BP 1: Dynamic Processes and Pattern Formation

Time: Monday 10:15–13:15 Location: HÜL 186

Invited Talk BP 1.1 Mon 10:15 HÜL 186

Taming a Heart Gone Wild — •Stefan Luther — Biomedical Physics Group, Max Planck Insitute for Dynamics and Self-Organization, Bunsenstrasse 10, 37073 Goettingen, Germany

Spatiotemporally chaotic wave dynamics underlie a variety of debilitating crises in extended excitable systems such as heart and brain. It is well known that control of spatiotemporal chaos requires multiple control sites. Creating such sites in living tissue, however, is a long-standing problem. Here we show that natural anatomical heterogeneities within cardiac tissue can provide a large and adjustable number of control sites for low-energy termination of malignant wave dynamics. This allows us to terminate ventricular fibrillation in canine cardiac tissue using small amplitude pulsed electric fields with up to two orders of magnitude lower energies than those used for defibrillating shocks. We quantify the physical mechanism underlying the creation of control sites using fully time resolved high-spatial resolution imaging of wave emission, high-resolution magnetic resonance imaging of cardiac structure, and cell culture experiments. Our method avoids the invasive implantation of multiple electrodes and, more importantly, has the potential to control the tissue where the chaotic state is most susceptible, i.e., at rotating wave cores. This approach promises to significantly enhance current technologies for the termination of life-threatening cardiac arrhythmias, a leading cause of mortality and morbidity in the industrialized world. Moreover, the method should be capable of regulating wave dynamics in other excitable systems, including the nervous system.

BP 1.2 Mon 10:45 HÜL 186

Simulation of wave propagation on moving heart geometry — •Stefan Fruhner[1,2], Steffen Bauer[2], Markus Bär[2], and Harald Engel[1] — [1]TU Berlin, Germany — [2]PTB Berlin, Germany

Cardiac contraction is controlled by electric waves propagating through the heart. Although realistic heart models often include detailed physiological knowledge about ionic dynamics of cardiac cells and accurately account for anatomical details like fibre orientation or heterogeneity of heart tissue, mechanical deformations of the heart during contraction usually is neglected. However, static heart models fail to describe the feedback between propagating waves of electric activity and cardiac contraction which might be essential for understanding the mechanism of cardiac arrhythmias like tachycardia and fibrillation. Based on magneto-resonance images two-dimensional finite-element meshes have been generated to simulate waves of electric activity propagating in a beating human heart. The approach offers the opportunity to calculate the mechanical stresses during cardiac contraction from experimental data without using detailed models on calcium dynamics and stress-activated channels in cardiac myocytes.

BP 1.3 Mon 11:00 HÜL 186

Pattern formation in myxobacteria driven by adventurous motility and cell shape — Fernando Peruani[1,2,3], Jörn Starruss[3], Vladimir Jakovljevic[4], Lotte Sogaard-Andersen[4], •Markus Bär[2], and Andreas Deutsch[3] — [1]ICS Paris, France — [2]Physikalisch-Technische Bundesanstalt, Berlin — [3]ZIH, TU Dresden, Dresden — [4]MPI for Terrestrial Microbiology, Marburg

Bacteria and other microorganisms exhibit a transition to multicellularity which starts with the onset of clustering. We study the combined effects of active, adventurous motion and anisotropic cell shape in assemblies of a mutant strain of myxobacteria that exhibit neither social motility nor so-called C-signalling. We observe a transition to clustering and collective motion, that is presumably caused by simple physical volume-exclusion interactions only. Our results show that in gliding bacteria, the combination of anisotropic cell shape and active motion, leads to an primitive effective alignment mechanism. The transition to clustering is predicted by a mathematical model and verified by comparison of cluster-size statistics predicted by the model with corresponding statistics taken from experimental data.

BP 1.4 Mon 11:15 HÜL 186

Generalized analysis of oscillatory systems in cell biology — •Martin Zumsande and Thilo Gross — Max-Planck-Institut für Physik komplexer Systeme, Nöthnitzer Straße 38, 01187 Dresden

We present a generalized approach for the modeling and analysis of oscillatory systems in cell biology. The advantage of this approach is that it does not require detailed knowledge of the functional form of rate laws, which is often not available. Instead, we investigate the system by parameterizing the Jacobian matrices of all steady states that are compatible with a given model structure. We then analyse the bifurcation landscape of the models via statistical sampling methods. This reveals Hopf bifurcations leading to oscillatory dynamics. By computing the first Lyapunov coefficient from a higher order expansion of the dynamics around the steady states we can distinguish between supercritical and subcritical Hopf bifurcations. The latter can lead to a catastrophic loss of stability, while in the former case, the loss of stability is a continuous, and hence reversible, transition. To illustrate our method we show results for small, toy model oscillators and a more complex model of a mammalian circadian oscillator.

15 min. break

BP 1.5 Mon 11:45 HÜL 186

Anti-spiral waves in glycolysis: How molecular enzyme properties determine the resulting spatio-temporal patterns — •Ronny Straube[1] and Ernesto M. Nicola[2] — [1]MPI for Dynamics of Complex Technical Systems, Sandtorstr. 1, 39106 Magdeburg, Germany — [2]MPI for Physics of Complex Systems, Noethnitzer Str. 38, 01187 Dresden, Germany

Spiral waves are probably the most common structure arising in pattern forming systems. Much less common are so called anti-spirals where, in contrast to "normal" spirals, the wave fronts propagate inwardly, i.e. towards the spiral core. Since their first discovery in chemical model systems [1,2] anti-spirals have now been generated in glycolysis using an extract of yeast cells (unpublished results), which represents a biological model system for the energy metabolism. Here, we explore theoretically the conditions for the occurrence of anti-spirals in two well-known glycolytic model systems: The Goldbeter model and the Selkov model. Interestingly, anti-spirals can only emerge in the Goldbeter model provided that the enzyme cooperativity, as measured by the number of enzyme subunits, is sufficiently large. This is in agreement with the observation that under physiological conditions the glycolytic enzyme phosphofructokinase is predominantly found in a tetrameric or octameric conformation.

[1] V. K. Vanag, I. R. Epstein. Science **294**, 835-837 (2001).
[2] X. Shao et.al. Phys. Rev. Lett. **100**, 198304 (2008).

BP 1.6 Mon 12:00 HÜL 186

Mechanically driven reaction-diffusion model for Hydra axis-definition — Jordi Soriano[1], •Sten Rüdiger[2], and Albrecht Ott[3] — [1]Universitat de Barcelona, Spain — [2]Humboldt-Universität zu Berlin, Germany — [3]Universität des Saarlandes, Saarbrücken, Germany

We have studied the relation between morphogenetic processes and mechanical properties during regeneration of the freshwater polyp Hydra. It has been known that the axis-defining step (symmetry-breaking) of regeneration requires mechanical inflation-collapse oscillations of the initial cell ball. We found evidence that axis definition is retarded if these oscillations are slowed down mechanically. We show that a reaction-diffusion mechanism provides a suitable scenario to describe the Hydra symmetry breaking. We employ a model in which the swelling of the initial Hydra cell ball induces changes in the diffusivity rates of activator and inhibitor. The mechanical stress provided by the oscillations drives the system to the Turing unstable regime. Once the organizer is constituted and a chemical gradient is established, the organizer locks and maintains the axis. Analytical considerations of the model show that the symmetry breaking time decreases with increasing swelling rate with the same behavior observed experimentally.

BP 1.7 Mon 12:15 HÜL 186

A Reaction-Diffusion System to Model Symmetry Breaking in C. elegans — •Philipp Khuc Trong[1,2,3], Nathan W. Goehring[2], Ernesto M. Nicola[1], and Stephan W. 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 — [3]University of Technology Kaiserslautern, Kaiserslautern, Germany

Prior to the first unequal cell division in the *Caenorhabditis elegans* embryo the PAR proteins become distributed asymmetrically in distinct anterior and posterior domains. Here we present a two-variable, mass conserved reaction-diffusion system in which PAR segregation can be triggered either convectively by cortical flows or spontaneously by random perturbations. We show that the spontaneous symmetry breaking is induced by a mechanism similar to a Turing instability. However, in our model the wavelength of the fastest growing spatial pattern is always equal to the system size. We explore the robustness of this mechanism as a function of the reaction rates and furthermore consider the volume differences between cell cortex and cytoplasm.

BP 1.8 Mon 12:30 HÜL 186

Dynamics of Blood Disorders — •Arne Traulsen[1], Jorge M. Pacheco[2], and David Dingli[3] — [1]Max-Planck-Institute for Evolutionary Biology, 24306 Plön, Germany — [2]App. Theor. Phys.-Group & Centro de Física Teórica e Computacional, Departamento de Física da Faculdade de Ciências, Complexo Interdisciplinar da Universidade de Lisboa, P-1649-003 Lisboa Codex, Portugal — [3]Division of Hematology, Mayo Clinic College of Medicine, Rochester, MN 55905, USA

Blood formation is characterized by a hierarchical architecture, with a small number of stem cells at the highest level. These cells differentiate more and more until they form the huge number of blood cells in the circulating blood. Based on a simple mathematical model for this hierarchy [1], we address the dynamics of different blood disorders. The leads to analytical estimates of the survival time of mutations in the system [2,3]. For chronic myeloid leukemia, the framework allows to describe the origin, development, response to therapy, and relapse after termination of therapy [4]. The resulting dynamics consistent with the available clinical data.

[1] D. Dingli, A. Traulsen, and J.M. Pacheco,PLoS One 2, 345 (2007)
[2] D. Dingli, J.M. Pacheco, and A. Traulsen, PRE 77, 021915 (2008)
[3] A. Traulsen J.M. Pacheco, and D. Dingli, Stem Cells 25, 3081 (2007)
[4] D. Dingli, A. Traulsen, and J.M. Pacheco, Clinical Leukemia 2, 133 (2008)

BP 1.9 Mon 12:45 HÜL 186

Spatiotemporal control of the energy metabolism in a thin layer of yeast cells by oxygen gradients — •Christian Warnke[1], Thomas Mair[2], Mathias Müller[1], Hartmut Witte[1], 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

The energy metabolism of cells can work both in absence (anaerobic) and in presence (aerobic) of oxygen. Specially, the anaerobic energy metabolism is represented by glycolysis, a pathway that is characterized by oscillatory behavior. Accordingly, spatiotemporal patterns, resulting from reaction-diffusion coupling, can be observed as well. We present an experimental method to produce spatiotemporal gradients of oxygen in planar yeast cell / Au electrode - interfaces that exhibit glycolytic oscillations. This planar interface allowed a stimulation by electrical pulses of energy metabolism by electrolytic reactions between the blank Au-metal and the electrolytic solution creating oxygen concentration close of the electrodes. The local oxygen pulses are aimed to perturb glycolytic oscillations by a short activation of the aerobic energy metabolism. Additionally, the studies were conducted at different temperatures using a Peltier element connected with the electrode-yeast-interface. We investigated the effect of these local perturbations on the temporal and spatiotemporal dynamics of glycolysis in yeast cells.

BP 1.10 Mon 13:00 HÜL 186

Entrainment in nonlinear oscillator model of insect flight — •Elena Y. Shchekinova[1], Jan Bartussek[2], and Martin Zapotocky[3] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Institute of Robotics and Intelligent Systems, ETH Zurich, Zurich, Switzerland — [3]Institute of Physiology, Academy of Science of the Czech Republic, Prague, Czech Republic

In the recent insect flight control experiments the wingbeat frequency transitions and short–time entrainment of the wingbeat cycle to the external stimulus was observed during tethered mechanically stimulated flight. Such an alternation of wing kinematics behavior is achievable due to the changes in the oscillatory combinatorial activity of the flight power and control muscles during flight.

We provide a minimal deterministic description of a synchronous activity of insect flight power and steering muscles. The oscillatory dynamics is modeled by a chain of coupled nonlinear oscillators in the regimes close to the dynamical instability threshold. By introducing small periodic parametric modulation in the model frequency transitions and entrainment to the external driving frequency is achieved. Our results aim to elicit entrainment and frequency transitions in wingbeat regimes observed during mechanically stimulated flight experiment.