BP 1: Statistical Physics in Biological Systems I (joint DY, BP)

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

Invited Talk BP 1.1 Mon 10:15 ZEU 250

High throughput microscopy for systems biology: from genome-wide profiling to the analysis of protein complexes — •Jan Ellenberg — EMBL, Heidelberg, Germany

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

BP 1.2 Mon 10:45 ZEU 250

The flow field of an individual bacterium and its implications for cell-cell and cell-surface interactions — Knut Drescher[1], •Jörn Dunkel[1], Luis Cisneros[2], Sujoy Ganguly[1], and Raymond Goldstein[1] — [1]DAMTP, University of Cambridge, Wilberforce Road, Cambridge CB3 0WA, UK — [2]Department of Physics, University of Arizona, 1118 E 4th St, Tucson, AZ 85721, USA

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

BP 1.3 Mon 11:00 ZEU 250

The energy-speed-accuracy tradeoff in sensory adaptation — Ganhui Lan[1], •Pablo Sartori[2], Silke Neumann[3], Viktor Sourjik[3], and Yuhai Tu[1] — [1]IBM T. J. Watson Research Center, Yorktown Heights, NY 10598, USA — [2]Max Planck Institute for the Physics of Complex Systems, Dresden 01187, Germany — [3]Zentrum fur Molekulare Biologie der Universitat Heidelberg, Heidelberg, Germany

Adaptation is a fundamental function of living systems. The benefits of adaptation in sensory systems are well known, but its costs remain poorly understood. By analyzing a stochastic model of the generic feedback circuit responsible for sensory adaptation, we show that adaptation processes are inherently dissipative and continuous energy consumption is required to stabilize the adapted state. We derive a universal relation among energy dissipation rate, adaptation speed, and the maximum adaptation accuracy from our model. We demonstrate how this general energy-speed-accuracy (ESA) relation applies to the E. coli chemosensory system, where hydrolysis of the S-adenosylmethionine (SAM) molecules drives the near-perfect adaptation of the system and maintains its high sensitivity in a wide range of backgrounds. We identify the key requirements for an adaptive network to achieve its maximum accuracy with a given energy budget. These requirements are met in the E. coli chemotaxis pathway, making it highly efficient. Moreover, direct measurements confirm that adaptation slows down as cells gradually de-energize in medium without nutrients.

BP 1.4 Mon 11:15 ZEU 250

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

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

15 min. break

BP 1.5 Mon 11:45 ZEU 250

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

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

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

BP 1.6 Mon 12:00 ZEU 250

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

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

interacting drug pair, conflicts are resolved by linearly interpolating the two single drug responses, while for the antagonistic drug pair, the drug that has the stronger impact on growth dominates the transcriptional response. Importantly, for a given drug pair, the same strategy of conflict resolution is used for almost all genes. These results provide a recipe for predicting gene expression responses to drug combinations, which may lead to a more rational design of combination treatments.

BP 1.7 Mon 12:15 ZEU 250

Modelling the dynamics of micro-swimmers — •Eva Baresel and Rudolf Friedrich — Insitute for Theoretical Physics, University of Münster, Wilhelm-Klemm-Str. 9, D-48149 Münster

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

BP 1.8 Mon 12:30 ZEU 250

Onset of Collective Motion due to Escape and Pursuit — •Pawel Romanczuk[1], Vishwesha Guttal[2], Lutz Schimansky-Geier[1], and Iain D. Couzin[2] — [1]Department of Physics, Humboldt Universität zu Berlin, Germany — [2]Department of Ecology and Evolutionary Biology, Princeton University, USA

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

[1] S. J. Simpson *et. al.*, Proc. Natl. Acad. Sci. USA, 103, 4152 (2006)

[2] P. Romanczuk *et. al.*, Phys. Rev. Lett., 102, 010602 (2009)

[3] S. Bazazi *et. al.*, Proc. Roy. Soc. B, doi 10.1098/rspb.2010.1447

BP 1.9 Mon 12:45 ZEU 250

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

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

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