BP 20: Statistical Physics in Biological Systems II (joint with DY)

Time: Wednesday 15:00–17:30 Location: H43

Topical Talk BP 20.1 Wed 15:00 H43

Challenges of Neurophysics — •Theo Geisel — Max Planck Institute for Dynamics and Self-Organization & Bernstein Center for Computational Neuroscience, Universität Göttingen

As you are reading these lines, millions of neurons are activated in your brain and communicate by sending short pulses to each other. It is a major aim of neurophysics to understand the collective dynamics of large biological neural networks and to determine how they carry out complex computations. Recent progress of experimental techniques allows monitoring the activity of large numbers of cells in parallel and with single cell resolution even in freely moving animals. These techniques together with targeted optogenetic stimulation promise to considerably advance our insight into the function of collective neuronal dynamics in the near future.

On the other hand, these networks exhibit features that let them elude standard theoretical treatment: E.g. the units of the network interact asymmetrically and at discrete times only, i.e. not continuously as in conventional many-body theory in physics. There are significant interaction delays, which formally make the systems infinite-dimensional. Complex connectivities give rise to novel multi-operator problems, for which new methods based on graph theory are devised to reach rigorous analytic results. The talk reviews challenges and recent progress in characterizing the dynamics and function of these networks.

BP 20.2 Wed 15:30 H43

Retinal light collectors enhance underwater vision — •Moritz Kreysing[1], Kristian Franze[2], Mike Francke[3], Andreas Reichenbach[3], and Jochen Guck[4] — [1]Systems Biophysics, Department of Physics, LMU München, Germany — [2]Department of Physiology, Development and Neuroscience, Cambridge University, UK — [3]Paul Flechsig Institute, University of Leipzig, Germany — [4]Biotechnology Center, TU Dresden, Germany

Vision at low light intensities relies on photoreceptors being able to detect individual photons. As an accepted rule, the light sensitive portions of vertebrate rods and cones, namely outer segments, increase in volume the darker the animals' habitat gets, in order to enhance the probability to capture incident photons. Consequently, the biggest outer segments are found in fish living in the deep sea. A peculiar exception to this rule are the eyes of some deep sea fish, as well as fish living in highly turbid rivers. In their retinas relatively short outer segments are bundled into spatially isolated groups, clearly not meant to maximize the probability of photon absorption. Based on a detailed morphological and optical study of multilayer light-collectors surrounding these segments [1], we argue that under extreme conditions in which quantum noise, i.e. the rate of spontaneous photo-pigment activation, becomes comparable to the rate of photon arrival, visual sensitivity cannot be achieved by large outer segments anymore. Instead the retinal focusing of light on very small receptors is the only way to lower the visual threshold further, or to see at near IR wavelengths. Reference: 1. M. Kreysing et al., Science 336(6089):1700-1703 (2012).

BP 20.3 Wed 15:45 H43

Monte Carlo simulation of the patterns of histone acetylation in response to MS-275 — •Davoud Pouladsaz[1] and Azadeh Ebrahimi[2] — [1]Department of Biological Physics, Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]Department of Neuropathology, Faculty of Medicine, University of Tübingen, Tübingen, Germany

Abnormal activities of histone decaetylases (HDACs) are considered to be associated with various neurological disorders, from oncogenesis, to neurodegenerative and psychiatric disorders. In this scheme, HDACs are potential targets for therapeutic development. HDAC inhibition has been reported in several studies to improve cognitive function and increase neural longevity. A novel HDAC inhibitor is MS-275, a benzamide derivative with in vivo antitumor activity and selectivity against HDAC1 and HDAC3. We perform computer simulations based on Monte Carlo method in order to describe the patterns of histone acetylation in the brain in response to MS-275. According to previous experimental results, MS-275 is a potent brain region-selective HDAC inhibitor. We theoretically produce similar acetylation profiles associated with the measurements in different regions of the brain, and calculate the changes in the acetylation by means of stochastic processes representing the inhibition of HDACs. The theoretical results show significant correlation to experimental measurements.

BP 20.4 Wed 16:00 H43

NAD(P)H Dynamics in Yeast Populations — •André Weber[1,2], Yury Prokazov[2], Werner Zuschratter[2], and Marcus J B Hauser[1] — [1]Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Germany — [2]Leibniz-Institut für Neurobiologie Magdeburg, Germany

NAD(P)H is the most important electron carrier in living cells and therefore it plays a key-role in numerous cellular processes. It is directly involved in glycolysis and Krebs cycle and its autofluorescence acts as an indicator for metabolic dynamics and enzyme activity in cells. The amount of NAD(P)H is reflected by its emitted light intensity. Furthermore, it is possible to discriminate between free and protein-bound NAD(P)H through fluorescence lifetimes. Using single photon counting fluorescence microscopy, we study glycolytic oscillations and metabolic changes in yeast cell populations via NAD(P)H imaging.

Yeast cells show synchronised glycolytic oscillations for high population densities which can be detected as global oscillations. These global oscillations become quiescent, when the population density drops below a critical value. Our results show that individual cells remain oscillatory even at very low cell densities (e.g. 1×10^5 cells/ml). The transition from global oscillations to a quiescent population signal is caused by the desynchronisation of the oscillations of individual cells. This is characteristic for a Kuramoto transition to incoherence. Spatially resolved measurements at low cell densities uncover that even cells that adhere to their neighbours oscillate with their own, independent frequencies and phases.

BP 20.5 Wed 16:15 H43

Description of polarity reorientation in the wing of the fruit fly by liquid crystal hydrodynamics — •Matthias Merkel[1], Andreas Sagenr[2], Raphael Etournay[2], Suzanne Eaton[2], and Frank Jülicher[1] — [1]Max-Planck-Institut für Physik komplexer Systeme, Dresden, Germany — [2]Max Planck Institute for Molecular Cell Biology and Genetics, Dresden, Germany

Epithelia are two-dimensional sheets of cells, which often exhibit large-scale patterns of planar cell polarity (PCP) in the tissue plane. Within a single cell, PCP is reflected in an anisotropic distribution of a class of proteins, called PCP proteins. We study PCP in the wing epithelium of the fruit fly. During development of the fly, two processes are observed: cell polarity reorients on large scales and a complex flow field reshapes the wing. This flow field includes a stereotypical pattern of tissue shear. We quantify polarity patterns in wild type and mutant wings. To interpret these patterns, we discuss a simple hydrodynamic model for polarity reorientation from liquid crystals theory. Our model consists of local polarity interactions and a coupling of polarity to tissue shear and tissue rotation. We find, that we can fit stationary states of our hydrodynamic description to the polarity patterns of the adult wings. These fits suggest that the sign of the coupling of polarity to tissue shear depends on the local expression of a PCP protein. We underpin our findings by numerical solutions of the polarity dynamics.

BP 20.6 Wed 16:30 H43

Optimization of shape for cargo transport with bead-spring microswimmers — •Jayant Pande and Ana-Sunčana Smith — Cluster of Excellence: EAM, and Institute for Theoretical Physics, Friedrich Alexander University Erlangen-Nürnberg, Germany

Microswimmers are entities that are capable of swimming in fluids at very low Reynolds numbers. A simple model of a microswimmer was introduced by Najafi and Golestanian, and consists of three spheres connected in series by two arms. This model could be used as a basis for constructing cargo-carrying micromachines, with the cargo making up the spheres in the swimmer. To determine whether other shapes for the bodies lead to more efficient swimming, we augment this model by replacing the spheres by general ellipsoids of revolution and including springs between these ellipsoids. The velocities of such three-ellipsoid swimmers acting under the influence of sinusoidal driving forces are calculated, assuming that either the deformations of the arms or the

driving forces are known. Comparing the velocities of different swimmers for a given cargo volume leads to a determination of the optimum body shapes and mechanism of propagation. We observe that a rich behaviour for the velocity curve is obtained, depending on the relative magnitudes of the spring constant and the fluid viscosity. The theoretical calculations are supported by simulations using a framework combining "waLBerla", a lattice-Boltzmann method based fluid solver, and "pe", a rigid body physics engine. The simulation results are found to agree well with the calculated values.

BP 20.7 Wed 16:45 H43

On the collective motion of Chlamidomonas cells — •Johannes Greber[1], Salima Rafai[2], Philippe Peyla[2], and Walter Zimmermann[1] — [1]Universität Bayreuth, D-95447 Bayreuth, Germany — [2]Universite Joseph Fourier, F-38402 Grenoble, France

Swimming Chlamydomonas cells have a n eyespot registrating light comming from a light source far away enabling the cell to orient its direction of motion towards the light. This motion is called phototaxis.

During the propelling process, each cell generates a flow field with an atracting part in the direction of motion and a repelling part perpendicular to this direction. Due to this flow field a stable collectiv motion of a cloud of cells is impossible as long as no direction of motion is prefered by the cells.

We present experimental results and a theoretical analysis based on a model called "Puller" on the collectiv motion of Chlamydomonas cells.

BP 20.8 Wed 17:00 H43

Elastic coupling effects in cooperative transport by molecular motors — •Florian Berger, Corina Keller, Stefan Klumpp, and Reinhard Lipowsky — Max Planck Institute of Colloids and Interfaces, Theory & Biosystems, 14424 Potsdam, Germany

Intracellular transport of cargos is achieved by the cooperative action of molecular motors, which pull the cargo along cytoskeletal filaments. To study this mechanism systematically in vitro, engineered constructs coupling a defined number of molecular motors have recently been introduced. These motors are elastically coupled via their common cargo, which may influence the motors' velocity and/or enhances their unbinding from the filament. Starting from the single molecule properties, we introduce a theoretical framework for cooperative transport which is consistent with recent experiments and provides novel testable predictions about the behavior of elastically coupled kinesin, dynein and myosin motors. Such an approach relates the single motor properties directly to the cooperative dynamics. As an example, we show that the overall cargo run length can either increase or decrease as a function of the single motor velocity depending on the single motor unbinding mechanism.

BP 20.9 Wed 17:15 H43

Teams of molecular spiders: Cooperative effects enhance the transport properties — •Matthias Rank, Louis Reese, and Erwin Frey — Arnold Sommerfeld Center for Theoretical Physics (ASC) and Center for NanoScience (CeNS), Department of Physics, Ludwig-Maximilians-Universität München

Molecular spiders are synthetic molecular motors based on DNA nanotechnology. While natural molecular motors have evolved towards very high efficiency, it remains a major challenge to develop efficient designs for man-made molecular motors. Inspired by biological motor proteins like kinesin and myosin, molecular spiders comprise a body and several legs. The legs walk on a lattice that is coated with substrate which can be cleaved catalytically. We propose a novel molecular spider design in which n spiders form a team. Our theoretical considerations show that coupling several spiders together alters the dynamics of the resulting team significantly. Although spiders operate at a scale where diffusion is dominant, spider teams can be tuned to behave nearly ballistic, which results in fast and predictable motion. Based on the separation of time scales of substrate and product dwell times, we develop a theory which utilises equivalence classes to coarse-grain the microstate space. In addition, we calculate diffusion coefficients of the spider teams, employing a mapping of an n-spider team on an n-dimensional random walker on a confined lattice. We validate these results with Monte Carlo simulations and predict optimal parameters of the molecular spider team architecture which makes their motion most directed and maximally predictable.