, UK — [3]Laboratory of Cellular and Molecular Systems, Department of Neuro- and Sensory Physiology, Georg-August-University, Göttingen, Germany

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 Foerster 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 GFP.

BP 12.16 Mon 17:15 P3

Upgrading a Commercial Confocal Microscope to CW-STED Super-Resolution — •Til Driehorst, Florian Rehfeldt, and Christoph F. Schmidt — Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany

Fluorescence microscopy is one of the most commonly used imaging techniques in the life sciences, particularly when investigating living organisms at the sub-cellular level. A major drawback is the diffraction-limited resolution. This limit has been overcome by several new methods such as stimulated emission depletion (STED) microscopy. Here we describe the upgrade of a Leica TCS SP5 X confocal microscope to super-resolution by implementing a custom-built STED system. Fluorophore excitation is done with a pulsed white light laser (WLL) source, while a 592 nm continuous wave (CW) laser is used for STED. The combination of a WLL source and 592 nm STED laser is well-suited for commonly used fluorescent markers such as the FITC and the yellow fluorescent protein (YFP) family.

BP 12.17 Mon 17:15 P3

Real-time 3-dimensional particle tracking with sub-nanometer accuracy at 5,000 frames per second — •Alexander Huhle, Sihwa Joo, Daniel Klaue, and Ralf Seidel — Biotechnologisches Zentrum, TU Dresden, Tatzberg 47/49, 01307 Dresden

Tracking the position of single spherical micrometer-sized particles in all 3 dimensions is crucial for modern force sensing techniques, such as optical and magnetic tweezers. It can be realized using either position sensitive devices in combination with focused laser illumination or a camera and wide-field illumination. While camera-based detection is

very simple to implement and offers the attractive possibility to determine 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. Computationally demanding parts of the tracking algorithm are carried out in the GPU that is specialized for highly parallelized execution. Tracking 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 overfocus. 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 microscopy with full accuracy — •Frederik Grüll, Manfred Kirchgessner, and Udo Kebschull — Kirchhoff Institute für Physics, Heidelberg University, Germany

In localization microscopy the resolution limit is improved by calculating the centroid of the image of each fluorescent point-like object. Current solutions 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 computer hardware.

BP 13: Posters: Biological Membranes

Time: Monday 17:15–20:00 Location: P3

BP 13.1 Mon 17:15 P3

Physical description of endosome dynamics — •Jonathan Edward Dawson[1], Lionel Foret[2], Roberto Villasen[3], Yannis Kalaidzidis[3], Lutz Brusch[4], Andreas Deutsch[4], Marino Zerial[3], and Frank Jülicher[2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Ecole Normale Superieure, LPS, Paris, France — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [4]ZIH-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 endocytosis. 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 endosomes strikingly display a broad power law, which is robust. Our theory can quantitatively reproduce the shape of steady distribution and their time dependence. We determine the kinetic parameters of early endosomal network in HeLa cells. Our theory predicts various scaling properties which have been observed in the experimental data.

BP 13.2 Mon 17:15 P3

Physical description of endosome dynamics — •Jonathan Edward Dawson[1], Lionel Foret[2], Claudio Collinet[3], Roberto Villasen[3], Yannis Kalaidzidis[3], Lutz Brusch[4], Andreas Deutsch[4], Marino Zerial[3], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Ecole Normale Superieure, LPS, Paris, France — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [4]ZIH-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 that are internalized into the cell by endocytosis. Dynamics of endosomal trafficking and sorting involves a large number of individual endosomes which exchange material by fusion and fission thereby establish a dynamic network. Using fluorescence microscopy and automated image analysis we quantify cargo distributions in a specific endosomal network and present a general theory that provide a quantitative description of cargo trafficking in the network. The steady state distribution of total fluorescence intensity of cargo molecules in endosomes display a power law. Our theory can quantitatively reproduce the shape of steady distribution and their time dependence. We determine the kinetic parameters of early endosomal network in HeLa cells. Our theory predicts various scaling properties which have been observed in the experimental data.

BP 13.3 Mon 17:15 P3

Shape and fluctuations of a membrane pinned to a patterned substrate — •Daniel Schmidt[1], Udo Seifert[1], and Ana-Sunčana Smith[2] — [1]II. Institut für Theoretische Physik, Universität Stuttgart — [2]Institut für Theoretische Physik and Excellence Cluster: Engineering 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 minimum at a finite distances from the substrate and thus induces membrane 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 tensions.

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

BP 13.4 Mon 17:15 P3

Dynamics of specific adhesion — •Timo Bihr[1], Ana-Sunčana Smith[2], and Udo Seifert[1] — [1]II. Institut für Theoretische Physik, Uni Stuttgart — [2]Institut für Theoretische Physik and 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 accounting 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 satisfy detailed balance.

We find that when the correlations between the bonds are weak, sparse arrangement of bonds are observed and the increase of the number of bonds in time is associated with a squeezed exponential. When the correlations between the bonds are strong, a domain grows radially 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 isolating membranes. In order to make experiments more effective it is desirable to construct several small arrays of pore-spanning lipid bilayers, which are individually addressable for electrical recordings.

We have therefore designed microchips for simultaneous electrical

recording and fluorescence microscopy to study ion channels. The substrates were produced using standard clean-room techniques. Apertures of micrometer size were etched into silicon nitride membranes forming several porous microarrays. Integrated Ag/AgCl electrodes surrounding each microarray were fabricated by chemical vapour deposition to make them individually addressable for electrical recordings and to be able to switch between the microarrays during the measurement. The substrates were further functionalized by depositing a titanium/gold layer on the microporous arrays. A self-assembled octadecane-thiol monolayer was grown via thiol-gold interaction to stabilize the lipid bilayers. Lipid bilayers were formed by GUV-spreading. The substrates and lipid bilayers were visualized by fluorescence microscopy and atomic force microscopy.

BP 13.6 Mon 17:15 P3

The process of symmetry break on two-dimensional, biofunctionalized surfaces — •Alexander Körner[1], Fernanda Rossetti[1], Christina Deichmann[2], Almut Köhler[2], Doris Wedlich[2], and Motomu Tanaka[1] — [1]Institut of Physical Chemistry, University of Heidelberg, Germany — [2]Institut of Zoology 2, Institut of Technology Karlsruhe, Germany

A challenge in developmental biology is to understand how tissue structures evolve from uniform cell ensembles. The initial step can be generalized as the break of symmetry, which can be characterized by changes in cell polarity. In-vivo studies suggested that a change in cell polarity is induced by the gradient of morphogens (e.g. Wnt), little is known about the quantitative mechanisms. The main focus of this study is to design a model system for the formation of central nerval systems in Xenopus. Our strategy is to use two-dimensional, model membranes functionalized with cell adhesion molecules (Xcadherin 11) to give a cue that guides the symmetry break in tissue explants (animal caps) in a quantitative manner. The precise control of the lateral density of cadherin on the membrane surface was confirmed from changes in the mass density detected by a Quartz Crystal Microbalance. The thickness, roughness, and electron density of supported membranes in the presence and absence of cadherin molecules were determined by high energy X-ray reflectivity measurements. After confirming the quantitative functionalization, we placed Xenopus animal cap onto supported membranes exposing Xcadherin 11, and found that cells injected with a promoter gene showed a sign of the change in their polarity.

BP 13.7 Mon 17:15 P3

Characterization of polymer-supported lipid membranes by X-ray and neutron reflectivity — •Fernanda F. Rossetti[1], Emanuel Schneck[1], Giovanna Fragneto[2], Oleg Konovalov[3], and Motomu Tanaka[1] — [1]Physical Chemistry of Biological Systems, University of Heidelberg, 69120 Heidelberg, Germany — [2]Institut Laue-Langevin, 6 rue Jules Horowitz, BP 156, 38042 Grenoble, France — [3]European Synchrotron Radiation Facility, Beamline ID 10B, 38043 Grenoble, France

Polymer-supported lipid membranes recently attracted increasing interest as planar models of cell membranes. Their major advantage over solid-supported membranes is a reduced frictional coupling between transmembrane proteins and the solid support, which reduces the risk of protein denaturation. However, the structures of such two-dimensional model membranes on the molecular level are still unknown. Here, we present a quantitative study–performed by X-ray and neutron reflectivity at the solid-liquid interface–of artificial and native lipid membranes prepared on polymer cushions made of ultrathin films of regenerated cellulose. The reflectivity results were consistent with the formation of homogeneous membranes over a macroscopically large area and allowed us to extract the properties of both the membrane and the cellulose layer. The interfacial forces acting between the membranes and the substrates were calculated by including contributions from Van der Waals, Helfrich and hydration forces. The resulting membrane-substrate equilibrium distance was found to coincide with the measured thickness of the hydrated cellulose films.

BP 13.8 Mon 17:15 P3

Confocal Raman Microscopy of Ternary Phase Domains in Model Membrane Systems — •Guillermo Beltramo, Magret Giesen, and Agnes Csiszár — Institute für Complexe Systeme Biomechanik ICS-7, Forschungszentrum Jülich, D 52425 Jülich, Germany

Recently lipid micro domains in cellular membranes as well as in model membranes like lipid bilayers and vesicles have been extensively investigated. The micro domains are formed due to a phase separation between areas of different cholesterol and lipid concentration. These membrane structures have been frequently studied using confocal fluorescence microscopy. Fluorescent dyes, however, may alter the properties of the molecules of interest. With the recent development of microscopic techniques, based on vibrational optical spectroscopy, novel means appeared to characterize lipid micro domains in model systems. Molecular vibrations are excited by non-elastically scattered photons. This is known as Raman effect: Laser light interacts with molecular vibrations in the molecule, resulting in a red-, respectively, blue-shift of the laser light. The energy shift gives detailed information on the chemical components in a membrane with high spatial and time resolution. In confocal Raman microscopy, the laser beam scans a sample volume and the membrane is imaged based on its vibrational properties. Hence, information about the membrane chemical composition is achieved bypassing the need for any staining procedures. In our work we present confocal Raman microscopy studies on model membranes composed of sphingomyeline, phospholipid, and cholesterol.

BP 13.9 Mon 17:15 P3

Self Organized Criticality and Fractal characteristics in Ion Channels: studies on Voltage Dependent Anion Channel — •Subhendu Ghosh[1], Jyotirmoy Banerjee[2], Smarajit Manna[2], Mahendra K. Verma[3], Naveen K. Bhatraju[4], and Mrinal K. Das[2] — [1]Max Planck Institute for the Physics of Complex Systems, 01187 Dresden, Germany — [2]Department of Biophysics University of Delhi South Campus New Delhi 110021, India. — [3]Indian Institute of Technology, Kanpur Kanpur 208016, India. — [4]School of Life Sciences University of Hyderabad Hyderabad, 500046, India

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.

BP 13.10 Mon 17:15 P3

Biophysical applications of Brewster angle microscopy and imaging ellipsometry - an overview — •Peter H. Thiesen[1], Dirk Hönig[1], and Michael Howland[2] — [1]Accurion GmbH, Stresemannstr. 30, 37079 Göttingen — [2]UC Davis, USA

Ellipsometry is a very sensitive optical method, which has been used for about a hundred years to derive information about surfaces. It makes use of the fact that the polarization state of light may change when the light beam is reflected from a surface. If the surface is covered by a thin film (or a stack of films), the entire optical system of film & substrate influences the change in polarization. It is therefore possible to deduce information about the film properties, especially the film thickness. By using imaging technology, one can extend the classical ellipsometer to a new form of visualization tool or a microscope with extreme sensitivity to thin films. The following examples give an idea about the capability of imaging ellipsometry in the field of lipid layers. One focus will be the current developement in Brewster angle microscopy.

BP 13.11 Mon 17:15 P3

Crystallinity of purple membranes comprising the chloride-pumping bacteriorhodopsin variant D85T — •Daniel Rhinow[1], Ivan Chizhic[2], Roelf-Peter Baumann[2], Frank Noll[2], and Norbert Hampp[2] — [1]Max-Planck-Institut für Biophysik, Max-von-Laue-Str. 3, 60438 Frankfurt — [2]Philipps-Universität Marburg, Fachbereich Chemie, Hans-Meerwein-Str., 35032 Marburg

Purple membranes (PM) from Halobacterium salinarum comprise bacteriorhodopsin (BR) and lipids only and form a 2-D crystalline lattice in the cell membrane. In PMs comprising the chloride-pumping BR-variant D85T 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 freeze-fracture electron microscopy to analyze structural transitions within PM-D85T statistically as well as on the single membrane level. PM-D85T is a model system to study membrane protein association upon substrate binding in a native environment.

BP 13.12 Mon 17:15 P3

Atomistic Simulations of Hydration Forces between Biological Surfaces — •Emanuel Schneck, Felix Sedlmeier, 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 hydrophilic 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 hydrophilic 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 Schneck[1], Bruno Demé[2], Christian Gege[1,3], and Motomu Tanaka[1,4] — [1]University of Heidelberg — [2]Intitut Laue-Langevin, Grenoble — [3]University of Konstanz — [4]Karlsruhe 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 Schwille, 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/polymers interacting with the non-supported membrane by means of single molecule tracking [1].

Electroformation on indium-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 $\sim$ 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.

[1] C. Herold, P. Schwille, E.P. Petrov, Phys. Rev. Lett. 104, 148102 (2010)

[2] M. I. Angelova, S. Soleau, P. Meleard, J. F. Faucon, P. Bothorel, Prog. Colloid Polym. Sci. 89, 127 (1992).

BP 13.15 Mon 17:15 P3

Lipid layer studies at the LISA liquid interface diffractometer at PETRA III — •Klaas Loger[1], Annika Elsen[1], Lars Joergensen[2], Benjamin Runge[1], Christian Koops[1], Matthias Greve[1], Oliver Seeck[3], Beate Kloesgen[2], Olaf Magnussen[1], and Bridget Murphy[1] — [1]IEAP, Christian-Albrechts-Universität zu Kiel, Leibnizstr. 19, D-24098 Kiel, Germany — [2]MEMPHYS, University of Southern Denmark, Campusvej 55, DK-5230 Odense M, Denmark — [3]PETRA III at DESY, Notkestr. 85, D-22603 Hamburg, Germany

Lipid monolayers and bilayers at liquid-air and liquid-liquid interfaces are important model systems for biological membranes. The study of their molecular structure and properties by x-ray scattering methods requires special diffractometers, capable of tilting the beam at precise angles down onto the interface. The new liquid interface scattering apparatus (LISA) for the High Resolution Diffraction Beamline at PETRA III uses a non-dispersive tilting double crystal monochromator which allows reflectivity measurements without moving the sample. Here we present dedicated instrumentation for model membrane studies, specifically a newly developed experimental sample environment and first results on lipid layers at liquid interfaces.

BP 13.16 Mon 17:15 P3

Phase separation and near-critical fluctuations in two-component lipid membranes: Monte Carlo simulations on experimentally relevant scales — •Jens Ehrig, Eugene P. Petrov, and Petra Schwille — Biophysics, BIOTEC, TU Dresden, Tatzberg 47/49, 01307 Dresden, Germany

By means of lattice-based Monte Carlo simulations, we address properties of two-component lipid membranes on the experimentally relevant spatial scales of order of a micrometer and time intervals of order of a second, using DMPC/DSPC lipid mixtures as a model system. We find that, within a certain range of lipid compositions, the phase transition from the fluid phase to the fluid-gel phase coexistence proceeds via near-critical fluctuations. The line tension characterizing lipid domains in the fluid-gel coexistence region is found to be ~ 2 pN. When approaching the critical point, the line tension, the inverse correlation length of fluid-gel spatial fluctuations, and the corresponding inverse order parameter susceptibility of the membrane vanish. All these results are in agreement with recent experimental findings for model lipid membranes. We observe transient subdiffusive behavior of lipids in the presence of near-critical fluctuations, which is a new result important for understanding the origins of subdiffusion in cell membranes. The effects of the interaction of the membrane with the cytoskeleton will be discussed as well.

[1] J. Ehrig, E. P. Petrov, and P. Schwille, *Biophys. J.* **99** (2010), doi:10.1016/j.bpj.2010.11.002.

[2] J. Ehrig, E. P. Petrov, and P. Schwille, arXiv:1009.4860.

BP 13.17 Mon 17:15 P3

Interaction of charged colloidal beads with oppositely charged freestanding lipid membranes — •Markus Anton, Christoph Herold, Eugene P. Petrov, and Petra Schwille — Biophysics, BIOTEC, TU Dresden, Tatzberg 47/49, 01307 Dresden, Germany

Membrane-mediated interactions are believed to be important in lateral organization of membrane proteins and peptides. A system consisting of charged (sub)micrometer-sized colloidal particles interacting with an oppositely charged lipid membrane can serve as a simple model of a membrane with interacting inclusions.

Previously it was reported [1] that negatively charged micron-sized latex beads can form stable ordered clusters at oppositely charged surfactant membranes. In contrast, no mutual attraction between smaller ($<$ 100 nm in diameter) negatively charged polystyrene beads on cationic freestanding lipid membranes was observed [2]. To resolve this controversy, we carry out a systematic investigation of the interaction of negatively charged polystyrene beads with positively charged lipid membranes as a function of the bead size, surface density of membrane-attached beads, and the membrane charge density using fluorescence video microscopy with a sub-second time resolution.

[1] H. Aranda-Espinoza et al., Science 285, 394 (1999); L. Ramos et al., Science 286, 2325 (1999)

[2] C. Herold, P. Schwille, E. P. Petrov, Phys. Rev. Lett. 104, 148102 (2010)

BP 14: Posters: Neurobiophysics, Theoretical Neuroscience, Sensory Transduction

Time: Monday 17:15–20:00 Location: P3

BP 14.1 Mon 17:15 P3

Optical properties of cells in the vertebrate retina — •Silke Agte[1,2], Sabrina Matthias[1], Stephan Junek[3], Elke Ulbricht[1], Ines Erdmann[1], Detlef Schild[3], Josef Käs[2], and Andreas Reichenbach[1] — [1]Paul-Flechsig-Institute for Brain Research, Department of Neurophysiology, Jahnallee 59, 04109 Leipzig, Germany — [2]Institute of Physics, Department of Soft Matter Physics, Linnèstrasse 5, 04103 Leipzig, Germany — [3]Center of Physiology and Pathophysiology, Department of Neurophysiology and Cellular Biophysics, Humboldtallee 23, 37073 Göttingen, Germany

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 overcomes 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 its part of the image via its 'individual' Müller cell-light guide.

BP 14.2 Mon 17:15 P3

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 decisive 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.

BP 14.3 Mon 17:15 P3

Analyzing Multi-electrode Array Measurements of Neurons — •Stephan Kramer[1], Kai Bröking[2], and Annette Witt[2] — [1]Institut f. Numerische u. Angewandte Mathematik, Uni Göttingen — [2]Max-Planck-Institut f. Dynamik u. Selbstorganisation, Göttingen

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 principle 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).

[1] S. Shoham et al., 2003. Robust, automatic spike sorting using mixtures of multivariate t-distributions. JNM 127 (2), 111 - 122

[2] D. Abrahams, A. Gurtovoy, 2004. C++ Template Metaprogramming: Concepts, Tools, and Techniques from Boost and Beyond, Addison-Wesley

BP 15: Single-Molecule Biophysics I

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

Invited Talk BP 15.1 Tue 10:15 ZEU 250

Single-molecule mechanics: theory, analysis, interpretation — •Olga Dudko — UC San Diego, La Jolla, California, USA

Single-molecule biophysical tools permit measurements of the mechanical response of individual biomolecules to external load, revealing details that are typically lost when studied by ensemble methods. An analytical theory of single-molecule force experiments will be presented. The proposed theoretical procedure, based on a picture of diffusive crossing of a free energy barrier, provides estimates of the intrinsic rate coefficient, the location of the transition state, and the free energy of activation. A quantitative, model-free relation between the data collected in two types of measurements - under constant force and under constant force ramp speed - is established. The theoretical procedure of analyzing and interpreting experimental data will be illustrated with the unzipping of individual nucleic acid-based structures by nanopores and optical tweezers and with the unfolding of individual proteins by an atomic force microscope. Effects of multidimensionality of the free energy landscape of the biomolecule on the nature of its response to force will be explored. The theory is applicable to biological contexts ranging from protein folding to ligand-receptor interactions.

BP 15.2 Tue 10:45 ZEU 250

A versatile first passage framework for the theoretical analysis of nanopore translocation experiments with structured polynucleotides — •Severin Schink[1], Karen Alim[2], and Ulrich Gerland[1] — [1]ASC and CeNS, Ludwig-Maximilians-Universität Munich, Germany — [2]Harvard School of Engineering and Applied Sciences, Harvard University, USA

Probing the structures and folding dynamics of DNA or RNA molecules by translocation through nanopores is an emerging new experimental approach of single-molecule biophysics. The nanopore allows single- but not double-strands to pass and thereby couples translocation to unfolding (and refolding) of the molecule. For the quantitative interpretation of these measurements, analysis based on theoretical models for the translocation process is required. The spectrum of available theoretical approaches ranges from generic Kramers rate theory to detailed simulations of both the basepairing and translocation dynamics. Here, we present a versatile mesoscopic framework, which is based on the construction of squence-dependent one-dimensional free energy landscapes starting from the known free energy parameters for RNA and DNA secondary structure formation. This approach has only a small number of adjustable parameters which can be calibrated using translocation experiments with simple sequences. The model then yields a baseline prediction for other sequences, based on which the corresponding experiments can be interpreted, both for constant force measurements as well as nanopore force spectroscopy data. We illustrate the use of our framework with several examples.

BP 15.3 Tue 11:00 ZEU 250

Folding quantization of a biopolymer translocating through nanopores based on multiscale simulations — •Maria Fyta[1,2], Simone Melchionna[1,3], Massimo Bernaschi[4], Sauro Succi[4,5], and Efthimios Kaxiras[1,5] — [1]Department of Physics and School of Engineering and Applied Sciences, Harvard University, Cambridge, MA, USA — [2]Physics Department, Technical University of Munich, 85748 Garching, Germany — [3]INFM-SOFT, Department of Physics, University of Rome La Sapienza, Rome, Italy — [4]Istituto Applicazioni Calcolo, CNR, Rome, Italy — [5]Initiative in Innovative Computing,

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 10^4 biopolymers provide valuable insight into the cooperation of the biopolymer and hydrodynamic motion. 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 value of the folding number, 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 Lipfert, Gary Skinner, Matthew Wiggin, Jacob Kerssemakers, and Nynke Dekker — 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 DNA. 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 straight-forward measurements of free rotation, termed freely-orbiting magnetic tweezers [2]. [1] Lipfert, et al. Nature Methods (2010) [2] Lipfert, Wiggin, et al. Nature Methods, under review

15 min. break.

BP 15.5 Tue 11:45 ZEU 250

Single-molecule spectroscopy on pigment proteins and bio-nano hybrids — •Marc Brecht[1], Robert Bittl[2], Jana Nieder[2], and Martin Hussels[1] — [1]Universität Tübingen Institut für Physikalische und Theoretische Chemie Auf der Morgenstelle 18 72076 Tübingen — [2]FU 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 line 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-nanostructures 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.

[1] Brecht, M. Radics, V. Nieder, J.B. and Bittl, R. (2009), PNAS, 106 (29):11857-11861 [2] Nieder, J.B. Bittl, R. Brecht, M. (2010) Angewandte Chemie,dx.doi.org/10.1002/anie.201002172

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 — •Hergen Brutzer, Friedrich W. Schwarz, and Ralf Seidel — 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 Holliday 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 movement, while 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 fluorescent 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 Jannasch[1], Marko Storch[2], Jonathon Howard[2], and Erik Schäffer[1] — [1]Nanomechanics Group, Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstr. 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 polyethylenglycol 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 Fenz[1], Cassandra Verheul[1], Ewa Snaar-Jagalska[2], and Thomas Schmidt[1] — [1]Leiden Institute of Physics, Leiden University, The Netherlands — [2]Leiden 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 yields two fractions of receptors prior to 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 Wrachtrup, and Michael Börsch — 3.Physikalisches Institut, Universität Stuttgart, Pfaffenwaldring 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 biological 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 Iiving 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.

BP 16: Biological Membranes I

Time: Tuesday 10:15–13:00 Location: ZEU 260

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 Salomé — 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 muopioid 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 — •Gernot Guigas[1], Diana Morozova[2], and Matthias Weiss[1] — [1]Experimental Physics I, University of Bayreuth — [2]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 mechanisms 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.

BP 16.4 Tue 11:15 ZEU 260

Bending and breaking the influenza lipid envelope — •Sai Li[1], Frederic Eghiaian[1], Christian Sieben[2], Andreas Herrmann[2], and Iwan Schaap[1] — [1]Drittes Physikalishes Institut, Georg-August-Universität Göttingen, Germany — [2]Division of Molecular Biophysics, Humboldt-Universität zu Berlin, Germany

Lysosomes, enveloped viruses, synaptic and secretory vesicles are all examples of natural nano-containers (diameter ~100 nm) which specifically rely on their lipid bilayer to protect and exchange their contents with the cell. We have used Atomic Force Microscopy (AFM) and Finite Element Modeling to investigate the mechanical properties of the influenza virus lipid envelope. The mechanical properties of small, spherical vesicles made out of PR8 influenza lipids were probed by an AFM tip applying forces up to 0.2 nN, which led to an elastic deformation up to 20% on average. We found that influenza liposomes were much softer than what would be expected for a gel phase bilayer and highly deformable. We observed that the stiffness of the influenza envelope increased weakly (within one order of magnitude) with temperature, which is consistent with previous suggestion that influenza lipids do not undergo a major phase transition. Influenza liposomes were in most cases able to withstand wall-to-wall deformation, and forces over 1 nN were generally required to rupture the influenza envelope. In contrast to other viruses that pack their contents in stiff protein shells, the influenza virus seems to rely mainly on its highly flexible lipid envelope to protect its genome.

15 min. break

BP 16.5 Tue 11:45 ZEU 260

Structure Formation in Membranes with Quenched Protein Obstacles — •Timo Fischer and Richard Vink — Institut für Theoretische Physik, Georg-August-Universität Göttingen, Friedrich-Hund-Platz 1, 37077 Göttingen

There is growing consensus that membrane lateral structure is heterogeneous, and characterized by micro-domains of different size and compositions. From equilibrium thermodynamics, the formation of micro-domains could be explained by critical fluctuations near a critical point of a demixing transition. Away from the critical point, one would either have a homogeneous mixture or a macroscopic demixing of the membrane components. Such a phase transition is indeed seen in model membranes, and was shown to belong to the Ising universality class. In the membranes of living cells, however, no macroscopic demixing is seen.

Using Monte-Carlo simulations of a simple model of a two-component membrane we investigate how randomly-distributed static obstacles, such as trans-membrane proteins coupling to the inner structure of the cell, influence the fate of the demixing transition. Our findings are compatible with a change in universality from Ising to random-field Ising (RFIM) [1]. This change in universality class elegantly accounts for the non-observation of macroscopic demixing in living cells, since the RFIM does not phase separate in two dimensions. Instead, we find equilibrium micro-structures, which suit well to the expected heterogeneous structure of the membrane.

[1] T. Fischer, RLC Vink, arXiv:1011.0538v1

BP 16.6 Tue 12:00 ZEU 260

Atomistic Simulations of Hydration Forces between Biological Surfaces — •Emanuel Schneck, Felix Sedlmeier, 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 hydrophilic 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 hydrophilic 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 16.7 Tue 12:15 ZEU 260

Molecular Dynamics simulations of phase separation of ternary lipid-cholesterol structure — •Davit Hakobyan and Andreas Heuer — WWU Münster, Institut für Physikalische Chemie, Corrensstraße 30, 48149 Münster, Germany

This project is supported by SFB 858

The separation of liquid-ordered and liquid-disordered phases of lipids in membranes is a subject of continued experimental and theoretical investigations. Yet, the driving force of phase separation is still to be understood. Comparison of energetic and entropic components between cholesterol-saturated lipid and cholesterol-unsaturated lipid complexes [1] indicates that phase separation is the consequence of a cooperative effect of lipids and cholesterols interactions. Here we present the results of coarse-grained (CG) simulations using MARTINI potential [2] for binary dipalmitoyl phosphatidylcholine (DPPC) /dilinoleyl phosphatidylcholine (DUPC) and ternary DPPC/DUPC/CHOL systems. Investigation of temporal evolution of order parameters as a function of nearest-neighbors shows rather clear distinction between systems with and without CHOL. For the former case the order parameter for the saturated DPPC is differentiated among nearest neighbors while for the latter case it is not, which might be thought of as a distinctive property of phase separated and mixed systems. The numerical analysis is complemented by studying a more detailed united atom model of the same system.

[1] Z. Zhang, et al., J. Phys. Chem. B, 111, 12888-12897, 2007.
[2] S.J. Marrink, et al., J. Phys. Chem. B, 111, 7812-7824, 2007.

BP 16.8 Tue 12:30 ZEU 260

Calculating Partition Coefficients From Atomistic Computer Simulations — •Axel Arnold[1], Thorsten Köddermann[2], and Dirk Reith[2] — [1]ICP, Universität Stuttgart, Germany — [2]Fraunhofer SCAI, St. Augustin, Germany

The partition coefficient (log POW) of a substance measures its solubility in octanol compared to water. This can be seen as a simple model for its solubility in biological membranes, which is a rough estimate for toxicity. If a substance is hardly soluble in octanol, it is practically impossible for it to enter (human) cells, and therefore it is less likely to be toxic. On the other hand, for novel drugs it might be important to penetrate the cell through the membrane, or even integrate into it.

Being able to determine the log POW *a priori* from computer simulations would therefore be an important step towards virtual drug design. Up to now, heuristic approaches based on functional groups are mostly used to estimate the log POW, and only there were only a few computer simulations studies trying to calculate the partition coefficient *ab initio*.

We present a method to reliably calculate log POW values from atomistic computer simulations. It is based on the calculation of solvation free energies using thermodynamic integration. First results demonstrate that this generic approach is able to predict log POW values for alcohols better than the classical heuristic methods.

BP 16.9 Tue 12:45 ZEU 260

The pico- to nanoscond dynamics in phospholipid bi- and monolayers — •Sebastian Busch[1] and Tobias Unruh[2] — [1]Technische Universität München, Forschungs-Neutronenquelle Heinz Maier-Leibnitz (FRM II) and Physik Department E13, 85748 Garching bei München, Germany — [2]Friedrich-Alexander-Universität Erlangen-Nürnberg, Lehrstuhl für Kristallographie und Strukturphysik, 91058 Erlangen, Germany

The dynamics of phospholipid molecules on the pico- to nanosecond time scale was studied with incoherent quasielastic neutron scattering.

Looking at stacks of bilayers [1], it was found that the observed motions of the molecules agree very nicely with preceding MD simulations [2]. The effect of several additives (except cholesterol) was negligible on this time scale [3].

In this contribution, we will concentrate on the evolution of the dynamics of the phospholipid molecules when going from stacks of bilayers to single bilayers (vesicles) and monolayers (as a stabilizing layer on oil-in-water dispersions).

[1] S. Busch et al., JACS 132(10):3232, 2010
[2] E. Falck et al., JACS 130(1):44, 2008
[3] S. Busch et al., BBA Biomembranes, in print, doi:10.1016/j.bbamem.2010.10.012

BP 17: Biophysics I: Bionics and Biomaterials (joint AG jDPG, BP)

Time: Tuesday 10:30–12:10 Location: HSZ 201

Invited Talk BP 17.1 Tue 10:30 HSZ 201

Quo vadis Bionik? Möglichkeiten und Grenzen naturinspirierter Technologie — •Christoph Neinhuis — Technische Universität Dresden, Institut für Botanik, Dresden, Deutschland

Die Bionik oder Biomimetik hat in den vergangenen Jahren eine erhebliche Popularität erlangt und wird, nachdem sie über Jahrzehnte ein Schattendasein geführt hat, heute mit erheblichen Mitteln gefördert. Es hat sich eine lebendige Wissenschaftsgemeinschaft der Erforschung biologischer Prinzipien zum technischen Nutzen verschrieben. Tatsächlich ist, trotz aller Anstrengungen, weltweit bis heute nur ein winziger Bruchteil der Organismen auf seine Eigenschaften hin untersucht und das wird auch auf absehbare Zeit so bleiben. Auf der anderen Seite ist trotz aller Förderung und der zunehmenden Anzahl von Forschern auf dem Gebiet die Zahl der tatsächlich realisierten Produkte relativ gering. Und es bleibt selbst bei den bekannten Beispielen immer die Frage, ob es sich tatsächlich um Bionik handelt.

Der Vortrag soll zum einen diesen Konflikt beleuchten, auf der anderen Seite aber die Möglichkeiten, die in der Suche nach Lösungen aus der Natur liegen beleuchten.

Invited Talk BP 17.2 Tue 11:00 HSZ 201

Mikrostrukturierte Haftoberflächen - Vom Vorbild Natur zu praktischen Anwendungen — •Eduard Arzt, Dadhichi Paretkar und Elmar Kroner — INM - Leibniz-Institut für Neue Materialien und Universität des Saarlandes, Saarbrücken, Deutschland

Die Evolution hat verschiedene Oberflächen hervorgebracht, die spezielle Funktionen in optischer, thermodynamischer, hydrodynamischer oder mechanischer Hinsicht erfüllen. Beispiele sind der Mottenaugen-Effekt, der Lotus-Effekt, der Haifischhauteffekt und neuerdings der Gecko-Effekt. Das gemeinsame physikalische Prinzip ist die gezielte Mikro- und Nanostrukturierung, die inzwischen auch im Labor nachgebildet werden kann. Dieser Vortrag behandelt grundlegende Prinzipien der physikalischen Haftung von fibrillären Haftoberflächen und beleuchtet die Mechanismen aus der Sicht der Kontaktmechanik. Schwerpunkt sind die Erfolge bei der Entwicklungen künstlicher Gecko-Oberflächen, die interessante Anwendungen im Haushalt, in der Biomedizin, sowie bei Hygiene- und Sportartikeln versprechen.

D. R. Paretkar, M. Kamperman, A. S. Schneider, D. Martina, C. Creton and E. Arzt, Bioinspired pressure actuated adhesive system, Mat. Sci. Eng. C, in press
M. Kamperman, A. del Campo, R. McMeeking and E. Arzt, Functional adhesive surfaces with Gecko effect: the concept of contact splitting, Adv. Eng. Mats. 12, 335-348 (2010)
G. Guidoni, D. Schillo, U. Hangen, G. Castellanos, E. Arzt, R. M. McMeeking, and R. Bennewitz, Discrete contact mechanics of a fibrillar surface with backing layer interactions, J. Mech. Phys. Sol., in press (2010)

C. Greiner, R. Spolenak and E. Arzt, Adhesion design maps for fibrillar adhesives: the effect of shape, Acta Biomater. 56, 597-606 (2009)
A. del Campo, C. Greiner and E. Arzt, Contact shape controls adhesion of bioinspired fibrillar surfaces, Langmuir 23, 10235-10243 (2007).

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 in an elastic 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: Single-Molecule Biophysics II

Time: Tuesday 14:00–15:15 Location: ZEU 250

Invited Talk 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 biophysics 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, Garcing, Germany

The friction forces and mobilities for the C_{16} 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 Carolin[1], Singer David[2], Hoffmann Ralf[2], and Kremer Friedrich[1] — [1]Leipzig University, Department of Molecular Physics, Leipzig, Germany — [2]Leipzig 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 t0, 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.

BP 19: Biological Membranes II

Time: Tuesday 14:00–15:15 Location: ZEU 260

BP 19.1 Tue 14:00 ZEU 260

Lipid Bilayer Membranes on Multistimuli-Responsive Poly(*N*-isopropylacrylamide) Copolymer Cushions — •Martin Kaufmann[1], Yunfei Jia[1], Carsten Werner[1,2], and Tilo Pompe[1] — [1]Leibniz Institute for Polymer Research Dresden, Germany — [2]Center of Regenerative Therapies Dresden, Germany

To mimic the native environment of a lipid bilayer in respect to the extracellular matrix or intracellular structures, we pursue the approach to use a thin polymer film as bilayer cushion support in order to prevent transmembrane proteins from pinning to the support. With the aim to actively tune transmembrane protein mobility, we first studied the characteristics of a bilayer membrane formed on a stimuli-responsive polymer cushion. Swelling characteristics of thin films of poly(*N*-isopropylacrylamid-*co*-carboxyacrylamid) were probed by ellipsometry and quartz crystal microbalance (QCM) and found to switch in thickness between 15 nm and 150 nm depending on monomer composition, *pH* and temperature. The mobility of lipid bilayer on top of the cushions, as analyzed by fluorescence recovery after photobleaching (FRAP), yielded higher lipid diffusion coefficients ((6.3 - 9.6) $\mu m^2 s^{-1}$) in comparison to solid glass supports ((3.0 - 5.9) $\mu m^2 s^{-1}$) independent of the swelling state of the polymer cushion. This finding revealed a very weak coupling of the lipid bilayer with the polymer cushion. Further, focus of interest is set on the impact of the tunable frictional drag between transmembrane adhesion receptors (integrins) and cushion support, which is expected to influence mobility, activation, and receptor clustering.

BP 19.2 Tue 14:15 ZEU 260

Lipid bilayers interacting with polymer chains — •Marco Werner[1,2] and Jens-Uwe Sommer[1,2] — [1]Leibniz-Institut für Polymerforschung Dresden, Germany — [2]Technische Universität Dresden - Institut für Theoretische Physik

We apply the bond fluctuation model [I. 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. Dominowski, 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 use the 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 biological 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 Händel[1], Undine Dietrich[2], Sergio Alonso[3], Markus Bär[4], and Josef Käs[5] — [1]Division of Soft Matter Physics, University of Leipzig, Germany — [2]Division of Soft Matter Physics, University of Leipzig, Germany — [3]Physikalisch-Technische Bundesanstalt, Berlin, Germany — [4]Physikalisch-Technische Bundesanstalt, Berlin, Germany — [5]Division 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 inclusions: application to membrane fusion — Giovanni Marelli[1], Jelger Risselada[2], and •Marcus Mueller[1] — [1]Insitut für theoretische Physik Frederich Hund Platz 1 37077 Goettingen — [2]Max 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 (eg., 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.

BP 20: Neurobiophysics

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

Invited Talk BP 20.1 Wed 10:15 ZEU 250

Quantitative universality and non-local interactions in neural pattern formation — •Matthias Kaschube — Lewis-Sigler Institute for Integrative Genomics and Physics Department, Princeton University, Princeton NJ, USA

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

Optically Clamping Neurons in vitro — •Kai Bröking[1,3,5], Ahmed ElHady[1,2,4,5], Ragnar Fleischmann[1], Theo Geisel[1,3,4,5], Walter Stühmer[2,4,5], and Fred Wolf[1,3,4,5] — [1]Max-Planck-Inst. für Dynamik und Selbstorganisation, Göttingen, Germany — [2]Max-Planck-Inst. für experimentelle Medizin, Göttingen — [3]Fakultät für Physik, Georg-August-Universität Göttingen — [4]Bernstein Center for Computational Neuroscience, Göttingen — [5]Bernstein Focus for Neurotechnology, Göttingen

Transfecting 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 $\lambda \approx 480$ nm 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] Boyden, E., et al., Nat Neurosci **8**, 1263-1268, doi:10.1038/nn1525

BP 20.3 Wed 11:00 ZEU 250

A nonlinear oscillator underlies flight control in flies — •Jan Bartussek[1], Kadir Mutlu[1], Martin Zapotocky[2], and Steven N. Fry[3] — [1]Institut für Neuroinformatik, Uni/ETH Zürich, Schweiz — [2]Akademie der Wissenschaften der Tschechischen Republik, Prag, Tschechien — [3]FB Bionik, 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 oscillated a tethered fly's body 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 — •Dominika Lyzwa[1], Hubert H. Lim[2], and J. Michael Herrmann[3] — [1]Dept. Nonlinear Dynamics, MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Dept. Otolaryngology, Hanover Medical University, Germany — [3]IPAB, School of Informatics, University of Edinburgh, U.K.

The inferior colliculus (IC) is an important stage in the auditory pathway. We study the spatio-temporal encoding taking place in the laminated central inferior colliculus. We analyze multi-unit activity (MUA) recorded from the IC in cats during acoustic stimulation with pure tones and in guinea pigs during stimulation with vocalizations of these animals as an example of natural stimulation.

Using linear discriminant analysis we obtain that for pure tone stimuli the classification into different stimulus categories is best for time intervals of the recording that contain the onset activity. The latency of the classification is found to be 5-10 ms, increasing from low to high stimulus tones. The information about the stimulus frequency is mostly contained in the first principal component of the response and at early latencies. In the recordings from the vocalization stimulation the dynamic correlations of the response properties from neuron populations along the tonotopic axis and in particular within an isofrequency lamina are investigated. The results from pure tone and natural stimulation are combined to give a phenomenological model of spatio-temporal encoding in the ICC.

15 min. break

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

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.

[1] Y. Shu, A. Hasenstaub, and D. A. McCormick, Nature 423, 288 (2003). [2] A. Weigenand et al, Proc. Biosignal 2010 [3] A. Compte, M.V. Sanchez-Vives, D.A. McCormick, and X. Wang, J. Neurophysiol. 89, 2707 (2003). [4] A. Weigenand et al., in preparation

BP 20.6 Wed 12:00 ZEU 250

How stochastic adaptation currents shape interspike interval statistics - theory vs experiment — •Tilo Schwalger[1], Karin Fisch[2], Jan Benda[2], and Benjamin Lindner[1] — [1]MPI Physik komplexer Systeme, Dresden, Germany — [2]Biozentrum 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. To this end, we consider an integrate-and-fire 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.: Schwalger T, Fisch K, Benda 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 Bauermeister[1], Tilo Schwalger[1], Alexander Neiman[2], and Benjamin Lindner[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden, Germany — [2]Department of Physics and Astronomy, Ohio University, Athens, Ohio 45701, USA

Stochastic oscillations are a ubiquitous phenomenon in neural systems. We study the role of these oscillations in an analytically tractable model, the stochastic perfect integrate-and-fire neuron with narrowband (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

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

London et al. [1] recently showed that triggering a single additional spike in a cerebral cortical neuron can cause an exponentially growing cascade of extra spikes in the network that largely decorrelate the network's microstate. The network mechanism involved in this extreme sensitivity of cortical networks is currently not well understood. Here, we show in a minimal model of cortical circuit dynamics that exponential state separation after single spike and even single synapse perturbations can occur although the dynamics is stable to infinitesimal perturbations and rate responses are extremely weak. We present a conciliatory picture of exponentially separating flux-tubes around unique stable trajectories constituting the networks' state spaces. [1] M. London, A. Roth, L. Beeren, M. Häusser and P. E. Latham, Nature 466, 123 (2010);

BP 20.9 Wed 12:45 ZEU 250

Plasticity in a Spiking Neural Network Model — •Cornelia Petrovic and Rudolf Friedrich — Westfälische Wilhelms-Universität Münster, Institut für Theoretische Physik

We study the influence of spike-timing-dependent plasticity (STDP) in a spiking neuronal network which consists of pulse-coupled phase oscillators introduced by Haken as the lighthouse model [1]. It is a single neuron model that falls between spiking neuron models and firing rate descriptions and thus combines "best of both worlds". In the limit of slow synaptic interactions it can be reduced to the classic Wilson-Cowan and Amari type firing rate models [2,3,4]. For fast synaptic dynamics, it shows some of the complex properties of spiking neural networks.

[1] H. Haken, Brain Dynamics, Springer-Verlag, New York, Berlin, 2002.
[2] H.R. Wilson and J.D. Cowan, Biophys. J., 12 (1972), pp. 1-24.
[3] S. Amari, IEEE Trans. Systems Man Cybernet., 2 (1972), pp. 643-657.
[4] C.C. Chow and S. Coombes, SIAM J.Appl. Dyn. Syst., 5 (4) (2006), pp. 552-574.

BP 21: Biopolymers and Biomaterials II (with CPP)

Time: Wednesday 10:15–13:00 Location: ZEU 260

Invited Talk BP 21.1 Wed 10:15 ZEU 260

Stretching Proteins out of equilibrium: how extracellular matrix proteins serve as mechanotransducers — •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 exterior 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 Deshpande[1], Dagmar Steinhauser[2], and Thomas Pfohl[1,2] — [1]Chemistry Department, University of Basel, Switzerland — [2]Max Plank 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 (L_p) increases proportionally with the number of filaments present in a bundle (n) as: $L_p \approx n^{1.3}$. In the next step, we try to form more complex networks using cross-linking proteins such as α-actinin, filamin, HMM 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 L_P. In the case of the intermediate filament (IF) protein vimentin, L_P was 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 ($L \approx L_P$) 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 λ. We combine IF data with literature data for actin. Thereby we can access both the channel dimension d and L_P, which define the scaling law connecting λ and L_P, $\lambda = a \cdot d^{2/3} \cdot L_P^{1/3}$. The scaling law is fully confirmed by our experiments. Additionally our dynamic measurements yield L_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 Caillerie[1], •Karin John[2], Chaouqi Misbah[2], Philippe Peyla[2], and Annie Raoult[3] — [1]L3S-R, BP 53 - 38041 Grenoble Cedex 9, France — [2]LSP, UJF Grenoble & CNRS, BP 87 - 38402 Saint-Martin-d'Hères, France — [3]LMAP5, 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, 10μs and <1nm, 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 pico-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 Hertrich, Martin Huth, and Bert Nickel — Ludwig-Maximilians-Universität, Department für Physik and CeNS, Geschwister-Scholl-Platz 1, 80539 München

The behaviour of cells in contact to interfaces varies significantly depending on the surface properties. Bioadhesive coatings can act as an interlayer between cells and anorganic interfaces 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. Madarasz and G. Menzo from the Hungarian Academy of Science (HAS).

[1] Huth, M, et al., Materials 2010, 3, 4994-5006.

BP 21.8 Wed 12:30 ZEU 260

Two-component Polymer Scaffolds for Controlled Three-dimensional Cell Culture — •Benjamin Richter[1,2], Franziska Klein[1], Thomas Striebel[1], Clemens Franz[1], Georg von Freymann[3], Martin Wegener[2], and Martin Bastmeyer[1] — [1]Zoologisches Institut, Karlsruher Institut für Technologie, 76131 Karlsruhe — [2]Angewandte Physik, Karlsruher Institut für Technologie, 76131 Karlsruhe — [3]AG 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 photoresist, 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 Hümbert, and Karin Jacobs — Deparment 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 subsurface 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 subsurface 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, much in the same way chemical composition, wetting properties or surface roughness are taken into account. An additional parameter to control is the proper immobilization of the bacteria on the AFM tip, with the help of which force/distance curves have been performed.

BP 22: Physics of Cells I

Time: Wednesday 15:00–17:45 Location: ZEU 250

Invited Talk BP 22.1 Wed 15:00 ZEU 250

The interplay between actin dynamics and membrane tension determines the shape of moving cells — •Kinneret Keren — Department of Physics, Technion- Israel Institute of Technology, Haifa, Israel.

A central challenge in cell motility research is to quantitatively understand how numerous molecular building blocks self-organize to achieve coherent shape and movement on cellular scales. We focus on one of the classic examples of such self-organization, namely lamellipodial motility, in which forward translocation 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.

BP 22.2 Wed 15:30 ZEU 250

A common mechanism connects diverse reaction-diffusion models of cellular symmetry breaking — •Ernesto M. Nicola[1], Philipp Khuc Trong[2,3], Nathan W. Goehring[2], and Stephan W. Grill[2,3] — [1]IFISC, Institute for Cross-Disciplinary Physics and Complex Systems (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain. — [2]Max-Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstrasse 108, 01307 Dresden, Germany. — [3]Max-Planck Institute for the Physics of Complex Systems, Noethnitzer Strasse 38, 01187 Dresden, Germany.

Polarity, the asymmetry in shape present in many cells, is a common feature of many different cell types and is a important mechanism to achieve functional specialization. The initial establishment of cell polarity can be considered as a symmetry-breaking process and has attracted much attention during the last years.

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.

BP 22.3 Wed 15:45 ZEU 250

Influence of cell shape on organelle organization — •Nina Malchus[1] and Matthias Weiss[1,2] — [1]DKFZ c/o BIOQUANT, Heidelberg, Germany — [2]University of Bayreuth, Bayreuth, 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 varitions in an ensemble of cells despite a common geometry and symmetry-dependent correlations between features of different organelles.

BP 22.4 Wed 16:00 ZEU 250

Single cell motility in flow: how parasites invade tissue — •Sravanti Uppaluri[1], Niko Heddergott[2], Eric Stellamanns[1], Stephan Herminghaus[1], Markus Engstler[2], and Thomas Pfohl[1,3] — [1]Max Planck Institute for Dynamics and Self Organization, Göttingen, Germany — [2]University of Würzburg, Germany — [3]University of Basel, Switzerland

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. 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 toward 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.

15 min. break

BP 22.5 Wed 16:30 ZEU 250

High-Precision Dynamics of Membrane Protrusions and Dorsal Ruffles in Mouse Fibroblasts — •Erik Bernitt[1], Pritpal Singh[2], Christina Oettmeier[1], Cheng-Gee Koh[2], and Hans-Günther Döbereiner[1] — [1]Institut für Biophysik, Universität Bremen, Germany — [2]School of Biological Sciences, Nanyang Technological University, Singapore

High-contrast microscopy techniques like total internal reflection fluorescence microscopy allow to accurately locate cellular structures. Cell dynamics can thus be precisely described using advanced localization algorithms in combination with an appropriate tracking method. We implemented a novel velocity chart method and applied it to spreading NIH 3T3 fibroblast cells. We could clearly identify a difference in cell spreading velocities of wildtype cells and cells that overexpress the PAK phosphatase POPX2. The precision of the method is thereby only limited by spatial and temporal resolution of the micrographs and thus superior to the traditional method of kymographs that relies on a preserved direction of structure propagation. We give a detailed analysis of experimental error in measuring membrane protrusion speeds. Further, we report on our latest advances in the quantification of the dynamics of dorsal ruffles that are a characteristic feature of POPX2-overexpressing cells. Function and mechanism of dorsal ruffles are still under discussion and quantitative dynamic data is missing. Therefore our data provides the basis for the establishment of models describing dorsal ruffle dynamics.

BP 22.6 Wed 16:45 ZEU 250

Spatio-Temporally Controlled Cues Mediating Cell Migration — Börn Meier and •Doris Heinrich — Faculty of Physics and Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 München, Germany

Cell migration relies on iterative pseudopod extension, which is based on internally controlled actin polymerization. In the chemotactic model organism Dictyostelium discoideum, robust intracellular feedback systems of complex protein interactions ensure directed cell migration towards an external chemotactic stimulus. Here, we investigate how external, spatiotemporally varying cues influence pseudopod generation and intracellular actin distribution in living cells. To relate the dynamics of pseudopod formation to the spatial distribution of chemotactic key players, we developed a microfluidic chamber with three independently tunable inlets to generate large scale spatiotemporally controlled gradient fields. For a quantitative description of cellular repolarization dynamics, we reverse the chemotactic gradient direction on freely tunable timescales. In response, we observe the time-resolved spatial distribution of actin polymerization in the evolving external gradient field. We can control cell migration by increasing the switching frequency of the gradient direction up to the point, where we chemically trap the cells.

BP 22.7 Wed 17:00 ZEU 250

Actin network growth in the tail of small propelled particles — •Julian Weichsel and Ulrich S. Schwarz — 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

pathogens like the Listeria bacterium and the Vaccinia virus as they propel themselves forward in the cytoplasm of the infected host cell. In fact even plastic beads, vesicles or oil droplets can be propelled in this way in in-vitro assays. We have shown before with stochastic network simulations and a rate equation theory that the steady state structure of the growing actin network in the lamellipodium can dramatically change as a function of network growth velocity [1]. Here we extend this description to curved obstacles in a piecewise-linear approximation in two dimensions. By using adequately rotated reference frames, we again find similar transitions in the actin network behind small propelled particles.

[1] Weichsel, J., and Schwarz, U. S. Two competing orientation patterns explain experimentally observed anomalies in growing actin networks. PNAS 107, 14 (2010), 6304–6309.

BP 22.8 Wed 17:15 ZEU 250

Cell-substrate impedance analysis of cellular motility — •Helmar Leonhardt, Matthias Gerhardt, and Carsten Beta — Institute of Physics and Astronomy, University of Potsdam, Germany

Electric cell-substrate impedance sensing (ECIS) measures the frequency dependent impedance of a small disc-shaped electrode to ac current in the presence of cells. Cells on the electrode restrict the current path, forcing it to pass through the gaps between neighboring cells or through the cell membranes. We have applied ECIS to motile cells of the social amoebae Dictyostelium discoideum. During starvation, Dictyostelium forms multicellular aggregates, which eventually turn into a migrating slug and later into a fruiting body to facilitate spore dispersal. The chemotactic motility of Dictyostelium cells requires the formation and retraction of pseudopodia, resulting in cyclic changes of cell shape and size, which lead to distinct periodicities in the impedance signal. Thus, while shape oscillations of single cells and 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.

BP 22.9 Wed 17:30 ZEU 250

Mechanical energetics of helical bacteria trapped in a light tube — Matthias Koch and •Alexander Rohrbach — University of Freiburg, Georges-Koehler-Allee 102, 79110 Freiburg, Germany

The wall-less, helical bacterium spiroplasma melliferum has an extreme structural simplicity and is among the smallest cells in size (˜200nm thin, 3-5μm long). However, they infect various plants and insects and thereby do tremendous harm to agriculture industry. It has been hypothesized only recently that spiroplasms are responsible for mad cow disease and Creutzfeldt-Jakob-disease. Their motility, defined by helicity changes, kinking and propelling is very complex, and enables propagation in complex environments.

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.

BP 23: Biopolymers and Biomaterials III (with CPP)

Time: Wednesday 15:00–17:45 Location: ZEU 260

BP 23.1 Wed 15:00 ZEU 260

Spontaneous Flows of Active Polar Gels between two Rotating Cylinders — Marc Neef[1], Sebastian Fürthauer[2], •Stephan Grill[2], Frank Jülicher[3], and Karsten Kruse[1] — [1]Theoretische Physik, Universität des Saarlandes, 66041 Saarbrücken — [2]Max Planck Institute of Molecular Cell Biology and Genetics, 01307 Dresden — [3]Max-Planck-Institute for the Physics of Complex Systems, 01187 Dresden

Active Biological matter, e.g. cell tissues or the cytoskeleton can flow spontaneously. In situations, where the material is confined, the flow pattern depends on the geometry of the domain and the boundary conditions, as well as on the system's active properties. We investigate the influence of these factors by theoretically analyzing the equations of motion for active polar fluids in the space between two coaxial cylinders that rotate at a given frequency. In striking contrast to the behavior of uniform flows in open geometries, we find that in the confined case, activity can also stabilize uniform flow patterns.

BP 23.2 Wed 15:15 ZEU 260

Brownian motion of stiff filaments in confined media — •Nikta Fakhri[1,4], Fred MacKintosh[2], Brahim Lounis[3], Laurent Cognet[3], and Matteo Pasquali[4] — [1]Fakultät für Physik, III. Physikalisches Institut - Biophysik , Georg-August-Universität, Göttingen, Germany — [2]Department of Physics and Astronomy, Vrije Universiteit, Amsterdam, The Netherlands — [3]Centre de Physique Moléculaire Optique et Hertzienne, Université Bordeaux, and CNRS, Talence, France — [4]Department of Chemical and Biomolecular Engineering, The Smalley Institute for Nanoscale Science and Technology, Rice University, Houston, Texas, USA

The thermal motion of stiff filaments in a crowded environment underlies the behavior of such disparate systems as polymer materials, nanocomposites, and the cell cytoskeleton. Despite decades of theoretical study, the fundamental dynamics of such systems remains a mystery. Using near-infrared video microscopy, we study the thermal diffusion of individual single-walled carbon nanotubes (SWNTs) confined in porous agarose networks. Surprisingly, we find that even a small bending flexibility strongly enhances their motion: the rotational diffusion constant is proportional to the filament bending compliance and is independent of the network porosity. This study establishes definitively the reptation dynamics of stiff filaments and provides a framework to tailor the mobility of SWNTs in confined environments.

BP 23.3 Wed 15:30 ZEU 260

Depletion forces between single actin filaments — Martin Streichfuss[1,2], •Tamas Haraszti[1,2], and Joachim P. Spatz[1,2] — [1]Max-Planck Institute for Metals Reseach, Stuttgart, Germany — [2]Biophysical Chemistry, 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 lamellopodia.

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 (Mg^{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.

BP 23.4 Wed 15:45 ZEU 260

Coarse Grained Simulations of Biopolymers: Effects of Finite Damping and Hydrodynamic Interactions — Uwe Winter and •Tihamer Geyer — Center for Bioinformatics, Saarland University, Saarbrücken

In the coarse grained Brownian Dynamics simulation method the many

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 integration of the equations of damped motion. In the resulting Langevin integration scheme our recently proposed approximate form of the hydrodynamic interactions between the particles [1] can be incorparated 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].

[1] Geyer, Winter, *J. Chem. Phys.* **130** (2009) 114905
[2] Winter, Geyer, *J. Chem. Phys.* **131** (2009) 104102

BP 23.5 Wed 16:00 ZEU 260

Transport of a semiflexible filament in a network — •Teresa Bauer[1], Felix Höfling[2], Erwin Frey[1], and Thomas Franosch[3] — [1]Arnold Sommerfeld Center (ASC) for Theoretical Physics and Center for NanoScience (CeNS), Fakultät für Physik, Ludwig-Maximilians-Universität München, Germany — [2]Max-Planck-Institut für Metallforschung, Stuttgart and Institut für Theoretische und Angewandte Physik, Universität Stuttgart, Germany — [3]Institut 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

BP 23.6 Wed 16:30 ZEU 260

Interplay of conformational degrees of freedom and crosslink binding in filamentous biopolymer bundles — •Claus Heussinger — 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 interplay of bundle conformational 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.

BP 23.7 Wed 16:45 ZEU 260

Interfacial effects on amyloid fibrilization — •Chiu Fan Lee[1], Létitia Jean[2], Chongsoo Lee[2], Michael Shaw[2], and David J. Vaux[2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Sir William Dunn School of Pathology, Oxford, UK

Amyloid accumulation is associated with pathological conditions, including type II diabetes and Alzheimer's disease. Lipids influence amyloidogenesis and are themselves targets for amyloid-mediated cell membrane disruption. Amyloid precursors are surface active, accumulating at hydrophobic-hydrophilic interfaces (e.g., air-water), where their biophysical and kinetic behaviors differ from those in the bulk solution with significant and underappreciated consequences. Using a combined experimental and theoretical approach, we demonstrate amyloid fibrilization is critically dependent on the presence of air-water interface (AWI). Furthermore, we showed that the role of membranes in amyloidogenesis has been previously underestimated; in an *in vivo*-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.

Reference: L. Jean, C. F. Lee, C. Lee, M. Shaw, D. J. Vaux. FASEB J. **24**, 309 (2010).

BP 23.8 Wed 17:00 ZEU 260

Keratin homogeneity in the tail feathers of peacocks — •Silvia Pabisch[1,2], Stephan Puchegger[1], Ingrid M. Weiss[3], Helmut O. Kirchner[3], and Herwig Peterlik[1] — [1]University of Vienna, Faculty of Physics, Vienna, Austria — [2]Vienna University of Technology, Institute for Materials Chemistry, Vienna, Austria — [3]INM-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 peacocks' 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 core are locked into a zip-like arrangement. Tensile and compression tests are additionally performed in-situ to follow the structural change as consequence of varying load.

[1] R.D.B. Fraser and D.A.D. Perry, J. Struct. Biol. 162 (2008) 1-13.

BP 23.9 Wed 17:15 ZEU 260

Thermophoresis quantifies the Conformation and Stability of Biomolecules — •Christoph Jens Wienken, Philipp Baaske, Stefan Duhr, and Dieter Braun — Systems Biophysics, LMU München, Germany

Stability and conformation of biomolecules is important in the field of biology, medical diagnostics and biotechnology. We developed a method which measures both parameters using Microscale Thermophoresis, an all-optical technique which only uses 250nl of sample. 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].

When measuring thermophoresis over temperature, information about the thermal stability of biomolecules are accessible. We find clear melting transitions and resolve intermediate conformational states. With this it is possible to analyze single nucleotide polymorphisms, DNA modifications and conformational states. The thermophoretic melting analysis is also applicable to proteins where unfolding patterns comparable to scanning calorimetry are found.

[1] Duhr,S & Braun,D Proc. Natl Acad. Sci. USA 103, 19678 (2006).
[2] Baaske,P et al. Angew. Chem. Int. Ed. 49, 2238 (2010).
[3] Wienken,CJ et al. Nat. Commun. 1:100 (2010).

BP 23.10 Wed 17:30 ZEU 260

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, Auf der Morgenstelle 10, Universität Tübingen, 72076 Tübingen, Germany

The liquid-liquid phase separation (LLPS) in concentrated protein solutions plays an important role for protein crystallization as well as protein-association related diseases, such as the sickle cell anemia and eye cataracts, etc [1]. Here, we show that the LLPS can be induced in protein solutions by using a multivalent salt like Yttrium Chloride (YCl_3). The phase diagram of proteins with YCl_3 in the c_p (protein concentration) - c_s (salt concentration) plane is determined. The protein solution undergoes a phase-separation upon adding salt up to a critical value c*. Further increasing c_s to c** the precipitates dissolve and the system turns back to a homogenous solution. This is a reentrant phase behavior [2]. In the condensed regime between c* and c** the system is thermodynamically equivalent to the phase behavior

of a hard sphere with short range interactions, which exhibits a stable 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 University Press, [2] F. Zhang et al., Phys. Rev. Lett. 101 (2008) 148101

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 Hellmann[1,2], Dieter W. Heermann[2], and •Matthias Weiss[1,3] — [1]Cellular Biophysics Group, German Cancer Research Center, D-69120 Heidelberg, Germany — [2]Institut für Theoretische Physik, Universität Heidelberg, D-69120 Heidelberg, Germany — [3]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 experimentally observed subdiffusive characteristics is most consistent with fractional Brownian motion, i.e. the motion of particles in a viscoelastic medium. Here, we show that biochemical reactions, e.g. (multiple) phosphorylation events, are massively influenced by the reactants' (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, multiple 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 — •Simone Herth[1], Miriam Giesguth[2], Günter Reiss[1], and Karl-Josef Dietz[2] — [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 difference between the overlap of the two metals and the reference points and not on the size of the system, thermo couples can also be nanostructured on chip or even onto a glass capillary.

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

BP 24.3 Thu 10:45 ZEU 250

High resolution imaging of the surface of single bacterial cells — •Dominik Greif, Daniel Wesner, Jan Regtmeier, and Dario Anselmetti — Experimental Biophysics & Applied Nanoscience, Bielefeld University, Universitaetsstr. 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 preparation procedures.

We systematically investigated the origin of surface morphology observed 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 environment to fixed bacteria in high vacuum. Stepwise, we applied different sample modifications (fixation, drying, metal coating, etc.) and characterized observed surface patterns. A detailed analysis revealed that the surface structure that is dominated by wrinkled protrusions in SEM images were not generated de novo but evolved from native structures on the surface of living bacteria [1]. In addition we evaluated the influence of osmotic stress to the surface morphology of living cells and also the contribution of exopolysaccharide and lipopolysaccharide (LPS) by imaging two mutant strains of the bacterium under native conditions [1]. Lastly, we could demonstrate that AFM images of living bacteria in culture medium allowed identification of surface features of the size of single proteins emphasizing the usefulness of AFM for high resolution cell imaging. [1] D. Greif et al., Ultramicroscopy 110 (2010) 1290-6

BP 24.4 Thu 11:00 ZEU 250

Fluoreszenz Messungen an Einzelzellen des Modelorganismus für die Photosynthese *Chlamydomonas reinhardtii* — •Andreas Garz[1], Michael Sandman[2], Heiko Lokstein[2], Martin Steup[2] und Ralf Menzel[1] — [1]Institut für Physik und Astronomie, Photonik — [2]Institut für Biochemie und Biologie, Pflanzenphysiologie, Universität Potsdam, Karl-Liebknecht-Str. 24/25, 14476 Potsdam

Die der Photosynthese zugrunde liegenden Mechanismen weisen nach wie vor viele ungeklärte Fragen auf. Innerhalb des interdisziplinären Forschungsverbundes GoFORSYS sollen die im Labor gewonnen Daten den bedeutendsten biochemischen Vorgang der Erde am Computer nachbilden.

In einem Teilprojekt untersuchen wir im Speziellen die regulierenden Mechanismen der Photosynthese, insbesondere deren Schutzmechanismen. Mittels des Prinzips der Puls-Amplituden-Modulation (PAM)-Fluorimetrie an einzelnen Zellen der Grünalge *Chlamydomonas reinhardtii* werden für diese das photochemische und nicht-photochemische Quenchen untersucht. Vorgestellt werden Fluoreszenzmessungen an einzelnen Zellen und die daraus abgeleitete photosynthetische Aktivität in Abhängigkeit des Zellentwicklungsstadiums und gezielt veränderter Umweltbedingungen.

BP 24.5 Thu 11:15 ZEU 250

Mechanics of Spindle Alignment in Saccharomyces cerevisiae — •Stephan Baumgärtner, Hannes Weisse, and Iva Tolic-Nørrelykke — Max-Planck-Institute for Cell Biology and Genetics, Dresden

Asymmetric cell devisions are an important process for cell differentiation in higher organisms. To study such divisons, the asymmetric dividing fungus Saccharomyces cerevisiae is an excellent model. It is essential for finishing cytokinesis to orient the mitotic spindle along the mother-bud axis 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). During a late PW, the aMTs grow inside the bud and get captured by the dynein anchor Num1 located in the bud cell cortex. Dynein translocates 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 $\geq 2\mu m$), 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 — Cavendish Laboratory, University of Cambridge, Cambridge, UK

The function of pluripotent stem cells (PSCs) is to commit to all types of tissue cells needed for an organism while self-renewing and maintaining 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 biological 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. These structural changes are a physical phenotype that we can use to deduce PSC state, and they can also be used as a biomarker for pluripotency and differentiation.

BP 24.7 Thu 12:00 ZEU 250

Anomalous diffusion of intracellular lipid granules — •Christine Selhuber-Unkel[1,2], Pernille Yde[2], Jae-Hyung Jeon[3], Vincent Tejedor[3], Kirstine Berg-Sorensen[4], Ralf Metzler[3], and Lene B. Oddershede[2] — [1]University of Kiel, Institute for Materials Science — [2]University of Copenhagen, Niels-Bohr-Institute — [3]Technical University Munich, Physik-Department — [4]Technical 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.

BP 24.8 Thu 12:15 ZEU 250

Physical description of centrosome assembly and disassembly — •David Zwicker[1], Markus Decker[2], Steffen Jaensch[2], Anthony A Hyman[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max 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 centrioles.

BP 24.9 Thu 12:30 ZEU 250

Spatial organization of the cell cytoplasm: Protein gradients and liquid-liquid phase separation in the C. elegans embryo — •Chiu Fan Lee[1], Clifford P. Brangwynne[2], Zdeněk Petrášek[3], Jöbin Gharakhani[1], Anthony A. Hyman[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [3]Biotechnologisches 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 a concentration gradient of the protein Mex-5. Using a combined experimental and theoretical approach, we show that the Mex-5 gradient is established by a 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.

BP 24.10 Thu 12:45 ZEU 250

Random cell movement promotes synchronization of the segmentation clock — •Koichiro Uriu[1,2], Yoshihiro Morishita[2,3], and Yoh Iwasa[2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Kyushu University, Fukuoka, Japan — [3]PRESTO JST, Japan

In vertebrate somitogenesis, the expression of segmentation clock genes show oscillation, synchronized over neighboring cells. Both experimental and theoretical studies have shown that the synchronization between neighboring cells is achieved by intercellular interaction via Delta-Notch signaling. However, the following question emerges: during somitogenesis, active cell movement is observed in the posterior presomitic mesoderm. Can a synchronized state be stably sustained under random cell movement? In this talk, we show that synchronized oscillation can be sustained under random cell movement. We also find that after disturbed initial condition, the synchronization of cells is achieved much faster with random cell movement. We also show that the anisotropy in the direction of cell movement and the shapes of tissues affect synchronization of the segmentation clock.

BP 25: Statistical Physics in Biological Systems III (joint DY, BP)

Time: Thursday 10:15–13:00 Location: ZEU 260

Invited Talk BP 25.1 Thu 10:15 ZEU 260

Bacterial Games — •Erwin Frey — Arnold-Sommerfeld-Center for Theoretical Physics and Center for NanoScience, Ludwig-Maximilians-Universitaet Muenchen, Theresienstrasse 37, D-80333 Muenchen

Microbial laboratory communities have become model systems for studying the complex interplay between nonlinear dynamics of evolutionary selection forces, stochastic fluctuations arising from the probabilistic nature of interactions, and spatial organization. Major research goals are to identify and understand mechanisms that ensures viability of microbial colonies by allowing for species diversity, cooperative behavior and other kinds of social behavior. A synthesis of evolutionary game theory, nonlinear dynamics, and the theory of stochastic processes provides the conceptual framework for a deeper understanding of these ecological systems. In this talk, we give an introduction into the modern formulation of these theories and illustrate their effectiveness focussing on selected examples of microbial systems. We also discuss current challenges and future perspectives in quantifying bacterial population dynamics, and how this might have an impact on research in non-equilibrium physics.

BP 25.2 Thu 10:45 ZEU 260

Transport efficiency governs the morphology of the plasmodial arterial network in slime moulds — •Werner Baumgarten and Marcus Hauser — Abteilung Biophysik, Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany

The plasmodium of the slime mould Physarum polycephalum is a single multi-nucleate giant amoeboid cell. It forms a characteristic two-dimensional arterial network, where the apical end of the plasmodium extends to search for new food sources, while the dense network of tubular arteries is in charge of transport of protoplasm throughout the giant cell. The tubular network forms a regular graph [1,2] and displays characteristic distributions of the lengths, widths, and surface area of the tubes [2]. With time, the originally dense network coarsens as tiny arterial segments are deleted. Taking into account the laminar flow inside the arterial network [3], the conductivity and drag inside the arteries are estimated. From these data it will be shown

that the evolution of the network strongly depends on the efficiency of the protoplasmic transport in the arteries.

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BP 25.3 Thu 11:00 ZEU 260

A Thermal Trap for DNA Replication — •Christof 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.

BP 25.4 Thu 11:15 ZEU 260

Negative design in protein folding: The role of correlations — •Jonas Minning[1], Ugo Bastolla[2], and Markus Porto[3] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Germany — [2]Centro di Biología Molecular 'Severo Ochoa', Madrid, Spain — [3]Institut 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 the REM approach might be generalized to include these correlations.

15 min. break

BP 25.5 Thu 11:45 ZEU 260

Assessing the asymptotic fitness distribution of beneficial mutations from incomplete data sets — •Ivan G. Szendro[1], Martijn Schenk[2], J. Arjan G.M. de Visser[2], and Joachim Krug[1] — [1]Institut für Theoretische Physik, Universität zu Köln — [2]Laboratory of Genetics, Wageningen University

Since seminal work by Gillespie [1] and Orr [2] it is expected that the distributions of fitness effects of beneficial mutations are determined by the universality classes of extreme value theory. More specifically, it is commonly assumed that the distributions of fitness fall into the Gumbel class, implying an exponential decay at large values. However, there have been recent claims that for some viruses the distribution belongs to the Weibull class [3].

In this contribution, we assess the effect of not observing existing beneficial mutations on the assignment of fitness distributions to one of the three extreme value classes. We assume that the probability to observe a specific mutant depends on its selective disadvantage with respect to the fittest observed mutants. In the light of our considerations, we analyze data collected in an experimental evolution study of the TEM-1 β-lactamase enzyme, which confers antibiotic resistance to *Escherichia coli*.

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BP 25.6 Thu 12:00 ZEU 260

Stochastic tunneling in a two-locus system with recombination — •Andrej Fischer, Ivan Szendro, Joachim Krug, and Alexander Altland — Institut für Theoretische Physik, Universität zu Köln, D-50973 Köln, Germany

The analysis of minimal models in population genetics is an important conceptual task. The effects of mutation, selection and drift (finite population size) on evolution are captured by Kimura's well-known one-locus model with two alleles. Here, we analyze a model that includes additionally the effects of epistasis and recombination in a two-locus setting. For sign epistasis, i.e. the over-compensation of an initial deleterious point mutation by a beneficial secondary mutation at the other locus, the fixation of the fittest genotype is dominated by the presence of several bottlenecks. The interplay of both finite size effects and meta-stability induced by recombination make for intricate fixation dynamics in this paradigmatic model system. Both analytical and numerical results are presented.

BP 25.7 Thu 12:15 ZEU 260

How to cross a fitness valley - A network approach — •Hinrich Kielblock[1], Marc Timme[1,2], and Stefan Grosskinsky[3] — [1]Network Dynamics Group, Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Bernstein Center for Computational Neuroscience Göttingen, Germany — [3]Centre for Complexity Science, University of Warwick, Conventry, UK

How fast does a population evolve from one fitness peak to another in a fitness landscape? This question has recently received much attention as the answer may strongly affect the speed of evolution.

Here we analyze the problem in the stochastic tunneling regime, where almost always almost all individuals are found near one fitness peak but once in a while the population switches to another peak. We derive an analytical expression for this switching time considering finite polulation sizes. We first analyze the dynamics of a population existing in only two different genotypes. The results of such a simple system enable us to derive a formula for an effective mutation rate between the peaks of a fitness valley. This effective rate makes it possible to determine the mean switching times in more complex setups, as e.g. multiple fitness valleys or other structures.

BP 25.8 Thu 12:30 ZEU 260

A dynamical phase transition in a model for evolution with migration — •Bartlomiej Waclaw, Rosalind Allen, and Martin Evans — Department of Physics & Astronomy, University of Edinburgh, JCMB, The King's Buildings, Mayfield Road, Edinburgh EH9 3JZ, United Kingdom

Migration between different habitats is ubiquitous among biological populations. Here I will discuss a simple model for evolution of asexual 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.

BP 25.9 Thu 12:45 ZEU 260

The role of population size in the evolution of microbial populations — •Joachim Krug[1], Kavita Jain[2], and Su-Chan Park[3] — [1]Institut für Theoretische Physik, Universität zu Köln, Cologne, Germany — [2]Theoretical Sciences Unit and Evolutionary and Organismal Biology Unit, Jawaharlal Nehru Centre, Bangalore, India — [3]Department 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)

Time: Thursday 10:30–11:30 Location: HSZ 201

Invited Talk BP 26.1 Thu 10:30 HSZ 201

The Hydrodynamics of Microswimmers — •Gerhard Gompper — 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].

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Invited Talk BP 26.2 Thu 11:00 HSZ 201

What sperm head wiggling can tell us about flagellar hydrodynamics — •B.M. Friedrich[1], I.H. Riedel-Kruse[3], J. Howard[4], and F. Julicher[2] — [1]Weizmann Institute of Science - Department of Materials and Interfaces, Rehovot, Israel — [2]Max-Planck-Institute for the Physics of Complex Systems, Dresden, Germany — [3]Stanford University, Stanford, USA — [4]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 cells 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 J. Gray, G. T. Hancock, J. exp. Biol. 32 (1955). B.M. Friedrich, I.H. Riedel-Kruse, J. Howard, F. Julicher, J. exp. Biol. 213 (2010).

BP 27: Physics of Cells III

Time: Thursday 14:00–17:00 Location: ZEU 250

Invited Talk BP 27.1 Thu 14:00 ZEU 250

Inelastic Mechanics of Biopolymer Networks — •Klaus Kroy — Intstitut 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 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 helical 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, Clemens Kaminski, Teresa Tiffert, and Virgilio Lew — Universität 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 homeostatic behaviour of malarial blood cells, providing an unprecedented wealth of information. The data are compared to predictions from a detailed physiological model of 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[1], Stefan Glorius[1], Stephanie Johne[1], Maria Kasimir[1], Martin Kaufmann[1], Lars Renner[1], Manfred Bobeth[2], Wolfgang Pompe[2], and Carsten Werner[1,3] — [1]Leibniz Institute of Polymer Research Dresden, Max Bergmann Center of Biomaterials, Germany — [2]Technische Universität Dresden, Institute of Materials Science, Germany — [3]Center for Regenerative Therapies Dresden, Germany

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 physicochemistry 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 myofibril assembly — •Benjamin M. Friedrich[1], Amnon Buxboim[2], Dennis E. Discher[2], and Samuel A. Safran[1] — [1]Department of Materials and Interfaces, Weizmann Institute of Science, Rehovot, Israel — [2]Group of Physics and Astronomy, University of Pennsylvania, Philadelphia, Pennsylvania, USA

Myofibrils are the force generating units in striated muscle cells and represent a crystal-like state of acto-myosin organization with characteristic, sarcomeric architecture. The assembly of these myofibrils is a multi-step process that starts with the formation of stress fiber-like, sarcomeric premyofibrils near the cell-substrate interface. A prerequisite for the subsequent fusion of neighboring premyofibrils into nascent myofibrils is the inter-fiber registry of their respective sarcomeric periodicity. Here, we propose that substrate-mediated elastic interactions drive neighboring premyofibrils into registry. Elastic interactions may thus guide myofibril assembly and provide a link between acto-myosin organization and mechanical properties of an extra-cellular substrate. Our theory can account for the non-monotonic dependence of myofibrillogenesis on substrate rigidity that was observed in recent experiments (Engler et al., J. Cell Biol. 166, 2004).

BP 27.6 Thu 15:30 ZEU 250

Contractile network models for adherent cells — •Philip Guthardt Torres[1,2], Ilka B. Bischofs[1,3], and Ulrich S. Schwarz[1,2] — [1]Bioquant, University of Heidelberg — [2]ITP, University of Heidelberg — [3]ZMBH, University of Heidelberg

Cells sense the geometry and stiffness of their environment by active contractility. Assuming a flat substrate, two-dimensional contractile network models can be used to understand how force is distributed throughout the cell. We show that the widely used Hookean spring networks do not correctly predict cell shape on patterned substrates. The observed circular shape feature is only predicted by actively contracting cable networks, which model both the filamentous mechanics of the actin 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 27.7 Thu 16:00 ZEU 250

High-Resolution Cell Mechanics with a Dual Optical Trap — •Florian Schlosser, Christoph F. Schmidt, and Florian Rehfeldt — Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany

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 *mechano*-sensing.

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

Here, we present data of contractile forces and elastic responses of 3T3 fibroblasts and use biochemical perturbations (e.g. blebbistatin, a potent non muscle myosin II inhibitor) to elucidate the contributions of the different cytoskeletal elements to the active and passive mechanical properties of a cell.

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 — Universität Leipzig, Faculty of Physics and Earth Science, Soft Matter Physics Division, Linnéstraße 5, 04103 Leipzig, Germany

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 27.9 Thu 16:30 ZEU 250

Responses of cytoskeletal waves to stimuli and possible implications for cell behaviour — •Alexander Dreher[1], Konstantin Doubrovinski[2], and Karsten Kruse[1] — [1]Theoretische Physik, Universität des Saarlandes, Postfach 151150, 66041 Saarbrücken, Germany — [2]Department of Molecular Biology, Princeton University, Princeton, NJ 08544, USA

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 cytokeletal 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. — •Kenechukwu David Nnetu, Tobias Kiessling, Roland Stange, and Josef Käs — Institut für Experimentelle Physik I, University of 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 regulated 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 bipolar 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 Location: ZEU 260

BP 28.1 Thu 14:00 ZEU 260

Evolution of complex chemical mixtures: a problem linked to the origin of life — •Eva Wollrab[1], Sabrina Scherer[1], Christian Lay[1], Manuel Worst[1], Philipp Zimmer[2], Karsten Kruse[2], and Albrecht Ott[1] — [1]Universität des Saarlandes, Biologische Experimentalphysik, 66123 Saarbrücken — [2]Universität 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 spectroscopy 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 Plitzko, Christian Guill, 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 Franke[1], Alexander Klözer[1], J. Arjan G. M. de Visser[2], and Joachim Krug[1] — [1]Cologne University, Cologne, Germany — [2]Wageningen 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 unversality 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 — •Erik A. Martens and Oskar Hallatschek — Group for Biophysics and Evolutionary Dynamics, Max Planck Institute for Dynamics and Self-Organization, 37073 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 strong 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 Rudolf[1], Neo Martinez[2], and Thilo Gross[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden — [2]Pacific 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 multicompartment 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.

Ref.:
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BP 28.7 Thu 15:45 ZEU 260

Stochastic slowdown in evolutionary processes — •Philipp M. Altrock, Chaitanya S. Gokhale, and Arne Traulsen — Max-Planck-Institute for Evolutionary Biology, Plön

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 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.

[1] Altrock, Gokhale, and Traulsen, Physical Review E 82, 011925 (2010)

BP 28.8 Thu 16:00 ZEU 260

Food Quality in Producer-Grazer Models — •Dirk Stiefs[1], George van Voorn[2], Bob Kooi[3], Ulrike Feudel[4], and Thilo Gross[1] — [1]Max-Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Wageningen University and Research Centre, Wageningen, The Netherlands — [3]Vrije Universiteit, Amsterdam, The Netherlands — [4]ICBM, Carl von Ossietzky Universität, Oldenburg, Germany

Stoichiometric constraints play a role in the dynamics of natural populations, but it is not yet resolved how stoichiometry should be integrated in population dynamical models, as different modeling approaches are found to yield qualitatively different results. We use the approach of generalized modeling to investigate the effects of stoichiometric constraints on producer-grazer systems. The stability of steady states can be analyzed by using a normalization technique to plot 3-dimensional bifurcation diagrams. Because we do not specify the functional 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 modeling assumptions and are hence not structurally stable.

BP 28.9 Thu 16:15 ZEU 260

Evolutionary Game Theory in Growing Populations — •Anna Melbinger, Jonas Cremer, and Erwin Frey — Ludwig-Maximilians Universität, Munich, Germany

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 here 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.

[1] Phys. Rev. Lett. 105, 178101 (2010)

BP 28.10 Thu 16:30 ZEU 260

A Non-Equillibrium Phase Transition in Expanding Populations — •Jan-Timm Kuhr and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München

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.

[1] O. Hallatschek and D. Nelson, Life at the front of an expanding population. Evolution, **64**, 193-206, (2010) – [2] M. Eden, A two-dimensional growth process, Proc. of the Fourth Berkeley Symposium on Mathematical Statistics and Probability, **4**, 223-239, (1960)

BP 29: Posters: Biopolymers & Biomaterials

Time: Thursday 17:15–20:00 Location: P3

BP 29.1 Thu 17:15 P3

Plasma-chemical oxidation of titanium implants enhances peri-implant bone volume and bone-implant contact in a rat model — •Christian Schrader[1], Michael Diefenbeck[2], Sergiy Zankovych[3], and Ulrich Finger[4] — [1]Innovent e.V. Technologieentwicklung, Jena, Germany — [2]Universitätsklinikum, Jena, Germany — [3]Institut für Materialwissenschaft und Werkstofftechnologie, Jena, Germany — [4]Königsee Implantate GmbH, Aschau, Germany

Orthopaedic and dental implants rely on an early force-fit bonding to the host bone for good clinical outcome. The implant anchorage has two structural components: Bone-implant bonding (osseointegration [OI]) and peri-implant trabecula bone [PIB]. OI is established by trabecular conjunctions with the PIB, which bridge the implant to the bony cortex and lead to a structural unit between implant and skeleton. Though several approaches to enhance OI and PIB-formation have been used with good results some stimuli still might bear the risk of complication. Our approach is to modify the titanium surface of the implant by Plasma Chemical Oxidation. It is a processing technique in which the surface of the implant is converted into an oxide coating. The coatings presented in this paper not only serve as a diffusion barrier they are also supplemented with useful compounds to assist early OI and to fulfil biocompatible features besides bio-inert ones related to optimised surface properties. It is now confirmed by in vivo testing with a modified rat tibial implantation model and its bilateral implantation of titanium cylinders. Future project plans include investigations into functional coatings providing antibacterial properties.

BP 29.2 Thu 17:15 P3

Combining microfluidics and SAXS to access intermediate fil-

ament assembly — •Martha Brennich[1], Jens Nolting[1], Christian Dammann[1], Bernd Nöding[1], Susanne Bauch[1], Harald Herrmann[2], and Sarah Köster[1] — [1]Courant Research Centre Nano-Spectroscopy and X-Ray Imaging, University of Göttingen, Germany — [2]Division of Molecular Genetics, German Cancer Research Center (DKFZ), Heidelberg, Germany

In cells, intermediate filaments (IFs) form a complex network that is part of the cytoskeleton.Vimentin is a member of the IF multi-gene family which is found in cells of mesenchymal origin like fibroblasts. We use this model system to study the first steps of the hierarchical self-assembly of protein-subunits to extended filaments *in vitro* upon changes in the concentration of monovalent ions. In microfluidic laminar flow mixers the ion concentration can be precisely adjusted by tuning the diffusion time scales of ions into a hydrodynamically focused protein jet. We determine the ion and protein concentration distributions by confocal microscopy and finite element method simulations. As the protein in the device flows along one spatial axis, the time axis for the assembly process is projected onto the protein flow axis and we observe different assembly states by collecting data at different positions in the device. We find that the mean square radius of gyration perpendicular to the filament axis increases as the precursor proteins aggregate laterally. This increase occurs on the same timescale (seconds) as the diffusion of salt into the protein jet indicating a diffusion limit to the reaction rate.

BP 29.3 Thu 17:15 P3

Effect of bias voltage on wear particle size distribution of DLC coatings in artificial hip joints — •Ying Ren[1], Ingo Erdmann[1], Friederike Deuerler[1], Berrin Küzün[2], and Volker Buck[2] — [1]Faculty D-Department of Mechanical Engineering, University of Wuppertal, — [2]Thin Film Technology Group, Faculty of Physics, University Duisburg-Essen and CeNIDE, 47057, Duisburg, Germany

Due to the biocompatibility, DLC is an inert and impervious material with properties suitable for use in the biomedical field, particularly in tribological implants such as hip joint replacements. Currently the lifetime of such joints is just about 15 years. Therefore some (10%) of patients require second replacements. It is currently 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 distribution 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.

BP 29.4 Thu 17:15 P3

Temperature-dependent Properties of Keratin 8/18 — •Ines Martin[1], Anke Leitner[1], Stephanie Portet[2], Michael Beil[3], Harald Herrmann[4], and Othmar Marti[1] — [1]Department of Experimental Physics, Ulm University, Ulm, Germany — [2]Department of Mathematics, University of Manitoba, Winnipeg, Canada — [3]Department of Internal Medicine I, Ulm University, Ulm, Germany — [4]Division of Molecular Genetics, German Cancer Research Center, Heidelberg, Germany

The cytoskeleton of epithelial cells consists of three types of filaments: microtubules, intermediate filaments and actin filaments. In our work, we have a closer look at intermediate filaments, which are responsible for the stiffness of cells and responses to mechanical stimuli.

The Keratin 8/18 dimer is a basic module of intermediate filaments. Its assembly process is a three step process which is highly sensitive to temperature changes and has very interesting kinetics. Therefore we assembled it in vitro at different temperatures (4°C, 21°C, 30°C, 37°C) and for different durations (10s, 1min, 10min, 20min). The resulting filaments were diluted to a suitable concentration for detection of single filaments and imaged with the help of Transmission Electron Microscopy. The samples were negatively stained with Uranylacetate to enhance the contrast.

With these pictures, the length and diameter of filaments of the different samples were measured and compared by fitting to existing models.

BP 29.5 Thu 17:15 P3

Effect of bias voltage on wear particle size distribution of DLC coatings in artificial hip joints — •Ying Ren[1], Ingo Erdmann[1], Friederike Deuerler[1], Berrin Küzün[2], and Volker Buck[2] — [1]Faculty D-Department of Mechanical Engineering, University of Wuppertal, 42119, Wuppertal, Germany — [2]Thin 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 distribution 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.

BP 29.6 Thu 17:15 P3

Effect of bias voltage on wear particle size distribution of DLC coatings in artificial hip joints — •Ying Ren[1], Ingo Erdmann[1], Friederike Deuerler[1], Berrin Küzün[2], and Volker Buck[2] — [1]Faculty D-Department of Mechanical Engineering, University of Wuppertal, 42119, Wuppertal, Germany — [2]Thin 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. Therefore some (10%) of patients require second replacements. It is currently 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 distribution 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.

BP 29.7 Thu 17:15 P3

Volume imaging of collagen fibrils within human cortical bone — •Stephanie Röper[1], Alexander M. Gigler[2], Christian Riesch[1], Anke Bernstein[3], and Robert Magerle[1] — [1]Chemische Physik, Technische Universität Chemnitz, 09107 Chemnitz — [2]CeNS und Dept. für Geo- und Umweltwissenschaften, Ludwig-Maximilians-Universität München, 80333 München — [3]Dept. für Orthopädie und Unfallchirugie, Muskulosketettales Forschungslabor, Universitätsklinikum Freiburg, 79106 Freiburg

Biological materials such as bone and teeth are nanocomposites of a soft organic matrix (mainly type I collagen) that is reinforced by a stiff inorganic component (hydroxylapatite). Nanotomography based on scanning probe microscopy is a serial reconstruction approach for high resolution volume imaging of these materials. A specimen cut from human cortical bone from the femur was first mechanically grinded and polished, then layer-by-layer ablated by etching with diluted solutions of formic acid and sodium hypochlorite, followed by flushing to stop the etching process, and imaged with tapping mode scanning force microscopy (SFM) after each etching step. The resulting series of SFM images show the arrangement of collagen fibrils with the typical periodic D-band pattern with 67 nm period. A high resolution volume image of the spatial arrangement of collagen fibrils within native cortical bone can be reconstructed by registration of neighboring slices.

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.

BP 29.8 Thu 17:15 P3

Enhancing mechanical properties of calcite by Mg substitutions: A quantum-mechanical study — •Pavlina Elstnerova[1], Martin Friak[1], Tilmann Hickel[1], Helge Otto Fabritius[1], Dierk Raabe[1], Andreas Ziegler[2], Sabine Hild[3], and Joerg Neugebauer[1] — [1]Max-Planck-Institut for Iron Research, Duesseldorf, Germany — [2]University of Ulm, Ulm, Germany — [3]Johannes Kepler University Linz, Linz, Germany

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. Examining the structural characteristics, 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, but also to increase local strains due to the large sizemismatch when substituting Ca atoms by Mg ones (Elstnerova et al., Acta Biomaterialia 6 (2010) 4506-4512).

BP 29.9 Thu 17:15 P3

Cooperative dynamics of microtubule ensembles under force — •Björn Zelinski[1] and Jan Kierfeld[2] — [1]Physics Department, TU Dortmund, Dortmund, Germany — [2]Physics Department, TU Dortmund, Dortmund, Germany

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.

BP 29.10 Thu 17:15 P3

Microrheology of composite networks of microtubules and F-actin — •Marcel Bremerich[1], Frederick C. MacKintosh[2], and Christoph F. Schmidt[1] — [1]3. Physikalisches Institut, Georg-August-Universität, 37077 Göttingen — [2]Department of Physics & Astronomy, Vrije Universiteit , 1081 HV Amsterdam

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.

BP 29.11 Thu 17:15 P3

Length Dynamics of Active Polar Filaments — •Christoph Erlenkämper and Karsten Kruse — Theoretische Physik, Universität des Saarlandes, 66123 Saarbrücken, Germany

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 lenghts and treadmilling velocities.

BP 29.12 Thu 17:15 P3

Measured and simulated valence band structure of cellulose and lignin — •Thomas Haensel[1], Syed Imad-Uddin Ahmed[1,2], and Markus Reinmöller[1] — [1]Institut für Physik and Institut für Mikro- und Nanotechnologien, TU Ilmenau, PF 100565, 98684 Ilmenau — [2]Ostfalia University of Applied Sciences, 38302 Wolfenbüttel

The regenerative biopolymers cellulose and lignin are available in large quantities. This makes them attractive for technical applications. Cellulose is used, for e.g. in the paper and textile as well as medical industry and in modern electronic devices. In the latter case they are utilized in batteries and solar cells as chemically inert isolating materials. In comparison, lignin is a waste product of the paper industry and is mainly used as fuel in combustion processes. It is also used as a filler in polymer compounds and applications in electronic devices are also targeted. While the structure and chemical composition of cellulose and lignin are well established, the molecular orbitals and valence band structures, which are important for understanding the electric properties, have not been thoroughly investigated. In this contribution, X-ray photoelectron spectroscopy (XPS) measurements of cellulose and lignin are combined with density functional theory (DFT) calculations of the basic units from cellulose and lignin to analyze their orbital and valence band structures. In particular, a structure at about 6 to 8 eV therein is attributed to oxygen rather than to carbon, as reported in literature. The results further indicate a significant dependence of the electronic properties on cross-linking and chemical processes leading to polymerisation.

BP 29.13 Thu 17:15 P3

The influence of van der Waals forces on protein adsorption kinetics — •Almuth Hoffmann, Hendrik Hähl, and Karin Jacobs — Department of Experimental Physics, Saarland University, D-66041 Saarbrücken, Germany

In contact with an aqueous solution of proteins, any surface is instantly covered by a thin layer of proteins. It is of great interest for many biological and biomedical applications to understand and control this adsorption process that depends on many parameters.

Concentrating on the influence of the substrate on the adsorption, the surface chemistry has been focus of many studies. Protein adsorption is mainly influenced by short-range forces arising from the surface chemistry and Coulomb interaction. Yet, it could be shown that van der Waals forces influence the adsorption kinetics. By a variation of the oxide layer thickness on a Si wafer, however, it could be shown that also van der Waals forces influence the adsorption kinetics [1,2].

Monte Carlo simulations explain the kinetics with a multi step process composed of the actual adsorption and subsequent surface processes. These simulations suggest that a variation of the van der Waals forces influences the time constant of the surface processes. Fitting the experimental curves with an appropriate model yields the time constants of the various processes involved and shows the influence of the vdW forces.

[1] A. Quinn et al., *EPL* **81** (2008) 56003.
[2] Y. Schmitt, H. Hähl et al., *Biomicrofluidics* **4** (2010) 032201.

BP 29.14 Thu 17:15 P3

Cyclic contraction of regenerated *Bombyx mori* silk fibroin nanofibers — Taiyo Yoshioka[1], Aurel Radulescu[2], Yutaka Kawahara[3], and •Andreas Schaper[1] — [1]Center for Materials Science, Philipps University, 35032 Marburg, Germany — [2]Department of Biological and Chemical Engineering, Gunma University, Gunma 376-8515, Japan — [3]Jülich Centre for Neutron Science at FRM II, 85747 Garching, Germany

Spider dragline silk is known to show significant shrinking (supercontraction) when the fiber is wetted under unrestrained conditions, restraining generates substantial stress (ca. 50MPa) accordingly.

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.

We report first observations of cyclic contraction by EtOH and water vapour treatment of electrospun nanofibers of regenerated *Bombyx mori* silk fibroin. Mechanical measurements and time-resolved microscope observations showed that the contraction behavior is significantly influenced by the structural state of the original fibers. This was proved by scanning and transmission electron microscopy and diffraction, wide-angle x-ray diffraction and small-angle neutron scattering. From our observations we derived a tentative model of the irreversible and the cyclic contraction mechanisms.

T.Y. is grateful to AvH Foundation for a fellowship.

BP 29.15 Thu 17:15 P3

Rule of mixing in composite cytoskeletal networks — •C. Heussinger[1], E.M. Huisman[2], C. Storm[3], and G.T. Barkema[2,4] — [1]Institute for Theoretical Physics, University of Goettingen, Germany — [2]Instituut Lorentz, Universiteit Leiden, The Netherlands — [3]Department of Applied Physics and Institute for Complex Molecular Systems, Eindhoven University of Technology, The Netherlands — [4]Institute 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, Universität 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 are interested in 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 multi-component 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 Alexander 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 biopolymers like actin filaments or microtubules 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 fluorescently labelled microtubule filaments attached to optically trapped 1μm spheres. We aim at building 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 protein adsorbates — •Hendrik Hähl[1], Florian Evers[2], and Karin Jacobs[1] — [1]Department of Experimental Physics, Saarland University, D-66041 Saarbrücken, Germany — [2]Faculty 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.

[1] Y. Schmitt, H. Hähl et al. *Biomicrofluidics* **4** (2010) 032201.

BP 29.19 Thu 17:15 P3

Investigation of the nanomechanical properties of in vitro assembled Keratin 8/18 networks — •Anke Leitner[1], Tobias Paust[1], Kirsten Dammertz[1], Harald Herrmann[2], Michael Beil[3], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University, Ulm, Germany — [2]Division of Molecular Genetics, German Cancer Research Center, Heidelberg, Germany — [3]Department 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 microrheology 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 Jayachandran[1] and Florian Rehfeldt[2] — [1]Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany — [2]Drittes 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.

BP 29.21 Thu 17:15 P3

About the stiffening-fluidization paradox in cell mechanics — Lars Wolff, •Andrea Kramer, and Klaus Kroy — ITP, Uni Leipzig

We examine the effect of inelastic breaking and reforming of transient bonds on the linear and nonlinear mechancis of biopolymer networks theoretically. We combine a natural mathematical representation of the kinetics of weak bonds with phenomenlogical models for the linear rheology, such as the Glassy Wormlike Chain or a generic power-law fluid, and thereby extend their range of validity to nonlinear experimental situations. We show that bond breaking can lead to robust non-Maxwellian absorption patterns in the linear and weakly nonlinear rheology, which are to a large extent independent of the particular viscoelastic model chosen. We further show that transient bond breaking and reforming can resolve the stiffening-fluidization paradox of cell mechanics, i.e. that a material vulnerable to transient bond breaking can show strain or stress stiffening *and* fluidization, depending on the particular experimental protocol.

BP 29.22 Thu 17:15 P3

Towards Non-Invasive Cell Sorting and Specific Insights into Differential Hsp70 Expression in Colon Carcinoma Sublines — •Patrice Donfack[1], Gabriele Multhoff[2], and Arnulf Materny[1] — [1]Center of Functional Materials and Nanomolecular Science, Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany — [2]Dpt. Radiation Oncology, Klinikum rechts der Isar, TU München, Germany

Raman scattering provides noninvasive discrimination and biomolecular insights into Hsp70 associated with human colon carcinoma sublines CX- and CX+ in-vivo. CX-/CX+ are different in Hsp70 membrane expression exhibiting biologically relevant chaperon functions with immunostimulatory effects. We have phenotypically characterized them by immunofluorescence and Raman spectroscopy, combined with robust clustering and multivariate analyses. Although, CX- and CX+ show similar Raman spectra due to their strong resemblance, their protein-dominated Raman spectra reveal changes in protein and amino acids. Also significant and specific changes in DNA/RNA nucleotides involve pyrimidine rings Raman hypochromic effects. Discriminating CX- from CX+ is ultimately achieved with one or two principal components, paving the way for label-free cell-sorting of the sublines. Changes in proteins point to tumor-specific interactions of regulatory proteins and changes in nucleobases indicate DNA-RNA/protein binding interactions. We suspect transcription deregulations as participating precursor onsets of different transport mechanisms leading to Hsp70 differential expression and associated CX-/CX+ phenotypic variation.

BP 29.23 Thu 17:15 P3

Viscoelastic in-vitro study of cellular actin structures — Timo Maier[1,2], •Tamás Haraszti[1,2], and Joachim P. Spatz[1,2] — [1]Max-Planck Institute for Metalsreseach, Stuttgart, Germany — [2]Biophysical Chemistry, University of Heidelberg, Heidelberg, Germany

Cellular actin structures are a crucial part of the cytoskeleton. These structures are determined by several factors, such as the presence of actin binding proteins (ABPs), ions and intracellular macromolecules. In their distinct forms of appearance they are able to adapt to physical and chemical changes and serve thus to sustain constitution and preservation of the cellular shape and motility.

In vitro biomimetic actin model networks open the possibility to analyse the physical and chemical properties in a controlled environment. We have previously developed a flow cell to form stress fiber like structures on pillar substrates. Shape of the filamentous topology is thereby controlled by the flow forces as well as crosslinker agents. Here we report the development of an *in situ* polymerization method within these microfluidic channels forming a refined mesh structure with a better visual resemblance to the actin cortex.

While in the last two decades, macro- and microrheological investigations of actin focused on the viscoelastic behaviour of three dimensional gels it is our ambition to determine distinctions in its characteristics due to the transition to two or one dimensional structures.

BP 29.24 Thu 17:15 P3

Single-walled carbon nanotubes as fluorescent probes — Alok Wessel, •Miquel Banchs Piqué, Nikta Fakhri, and Christoph Schmidt — III. Physikalisches Institut, Göttingen, Germany

Single-walled carbon nanotubes (SWNTs) have unique mechanical and optical properties. Typical SWNTs have a diameter of about 1 nm and a length on the order of microns. Depending on lattice structure SWNTs are conducting or semiconducting. Two-thirds of SWNT species have semiconducting properties. Individual and chemically intact SWNTs show band-gap fluorescence in the near-infrared (NIR) region between 900 to 1600 nm. The emission wavelengths are characteristic of their chirality and diameter. Since biomolecules and cells are relatively transparent in NIR range, the sharp spectra of SWNTs can be detected in complex biological media. We utilize the intrinsic near-infrared (NIR) fluorescence of water solublized SWNTs to image individual SWNTs and study their photostability i.e. resistance to photobleaching and lack of blinking.

BP 29.25 Thu 17:15 P3

Determination of the crystalline part within the cuticle of the isopods Porcellio scaber and Tylos europaeus determined by Raman spectroscopy — Katja Huemer[1], •Sabine Hild[1], Bastian Seidel[2], and Andreas Ziegler[2] — [1]Institute of Polymer Science, Johannes Kepler University, Altenbergerstrasse 69, 4040 Linz, Austria — [2]2 Central Facility for Electron Microscopy, University of Ulm, Albert-Einstein-Allee 11, 89069 Ulm, Germany

The exceptional properties of biological composites, such as the exoskeleton of crustaceans, are based on a complex hierarchical architecture of inorganic and organic components which are organized at different structural levels ranging from the nano- to the meso-scale. The cuticle of crustaceans is an excellent model to study biological composite materials that consists of an organic matrix composed of chitin-protein fibers associated with various amounts of crystalline and amorphous calcium carbonate (ACC). Using the combination of SEM and sacnning confocal Raman microscopy (SCRM) for isopods, a subgroup of the Crustaceans- is was possible to show that mineral phases have a layered arrangement where calcite is restricted to the outer area of the cuticle and ACC is localized in the middle having only little overlap with the crystalline layer. Additionally, to the compositional distribution the SCRM investigations reveal the oriented growth of nanocrystalline calcite within the outer part of the crystalline layer of the cuticle, with homogenous layers seen for Porcellio scaber and a specific orientation pattern seen for Tylos europaeus.

BP 29.26 Thu 17:15 P3

Mechanical measurements reveal high bending but low twisting rigidity of 3D DNA-origami — •Dominik Kauert[1], Tim Liedl[2], and Ralf Seidel[1] — [1]Biotechnology Center, TU Dresden — [2]Ludwig-Maximilians-Universität München

DNA-origami is a recently developed method to design and assemble DNA nanostructures of arbitrary shape and property. The understanding of their mechanical behavior is crucial to develop a toolbox of these nanostructures for a broad range of applications. We used magnetic tweezers that support also direct torque measurements to determine the bending and torsional rigidities of DNA multi-helix bundles assembled by the origami method. In particular we investigated 4-helix bundles of 480nm and 6-helix bundles of 400nm length. To analyze the measurements Monte Carlo simulations and numerical finite-element-modeling was applied. The bending rigidity was found increased about 15-fold and 40-fold for 4-helix bundles and 6-helix bundles compared to double-strand DNA, respectively. In contrast, the torsional rigidity increased only 4-fold and 6-fold for 4-helix bundles and 6-helix bundles. We also show the importance of a rigid attachment of the multi-helical structures, necessary to effectively use their rigid properties.

BP 29.27 Thu 17:15 P3

Homogeneous Hydroxyapatite Surfaces for Dental Studies — •Christian Zeitz[1], Stefan Fünfschilling[2], Samuel Grandthyll[1], Jörg Schmauch[1], Frank Müller[1], Mathias Werth[1], and Karin Jacobs[1] — [1]Saarland University, Department of Experimental Physics, D-66041 Saarbrücken — [2]Institute for Ceramics in Engineering, D-76131 Karlsruhe

Due to its biocompatibility, hydroxyapatite (HAP) has become a versatile material for various biomedical applications. However, a comprehensive explanation for the cell or tissue interactions with HAP is still missing, as is e.g. the influence of surface roughness or fluorida-

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. Schwarz, 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 artherothrombosis. Despite of their important function in mammals, the composition of platelets is simple as they lack a nucleus. This renders them a convenient modell 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 $0.5\,\mu m$ to $2.5\,\mu m$ 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

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

Force Generation in Contractile Cells — •Sarah Schwarz G. Henriques[1], Hansjörg Schwertz[2], Alexander Strate[3], and Sarah Köster[1] — [1]CRC Physics, University of Göttingen, Germany — [2]Division of Vascular Surgery, University of Utah, USA — [3]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 microscopy 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 Martini[1], Michael Beil[2], Thomas Schimmel[3,4], and Othmar Marti[1] — [1]Department of Experimental Physics, Ulm University — [2]Department of Internal Medicine I, Ulm University Hospital — [3]Forschungszentrum Karlsruhe — [4]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 hundreds 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[1,3], Dorothee Staiger[2], and Peter Reimann[1] — [1]Theorie der Kondensierten Materie, Fakultät für Physik, Universität Bielefeld — [2]Molekulare 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 Ebrahimian — 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 1um diameter magnetic particles were injected into living cells of a fungus (*Mucor mucedo*),a protoplast of Cress (*Arabidopsis thaliana*), and a epidermis protoplast of barley (*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 Human Umbilical Vein Endothelial Cells (HUVEC): projecting 2D trajectories into 1D — •Marion Vollmer[1], Matthias Himmelstoss[1], Stefan Zahler[2], and Doris Heinrich[1] — [1]Faculty of Physics and Center for NanoSciences (CeNS), Ludwig-Maximilians-University, Geschwister-Scholl-Platz 1, 80539 Munich, Germany. — [2]Center for Drug Research, Pharmaceutical Biology, Ludwig-Maximilians-University, 81377 Munich, Germany.

Intracellular transport is a regulated process to orchestrate the localisation of vesicles to subcellular compartments. Vesicles attach to microtubules (MT) via motor proteins and are transported to their destination. This directed transport is intercepted by the dissociation of the vesicles from the MT leading to diffusive motion. To distinguish between directed and diffusive motion in the cell, our group developed the TRAnSpORT algorithm [1], based on the analysis of the mean square displacement (MSD). To calculate the vesicular run lengths more precisely we projected 2D trajectories into 1D, thereby reconstructing the MT virtually. This approach was tested in HUVEC that were grown on prepatterned surfaces, generating elongated, quasi-1D cell shapes and which were treated with low doses of the antimicrotubule drug vinblastine. Compared to untreated cells, vesicles in treated HUVEC showed a reduced run length and velocity, indicating the reduction of directed transport processes. This suggests, that the 1D projection is a precise tool to analyse curvilinear trajectories with changing directions of motion. [1] Arcizet et al., PRL, 101(24):248103, 2008.

BP 30.9 Thu 17:15 P3

Mechanical Characteristics of Primary Cilia — •Christopher Battle and Christoph F. Schmidt — Drittes Physikalisches Institut, Georg-August Universitaet, Goettingen, 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[1,2], Mikael Simons[2], and Iwan A. T. Schaap[1] — [1]Georg-August-Universität, Göttingen, Germany — [2]Max-Planck Institute for experimental Medicine, 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 is 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 — •Haugen Grefe and Hans-Günther 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 preparation behind 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 dyed 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 *Physarum polycephalum* on different length scales — •Christina Oettmeier, Erik Bernitt, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen, Germany

The amoeboid slime mold *Physarum polycephalum* is a big single-celled organism with several hundred or thousands of nuclei. It can reach sizes of 10 to 100 cm or larger. *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 spherical shape, were used as the starting form to grow networks. 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 m/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[1], Tina Freisinger[2], Jared L. Johnson[3], Roland Wedlich-Söldner[2], and Erwin Frey[1] — [1]Department of Physics, Ludwig-Maximilians-Universität München, Theresienstraße 37, D-80333 München, Germany — [2]Max Planck Institute of Biochemistry, Am Klopferspitz 18, D-82152 Martinsried, Germany — [3]Department of Chemistry and Chemical Biology, Cornell University, Ithaca, New York 14853

Cell polarization is a prerequisite for processes such as cell motility, proliferation, and stem cell differentiation. The yeast Saccharomyces cerevisiae is able 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 Pawlizak, Anatol Fritsch, Mareike Zink, and Josef A. Käs — 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 correlated with a loss of epithelial characteristics and the acquirement 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 Reverey[1], Matthias Leippe[2], and Christine Selhuber-Unkel[1] — [1]Institute for Materials Science, Biocompatible Nanomaterials, Christian-Albrechts-University, Kaiserstr. 2, 24143 Kiel, Germany — [2]Zoological 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 induced 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 amoebae. 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 Fröhlich[1], Tobias Paust[1], Michael Beil[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Department 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. Becauce 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 Theves 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 inline holography (DIH) 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 Paust[1], Thomas Föhlich[1], Samuel Vollmer[1], Tobias Pusch[1], Paul Walther[2], Michael Beil[3], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Central Electron Microscopy Unit, Ulm University — [3]Department 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 Paust[1], Anke Leitner[1], Michael Beil[2], and Othmar Marti[1] — [1]Institute of Experimental Physics, Ulm University — [2]Department 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 medium and compute the unilateral 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 frequency-dependent storage and loss moduli of the system. In that way one 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 Bonny[1], Elisabeth Fischer-Friedrich[2], and Karsten Kruse[1] — [1]Theoretische Physik, Universität des Saarlandes, 66041

Saarbrücken — [2]Department of Chemical Physics, Weizmann Institute of Science, Rehovot 76100 Israel

The position of the division site in the rod-like bacterium E. coli is determined by the Min proteins. In a wild-type bacterium, prior to division, the Min proteins organize into a standing wave with a single node in the cell center, thereby selecting the cell center as division site. If the bacterium is prevented from dividing and grows longer, we see that in a considerable fraction of bacteria, the pattern changes first into a travelling wave that starts at one cell pole and disappears at the opposite pole before re-emerging at the original pole. After a further increase in cell size, the pattern changes again into a standing wave, now with two nodes. In our work, we present an experimental and a theoretical investigation of these transitions.

BP 30.21 Thu 17:15 P3

Regulation of Dynamic Cell Response with Laterally Confined Domains Embedded in Supported Membranes — •Thomas Kaindl[1], Stefan Kaufmann[1], Oleg Konovalov[2], Ana Martin-Villalba[3], and Motomu Tanaka[1] — [1]PCI, Universität Heidelberg, Germany — [2]ESRF, Grenoble, France — [3]DKFZ, Heidelberg, Germany

Highly uniform and strongly correlated domains of synthetic, fluorinated lipids were incorporated into solid supported lipid membranes to act as the confined, multivalent sites to regulate cell surface interactions. It was demonstrated that fluorinated lipids form monodispersive domains whose domain size and inter-domain correlation can 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.

BP 30.22 Thu 17:15 P3

The Role of Microtubules in Cell Motility — •Matthias Rakowski, Börn Meier, and Doris Heinrich — Faculty of Physics and Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München, Geschwister-Scholl-Platz 1, 80539 München, Germany

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 Dictyostelium discoideum cells, few address migration with depleted microtubules. We implemented an analysis method based on examination of increasing (gain) and decreasing (loss) cell areas between distinct time steps. This analysis is combined with skeletonisation, a morphological operation on binary images to transform a shape to a line as shown in Yuan Xiong et al [1]. This operation emphasizes geometrical and topological properties. Our statistical analysis of pseudopod dynamics, in terms of angle distributions, pseudopod lifetime, and the distinction between directed and random phases of migration obtained by our Transport-algorithm [2], permits an accurate description and quantification of cell migration and therefore will help to elucidate the role of microtubules in cell motility.

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

BP 30.23 Thu 17:15 P3

Optical trapping and motility of trypanosomes — •Eric Stellamanns[1], Sravanti Uppaluri[1], Niko Heddergott[3], Markus Engstler[3], and Thomas Pfohl[1,2] — [1]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]Department of Chemistry, University of Basel, Basel, Switzerland — [3]Department of Zoology, University of Würzburg, Würzburg, Germany

Trypanosomes are unicellular human bloodstream parasites and the causative agent of the so called African sleeping sickness. They are spread by the bite of the tsetse fly and represent a thread to an estimated number of 60 million people in 36 sub Saharan countries. Motility is of paramount importance to cell survival and hence pathogenicity of the parasite. Using optical tweezing methods in microfluidic cell culture environments we are able to analyze cellular motility to a great detail and measure the forces they generate. We find that trypanosome propagation forces are dependent on cell cycle and growth of the flagellum. Furthermore we describe that motility has a broad spectrum not only over the population but also on the single cell level.

BP 30.24 Thu 17:15 P3

Rheology of suspended cells: microscopic mechanisms and biological relevance — Franziska Lautenschläger, Andrew Ekpenyong, Danielle Kaminski, Graeme Whyte, and •Jochen Guck — Cavendish Laboratory, 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 confounded by stress 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, corresponding changes during differentiation and in laminopathies.

BP 30.25 Thu 17:15 P3

Nonlinear Cellular Deformation Response to Optical Forces — •Tina Händler, Tobias Kiessling, Roland Stange, and Josef Käs — University of Leipzig, Germany

A number of diseases are caused by alterations in the cytoskeleton, a highly dynamic protein network that spans the whole cell. The mechanical properties of the cytoskeletal proteins determine the cellular mechanics. Therefore, changes in these proteins are reflected in the cells' response to an applied stress. With an Optical Stretcher, global deformation behavior of suspended cells can be investigated. Optically induced forces are employed to mechanically characterize cells over a wide range of stress, accounting for the proteins' distinct elastic properties depending on their concentration and the mechanical stress they are subject to. At very small stresses, most cells show a linear deformation behavior that is dominated by the actin cortex. Being subject to larger stresses, cells are deforming non-linearly even at relatively small stresses, resulting in a rupture-like, visible restructuring of the cytoskeleton. However, the cells do not completely lose their mechanical integrity, indicating that other cytoskeletal components might account for the cells' viability after the rupture event under physiological circumstances. Modifying the cytoskeletal proteins with chemical agents allows a differentiated investigation of the observed phenomena and helps to understand how cells regulate their mechanical properties.

BP 30.26 Thu 17:15 P3

Flexible three-dimensional scaffolds for cell adhesion studies — •Thomas Striebel[1,2], Franziska Klein[1], Denis Danilov[1], Thomas Boehlke[1], Martin Wegener[1], Martin Bastmeyer[1], and Ulrich S. Schwarz[2] — [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.

[1] F. Klein, T. Striebel, J. Fischer et al., Adv. Mater. 2010, 22(8), 868-71.

BP 30.27 Thu 17:15 P3

Flow-Alignment Coupling in the Cortex of C. Elegans Embryo — •Guillaume Salbreux[1,2], Sundar Naganathan[2], Jean-Francois Joanny[3], Frank Julicher[1], and Stephan W. grill[1,2] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max Planck Institute for Cell Biology and Genetics, Dresden, Germany — [3]Institut Curie, Paris, France

In the nematode C.Elegans embryo, anteroposterior polarization is ensured by a cortical flow powered by myosin activity (Mayer&Al, 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 alignement 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 a coupling between flow and 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 microtubules role in nuclear centering of S. pombe — •Damien Ramunno-Johnson[1], Nicola Maghelli[1], Vladimir Krstic[1], Nenad Pavin[1,2], Alexander Krull[1], Frank Jülicher[2], and Iva Tolić-Nørrelykke[1] — [1]MPI-CBG, Dresden, Germany — [2]MPI-PKS, Dresden, Germany

In the fission yeast *Schizosaccharomyces pombe*, the nucleus ia positioned at the cell center. Since the nucleus determines the cell division site, nuclear centering is crucial for symmetrical cell division. Microtubules push against the cell ends and exert force on the nucleus, but how the cell regulates the centering remains unknown. Here we tackle this problem by using a combination of live cell imaging and theoretical modeling. We show that the nuclear centering efficiency is affected by the microtubule catastrophe rate.

To explore the effects of microtubule dynamics on nuclear centering, a mutant *S. pombe* strain was created to investigate of the role of kinesin-8 in microtubule catastrophe regulation. We found that centering functions better in the wild type. It is necessary to model this system as a dashpot and a spring in parallel. Taken together, our experimental and theoretical results provide a novel centering mechanism where kinesin-8 motors increase the efficiency of nuclear centering.

BP 30.29 Thu 17:15 P3

Quantification of adhesion of malaria infected erythrocytes on functionalized surfaces mimicking placental tissues. — •Harden Rieger[1,2], Hiroshi Yoshikawa[1], Michael Lanzer[2], and Motomu Tanaka[1] — [1]Physical Chemistry of Biosystems, Institute of Physical Chemistry, University of Heidelberg, D69120 Heidelberg, Germany — [2]Department of Infectious Diseases, Parasitology, University of Heidelberg, Medical School, D69120 Heidelberg, Germany

Pregnancy-associated malaria is a serious health issues in tropical countries, as it causes an increase of newborn and maternal mortality. It has been demonstrated that the glycoaminoglycans, such as chondroitin sulfate A (CSA), play a major role in the adhesion of infected erythrocytes to placental tissue, but a quantitative study showing their relative contributions is still missing. The primary aim of this study is to design a quantitative model of placenta surface by functionalization of planar lipid bilayer membranes with CSA at defined surface densities. By controlling the self-assembling of anchor molecules, the average distance of CSA <d> can be regulated within nm accuracy. The specific adhesion of infected erythrocytes was firstly demonstrated on the membrane with <d> = 5.4 nm: In contrast, healthy erythrocytes show no detectable adhesion on the same surface. Furthermore, we found that the infected cells can detect a small change in <d>, undergoing a very sharp binding-unbinding transition. The strength of cell adhesion was quantitatively measured by two means: (a) analysis of cell shape near the surface and (b) a non-invasive assay that utilizes intensive shock wave generated by a ps laser pulse.

BP 30.30 Thu 17:15 P3

Direct quantitative evidence for the presence of optical elements in the vertebrate retina — •Moritz Kreysing, Zuzanna Blaszczak, Lars Boyde, Kevin Chalut, Kristian Franze, and Jochen Guck — Department of Physics, University of Cambridge, J.J. Thomson Avenue, Cambridge CB3 0HE, UK

The vertebrate retina is an optics puzzle: light, before reaching the photoreceptor cells, needs to propagate through hundreds of microns of living neuronal tissue. Whereas the retina is commonly said to be transparent, little is actually known about its optical transmission characteristics. In recent years we have been reporting on both the optical properties of retinal glia cells as well as photoreceptor nuclei which seemingly have developed specific optical properties that facilitate efficient light transmission in addition to their usual biological function. With the current study we present the direct and quantitative observation of light modulation due to the presence of these optical elements inside the inner retina. A discussion of the implications of our finding for the understanding of the visual process concludes the talk.

BP 30.31 Thu 17:15 P3

Dynamics of P-granule formation and localization in C.elegans embryos — •Jöbin Gharakhani[1], Chiu Fan Lee[1], Clifford P. Brangwynne[1,2], Anthony A. Hyman[2], and Frank Jülicher[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Max 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[1,2], Iana Kalinina[3], Amitabha Nandi[1], Alexander Krull[3], Benjamin Lindner[1], and Iva M. Tolic-Norrelykke[3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Faculty of Science, Zagreb, Croatia — [3]Max 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 nucleoplasm. 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.

BP 30.33 Thu 17:15 P3

Forces in cellular growth and division — •Nils Podewitz — Group for Biophysics & Evolutionary Dynamics, MPI for Dynamics & Self-Organization, Göttingen, Germany

When cells grow and divide to from clusters, colonies or dense tissues, they exert mechanical forces onto their surroundings in order to free space for new cells. Obviously there is a maximal force at which cells will stop growing. Until now it is not fully understood why they stop growing and what these stall forces are.

To study this phenomenon we encaged yeast cells in a microfluidic chamber made of an elastic polymer. The deformation of the chamber wall then let us deduce the pressure exerted by the cells, providing us with a relation between cell growth and the forces involved.

Our findings could be relevant to the early stages of biofilm formation as well as allowing insight into tissue dynamics in higher organisms.

BP 31: Posters: Biological Machines & Motor Proteins

Time: Thursday 17:15–20:00 Location: P3

BP 31.1 Thu 17:15 P3

Neck-linker-length dependence of processive Kinesin-5 motility — •André Düselder, Christina Thiede, Stefanie 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 Henschel[1], Alessandro Esposito[2], Christoph Friedrich Schmidt[1], Fred Sylvester Wouters[3], and Dieter Robert Klopfenstein[1] — [1]Drittes Physikalisches Institut, Biophysics, Georg-August-University Göttingen, Göttingen, Germany — [2]MRC Cancer Cell Unit, Hutchison/MRC Research Centre, Cambridge, UK — [3]Laboratory 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 Foerster 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 31.4 Thu 17:15 P3

A tetrameric chimera made from a kinesin-1 and a kinesin-5 shows interesting motility properties — •Alok D. Wessel, Christina Thiede, Stefan Lakämper, Stefanie Reiter, and Christoph F. Schmidt — Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Germany

X. laevis Eg5 is a mitotic kinesin-5 that drives relative sliding of antiparallel microtubules (MT) by the processive action of its two opposing sets of dimeric motors. In order to obtain a tetrameric model system with clearly defined properties and motile phases, we have constructed a tetrameric chimera by replacing the Eg5-motor domain and neck-linker by the homologous regions of D. melanogaster Kinesin 1 (DK4mer).

In surface-gliding assays, Dk4mer showed fast motility (553 +- 31 nm/s). Single GFP-tagged DK4mer motors moved processively along the MT at comparable speeds (499 +- 3 nm/s). We observe clearly distinguished directional and diffusional episodes and an overall run length of ~9 microns on average. We further performed relative sliding assays using DK4mer and polarity labeled MTs and show that DK4mer is capable of sliding MT apart simultaneously using both pairs of motor domains. The exact sliding speed was found to depend on ionic conditions. Direction of sliding appeared to alternate. This phenomenon could be due to additional surface-bound motors, to 1D diffusional motion or to an unlikely reversion of motor direction.

BP 32: Posters: Other Topics in Biological Physics

Time: Thursday 17:15–20:00 Location: P3

BP 32.1 Thu 17:15 P3

The Nanowizard3 The Most Flexible, High Resolution AFM With True Optical Integration — •Gerd Behme — JPK Instruments, Berlin, Deutschland

The NanoWizard3 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 NanoWizard3 AFM head, which gives the lowest noise level in the cantilever deflection detection system available commercially. The NanoWizard3 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 Mul-

tiplex Sensing Systems — •Sebastian Friede, Tobias Niebling, Faheem Amin, Wolfgang J. Parak, and Wolfram Heimbrodt — Fachbereich Physik und WZMW, Philipps Universität Marburg, Renthof 5, 35037 Marburg.

Modern biological sensing systems are using the spectral diversity of fluorescence dyes mostly. An alternative concept for realizing e.g. ion-sensitive sensor systems is the multiplex sensing approach in combination with temporal resolved spectroscopy. Therefore two dyes are bound to a nanoparticle: an ion sensitive dye and a reference-dye. Avoiding spectral overlaps of the reference dyes and the sensing dyes, spectral similar dyes are chosen as reference-dyes for all sensing systems. In order to determine the concentrations of multiple species of ions there is a need to distinguish the luminescence intensities of the used dyes, specially those of the reference dyes. To do so, the fluorescence lifetimes of the reference dyes can be modified by using different kinds of nanoparticles. Bearing in mind the Stokes-shift, semiconductor-quantum dots with the right-tuned emission wavelenght can act as energy-donors for fluorophores and so enhance the fluorophore fluorescence-lifetimes. In contrast, the fluorescence lifetime of dye functionalized gold-cored hybrid systems is affected differently. We could show that a clear distinction of the reference dyes of the different sensor-particles is possible by measuring the fluorescence lifetimes of the dyes.

BP 32.3 Thu 17:15 P3

The effect of glycerol and DMSO on the phase behavior of lysozyme — •Christoph Gögelein[1], Gerhard Nägele[2], Dana Wagner[3], Frederic Cardinaux[3], and Stefan U. Egelhaaf[3] — [1]Max-Planck-Institut für Dynamik und Selbstorganisation, Bunsenstr. 10, 37073 Göttingen — [2]Forschungszentrum Jülich, 52425 Jülich — [3]Heinrich-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 by screening the protein electrostatic charges. 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.

[1] H. Sedgwick, J. E. Cameron, W. C. K. Poon, and S. U. Egelhaaf, J. Chem. Phys. 127 (2007), 125102.

BP 32.4 Thu 17:15 P3

Under-filling trapping objectives optimizes the use of available laser power in optical tweezers — •Mohammed Mahamdeh[1], Citlali Pérez Campos[2], and Erik Schäffer[1] — [1]Nanomechanics Group, Biotechnology Center, TU Dresden, Tatzberg 47-51, 01307 Dresden, Germany — [2]Max Planck Institute of Molecular Cell Biology and Genetics, Pfotenhauerstraße 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 0.5–2 μm 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 0.85 μm 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 finding suggests that apart from the choice of optimal microsphere size, under-filling the objective is key for optimal performance of an optical trap.

BP 32.5 Thu 17:15 P3

A simple three-point-force model for Chlamydomonas Reinhardti — •Ruud Boesten[1,2], Holger Stark[1], and Ignacio Pagonabarraga[3] — [1]TU Berlin, Germany — [2]TU Eindhoven, Netherlands — [3]University of Barcelona, Spain

There is an abundance of swimming organisms on the micrometer scale. From unicellar algae in the oceans, to pathogenic bacteria in human blood vessels. The motility of these microorganisms affects macroscopic properties. For suspensions of Bactilus Subtili a decrease of the viscosity has been measured with respect to the viscosity of the suspending medium [1]. In contrast, for suspensions of Chlamydomonas Reinhardti (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)
[2] Rafai et al., PRL 104, 098102 (2010)
[3] Guasto et al., PRL, 105, 168102 (2010)

BP 32.6 Thu 17:15 P3

Sequential gene-regulatory logic: Design schemes and quantitative characteristics — •Patrick Hillenbrand, Georg 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 its state, and to perform the operations 'set', 'reset', and 'toggle'. 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.

BP 32.7 Thu 17:15 P3

Measuring the non-harmonic potential of an optical trap — •Marcus Jahnel[1,2], Martin Behrndt[1,2], Anita Jannasch[3], Erik Schäffer[3], and Stephan W. Grill[1,2] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [2]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [3]Biotechnology 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.

BP 32.8 Thu 17:15 P3

Grating-based X-ray phase contrast tomography of human cerebellum — •Georg Schulz[1], Timm Weitkamp[2], Irene Zanette[3], Franz Pfeiffer[4], Christian David[5], Elena Reznikova[6], and Bert Müller[1] — [1]BMC, University of Basel, Switzerland — [2]Synchrotron Soleil, Gif sur Yvette, France — [3]ESRF,

Grenoble, France — [4]Department of Physics / Biophysics, TUM, Garching, Germany — [5]LMN, PSI, Villigen, Switzerland — [6]IMT, KIT, Karlsruhe, Germany

Here, we demonstrate that grating-based X-ray tomography provides much better contrast and spatial resolution than MRI microscopy for the human cerebellum. Using a grating interferometer, which consists of a beam-splitter and an analyzer absorption grating, one can detect deflection angles differences of approximately 20 $nrad$. The experiments performed with a photon energy of 23 keV at the beamline ID19 (ESRF Grenoble, France) reached a measurement sensitivity of the real part of the refractive index of $2.3{\cdot}10^{-10}$ corresponding to an electron density sensitivity of 0.15 electrons per nm^3 and a mass density sensitivity of 0.25 $mg\ cm^{-3}$ for such aqueous specimens. The spatial resolution using the FReLoN camera with a pixel size of 5 μm was sufficient to identify individual Purkinje cells within the brain tissue without using any contrast agent. This achievement is regarded as an important milestone in three-dimensional imaging of soft tissue post mortem.

BP 32.9 Thu 17:15 P3

A Riemannian geometric approach to human arm dynamics, movement optimization and invariance — •Armin Biess[1], Tamar Flash[2], and Dario G. Liebermann[3] — [1]Max-Planck-Institute for Dynamics and Self-Organization, 37073 Göttingen, Germany — [2]Department of Applied Mathematics and Computer Science, The Weizmann Institute of Science, Rehovot 76100, Israel — [3]Physical 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 familiy 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.

BP 33: Biological Machines & Motor Proteins

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

Invited Talk BP 33.1 Fri 10:15 ZEU 250

Clamping DNA Strands Together: The Mechanics of Single-strand Annealing — •Erik Schäffer and Marcel Ander — Biotechnology Center (BIOTEC), TU Dresden, Dresden, Germany

Homologous recombination is the fundamental biological process for exchanging DNA segments. It serves to repair DNA breaks, re-launch stalled replication forks, and maintains genetic diversity by mediating gene transfer mechanisms. Two mechanisms are known: strand invasion and single-strand annealing. While the former ATP-dependent mechanism promoted by RecA/Rad51 has been characterized to some extent, the latter ATP-independent mechanism is not understood on the molecular level. Using optical tweezers, we investigated the single-strand annealing mechanism using Redß as a model system. We discovered that despite Redß's efficiency in promoting single-strand annealing, it defaults to kinetic inhibition of DNA annealing. Instead, it is active towards the 3'-end of a single-stranded DNA in the following way: If sufficient complementarity towards another single-stranded DNA is given, presumably a monomer of Redß nucleates clamping of DNA strands. The clamping leads to a large energetic gain and resistance against DNA unzipping. Sequence conservation patterns suggest the existence of three distinct superfamilies: Redß, ERF, and Rad52. For the human version of the latter, we have also indications for the clamping mechanism suggesting that it is perhaps the underlying general mechanism of DNA single-strand annealing, irrespective of the protein family.

BP 33.2 Fri 10:45 ZEU 250

Exceptional *in vitro* and *in vivo* motility of the S. cerevisiae Kinesin-5 Cin8 — •Christina Thiede[1], Adina Gerson-Gurwitz[2], Natalia Movshovich[2], Vladimir Fridman[3], Maria Podolskaya[3], Tsafi Danieli[4], Stefan Lakämper[1], Christoph F. Schmidt[1], and Larisa Gheber[2,3] — [1]Drittes Physikalisches Institut, Georg-August-Universität Göttingen, Göttingen, Germany — [2]Department of Chemistry, Ben-Gurion University of the Negev, Beer-Sheva, Israel — [3]Department of Clinical Biochemistry, Ben-Gurion University of the Negev, Beer-Sheva, Israel — [4]Protein Expression Facility, Wolfson Centre for Applied Structural Biology, Hebrew University of Jerusalem, Jerusalem, Israel

Members of the conserved Kinesin-5 family fulfill essential roles in mitotic spindle morphogenesis and dynamics. The mechanisms that regulate Kinesin-5 function are not well understood. In this study, we have examined *in vitro* and *in vivo* functions and regulation of the *Saccharomyces cerevisiae* Kinesin-5 Cin8. Using *in vitro* single-molecule fluorescence motility assay in whole-cell extracts, we found that Cin8 motility is exceptional in the Kinesin-5 family. In high salt, Cin8 moved fast along microtubules ($\sim$ 22 μm/min) for a Kinesin-5. In low salt, Cin8 was slower and moved more diffusively. We further found that a unique 99 amino acid insert, located in the Cin8 motor domain, increased Cin8 binding to microtubules, affected its motile properties and *in vivo* controlled its localization and function during anaphase spindle elongation.

BP 33.3 Fri 11:00 ZEU 250

Cooperative Transport by Two Molecular Motors — •Florian Berger[1], Corina Keller[1], Melanie J. I. Müller[1,2], Stefan Klumpp[1], and Reinhard Lipowsky[1] — [1]Max Planck Institute of Colloids and Interfaces, 14424 Potsdam, Germany — [2]Department of Physics, Harvard University, Cambridge, MA 02138, USA

Intracellular transport of cargos is achieved by molecular motors, which pull the cargo along cytoskeletal filaments. Due to the thermal environment, these motors unbind from the filament resulting in a finite run length of the cargo. Assuming non-interacting motors the run length increases exponentially with the number of motors attached to the cargo [1]. However, in a recent in vitro experiment two kinesins coupled via a DNA interfere in such a way that they pull each other from the filament [2]. Using a discrete stochastic model based on well established single motor properties together with a spring like coupling, we study the origin of this interference in a motor pair of two identical motor proteins. Additionally, we consider a cargo transported by one active microtubule based motor, kinesin-1, and one diffusive actin based motor, myosin V resulting in an enhanced processivity of the cargo in agreement with a recent in vitro experiment [3].

[1] S. Klumpp, and R. Lipowsky, PNAS 102:17284 (2005)
[2] A. R. Rogers et al., PCCP 11:4882 (2009)
[3] F. Berger, M. J. I. Müller, and R. Lipowsky, EPL 87:28002 (2009)

BP 33.4 Fri 11:15 ZEU 250

Using single-molecule FRET to determine the stepsize of the rotating c-ring of F_oF_1-ATP synthase with DCO-ALEX — •Eva Hammann, Stefan Ernst, Andrea Zappe, Jörg Wrachtrup, and Michael Börsch — 3.Physikalisches Institut, Universität Stuttgart, Pfaffenwaldring 57, 70569 Stuttgart, Germany

ATP production is essential for life. The enzyme F_oF_1-ATP synthase performs this task by proton-driven internal subunit rotation. F_oF_1-ATP synthases comprise a membrane-embedded F_o part and a protruding F_1 part in the inner membranes. The F_1 part consists of 5 different subunits with the stoichiometry $\alpha_3\beta_3\gamma\delta\epsilon$. The α- and β-subunits form three catalytic binding sides for the reaction of ADP and phosphate to ATP and for the reversed ATP hydrolysis direction. The F_o part consists of three different subunits. The a- and b_2- , δ-, α- and β-subunits form a stator part. The 10 c-subunits (in E. coli bacteria) are arranged in a ring and form the rotary motor with the γ- and ϵ-subunits. The driving force is a proton current through the a-subunit and the c-ring. The rotation of the c-ring can be visualized by labeling

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 Neetz[1], Stefan Diez[1,2], and Iva Tolic-Norrelykke[1] — [1]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden — [2]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 in 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 Niedermayer[1], Antoine Jegou[2], Emmanuele Helfer[2], Guillaume Romet-Lemonne[2], Marie-France Carlier[2], and Reinhard Lipowsky[1] — [1]Abteilung Theorie und Bio-Systeme, Max-Planck-Institut für Kolloid- und Grenzflächenforschung, 14424 Potsdam, Germany — [2]Laboratoire d'Enzymologie et Biochimie Structurales, CNRS, 91198 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 Henschel[1], Alessandro Esposito[2], Christoph Friedrich Schmidt[1], Fred Sylvester Wouters[3], and Dieter Robert Klopfenstein[1] — [1]Drittes Physikalisches Institut, Biophysics, Georg-August-University Göttingen, Göttingen, Germany — [2]MRC Cancer Cell Unit, Hutchison/MRC Research Centre, Cambridge, UK — [3]Laboratory 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 Foerster 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 Nadrowski[1,2], Thomas Effertz[2], and Martin Göpfert[2] — [1]Theoretische Physik, Universität des Saarlandes, Campus E2.6, 66123 Saarbrücken — [2]Abt. Zelluläre Neurobiologie, Universität Göttingen, MPI für Experimentelle Medizin, Hermann-Rein-Str. 3, 37075 Götingen

Hearing relies on dedicated mechano-electrical transduction (MET) channels that convert stimulus forces into electrical signals. We present a physical model hat 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 parallely arranged channel populations, one of them constituted by NompC. We further show evidence that NompC might be specifically needed to detect low stimuli 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 Kohler[1,2] and Alexander Rohrbach[1,2] — [1]Bio and Nano-photonics, IMTEK, University of Freiburg, Germany — [2]BIOSS 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 inside living cells during filopodial retraction likely belonging to actin-based molecular motors [1]. Steps remain clearly visible even at force regimes clearly beyond the stall force of a single myosin motor. This indicates a kind of inter-motor coupling, a phenomenon which will be presented in this talk and which we try to explain by a stochastic multi-state model.

[1] Kress, H. et al., pnas, 104, 2007, 11633-11638

BP 34: New Technologies

Time: Friday 10:15–13:00 Location: ZEU 260

Invited Talk BP 34.1 Fri 10:15 ZEU 260

Super-resolution fluorescence imaging of cellular structure and dynamics — •Markus Sauer, Sebastian van de Linde, Teresa Klein, Anna Löschberger, Thorge Holm, and Sven Proppert — 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 photoswitching 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 Müller[1], Dimitar Stamov[1], Carsten Werner[1,2], and Tilo Pompe[1] — [1]Leibniz Institute of Polymer Research Dresden, 01069 Dresden, Germany — [2]Center 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 specialised 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 ECMs 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 nanometer 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 biostructural 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. Dynamics can be monitored on a scale from pico- 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.

[1] S. Domingo Köhler, A. Weber, S. P. Howard, W. Welte, and M. Drescher, Protein Science 19 (2010) 625-630 [2] M. Robotta, P. Braun, B. van Rooijen, V. Subramaniam, M. Huber, and M. Drescher, ChemPhysChem (2010) accepted [3] V. Singh, M. Azarkh, T. Exner, J. Hartig, M. Drescher Angewandte Chemie Int. Ed. 48 (2009) 9728-9730

BP 34.4 Fri 11:15 ZEU 260

Optical manipulation of neuronal networks bursting dynamics — •Ghazaleh Afshar[1,3], Ahmed El Hady[1,2,3], Theo Geisel[1,3,4,5], Walter Stuehmer[2,3,4], and Fred Wolf[1,3,4,5] — [1]Max Planck Institute for Dynamics and Self organization, Göttingen, Germany — [2]Max Planck Institute of Experimental Medicine, Göttingen, Germany — [3]Bernstein Focus for Neurotechnology, Göttingen, Germany — [4]Bernstein Center for Computational Neuroscience, Göttingen, Germany — [5]Faculty 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 stimulus, 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 Brinkmann[1,2,3,4], Sylwia Sekula[1], Michael Hirtz[1], and Harald Fuchs[1,2,3] — [1]Institut für Nanotechnologie, Karlsruher Institut für Technologie, 76128 Karlsruhe — [2]Physikalisches Institut, Westfälische Wilhelms-Universität Münster, 48149 Münster — [3]Center for Nanotechnology (CeNTech), 48149 Münster — [4]Institut 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 quell-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 polydimethysiloxane (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 Gaertner[1], Peter Cimalla[1], Lilla Knels[2], Sven Meissner[1], Wolfgang M. Kuebler[3], and Edmund Koch[1] — [1]TU Dresden, Faculty of Medicine Carl Gustav Carus, Clinical Sensoring and Monitoring, Dresden, Germany — [2]TU Dresden, Faculty of Medicine Carl Gustav Carus, Department of Anatomy, Dresden, Germany — [3]Institute for Physiology, Charité Berlin, Germany and 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 — •Cristian 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 recuperates 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 Krywka[1], Stephan Roth[2], Ralph Döhrmann[2], and Martin Müller[3] — [1]Christian-Albrechts-Universität zu Kiel, Institut für Experimentelle und Angewandte Physik, Leibnizstraße 19, D-24118 Kiel — [2]DESY, Notkestraße 85, D-22607 Hamburg — [3]Helmholtz-Zentrum Geesthacht, Institut für Werkstoffforschung, Max-Planck-Straße 1, D-21502 Geesthacht

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 targetting 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 targetted 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[1], Athina Zouni[2], Hans Joachim Eichler[1], and Gernot Renger[2] — [1]Institute of Optics and Atomic Physics, Berlin Institute of Technology — [2]Max-Volmer-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 excitation energy transfer (EET) 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 core complexes from Thermosynechococcus elongatus by using the technique of time correlated single photon counting with picosecond resolution. The obtained fluorescence decay curves were analyzed within the 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 EET 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: SYBE: Statistical Physics and Biological Evolution

Time: Friday 10:30–12:30 Location: TRE Ma

Invited Talk BP 35.1 Fri 10:30 TRE Ma

Microbial evolution in spatially-structured environments — •Arjan de Visser — Laboratory of Genetics, 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 freezer 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 environmental structure for microbial evolution.

Invited Talk 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.

[1] O. Noivirt-Brik, R. Unger and A. Horovitz, BMC Struct. Biol. **9**, 4 (2009).

[2] O. Noivirt-Brik, A. Horovitz, and R. Unger, PLoS Comput. Biol. **5**, e1000592 (2009).

Invited Talk BP 35.3 Fri 11:30 TRE Ma

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 publically 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 BP 35.4 Fri 12:00 TRE Ma

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.