# BP 17: Poster II

Time: Wednesday 17:15–19:45 Location: P3

BP 17.1 Wed 17:15 P3

**Elastic properties of human cancer cells** — •Carsten Hentschel[1], Hendrik Hölscher[2], Stefan Schneider[2], and Kristina Riehemann[1] — [1]Center for Nanotechnolgy (CeNTech)/University of Münster, Heisenbergstraße 11, 48149 Münster — [2]Affilitation

In the past decade the analysis of biomechanical properties of cancer cells became a tool to determine the invasiveness of a tumor. Atomic force microscope (AFM) has developed to a powerful tool to measure biophysical parameters by using force spectroscopy on living cells in liquid. The force spectroscopy in contact mode can be applied to gain more information about the structure and physical properties (e.g. elasticity) of cells. Different approaches have been shown to get this information [1]. But reproducible results in this area remains to be scarce

We optimized existing methods and showed highly reproducible results demonstrating the elasticity of different celllines strongly correlated to their invasiveness making this methods usefull for clinical applications.

[1] Acta Biomaterialia 3, S. Suresh, 413- 438 (2007)

BP 17.2 Wed 17:15 P3

**Force Measurements in Mitotic Spindles** — •Aaron Lindner[1], Bastian Rühle[1], Francois Nédelec[2], and Joachim Spatz[1,3] — [1]University of Heidelberg — [2]European Molecular Biology Laboratory, Heidelberg — [3]MPI for Metals Research, Stuttgart

The mitotic spindle is responsible for chromosome alignment and segregation during cell division. It is a complex, microtubule-based assembly of different molecular motors and other proteins. In spite of its essential role in cell proliferation, the mechanics of mitotic spindles is not sufficiently well understood. In this project, the pulling strength of mitotic spindles will be determined experimentally.

Bipolar mitotic spindles can be assembled in vitro around chromatinylated, DNA covered microspheres in a cell-free model system which is gained from Xenopus laevis oocytes. In this work, the DNA covered microspheres are attached on functionalized polymer pillars. This yields a regular pattern of bipolar spindles on a force-sensing material.

Spindle pulling forces are expected to be in the range of one nanonewton, which is for the required geometric parameters below the detection limit of existing polymer pillar technologies. That is why for the first time the pillars were made of hydrogel. The Young's modulus of this hydrogel can be varied by altering the water content during polymerization. So it is possible to adjust the stiffness of the pillars to the experimental needs without changing the geometry. With this method, forces of less than 1nN can be detected by observing the pillar bending.

BP 17.3 Wed 17:15 P3

**Towards measuring the centering forces acting on the mitotic spindle in the *C. elegans* embryo** — •Horatiu Fantana and Jonathon Howard — MPI of Molecular Cell Biology and Genetics, Pfotenhauerstraße 108, 01307 Dresden, Germany

The cytoskeleton is a highly dynamic and adaptable protein scaffold that determines the shape and internal organization of cells. In this project we want to investigate the mechanical properties of the microtubule cytoskeleton by applying forces to a dynamic microtubule array *in vivo* and measuring its displacement.

A prominent example for such an array is the mitotic spindle, which is responsible for chromosome segregation and cleavage plane specification during mitosis. At the beginning of mitosis, the spindle moves to the center of the cell. How does the spindle find the center and what keeps it there? Using magnetic tweezers, we plan to displace the spindle and measure the magnitude of the restoring forces acting on the spindle poles in the one-cell *C. elegans* embryo. Does the restoring force increase in proportion to the displacement? If so, then this tells us that the centering process acts like a spring, supporting some models for centering. Does the centering stiffness depend on whether the displacement is parallel or perpendicular to the long axis of the cell? This may give insight into the molecular mechanism underlying centering. What is the magnitude of the centering force? This will tell us something about the number of force-generating processes involved in centering. The results should provide a good basis for modeling and better understanding the centering process.

BP 17.4 Wed 17:15 P3

**Manipulation of stretch-activated calcium channels with the optical stretcher** — •Markus Gyger, Christoph Schneider, Susanne Ebert, and Josef Käs — Universität Leipzig, Germany

Cellular response to deforming forces can be measured with the optical stretcher. Cells are trapped by two anti-parallel laser beams. By increasing the laser power the momentum transfered to the cell surface causes visible deformations. This can be used to probe the global mechanical behaviour of single cells in suspension. For low stresses and small deformations most of the cells deform viscoelasticly. However, for higher stretching powers the cells start to counteract the deformations. Sometimes this active response to deformation results in a contraction of the cell relative to its initial, undeformed state. This raises interesting questions regarding the mechanisms by which cells register and respond to the applied forces. Under physiological conditions many cells react to mechanical stimuli. As a prominent example, hair-cells in the Cochlea of vertebrate ears are known to open transmembrane calcium channels upon mechanical stresses. Calcium is one of the most important second messengers and is involved in most of the known mechano-activated cell responses. Since its normal concentration in the cell soma is very low and increases only by influx from outside the cell or release from intracellular calcium stores upon stimulus, the influx can be made visible by appropriate fluorescent dyes. The aim of this work is to investigate the dependence of calcium influx on the forces applied to the cell surface by the optical stretcher in order to gain insight into the mechanisms of active responses to stretching.

BP 17.5 Wed 17:15 P3

**Mechanics in Neuronal Development** — •Kristian Franze[1], Hanno Svoboda[1], Pouria Moshayedi[1], Andreas Christ[1], James Fawcett[1], Josef Kas[2], Christine Holt[1], and Jochen Guck[1] — [1]University of Cambridge, UK — [2]University of Leipzig, Germany

The neuronal preference for soft substrates and the softness of radial glial cells, along which neurons preferentially grow, strongly point towards a role of mechanics in neuronal guidance. Here we show how neurons detect and avoid stiff substrates and how their mechano-responsiveness is used to guide their axons.

In vitro, neurons continuously probe the mechanical properties of their environment. Growth cones visibly deformed substrates with a compliance commensurate with their own. Externally applied mechanical stress exceeding the threshold of ˜300 Pa caused a calcium influx through mechanosensitive ion channels in the growth cone membrane that triggered neurite retraction. Subsequently, neuronal processes re-extended, thereby enabling exploration of alternative directions. To study the physiological consequences of this mechano-responsiveness, Xenopus eye primordia were cultured on polyacrylamide gels of various compliances. If the outgrowing retinal axons grew either on soft or on stiff substrates, they spread over a wide area. In contrast, on substrates of intermediate compliance they fasciculated and grew into one common direction, resembling an optic nerve. Hence, neurons may actively use mechanics as previously unknown guidance cue. This knowledge may ultimately help in finding new implants that promote axonal regeneration in the injured nervous system.

BP 17.6 Wed 17:15 P3

**Modelling control of cellular force distributions by adhesion geometry and rigidity** — •Ilka Bischofs[1], Sebastian Schmidt[2], and Ulrich Schwarz[2,3] — [1]Lawrence Berkeley Lab, Berkeley, USA — [2]University of Heidelberg, Heidelberg, Germany — [3]University of Karlsruhe, Karlsruhe, Germany

Adhesion geoemetry and matrix rigidity are important decision factors governing adherent cell morphology and cell differentiation. Both have been shown experimentally to control cellular adhesion forces which affect the status of the cytoskeletal machinery and feed into cell differentiation pathways. Here we present a mechanical contour model based on line and surface tensions that predicts cellular force distributions from the shape and rigidity of the adhesive patterns. For cells constrained to adhesive islands, forces scale with island curvature and preferentially localize to corners. For cells adherent to discrete

sites, line tension is the primary force determinant. Forces increase with increasing distance between adhesion sites because surface tension effects result in steeper pulling directions. Substrate compliance counteracts the positive distance effect while the elastic nature of line tension enhances it. The model compares well to experimental observations suggesting that contour forces play an important role in establishing the basic force pattern that might be subsequently amplified by the generation of discrete internal structures such as stress fibers.

BP 17.7 Wed 17:15 P3

**Influence of Mn2+ and Mg2+ on the interaction between integrin $\alpha 7\beta 1$ and invasin studied by dynamic force spectroscopy** — •Agnieszka Ligezowska[1], Kristian Boye[2], Johannes Eble[3], Bernd Hoffmann[4], Beate Klösgen[2], and Rudolf Merkel[4] — [1]Department of Physics, Jagiellonian University, Cracow, Poland — [2]Memphys Center for Biomembrane Physics, University of Southern Denmark, DK-5230 Odense, Denmark — [3]Institut für Physiologische Chemie und Pathobiochemie, Westfälische Wilhelms-Universität Münster, D-48149 Münster, Germany — [4]Institut für Bio- und Nanosysteme, Forschungszentrum Jülich, D-52425 Jülich, Germany

The ligand binding function of integrins, a group of transmembrane proteins mediating cell-matrix adhesion in animals, is known to be influenced by divalent cations. We have applied the Biomembrane Force Probe technique to study this phenomenon for a soluble variant of integrin $\alpha 7\beta 1$ and one of its ligands, invasin 497, an outer membrane protein of Yersinia bacteria. In a dynamic force spectroscopy approach, we show that the binding affinity of $\alpha 7\beta 1$ is promoted by divalent manganese and magnesium ions and that these ions work to enforce the binding strength in a synergistic manner. Single bond events could be studied by successive addition of free invasin to the measurement buffer which reduced the number of available binding sites and thus diminished the likelihood of multiply bond formation. Combining force-induced bond dissociation with free ligand binding enabled simultaneous studies of Mn2+ and Mg2+ influence in both, equilibrium and non-equilibrium conditions.

BP 17.8 Wed 17:15 P3

**Biomembrane adhesion on micropatterned substrates: A tool for thermal fluctuation analysis** — •Cornelia Monzel[1], Susanne Fenz[1], Sabine Dieluweit[1], Kheya Sengupta[2], and Rudolf Merkel[1] — [1]Institute of Bio- and Nanosystems 4: Biomechanics, Research Centre Jülich, Germany — [2]CINAM/CNRS-UPR3118, Luminy, Marseille, France

Cell adhesion is a complex process involving a manifold of forces. Much is known about the specific binding between biomolecules which affect cell adhesion. However, contributions due to generic interactions or repulsive thermal fluctuations are as yet barely understood. Therefore, we developed a simplified model system which permits us to do quantitative analysis of membrane fluctuations. Here, cell adhesion was mimicked by a system consisting of giant unilamellar lipid vesicles, with the specific binding being mediated by the biotin-neutravidin complex. Micropatterns of adhesion-competent and repulsive areas were produced on glass surfaces by microcontact printing. This technique provided us with the means to confine the membrane in a controlled manner. The adhered vesicle exhibited areas of fluctuating and fixed membrane corresponding to the underlying pattern. From Dual-Wavelength Reflection Interference Contrast Microscopy (DW-RICM) analysis, we reconstructed the membrane height distribution and quantified the membrane fluctuations with nano-metric accuracy. We calculated the fluctuation spectrum and the effective potential in which the membrane fluctuates.

BP 17.9 Wed 17:15 P3

**Quantification of cell adhesion strength on self assembled monolayers with tuneable surface properties** — •Christof Christophis, Michael Grunze, and Axel Rosenhahn — Angewandte Physikalische Chemie, Universität Heidelberg, Im Neuenheimer Feld 253, 69120 Heidelberg

Besides selective receptor interactions, physico-chemical surface properties play an important role in adhesion, proliferation, survival and even differentiation of mammalian cells. Self assembled monolayers are a versatile tool to tune surface properties in a well defined manner and it has been found that cell behavior is directed even by such thin coatings. To obtain quantitative data for cell adhesion on self assembled monolayers we use time lapse microscopy in combination with microfluidically cultivated cells. Cell adhesion kinetics is determined by image analysis while cell adhesion strength is quantified by application of a well defined liquid flow. The microfluidic system is fabricated in polydimethylsiloxane (PDMS) and integrated in a reusable device where any surface of interest can be used. This experimental design in combination with a well developed preparation protocol allows adhesion strength characterization e.g. for fibroblast cells with high reproducibility and small error bars.We show results on the adhesion of rat embryonic fibroblasts to ethylene glycol terminated self assembled monolayers in dependence of ethylene glycol chain length and end group termination. Interfacial properties including wetting and hydration are thus manipulated in a controlled way and cell response is quantified.

BP 17.10 Wed 17:15 P3

**AFM as a chance for studying in situ protein adsorption and bacterial adhesion** — •Peter Loskill, Yvonne Schmitt, and Karin Jacobs — Saarland University, Experimental Physics, D-66041 Saarbruecken, Germany

The interaction of proteins and of microorganisms with biological or artificial surfaces is a key factor in disease pathogenesis. To reveal the interactions, we follow two pathways: One ansatz is to characterize protein adsorption on a fundamental level via AFM in non-contact mode imaging, another is to directly probe bacterial adhesion by AFM - force spectroscopy. For proteins like amylase we have probed the adsorption kinetics by ellipsometry. Surprisingly, the kinetics is not only depending on surface chemistry, but also on the sub-surface composition [1,2]. In situ AFM scans of protein adsorption reveal the spatial statistics of adsorption sites and allow for a characterization of the mobility of proteins on the surface and the role of protein-protein interactions. Characterizing bacteria/substrate interaction, we use staphylococcus aureus as a model system. S. aureus is known to build complex cell consortia consisting of multilayered organisms, forming a biofilm. Wall-bound and secreted proteins mediate attachment. Since the bacterial cell wall cannot be treated as a homogeneous surface, it is necessary to differentiate between local and global adhesion measurements. To investigate the global adhesion properties of a bacterium in a planktonic state we directly use them as AFM probes.

[1] A. Quinn et al., Europhysics Lett. 81 (2008) 56003
[2] M. Bellion et al., J. Phys.: Condens. Matter 20 (2008) 404226

BP 17.11 Wed 17:15 P3

**Cell Adhesion and Cell Detachment Forces on Micro-Nanopatterned Substrates** — •Janosch Deeg[1,2], Ilia Louban[1,2], Daniel Aydin[1,2], and Joachim Spatz[1,2] — [1]University of Heidelberg, Dept. of Biophysical Chemistry, Im Neuenheimer Feld 253, D-69120 Heidelberg — [2]Max-Planck-Institute for Metals Research, Dept. of New Materials & Biosystems, Heisenbergstr. 3, D-70569 Stuttgart

Au-nanopatterned substrates, produced by micellar block copolymer nanolithography, are used to make adhesion ligands of a cell be positioned like the quasi-hexagonal ordered Au-nanoparticles on the surface. By tuning the spacing of these biofunctionalized nanoparticles, one is able to control the distance between adjacent binding sites. Former experiments have shown that an interparticle distance of more than 73 nm strongly reduces cell spreading, cell detachment forces and the formation of adhesion clusters. Microstructuring of these patterns divides the surface into regions with and without Au-particles due to vary the global density, meaning in this case binding sites per area, not only by changing the distance between these sites, but by creating entire micrometer sized parts without particles next to nanostructured ones. This diploma thesis is mainly interested in how far the detachment force of adherent cells depends on the amount of available integrin binding sites per area in comparison to their distance. The cell detachment force is measured with an AFM by immobilizing the cell on the functionalized tipless cantilever and subsequently detaching it from the surface. We expect to gain a deeper understanding about the effect of integrin spacing and density on cell adhesion strength.

BP 17.12 Wed 17:15 P3

**Cell Motility in Microstructured 3D Topologies** — •Sofia Capito, Delphine Arcizet, Joachim Rädler, and Doris Heinrich — Lehrstuhl für Physik weicher Materie und Biophysik, Biophysics of Cell Dynamics, Fakultät für Physik, Center for NanoScience (CeNS), Ludwig-Maximilians-Universität München

Living cells sense mechanical and chemical properties of their environment and especially motile cells react to the surrounding 3D topographical conditions.

Whereas most of the current in vitro experiments are carried out on

a flat substrate, we investigate cells in 3D surface topologies with fluorescence microscopy techniques. We fabricate well-defined microstructured substrates, consisting of PDMS pillar arrays with varying properties, such as pillar distance, diameter, and density. We study the influence of the substrate topography on cell velocity, motion persistence, and branching of the cells, and aim at controlling and predicting cellular migration in this model 3D environment. The amoeba Dictyostelium discoideum (Dd) is used as a model organism, exhibiting similar motility to neutrophils.

First results indicate that the substrate topography significantly influences Dd cell motility. The calculated mean square displacement (MSD) of the cell center of mass reveals an overdiffusive cell migration behavior in the pillar field, as opposed to a pure random walk on a flat surface.

Further work will concentrate on identifying the intracellular signaling, which triggers cell reaction to 3D topography.

BP 17.13 Wed 17:15 P3

**The first passage problem for diffusion through a cylindrical pore with sticky walls** — •Nicholas Licata and Stephan Grill — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

We formulate a simple model to calculate first passage times for diffusion through a cylindrical pore with sticky walls. A particle diffusively explores the interior of the pore through a series of binding and unbinding events with the cylinder wall. Through a diagrammatic expansion we obtain first passage time statistics for the particle's exit from the pore. Connections between the model and nuclear transport are discussed.

BP 17.14 Wed 17:15 P3

**Protein diffusion in crowded and charged solutions: A light scattering and neutron spin echo study** — •Marcus Hennig[1,2], Felix Roosen-Runge[1,2], Fajun Zhang[1], Stefan Zorn[1], Maximilian Skoda[3], Robert M. J. Jacobs[4], Peter Fouquet[2], Tilo Seydel[2], and Frank Schreiber[1] — [1]Institut für Angewandte Physik, Universität Tübingen, Germany — [2]Institut Laue-Langevin, France — [3]ISIS, Didcot, UK — [4]Chemistry Research Laboratory, Oxford, UK

Globular proteins under physiological conditions occur in crowded solutions with a protein volume fraction attaining up to approximately 40%. A recent finding of reentrant condensation of proteins induced by polyvalent salts underlines the necessity to examine salt-induced charge effects in order to understand the biological function and dynamical behavior of solvated proteins.

We review different existing models to interpret protein diffusion data in "crowded" solutions and we also consider the effect of charges. We discuss these models in the context of a combined light scattering and neutron spin-echo study of the short-range and long-range nanosecond diffusion of the model globular protein bovine serum albumin (BSA) in aqueous solution as a function of the NaCl salt concentration. The interpretation of the data on the BSA model system is put in the context of existing studies on related systems and of the relevance of charges for protein diffusion and protein function under physiological conditions.

BP 17.15 Wed 17:15 P3

**Microscopic origins of anomalous diffusion - insights from studies on crowded solutions** — •Jedrzej Szymanski and Matthias Weiss — Deutsches Krebsforschungszentrum, Heidelberg, Germany

Subdiffusive motion of macromolecules has been observed in many crowded environments, ranging from polymer and protein solutions to intracellular fluids. A clear understanding of the microscopic origin of the subdiffusive motion, however, has been lacking. To address this point, we have used fluorescence correlation spectroscopy (FCS) to study the diffusion of tracer molecules in crowded solutions with varying composition. We combined this approach with model simulations on percolation-like motion and continuous time random walks (CTRWs). Aiming at discriminating these two fundamentally different processes that may underlie the observed anomalous diffusion in FCS, we compared the experimentally determined distributions of the anomaly degree and the apparent mobility with the simulation data. As a result, the experimental data for crowding-induced subdiffusion are most consistent with a percolation-like motion but deviate strongly from the predictions of a CTRW. Hence, subdiffusion in crowded media, e.g. in the cytoplasm of living cells, most likely arises due to a stochastic process with a Gaussian-like propagator.

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**Water diffusion through OmpF channels using molecular dynamics simulations** — •Mihai Tomozeiu, Soroosh Pezeshki, and Ulrich Kleinekathöfer — Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany

Outer membrane protein F (OmpF) is one of the most prevalent porins of Escherichia coli. The protein is the main channel for the translocation for small molecules between the interior of the bacteria and its surroundings. One of its main functions is to control the osmotic pressure between the two media. The water diffusion through the channel is studied using molecular dynamics simulations in equilibrium conditions. Temperatures used for the simulations range from a few degrees above the melting point of water up to 363 K. As an additional control parameter, a strong electric field was applied along the channel axis to check if at this level, the electric field has any measurable influence on the water permeation. Due to the charge distribution of the protein the applied voltage drop over the channel was limited to one volt so that membrane and protein are not yet damaged in the simulations.

BP 17.17 Wed 17:15 P3

**Theoretical description of endosome dynamics** — •Jonathan Edward Dawson[1], Lionel Foret[1,2], Claudio Collinet[3], Yannis Kalaidzidis[3], Lutz Brusch[4], Perla Zerial[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 Supérieure, Laboratoire de Physique Statistique, Paris, France — [3]Max Planck Institute of Molecular Cell Biology and Genetics, Dresden, Germany — [4]ZIH-Technical University Dresden,Germany

We present a theoretical study to describe the collective dynamics of a population of endosomes in a cell. Endosomes are vesicular structures that form networks that sort and transport cargo molecules internalized into the cell by endocytosis. Endosomes undergo fusion and fission thereby changing their size and cargo content. We develop a mean field theory that describes the time evolution of the distribution of endosomal markers or cargo in the network. We calculate these distributions using both analytical and numerical methods. Experimentally these distributions can be determined using fluorescence microscopy. The steady state distribution of total fluorescence intensity of the cargo molecules shows charasteristic and robust features. Our theory is able to quantitatively reproduce the shape of steady state distributions and their time dependence. We determine the kinetic parameters of the early endosomal network in HeLa cells and provide an explanation for observed power law distributions.

BP 17.18 Wed 17:15 P3

**Protein translocation across artifical membrane channels** — •Stefan Bommer and Patrick Huber — Technische Physik, Universität des Saarlandes, Saarbrücken

Protein translocation across biological membranes is a fundamental process in cell biology. Many qualitative and semi-quantitive aspects of the translocation process have been analyzed over the last 35 years. The bacterial plasma membrane, the membrane of the endoplasmic reticulum, the inner and outer membranes both of mitochondria and chloroplasts all contain protein translocons. They all have one structural feature in common: a narrow aqueous channel as central subunit.

To better understand the collective, physical mechanisms of protein transport across bio-membranes we performed rigorous experimental protein permeation experiments through artificial, tunable channels in solid-state membranes using folded and unfolded cytochrome c supported by Brownian-Dynamics-Simulations that mimic the experimental geometry.

BP 17.19 Wed 17:15 P3

**Vesicle Transport in Guided Neuronal Axons** — •Carina Pelzl[1,2], Guido Piontek[3], Jürgen Schlegel[3], Joachim Rädler[1,2], and Doris Heinrich[1,2] — [1]Department of Biophysics, Ludwig-Maximilians-Universität München — [2]Center of NanoScience (CeNS) — [3]Institut für Allgemeine Pathologie und Pathologische Anatomie der Technischen Universität München, Klinikum rechts der Isar

Cellular vesicle transport is crucial to many physiological and pathological events. Several neuronal diseases like Amyotrophic Lateral Sclerosis (ALS) and Alzheimer's are caused by disrupted transport along microtubules.

This work focuses on the retrograde transport of vesicles in PC12 cells and primary ALS neurons. These systems are interesting for their

geometrical simplicity, since the microtubules in an axon are almost parallel. In order to further reduce the possible parameters, we force the axons in a perfectly 1D geometry by guiding dendrite outgrowth along predefined nanostructures.

To analyze the vesicle motion within an axon, we use a recently developed algorithm [1], based on a time-resolved mean square displacement (MSD) analysis, to distinguish between active and passive phases with a high temporal resolution.

In this way we can compare naturally occuring 1D transport in living cells to theoretical models. Furthermore, we aim at investigating degeneracies in ALS neurons.

[1] Arcizet et al., Temporal Analysis of Active and Passive Transport in Living Cells, Phys.Rev.Let, in press

BP 17.20 Wed 17:15 P3

**Influence of a repulsive short-range interaction on the transport properties of a driven two-channel system** — •Anna Melbinger[1], Tobias Reichenbach[2], Thomas Franosch[1], and Erwin Frey[1] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC), Center for NanoScience (CeNS), Department of Physics Ludwig-Maximilians-Universität, München, Germany — [2]The Rockefeller University, New York, U.S.A.

We investigate the behavior of a two-channel driven diffusive system where particles on different lanes interact via a repulsive short-range interaction. This system is motivated by biological transport phenomena happening in each cell. The coupling incoperates the effect of large cargos attached to motor proteins which cause an obstruction stemming from the excluded volume. In addition, the model serves as a classical description for spin currents where particles with two internal states are driven through a lattice. Depending on the strength of coupling, the behavior of the system can be divided into three regimes of qualitatively different behavior. While the model can be mapped on a one-channel problem for small and for large potentials, a new and rich phase behavior emerges for an intermediate strength of coupling. In this regime, the transport properties of the system are influenced in a nontrivial way. We rationalize our observations in an analytic approach employing a one-site cluster approximation, and connect the current-density relation with the phase diagrams using the Extremal Current Principle. Our results are confirmed by stochastic simulations.

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**Rheology and Transport Processes in Living Cells** — •Jean Mahowald, Delphine Arcizet, Joachim Oskar Rädler, and Doris Heinrich — Biophysics of Cell Dynamics Group, Lehrstuhl für Physik weicher Materie and Center of NanoScience (CeNS), Fakultät für Physik, Ludwig-Maximilians-Universität München, D-80539 München, Germany

Transport processes play a major role for the viability of cells. Living cells need to continuously uptake nutrients, which are engulfed in lipidic vesicles by endocytosis, and transported towards intracellular compartments. Transport throughout the cell consists of successive phases of diffusion phenomena (Brownian motion, subdiffusion or enhanced diffusion) and active transport along the microtubules by molecular motors.

We investigate the rheology and transport processes in Dictyostelium discoideum cells by magnetic tweezers, which are an interesting model organism due to their cytoskeleton simplicity and the variety of mutant strains available. Super paramagnetic micrometer beads engulfed by the cells are subjected to force pulses of 5 seconds and up to 200 pN. The recorded tracer path is providing real-time information about the transport phenomena. Our home-made algorithm allows us to dissect the bead path into phases of pure diffusion and directed active motion.

We observe that the average duration of diffusive transport events is significantly lowered by the application of an external force. Detailed information about the role of the different cell components in the active processes is obtained by modifying cytoskeleton properties.

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**Characterisation of Staphylococcus aureus Wall Teichoic Acids and their functional components with Vibrational and Photoemission Spectroscopy in thin films** — •Florian Latteyer[1], Timo Birkenstock[2], Heiko Peisert[1], Andreas Peschel[2], and Thomas Chassé[1] — [1]University of Tübingen, Institute for Physical and Theoretical Chemistry, Auf der Morgenstelle 8, D-72076 Tübingen — [2]University of Tübingen, Medical Microbiology and Hygiene Department, Elfriede-Aulhorn-Str. 6, D-72076 Tübingen

Staphylococcus aureus plays in medical applications a key role. The biofilm formation on surfaces, especially on implants and catheters, is liable for infections in humans. It could be shown in the past that wall teichoic acids, as a part of the bacterial cell wall, are responsible for the initial biofilm formation and hence for the adsorption on surfaces. By genetical manipulation of S. aureus d-Alanine has been removed as part of the wall teichoic acid. After the elimination of d-Alanine no adsorption and biofilm formation on surfaces was monitored. D-alanine is therefore supposed to be as an adsorption anchor. In this work we present IR-, Raman and XPS spectra of wall teichoic acids measured on Si substrates. D-alanine has been identified with his zwitterionic structure in the wall teichoic acid and hence contribute a positive charge to the structure. Thin films of d-Alanine and Glycerolphosphat are prepared and compared with the wall teichoic acid spectra. Structural characteristics of both molecules are investigated and compared with the spectra of the wall teichoic acid. During the investigation of D-alanine with soft x-rays a decomposition was monitored.

BP 17.23 Wed 17:15 P3

**Simulating E.coli's Major Efflux Pump: The Extrusion Mechanism for Substrates** — •R. Schulz[1], A. Vargiu[2], P. Ruggerone[2], M. Schreiber[3], and U. Kleinekathöfer[1] — [1]Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany — [2]University of Cagliari, 09042 Monserrato (CA), Italy — [3]Technische Universität Chemnitz, 09107 Chemnitz, Germany

Bacteria, such as E. coli, use multidrug efflux pumps to export toxic substrates through their cell membranes. The RND transporter of the AcrAB-TolC efflux pump is able to export structurally and chemically different substrates. This is one reason of the increasing antibiotic resistance of bacteria. The energy is converted in the transmembrane domain and transduced towards the periplasmic part and used there to initiate a three-cyclic peristaltic pumping [1]. The effects of conformational changes on the extrusion of drugs, which have been located into one of the proposed binding pockets, are assessed using different computational methods like targeted molecular dynamics (TMD). The mechanism of pumping is investigated in greater detail than ever before [2]. Within TMD, a linear transition between two conformations is described. To investigate the effect of the conformational changes a feasible substrate, doxorubicin, has been placed into one of the binding pockets. Previously, the conformational changes of TolC which lead to an opening of the aperture have been investigated [3].

[1] M. Seeger et al., Current Drug Targets **9**, 729 (2008)
[2] G. Sennhauser et al., PLoS Biology **5**, 106 (2007)
[3] R. Schulz et al., Biophysical Journal (accepted)

BP 17.24 Wed 17:15 P3

**Phenotype Decision in *B. subtilis*: Low Number Fluctuations Enhanced by Non-linear Dynamics** — •Jan-Timm Kuhr[1,3], Madeleine Leisner[2,3], Joachim O. Rädler[3], Berenike Maier[2,3], and Erwin Frey[1,3] — [1]Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), LMU, Germany — [2]Institut für Allgemeine Zoologie und Genetik, Westfälische Wilhelms Universität, Germany — [3]Department für Physik, Ludwig-Maximilians-Universität München, Germany

Clonal populations of the bacterium *B. subtilis* exhibit a variety of phenotypes, depending on the environment. If starved 15-20% of all cells become "competent", gaining the ability to incorporate external DNA into their genome. Competent individuals can adapt quicker to stress conditions than the residual population. Whether to become competent or not is decided on the single cell level.

To elucidate switching to competence we performed single cell experiments and set up a theoretical model incorporating non-linear feedback dynamics and low number fluctuations. Identifying the master regulator protein comK and its corresponding mRNA as the main players, we can describe switching by an effective two-species system: switching is induced by fluctuations and subsequent relaxation to one of two stable fixed points. Deterministic switching, as encountered in mutant strains, is easily explained by disappearance of one fixed point.

Using well-motivated rate constants we quantitatively reproduce our experimental results and give an intuitive picture of stochastic single cell phenotype decision.

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**Understanding the effect of virus infection on cellular architecture** — •Julian Weichsel[1,3], Nikolas Herold[2], Maik Lehmann[2], Hans-Georg Kräusslich[2], and Ulrich S. Schwarz[1,3] — [1]Bioquant, Ruprecht-Karls-University of Heidelberg, Im Neuenheimer

Feld 267, 69120 Heidelberg, Germany — [2]Department of Virology, Universitätsklinikum Heidelberg, Im Neuenheimer Feld 324, 69120 Heidelberg, Germany — [3]University of Karlsruhe, Theoretical Biophysics Group, Kaiserstrasse 12, 76131 Karlsruhe, Germany

The filament networks of the cytoskeleton are responsible for a variety of essential cellular processes, including force generation, shape changes and intracellular transport by motor proteins. Therefore even subtle changes in the network architecture are potentially able to affect vital functions of the cell. This fact is exploited by different viruses in different ways. In order to quantify the effect of virus infection on cellular architecture, we have used image processing to compare cells treated with drugs or virus particles to their wildtype analogues. A large number of automated high-throughput fluorescence images have been processed and structure parameters of the actin cytoskeleton have been extracted. This procedure can also be used to parameterize theoretical models for the actin cytoskeleton. We have implemented a random fiber network which is characterized by fiber density and length. In computer simulations we find that small changes in the microscopic parameters can lead to dramatic effects for the transport and mechanical properties of the overall network.

BP 17.26 Wed 17:15 P3

**Mechanical properties of non-enveloped viruses** — •Bodo D Wilts[1], José L Carrascosa[2], Charles M Knobler[3], Iwan A T Schaap[1], and Christoph F Schmidt[1] — [1]3. Physikalisches Institut, Fakultät für Physik, Georg-August-Universität, 37077 Göttingen, Germany — [2]Centro Nacional de Biotecnología, CSIC, Campus de la Universidad Autónoma de Madrid, Spain — [3]Department of Chemistry and Biochemistry, University of California, Los Angeles, USA

Non-enveloped viruses protect their genome with a closed protein shell that forms a small and rigid nano-container. The simplest viruses self-assemble in an iscosahedral symmetry that can consist of as few as 60 identical protein subunits.

We have used atomic force microscopy to image, and to probe the mechanical properties of two different viruses by indentation experiments:

i) CCMV (Bromoviridae), a 28 nm diameter plant-infecting virus which has the special ability to change it size under certain conditions. CCMV self-assembles around anionic polymers (such as DNA) and is therefore interesting for nano-technological applications. We have set out to test the variability of the viral mechanics under different buffer conditions.

ii) $\phi$29 (Podoviridae), an elongated 42*52 nm bacteriophage with a tail that is used for insertion of the viral DNA into the host bacterium.

Furthermore, we have modeled the measured elastic response of the viruses by finite element methods to compare it with the empirical data.

BP 17.27 Wed 17:15 P3

**Optical properties of light-harvesting systems determined by molecular dynamics simulations** — •Carsten Olbrich[1], Michael Schreiber[2], and Ulrich Kleinekathöfer[1] — [1]Jacobs University Bremen, Campus Ring 1, 28759 Bremen, Germany — [2]Technische Universität Chemnitz, Fakultät für Naturwissenschaften, 09107 Chemnitz, Germany

Harvesting sun light to gain energy for life is initially done by light-harvesting antenna complexes containing chlorophyll and carotenoid molecules. Starting from the available crystal structure of the light-harvesting systems 2 (LH2) of purple bacterium, we applied all-atom classical molecular-dynamics (MD) simulations to the LH2 ring embedded in a membrane. Thus obtained thermal fluctuations of the nuclear positions provide the input for quantum chemical calculations. To obtain the energies of the $Q_y$ excited states of the single Bacteriochlorophyll (BChl) molecules, the semi-empirical ZINDO/CIS method is used to be able to analyze longer time series as was previously possible with the CIS method [1]. To include solvent effects to the excited state dynamics, the surrounding atoms of the BChls are treated as classical point charges in the QM calculations. Using the nuclear motion and the obtained energy differences between ground and $Q_y$ excited states with a time-dependent Hamiltonian, we are able to calculate optical properties of the analyzed system.

[1] A. Damjanović, I. Kosztin, U. Kleinekathöfer and K. Schulten, Phys. Rev. E **65**, 031919 (2002).

BP 17.28 Wed 17:15 P3

**Novel PSs for PDT: time-resolved detection of $^1O_2$-phosphorescence allows to determine the PS's localisation** — •Christoph Feest[1], Annegret Preuss[1], Beate Röder[1], and Ursula Simonis[2] — [1]Institut für Physik, Humboldt-Universität zu Berlin — [2]Department of Chemistry and Biochemistry, San Fransisco State University

Novel photosensitisers (PS) for Photodynamic Therapy (PDT) have been designed to specifically localize at mitochondria as they play a key role in programmed cell-death (apoptosis). The PSs are based on a Tetraphenylporphyrin core and have specific substitutions that modulate their physico-chemical properties and allow for specific intracellular localisation. The photophysical parameters of all compounds were determined in solution. Additionally, the PDT relevant singlet oxygen ($^1O_2$) generation was investigated in vitro using flash-photolysis and time resolved $^1O_2$ luminescence detection. A new setup was successfully used for evaluation of $^1O_2$ consumption during low-dose irradiation of cells. The intracellular localization was investigated *in vitro* using CLSM and FLIM technique. In the future, the combination of these optical methods for investigation of light-induced photosensitized processes may enable us to precisely determine the intracellular site of the photodynamic action.

BP 17.29 Wed 17:15 P3

**Theoretical simulation of Protein Kinase C (PKC) membrane translocation** — •Mike Bonny, Martin Peglow, Karsten Kruse, and Heiko Rieger — Universität des Saarlandes, Theoretische Physik

Conventional protein kinases C (cPKCs) play an essential role in signal transduction and in gene regulation. PKC$\alpha$, a member of the cPKC-family, translocates to the plasma membrane after activation via $Ca^{2+}$-ions in cytoplasm and creates local pattern, so-called local translocation events, with limited spatial spreads ($< 4\mu m$), comprising two groups of lifetimes; brief events ($400-1500$ms) and longlasting events($> 4$s).

In our work, we use a mean-field description as well as a three dimensional stochastic reaction-diffusion model. If on assumes interactions among the PKC$\alpha$ molecules in the membrane both models show similar results and are able to explain the two groups of lifetimes and the limited spatial spread of membrane-bound PKC$\alpha$ molecules.

BP 17.30 Wed 17:15 P3

**Inflammatory activation of macrophages by specific kinds of nanoparticles** — •Kristina Riehemann[1], Kathrin Hardes[1], Stefan Gerbes[2], and Mirko Bukowski[2] — [1]Center for Nanotechnolgy (CeNTech)/University of Münster, Heisenbergstraße 11, 48149 Münster — [2]INM - Leibniz Institute for New Materials, Campus D2 2, 66123 Saarbruecken, Germany

Nanoparticles (NP) find more and more their way to clinical applications. Unfortunately negative side effects may happen e.g. through the activation of the immune system through complementary activation or by generation of autoimmune diseases. Macrophages are involved in the innate immunity of the body. Their reaction on NP is important for further acceptance of the particles by the immune system. We investigated the interaction of NPs with primary cell cultures of macrophages derived from peripheral blood and different kinds of macrophage cell-lines. The synthesised NP we used where SiO2- Particles which differed in size, surface charge and *chemistry. Some particles where modified with polyethyleneglycole(PEG)-chains on their surface. We have shown that dependent on their surface structure NP can activate macrophage as shown by the secretion of inflammation mediators like IL1, iNOS and H2O2.

BP 17.31 Wed 17:15 P3

**Quantification of hematopoietic stem cell chemotaxis by microstructured channel systems and ELISA** — •Christina Leinweber[1], Rainer Saffrich[2], Wolfgang Wagner[2], Axel Rosenhahn[1], Anthony D. Ho[2], and Michael Grunze[1] — [1]Angewandte Physikalische Chemie, Universität Heidelberg, Germany — [2]Abteilung Innere Medizin V, Universitätsklinikum Heidelberg, Germany

The chemical communication between mesenchymal stromal cells (MSC) and hematopoietic stem cells (HSC), playing an important role in modern leukemia therapy, is not yet understood in detail. It is supposed that HSC migrate towards bone marrow, the so called homing process, guided by a concentration gradient of chemokines which are expressed by marrow cells. We investigate these chemotactic motions of HSC and malignant hematopoietic cell lines using microstructured chip systems. By varying the channel geometries defined concentration gradients are generated that allow to study single parameters, e.g. mi-

gration kinetics, thresholds, sensing sensitivity and swarm behaviour. The first migration experiments in microwells and microstructured systems are presented. Stem cell migration is most likely controlled via SDF-1 as chemokine involved in the signalling process. In order to quantify the role of SDF-1 in greater detail we additionally performed ELISA experiments to study the expression of SDF-1 by MSCs. The correlation of migration kinetics and bioanalytical data is an important part of understanding stem cell homing and will be also the basis for mathematical simulations later on.

BP 17.32 Wed 17:15 P3

**Controlling cell signalling with magnetic nanoparticles** — •Verena Schittler[1,2], Delphine Arcizet[1,2], Yoshihiko Katayama[3,2], Don Lamb[3,2], Stefan Zahler[4], Joachim Rädler[1,2], and Doris Heinrich[1,2] — [1]Department für Physik, Ludwig-Maximilians-Universität, Munich — [2]Center of NanoScience (CeNS) — [3]Department Chemie und Biochemie, Ludwig-Maximilians-Universität, Munich — [4]Department Pharmazie, Ludwig-Maximilians-Universität, Munich

In recent years, numerous biomedical applications for superparamagnetic iron oxide nanoparticles have emerged as targeted drug delivery and magnetic resonance imaging. Labelling these nanoparticles by lipophilic dyes to visualize the nanoparticles via fluorescence microscopy offers new potential for imaging.

Our research is focused on cell control by fluorescent magnetic nanoparticles in living cells and we study the impact of external magnetic forces on transport properties inside the cell and on cell migration as a whole. So far, we investigated the internalisation in Dictyostelium discoideum cells and in human mammary epithelial cells (HMEC) with and without force field. The fluorescence of the particles allows us to visualize this step. To analyse further the intracellular diffusion and active transport by molecular motors of the particles, we use a 3D-tracking setup which offers the possibility to follow the particles online also in the z-direction. We aim at a better understanding of cell migration by stimulating magnetically labelled cells with external magnetic forces and investigate exact mechanisms in magnetotactic response.

BP 17.33 Wed 17:15 P3

**Formation of Domains in Bacterial Flagella** — •Reinhard Vogel and Holger Stark — TU Berlin

Many types of bacteria swim by rotating a bundle of helical filaments also called flagella. Each filament is driven by a rotatory motor. When its sense of rotation is reversed, the flagellum leaves the bundle and undergoes a sequence of configurations characterised by their pitch, radius and helicity (polymorphism). Finally the flagellum assumes its original form and returns into the bundle.

In general, the helical shape of the bacterial flagellum can assume 11 different configurations depending, e.g., on mechanical loading, temperature, and chemical composition of the solution. In recent optical tweezer experiments, Darnton and Berg [1] pulled at the flagellum and induced transformations between different helical configurations but they also observed the simultaneous occurence of two configurations separated by a transition region. We investigate this domain formation by extending the linear elasticity theory of thin helical rods. We compare two types of elastic free energy with two stable helical states. One is a polynomial of degree four, the other a composition of two harmonic potentials. For realistic parameter values, we discuss the force extension curve for both free energies as a function of pulling speed and explore the influence of thermal noise. Especially for the second free energy, the force extension curve exhibits sharp transitions between two helical configurations reminiscent to experiments.

[1] N.C.Darnton H.C. Berg, Biophys. J. 92, 2230-2236 (2007)

BP 17.34 Wed 17:15 P3

**A hydrodynamic model of bacterial motors** — •Johannes Greber — Institut für Theoretische Physik WWU Münster

We consider a simple model for bacterial motors moving in two dimensional fluids. The objects are rigidly connected point vortices. We investigate in detail a case of propelling objects and perform an analysis of the collision process between two counterpropagating swimmers.

BP 17.35 Wed 17:15 P3

**4D-Tracking of pathogens by digital in-line holography** — •Sebastian Weisse[1], Matthias Heydt[1], Niko Heddergott[2], Markus Engstler[2], Michael Grunze[1], and Axel Rosenhahn[1] — [1]Angewandte Physikalische Chemie, Universität Heidelberg, Im Neuenheimer Feld 253, 69120 Heidelberg, Germany — [2]Institut für Mikrobiologie und Genetik, Technische Universität Darmstadt, Schnittspahnstraße 10, 64287 Darmstadt, Germany

Digital in-line holography is based on the original idea of D. Gabor's 'new microscopic principle'. An interference pattern of the so-called 'source wave' and the so-called 'object wave' is recorded. It contains three dimensional information of the object encoded in phase and amplitude. From a time series of such holograms, three dimensional trajectories of moving microorganisms can be retrieved.

We have built a portable, temperature-controllable digital in-line holographic microscope to study the motion patterns of the blood parasite *Trypanosoma brucei*, the causative agent of African sleeping sickness under physiological conditions. Its cork-screw-like self-propulsion in the bloodstream of a mammalian host is essential for the clearing of immunglobulins from the cell surface by hydrodynamic drag force. Motility is therefore pivotal to evade the host's immune system. So far, the locomotion of the parasite has only been studied in 2D. Using our system parasites were tracked at varying temperatures and viscosities with high spatial and temporal accuracy in 3D. The ability to track different cell strains under varying physical conditions will lead to a deeper understanding of their locomotion and thus their pathogenesis.

BP 17.36 Wed 17:15 P3

**Looking at cell motility in blood flow** — •Sravanti Uppaluri[1], Eric Stellamanns[1], Dagmar Steinhauser[1], Markus Engstler[2], and Thomas Pfohl[1] — [1]Max Planck Institute for Dynamics and Self Organization — [2]Darmstadt University of Technology

Entry of African trypanosomes, bloodstream parasites responsible for sleeping sickness, into the brain drastically diminishes disease prognosis. With an average swimming speed of 20$\mu$m/s, trypanosomes are able to penetrate the blood brain barrier despite significantly higher blood flow rates around the brain. This suggests that trypanosomes may have the ability to preferentially position themselves along the width of a blood vessel even at local flow velocities of up to 1mm/s. Using microfluidic techniques, we emulate blood vessels and thereby study the trypanosome's behaviour in Poiseuille flow. We examine the parasite's position distribution along the width of the 'blood vessel' in increasing flow rates. We demonstrate the trypanosomes' ability to make turns at relatively high flow velocities and penetrate confined gaps. Further, chemical gradients are established within the microfluidic device to investigate the chemotactic response of trypanosomes in flow. These experiments should lead to the development of a microfluidic assay to test for membrane crossing of motile cells.

BP 17.37 Wed 17:15 P3

**Survival of heterogenous populations in fluctuating environments** — •Florentine Mayer and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics and CeNS, Department of Physics, Ludwig-Maximilians-Universität München, Theresienstr. 37, 80333 München

Organisms must rapidly adapt to fluctuating environments to survive. In bacterial populations this is often achieved by phenotypic diversity, where bacteria can switch between different phenotypic states. Survival of the population can increase if each of these phenotypes is adapted to different environmental conditions. We investigate a spatial cellular automaton model for a bacterial biofilm, where each bacterium can take two different phenotypes, whose growth and death rates depend on the environmental conditions. Employing stochastic simulations we explore the spatio-temporal dynamics of the population and the ensuing stationary states. We find a transition between an active and an absorbing state, which is characterized by a probability distribution for extinction times with an anomalous long time tail. Further properties of the stationary states, such as the cluster size and cluster mass distribution are analyzed in detail.

BP 17.38 Wed 17:15 P3

**Competition between sexual and asexual reproduction: geographic parthenogenesis in structured resource space** — •Yixian Song[1], Irene Ament[3], Stefan Scheu[2], and Barbara Drossel[1] — [1]Institut für Festkörperphysik, Technische Universität Darmstadt, Deutschland — [2]Institut für Zoologie, Technische Universität Darmstadt, Deutschland — [3]Institute for Physical Chemistry, Johannes Gutenberg Universität, Mainz, Deutschland

In spite of the twofold cost of sex due to the production of males about 95% of species are sexual. Since the paradox of sexuality was pointed out by Darwin(1859), many explanations were suggested, e.g. Muller's ratchet(1964),Williams' Lottery model(1975), Bell's Tangled

Bank(1982), and related models. The recently introduced Scheu-Drossel model(2007) is based on the fundamental fact of limited and structured resources. In this model asexual species win over sexual species only when mortality rates are large, resources regrow fast, many different genotypes are allowed to coexist at the same place, or when resource diversity is small. By adding spatial structure into this model, we obtained a pattern resembling geographic parthenogenesis. "Geographic parthenogenesis"describes the fact that many species reproduce asexually at the boundaries of ranges, i.e. in northern regions, at high elevations, or the transition to deserts. By including a gradient in the rate of mortality or resource diversity in our computer simulations a stable distribution was obtained, with sexuals prevailing in regions of low mortality and high resource diversity, while asexuals prevailing at the boundary, where mortality is high or resource diversity low.

BP 17.39 Wed 17:15 P3

**Spatial desynchronization of glycolytic waves as revealed by Karhunen-Loève analysis** — Satenik Bagyan[1], Ronny Straube[2], •Marcus J.B. Hauser[1], and Thomas Mair[1] — [1]Otto-von-Guericke University, Institute of Experimental Physics, Biophysics Group, Universitätsplatz 2, 39106 Magdeburg, Germany — [2]Max-Planck-Institute for Dynamics of Complex Technical Systems, Department of Systems

Glycolysis is the central pathways of the energy metabolism in almost all living beings. The dynamics of glycolytic waves in a yeast extract have been investigated in an open spatial reactor. A transition from inwardly moving target patterns to outwardly moving spiral or circular shaped waves has been observed during the course of the experiments. These two phases are separated by a transition phase of more complex spatio-temporal dynamics. The dynamics of the patterns observed at these three intervals was analysed at different spatial scales by means of a Karhunen–Loeve (KL) decomposition. During the initial phase of the experiment the patterns are sufficiently described by the 2 dominant spatially invariant KL modes independently of the spatial scale. However, during the last stage of the experiment this spatial invariance is lost and at least 6 KL modes are required to account for the observed patterns at spatial scales larger than 3 mm while for smaller scales 2 KL modes are still sufficient. This indicates that in the course of the experiment the local glycolytic oscillators become desynchronized at spatial scales larger than 3 mm. We discuss possible reasons for the desynchronization of the glycolytic waves.

BP 17.40 Wed 17:15 P3

**Recording of glycolytic oscillations by electrical measurements at planar yeast cell/electrode-interfaces** — •Christian Warnke[1], Mathias Müller[1], Michael Charpentier[1], Hartmut Witte[1], Thomas Mair[2], Marcus J. B. Hauser[2], and Alois Krost[1] — [1]Otto-von-Guericke-Universität Magdeburg, Inst. Exp. Phys., Abt. Halbleiterepitaxie — [2]Otto-von-Guericke-Universität Magdeburg, Inst. Exp. Phys., Abt. Biophysik

One example for temporal macroscopic oscillations is glycolysis in yeast cells. For studying and recording the glycolytic oscillations the measurement of the NADH-fluorescence is used as a standard method. An alternative detection method of glycolytic oscillations of yeast cells and yeast extract is the use of impedance measurements by a planar yeast cell/blank electrode interface [1]. This interface was developed further by the isolation of the utilized Ti-Au-electrodes on glass substrates with $Ta_2O_5$ and $SiO_2$ layers. As an other alternative approach we used the source-drain-current of an AlGaN/GaN High Electron Mobility Transistor (HEMT) to detect electrical signals from yeast cells. We found oscillations of the electrical measurement parameters with the same temporal dynamics as the glycolytic ones. In order to identify the underlying processes in yeast cells responsible for the electrical signals, we analyzed theses oscillations at different electrical conductivities of the cell membranes.

[1] Reiher, A. et al.: Electrical stimulation of the energy metabolism in yeast cells using planar Ti-Au-Electrode interface, J. Bioenerg. Biomembr. 38 (2006), 143-148.

BP 17.41 Wed 17:15 P3

**Modeling of spatio-temporal dynamics in glycolysis with inhomogeneous periodic influx of substrate** — •Anastasia Lavrova[1], Eugene Postnikov[2], Thomas Mair[3], and Lutz Schimansky-Geier[1] — [1]Institute of Physics, Humboldt-University at Berlin, Berlin, Germany — [2]Department of Theoretical Physics, Kursk State University, Kursk, Russia — [3]Institute of Experimental Physics,Otto-von-Guericke-University Magdeburg, Germany

Spatio-temporal dynamics in glycolysis has been observed in the yeast extracts. It has been shown that waves can be induced by local perturbation on the activity of key enzyme, phosphofructokinase (PFK). [Bagyan et al, 2005]. Since the propagation dynamics and shape of traveling reaction-diffusion waves can contain information about the state of the system, it has been suggested that they can play an important role for biological information processing [Mair et al,2000].

In the present work we consider the Selkov model extended with diffusion terms which describes glycolytic phase waves observed in yeast extracts. It has been shown that the slightly non-uniform influx can provide a rich assortment of wave patterns such a traveling waves with a phase reversal, spatial-temporal beats, etc. With the introduction of non-stationary periodic influx it is possible to control the direction and the velocity of waves.

We discuss mechanisms of the waves propagation depending on the inhomogeneous periodic substrate influx.

BP 17.42 Wed 17:15 P3

**Network Topology of Physarum Polycephalum** — •Siddharth Deshpande, Christina Oettmeier, and Hans-Günther Döbereiner — Institut für Biophysik, Universität Bremen

The vein network of the unicellular slime mold Physarum Polycephalum shows a characteristic structure. We study vein creation and network formation. Mainly, we are interested in the distribution of nodes and links as a function of time and growth conditions. Network topology is observed from nanometer to millimeter length scales using Zeiss objectives with various magnifications. Further, we have developed a special macro-observation setup via a Canon digital camera.

BP 17.43 Wed 17:15 P3

**Stability analysis and maneuver of gene regulation networks** — •Joseph Zhou and Thilo Gross — Max Planck Institute for the Physics of Complex Systems, Noethnitzer Strasse 38, Dresden

A gene regulation network can be viewed as a complex system with the ability to switch back and forth between different gene expression patterns due to a variety of intrinsic or extrinsic perturbation signals. More and more evidences show that malfunctioning cells, such as cancer cells, are not just the accumulation of random delirious gene mutations. Instead, it has an erroneous re-access of proliferating embryonic programs as local attractors which are embedded in the gene regulation network. Could we induce these cells out of these attractors by systematically over-expressing a well-designed combination of genes? For example, the current research of Induced pluripotent stem cell (iPS) is more an art of cell biologists than a well-founded science. The protocol of the combination of different genes, the ratio of these components, the timing and duration of over-expressing these genes is totally dependent on the try-and-error and past know-hows. It is badly needed to perform a systematic gene regulation network study to give some sound guidance for the cell reprogramming. In this research, we emply a general dynamic system model for a cell reprogramming from adult pancreatic exocrine cells to beta-cells to address questions above.

BP 17.44 Wed 17:15 P3

**Dynamics of biological networks** — •Eva Gehrmann and Barbara Drossel — Institut fur Festkorperphysik, Technische Universitat Darmstadt

We study the dynamical and functional properties of selected biological networks. To this aim, we use the generalized method proposed by Steuer et al. 2006, which does not refer to an explicit set of differential equations, but is based on those quantities that determine the system's Jacobian J. By varying the parameters and the representation of the system, we identify which features are necessary for observing a certain dynamical behaviour.

BP 17.45 Wed 17:15 P3

**Extraction of deep sources from human EEG** — •Philipp Stern[1], Andreas Galka[2], and Jens Christian Claussen[3,1] — [1]Theor. Phys. & Astrophys., CAU Kiel — [2]Klinik f. Neurologie, Univ.-Klinikum S.-H. — [3]Neuro- und Bioinformatik, U zu Lübeck

Noninvasive brain imaging methods do not allow for a time resolution comparable with EEG or invasive measurements. As many dynamical collective phenomena in the brain are observed in the 0.5-50Hz frequency range, noninvasive methods based on EEG measurements are the standard for clinical and behavioral studies as anaesthesia mon-

itoring, sleep research, and diagnostics of neural disorders as tremor and epilepsy. In this study [1] we employ the Kalman filter method for the inverse problem of EEG measurement [2] to extract time series from localized deep brain regions as the thalamus. We discuss the abilities and limitations of the approach.

[1] Philipp Stern, Diploma thesis, CAU Kiel (2008)
[2] Andreas Galka, Okito Yamashita, Tohru Ozaki, Rolando Biscay, Pedro Valdes-Sosa, NeuroImage 23, 435 (2004)

BP 17.46 Wed 17:15 P3

**Clusters of sustained activity in sparse networks - the influence of topology on networks bursts** — •Olav Stetter[1], Anna Levina[1,2], and Theo Geisel[1,2] — [1]Max-Planck-Institute for Dynamics and Self-Organization, Göttingen, Germany — [2]BCCN Göttingen, Germany

Recent studies demonstrated the dependence of the avalanche size in neuronal networks on the number and strength of its connections. In different experimental settings a similar dependence of the averaged network activity on the size of an external stimulus has been shown.

Additionally, in these experiments the temporal order of activation is shown to be non-random: There exists a topological hierarchy with a number of neurons that are more likely to take part in an early phase of synchronized network activity ("burst"). Their activity can in fact be used to predict the following network behavior.

Here we ask what characterizes these burst initiation zones. We use a simplified, analytically tractable model and concentrate on relations between the average number of neurons that take part in an avalanche (related to measurements using fluorescent dye imaging) and parameters of the network. We observe that certain classes of topological structures can enable the model network to exhibit sustained activity which then leads to an activation of large parts of the network. The likelihood of such sustained activity depends on characteristics of the network such as the number and strength of connections and the dependence of connection probability on the distance (related to the degree-degree correlation).