DY 38: Statistical Physics of Biological Systems II (Joint Session with DY)

Joint session with DY organized by BP.

Time: Wednesday 11:30–12:30 Location: H43

DY 38.1 Wed 11:30 H43

Receptor arrays optimized for sensing natural odors — •David Zwicker[1], Arvind Murugan[1,2], and Michael P. Brenner[1] — [1]School of Engineering and Applied Sciences, Harvard University — [2]Department of Physics and the James Franck Institute, University of Chicago

Natural odors typically consist of many molecules at different concentrations, which together determine the odor identity. This information is encoded in the collective response of olfactory receptors and subsequently interpreted by the brain. However, it is unclear how the receptors can measure both the composition of the odor and the concentrations of its constituents. I will discuss a theoretical model of receptor arrays from which we derive design principles for optimally communicating the odor information. These principles can be summarized as two possibly conflicting goals: (i) each receptor should respond to half of all odor mixtures; (ii) activity patterns of different receptors should be orthogonal. We show that there is a family of receptor arrays that satisfy these conditions and thus transfer the odor information near-optimally. Within this family, we can then discuss additional optimization goals, like the accuracy of concentration measurements and the capability for discriminating mixtures. Taken together, we can predict the performance and properties of receptor arrays based on a few, measurable quantities. Our work can thus be used to infer information about the receptors from physiological measurements. Moreover, we can use our results to improve artificial sensor arrays.

DY 38.2 Wed 11:45 H43

Making a loop - from polymer conformation to single file diffusion and back — •Wenwen Huang[1], Yen Ting Lin[1,2], Daniela Frömberg[1], Frank Jülicher[1], and Vasily Zaburdaev[1] — [1]Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — [2]School of Physics and Astronomy, University of Manchester, M139PL, Manchester, United Kingdom.

In this contribution, we show that the conformations of a pinned polymer loop embedded in a heat bath with a constant external force field can be modeled by an asymmetric exclusion process (ASEP) with reflecting boundary conditions. This correspondence allows us to find the exact solution for both systems' equilibrium statistics, which is well approximated by the Fermi–Dirac distribution. Moreover, we can quantify not only the behavior of average positions of the particles of the ASEP and the corresponding monomers of the polymer loop, but also their fluctuations. The condition of forming a loop and the corresponding constraint in the ASEP model lead to explicit dependence of the fluctuations on the position of the particles in ASEP and the monomers of the polymer. To close the loop of analogies we show that the kinetic Monte Carlo simulations, which can be performed for the ASEP with a well defined physical time, can be related to the non-equilibrium dynamics of polymer loops.

DY 38.3 Wed 12:00 H43

Evolutionary emergence of phenotype switching — Pintu Patra[1,2] and •Stefan Klumpp[1,3] — [1]Max-Planck-Institut für Kolloid- und Grenzflächenforschung, Potsdam, Germany — [2]Rice University, Houston, Texas, USA — [3]Institut für Nichtlineare Dynamik, Universität Göttingen, Göttingen, Germany

Bacterial persistence (phenotypic tolerance to antibiotics) provides a prime example of bet-hedging, where normally growing cells generate slow-growing but antibiotic-tolerant persister cells to survive through periods of exposure to antibiotics. The population dynamics of persistence is explained by a phenotype switching mechanism that allows individual cells to switch between these different cellular states with different environmental sensitivities. We report a theoretical study based on an exact solution for the case of a periodic variation of the environment to address how phenotype switching emerges and under what conditions switching is or is not beneficial for long-time growth [1]. Specifically we report a bifurcation through which a fitness maximum and minimum emerge above a threshold in the duration of exposure to the antibiotic. Only above this threshold, the optimal phenotype switching rates are adjusted to the time scales of the environment, as emphasized by previous theoretical studies, while below the threshold a non-switching population is fitter than a switching one. Whether the transition is continuous or discontinuous depends on how the phenotype switching rates are allowed to vary. [1] P. Patra and S. Klumpp, Phys. Biol. 12, 046004.

DY 38.4 Wed 12:15 H43

The statistical physics of hematopoiesis: from stem cell engraftment to ageing and disease — •Peter Ashcroft[1], Sebastian Bonhoeffer[1], Philipp Rauch[2], and Markus Manz[2] — [1]ETH Zurich, Zurich, Switzerland — [2]University Hospital Zurich, Zurich, Switzerland

Hematopoietic stem cells (HSCs) maintain blood production. The hematopoietic system has the highest turnover and proliferation rate of cells in the body, however, hematologic malignancies are not the most frequent forms of human cancer. A fine tuned system with many layers of control has evolved that limits and eliminates potentially malignant clones. The overall aim of our research is to obtain a clear, quantitative understanding of the hematopoietic system and the emergence of disease through combined theoretical and experimental work. Here we will describe the theoretical approach. We use techniques from statistical physics and probability theory to analyse the structure of the hematopoietic system at different scales. Experimental investigations of HSCs often involve the transplantation of low numbers of stem cells into a host. We construct and analyse an individual-based model of this process, and determine the probability that donor cells successfully engraft in the host. These donor cells could also represent the invasion of malignant cells and the initiation of blood-based diseases. We also investigate the structure of the hematopoietic tree and the influence this has on the proliferation of diseased cells. Finally, we describe the impact that stem cell ageing has on the hematopoietic system's ability to maintain a healthy supply of blood to the body.