DY 50: Statistical Physics of Biological Systems I (Joint Session BP/DY)

Time: Thursday 15:00–17:30 Location: ZEU 250

DY 50.1 Thu 15:00 ZEU 250

Inference of chemotactic strategies of *E. coli* and *Pseudonomas putida* using Kramers-Moyal coefficients — •Maximilian Seyrich[1], Oliver Pohl[1], Marius Hintsche[2], Zahra Alirezaei[2], Carsten Beta[2], and Holger Stark[1] — [1]Institut für Theoretische Physik, Technische Universität Berlin, 10623 Berlin, Germany — [2]Institut für Physik und Astronomie, Universität Potsdam, 14476 Potsdam, Germany

Bacteria like *E. coli* and *Pseudomonas putida* move with alternating runs and tumbles that occur with a mean tumble rate. In the presence of gradients of a chemoattractant, they both perform chemotaxis. We set up a random-walk model that describes runs and tumbles as a stochastic process of the bacterium's swimming direction and speed. The dynamics include rotational Brownian motion and shot noise for the swimming direction to initiate tumbling, while thermal and shot noise together with a mean reverting drift-term analogously to an Ornstein-Uhlenbeck process governs the speed dynamics. In order to infer the parameters of our model, generalized Kramers-Moyal coefficients are calculated for our model and matched to the ones determined from experimental trajectories. In contrast to common tumbling recognition algorithms no free parameters need to be preset. We first show that our method identifies the classical bacterial chemotaxis strategy of *E. coli* and *P. putida*, i.e., the tumble rate decreases along the chemical gradient. We also find evidence that a subpopulation of *E. coli* reduces its mean tumble angle when swimming in this direction.

DY 50.2 Thu 15:15 ZEU 250

Genotypic complexity of Fisher's geometric model — Sungmin Hwang[1], Su-Chan Park[2], and •Joachim Krug[1] — [1]Institute for Theoretical Physics, University of Cologne, Cologne, Germany — [2]Department of Physics, The Catholic University of Korea, Bucheon, Republic of Korea

Biological evolution can be conceptualized as a dynamical process in the space of gene sequences guided by the fitness landscape, a mapping that assigns a measure of reproductive value to each genotype [1]. The relationship between genotype and fitness is generally complex, as it is mediated by the multidimensional organismic phenotype that interacts with the environment and thereby determines reproductive success. A simple mathematical framework for exploring this relationship is provided by Fisher's geometric model, which describes the phenotype as a vector in an n-dimensional Euclidean trait space with a unique optimum located at the origin [2]. Genetic mutations are encoded as random phenotypic displacements, and complex fitness landscapes arise from the projection of the discrete network of genotypes onto the continuous trait space. The talk will discuss the properties of these fitness landscapes from the viewpoint of statistical physics, focusing in particular on the exponential growth of the number of local fitness peaks as a measure of genotypic complexity.

[1] J.A.G.M. de Visser, J. Krug, Nat. Rev. Genet. 15:480 (2014).
[2] R.A. Fisher, The Genetical Theory of Natural Selection. Clarendon Press, Oxford (1930).

DY 50.3 Thu 15:30 ZEU 250

Statistical description of normalized odor representations — •David Zwicker — Harvard University, Cambridge, USA

Natural odors comprise many molecules at different concentrations and it is unclear how such odors are discriminated by relatively few olfactory receptors. One problem is that the correlations present in natural odors cannot be removed by local computations, like center-surround inhibition in vision. Instead, the global inhibition present in the olfactory system leads to normalized odor representations, where the odor intensity is separated from its identity, encoded by the relative concentrations of the odorant molecules. This separation is useful to robustly identify odors at different intensities, but how such global inhibition influences the neural representations of odors is unclear.

In this presentation, I discuss a simple theoretical model of the olfaction system that focuses on global inhibition. The model leads to sparse odor representations and reveals two generic consequences of global inhibition: (i) odors with many molecular species are more difficult to discriminate and (ii) receptor arrays with heterogeneous sensitivities perform badly. Comparing these predictions to experiments will help us to understand the role of global inhibition in shaping normalized odor representations.

DY 50.4 Thu 15:45 ZEU 250

Magnetosensing with ion channels and the origin of anomalous gating kinetics — •Igor Goychuk — Institute for Physics and Astronomy, University of Potsdam, Karl-Liebknecht-Str. 24/25, 14476 Potsdam-Golm, Germany

It was earlier proposed by J. Kirschvink *et al.* that magnetosensitive ion channels can be involved in sensing weak magnetic fields by various animals, with a magnetic nanoparticle coupled to a gate of an ion channel and serving as sensor. I consider a generalization of this hypothesis, where a magnetic nanorod made of several magnetosomes is elastically coupled to a cluster of ion channels [1]. Magnetic nanorod reorients in viscoelastic cytosol following a Generalized Langevin equation dynamics and a gating spring instability leads to bistable open-shut dynamics in such a hypothetical magnetosensory complex. Is the proposed mechanism feasible for realistic parameters? It is shown that YES, and interestingly enough the open-shut dynamics can exhibit both stretched-exponential and power law features in the residence time distributions. Beyond this particular context of magnetosensing, viscoelasticity of the medium in which the sensory part of ion channel moves is proposed as a generic mechanism to explain the origin of anomalous gating kinetics observed in several naturally occurring ion channels.

[1] I. Goychuk, Phys. Rev. E **92**, 042711 (2015).

DY 50.5 Thu 16:00 ZEU 250

Quorum sensing in stochastic many-particle models of microbial populations — •Johannes Knebel[1], Matthias Bauer[2], Matthias Lechner[1], Peter Pickl[1], and Erwin Frey[1] — [1]Ludwigs-Maximilians Universitity, Munich — [2]Max Planck Institute for Intelligent Systems, Tuebingen

Autoinducers are small signaling molecules that mediate intercellular communication in microbial populations and trigger coordinated gene expression via "quorum sensing". Elucidating the mechanisms that control autoinducer production is pertinent to understanding collective microbial behaviors such as virulence and bioluminescence. Recent experiments indicate that autoinducers can be heterogeneously produced in clonal populations. Here we ask how phenotypic heterogeneity is established and how the autoinducer concentration in the population is regulated at the same time. In our conceptual model, cells synthesize and excrete autoinducers, and replicate and adapt in this environment. The model reveals that heterogeneous autoinducer production is facilitated by the coupling of ecological and evolutionary dynamics through quorum sensing. To capture the emergent dynamics, we derived a macroscopic mean-field equation from the microscopic stochastic many-particle process in the spirit of the kinetic theory in statistical physics. This mean-field equation reduces to the continuous replicator equation when quorum sensing is absent and, notably, admits bimodal stationary distributions when quorum sensing is present. Our analysis explains phenotypic heterogeneity through quorum sensing and the observed phase transitions to homogeneity.

DY 50.6 Thu 16:15 ZEU 250

Dynamics of population fronts in the presence of finite-sized heterogeneities — •Wolfram Möbius[1,3], Kim M. J. Alards[1], Francesca Tesser[1], Roberto Benzi[2], David R. Nelson[3], and Federico Toschi[1] — [1]Technische Universiteit Eindhoven, Eindhoven, The Netherlands — [2]Universita' di Roma "Tor Vergata" and INFN, Rome, Italy — [3]Harvard University, Cambridge, MA, USA

Populations spread on surfaces through the combined effect of dispersal and population growth on a wide range of length and time scales, yet the effect of heterogeneous environments on this spreading process is not well understood. We here investigate the effect of finite-sized features which affect dispersal or growth of the population locally. With an individual-based simulation we investigate the effect of individual features on the population front and identify a regime within which a local front speed is sufficient to predict the resulting front. Using least-time arguments we are able to describe the front dynamics for individual features and characterize how width and length of the features determine front shape at long times. These findings combined

with numerical solutions of the Eikonal equation allow us to characterize the resulting effective front speed for dilute to dense random sets of features. The results advance our understanding of population and other fronts in two-dimensional irregular environments.

DY 50.7 Thu 16:30 ZEU 250

Universality in the clonal dynamics in developing tissues — •Steffen Rulands[1,2], Samira Chabab[3], Fabienne Lescroart[3], Cedric Blanpain[3], and Benjamin David Simons[1] — [1]University of Cambridge, Cambridge, United Kingdom — [2]MPI-PKS, Dresden, Germany — [3]Université libre de Bruxelles, Brussels, Belgium

Lineage tracing studies based on transgenic animal models have led to advances in our understanding of cellular identity, hierarchy and function. They provide insights into the development, maintenance and regeneration of tissues, and factors leading to dysregulation in diseased states. However, large-scale cell rearrangements, particularly in growing tissues may render the retrospective analysis of lineages highly problematic. Drawing on studies of heart development, we show how such effects may lead to the emergence of universal scaling distributions. By mapping the problem of clonal evolution onto the theory of aerosols, we elucidate the origin and range of possible scaling behaviors. In generalizing our studies to other tissue types and contexts, we show how the identification of universal scaling dependences allows biological information on cell fate behavior to be distilled.

DY 50.8 Thu 16:45 ZEU 250

Incorporating sleep regulation and thalamocortical interactions in a cortical meanfield model — •Michael Schellenberger Costa[1], Arne Weigenand[1], Hong-Viet V. Ngo[2], Lisa Marshall[3], Jan Born[2], Thomas Martinetz[1], and Jens Christian Claussen[4,1] — [1]INB, U Lübeck — [2]Med. Psych. and Behav. Neurobiol., U Tübingen — [3]Neuroendocrinology, U Lübeck — [4]Comp. Syst. Biol, Jacobs University Bremen

Few models accurately reproduce the complex rhythms of the thalamocortical system, as well as the dynamical patterns of sleep regulation. Here, we build upon previous work on a meanfield (neural mass) model of the sleeping cortex [1] and investigate the effect of neuromodulators on the dynamics of the cortex and the corresponding transition between wakefulness and the sleep stages [2]. We show that our simplified model generates essential features of human EEG over a full day. This approach builds a bridge between sleep regulatory models and EEG generating neural mass models. Based on model [1|, we also suggest a new interpretation of the mechanisms responsible for the generation of KCs and SOs [3]. A KC corresponds to a single excursion along the homoclinic orbit, while SOs are noise-driven oscillations around a stable focus. The model generates both time series and spectra that strikingly resemble real EEG data and points out differences between the stages of natural sleep.

[1] A. Weigenand et al., PloS Comp Biol (2014) [2] M. Schellenberger Costa et al., J. Comp. Neurosci. (2016) [3] M. Schellenberger Costa et al., PloS Comp Biol (2016)

DY 50.9 Thu 17:00 ZEU 250

Modeling the spread of West Nile Virus in Germany — •Suman Bhowmick[1], Philipp Lorenz[2], Philipp Hövel[2], and Hartmut H. K. Lentz[1] — [1]Institute of Epidemiology, Friedrich-Loeffler-Institute, Südufer 10, 17493 Greifswald — [2]Institute of Theoretical Physics, Technische Universität Berlin, Hardenbergstraße 36, 10623 Berlin

West Nile virus (WNV) is an arthropod-borne virus (arbovirus) spreading in transmission cycle between mosquitoes and birds. In addition, horses and human are also the victims of WNV, being infected by blood feeding mosquitoes. In our current endeavour, a dynamic model has been devised to decipher the intricacy of the spreading dynamics of the West Nile virus.

The model which is of SEIR (susceptible-exposed-infected-removed) type, comprises of 19 compartments. In this model, we tried to couple the terrestrial and aqueous stages of mosquitoes through a single ODE, for the simplicity. In addition to the local spreading dynamics, spatial spread through aerial movement (diffusion) and bird migration shall be included in the model.

As results, we will present solutions of the local infection model as well as an analytical expression for the basic reproduction number R_0. The seasonal and environmental impacts are also taken into the considerations. The associated map of the basic reproduction number R_0 will be investigated further along with the ODE coupled with network.

DY 50.10 Thu 17:15 ZEU 250

Burst-Noise induced bifurcations in the Schlögl-Model — •Johannes Falk, Marc Mendler, and Barbara Drossel — TU Darmstadt, Germany

We investigate the influence of intrinsic noise on stable states of a one-dimensional dynamical system that shows in its deterministic version a saddle-node bifurcation between monostable and bistable behaviour. The system is a modified version of the Schlögl model, which is a chemical reaction system with only one type of molecule. The strength of the intrinsic noise is varied without changing the deterministic description by introducing bursts in the autocatalytic production step. We study the transitions between monostable and bistable behavior in this system by evaluating the number of maxima of the stationary probability distribution. We find that changing the size of bursts can destroy and even induce saddle-node bifurcations. This means that a bursty production of molecules can qualitatively change the dynamics of a chemical reaction system even when the deterministic description remains unchanged.