DY 53: Statistical Physics of Biological Systems III (joint session BP/DY)

Time: Friday 9:30–13:00 Location: H 2032

DY 53.1 Fri 9:30 H 2032

The Sun within: active processes from two-temperature models — •Faezeh Khodabandehlou and Christian Maes — Department of Physics and Astronomy KU Leuven, Leuven, Belgium

We propose an embedding of standard active particle models in terms of two-temperature processes. One temperature refers to an ambient thermal bath, and the other temperature effectively describes "hot spots," i.e, systems with few degrees of freedom showing important population homogenization or even inversion of energy levels as a result of activation. As a result, the effective Carnot efficiency would get much higher than for our standard macroscopic thermal engines, making connection with the recent conundrum of hot mitochondria. Moreover, that setup allows to quantitatively specify the resulting nonequilibrium driving, useful in particular for bringing the notion of heat into play, and making easy contact with thermodynamic features. Finally, we observe that the shape transition in the steady low-temperature behavior of run-and-tumble particles (with the interesting emergence of edge states at high persistence) is stable and occurs for all temperature differences, including close-to-equilibrium.

DY 53.2 Fri 9:45 H 2032

Irreversibility across a nonreciprocal PT-symmetry-breaking phase transition — •Henry Alston[1], Luca Cocconi[2], and Thibault Bertrand[1] — [1]Imperial College London, London, UK — [2]Max Planck Institute for Dynamics and Self-Organization, Gottingen, Germany

Nonreciprocal interactions are commonplace in continuum-level descriptions of both biological and synthetic active matter, yet studies addressing their implications for time-reversibility have so far been limited to microscopic models. We derive a general expression for the average rate of informational entropy production in the most generic mixture of conserved phase fields with nonreciprocal couplings and additive conservative noise. For the particular case of a binary system with Cahn-Hilliard dynamics augmented by nonreciprocal cross-diffusion terms, we observe a non-trivial scaling of the entropy production rate across a parity-time symmetry breaking phase transition. We derive a closed-form analytic expression in the weak-noise regime for the entropy production rate due to the emergence of a macroscopic dynamic phase, showing it can be written in terms of the global polar order parameter, a measure of parity-time symmetry breaking.

Invited Talk DY 53.3 Fri 10:00 H 2032

Bacterial transport in dilute and porous environments — •Christina Kurzthaler — Max Planck Institute for the Physics of Complex Systems, Dresden, Germany

Unraveling the motion of microorganisms in dilute and porous media is important for our understanding of both the molecular basis of their swim gait and their survival strategies in microbial habitats. First, I will show that by using renewal processes to analyze experimental measurements of wild-type E. Coli, we can provide a quantitative spatiotemporal characterization of their run-and-tumble dynamics in bulk [1]. We further demonstrate quantitatively how the persistence length of an engineered strain can be controlled by a chemical inducer and characterize a transition from perpetual tumbling to smooth swimming. Second, I will address how this run-and-tumble gait evolves towards a hop-and-trap motility pattern of agents moving in a porous environment [2]. Using computer simulations, we discover a geometric criterion for their optimal spreading, which emerges when their persistence lengths are comparable to the longest straight path available in the porous medium. Our criterion provides a fundamental principle for optimal transport in densely-packed biological and environmental settings, which could be tested experimentally by using engineered cells and may provide insights into microbial adaption mechanisms.

[1] arXiv:2212.11222 (2022) [2] Nat. Commun. 12, 7088 (2021)

DY 53.4 Fri 10:30 H 2032

Signature of (anti)cooperativity in the stochastic fluctuations of small systems: application to the bacterial flagellar motor — •María-José Franco-Oñate[1], Andrea Parmeggiani[2], Jérôme Dorignac[2], Frédéric Geniet[2], Jean-Charles Walter[2], Francesco Pedaci[3], Ashley Nord[3], John Palmeri[2], and Nils-Ole Walliser[2] — [1]MPI Physics of Complex Systems, Dresden, Germany — [2]Laboratoire Charles Coulomb (L2C), Montpellier, France — [3]Centre de Biologie Structurale (CBS), Montpellier, France

The cooperative binding of molecular agents onto a substrate is pervasive in living systems. To study whether a system shows cooperativity, one can rely on the fluctuation analysis of quantities such as the number of substrate-bound units.

Using a general-purpose grand canonical Hamiltonian description of a small one-dimensional (1D) lattice gas with nearest-neighbour interactions as a prototypical example of a cooperativity-influenced adsorption processes, we elucidate how the strength of the interaction potential between neighbouring bound particles on the lattice determines the intensity of the fluctuations of the mean occupancy at steady state.

We then employ this relationship to compare the theoretical predictions of our model to data from single molecule experiments on bacterial flagellar motors (BFM). In this way, we find evidence that cooperativity controls the mechano-sensitive dynamical assembly of the torque-generating units, the so-called stators, onto the BFM.

DY 53.5 Fri 10:45 H 2032

A power-law growth model of pancreatic cancer precursor lesions — Ashley L. Kiemen[1], Denis Wirtz[1], and •David Zwicker[2] — [1]Departments of Pathology, Johns Hopkins University School of Medicine, Baltimore, MD, USA — [2]Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany

Pancreatic cancer often originates from microscopic precursor lesions in the pancreatic ducts. Recent evidence showed that even healthy people possess more and larger lesions than previously believed. A better understanding of the growth of these lesions may thus improve our ability to understand how a minuscule fraction transitions to invasive cancer. Using advanced imaging, we quantified >1,000 lesions and found that lesion size is distributed according to a power law with a fitted exponent of -1.7 over more than three orders of magnitude. To explain these data, we analyze several models of lesion growth and fit the predicted size distributions to the observed data. Our analysis suggests that lesions either (i) grow sub-exponentially and frequently seed new lesions or (ii) grow super-exponentially and frequently merge. Independent genomic mapping of lesions supports both alternatives, suggesting both are relevant. Our work demonstrates how combining experimental measurements of human tissues with dynamic modeling can improve understanding of cancer tumorigenesis.

15 min. break

DY 53.6 Fri 11:15 H 2032

Exclusion model of mRNA translation with collision-induced ribosome drop-off — Johannes Keisers[1] and •Joachim Krug[2] — [1]Centre de Biologie Structurale (CBS), Université de Montpellier, 34090 Montpellier, France — [2]Institute for Biological Physics, University of Cologne, 50937 Köln, Germany

The translation of messenger RNA transcripts to proteins can be modeled as a one-dimensional totally asymmetric exclusion process with extended particles. In this contribution we focus on the effects of premature termination of translation through the irreversible detachment of ribosomes. We consider a model where the detachment is induced by the unsuccessful attempt to move to an occupied site [1]. The model is exactly solvable in a simplified geometry consisting of the translation initiation region followed by a single slow site representing a translation bottleneck. In agreement with a recent experimental study, we find a non-monotonic dependence of the protein production rate on the initiation rate, but only if the leading particle in a colliding pair detaches. The homogeneous version of the model is related to an asymmetric reaction-diffusion model with a localized input of particles. We exploit this connection to show that, for long transcripts, the ribosome density decays asymptotically as the inverse square root of the distance to the initiation site.

[1] J. Keisers, J. Krug, J. Phys. A 56 (2023) 385601

DY 53.7 Fri 11:30 H 2032

Boundary geometry drives three-dimensional defect transitions in a polar fluid — •Pamela Guruciaga[1], Takafumi Ichikawa[2], Takashi Hiiragi[2,3], and Anna Erzberger[1,4] —

[1]European Molecular Biology Laboratory, Heidelberg, Germany — [2]Kyoto University, Kyoto, Japan — [3]Hubrecht Institute, Utrecht, The Netherlands — [4]Heidelberg University, Heidelberg, Germany

Motivated by observations of an interplay between apico-basal polarity and boundary geometry in mouse embryo morphogenesis, we develop a minimal model to address the role of boundaries—with emphasis on their geometry—in the surface-induced ordering of a 3D polar fluid. We find that, although material parameters are responsible for the creation of defects in the order parameter field, their location and structure are determined by the system geometry. We test our results in the experimental context of the mouse epiblast, where cells gradually align along their apico-basal axis and eventually form a fluid filled cavity (lumen) at their apical sides. Since field defects represent regions where the apical sides of the cells meet, changes in defect position can be relevant to lumen formation in the biological system. We compare our predictions with imaging data of the morphogenetic process for wild-type and genetically perturbed mice, finding a remarkable quantitative agreement without any fitting parameters. Our work provides insights into luminogenesis and embryonic viability, while paving the way for defect control by geometry manipulation in more general settings.

DY 53.8 Fri 11:45 H 2032

Optimal Memoryless Chemotaxis — •Jacob Knight[1], Paula García-Galindo[2], Johannes Pausch[1], and Gunnar Pruessner[1] — [1]Department of Mathematics, Imperial College London, South Kensington, London SW7 2BZ, UK — [2]Department of Chemical Engineering and Biotechnology, University of Cambridge, Philippa Fawcett Drive, Cambridge CB3 0AS, UK

A wide array of biological systems can navigate in shallow gradients of chemoattractant with remarkable precision. Whilst previous models approach such systems using coarse-grained chemical density profiles, we construct a model consisting of a chemotactic cell responding to *discrete* cue particles, giving rise to novel phenomenology. For a cell without internal memory, we derive an effective velocity with which the cell approaches the source. This effective velocity is independent of the chemoattractant diffusivity, which can be tuned such that the cell can navigate in arbitrarily shallow chemical gradients. The effective velocity becomes negative beyond some homing radius, which represents an upper bound on the distance within which chemotaxis can be reliably performed.

DY 53.9 Fri 12:00 H 2032

Two-stage adaptive evolution in a rugged yet highly-accessible fitness landscape model with delayed commitment — •Muhittin Mungan[1], Suman G. Das[2], and Joachim Krug[1] — [1]Institute for Biological Physics, University of Cologne, Köln, Germany — [2]Institute of Ecology and Evolution, University of Bern, Bern, Switzerland

We study an empirically-motivated theoretical fitness landscape model of antibiotic-resistance evolution in bacteria [1]. The fitness of a genotype at any concentration depends on two parameters, the resistance level and the drugless growth rate, with a tradeoff between these. For intermediate concentrations fitness landscapes are rough while the fitness peaks are nevertheless highly accessible. Adaptation on such landscapes occurs in two stages. At first there is rapid accumulation of mutations and fast growth of fitness and resistance level along with a decrease in the drugless growth rate. Next there is slow growth of fitness and resistance level, and recovery of the drugless growth rate through the reversion of some of the mutations. We numerically demonstrate a robust pattern of evolution with qualitative features that are largely independent of specific model assumptions. The basins of individual fitness peaks overlap strongly, so that commitment to a peak is delayed substantially. An analytically tractable special case reproduces our findings rather well, shedding light on the nature of adaptive evolution, basins of fitness peaks and delayed commitment.

[1] S.G. Das et al. eLife 9:e55155 (2020)

DY 53.10 Fri 12:15 H 2032

Optimal memory with niche construction — •Edward Lee[1], Jessica Flack[2], and David Krakauer[2] — [1]Complexity Science Hub Vienna, Vienna, Austria — [2]Santa Fe Institute, Santa Fe, USA

Adaptation to changing environments is a universal feature of life and can involve the organism evolving or learning in response as well as actively modifying the environment to control selection pressures. The latter case couples the organism and environment together. Then, how quickly should the organism adapt in response to the changing environment? We formulate this question using a simple model of adaptive costs that considers timescales of memory and environment. We derive a general, sublinear scaling law for optimal memory as a function of environmental persistence, which encapsulates the trade-off between remembering vs. forgetting. The scaling holds for finite memory but a wide range of mediating factors. We then explore strategic game dynamics, uncovering a ratcheting mechanism that promotes reducing environmental volatility when niche constructors can monopolize benefits; conversely, niche destructors can dominate by degrading a shared environment. Finally, we compare the results with metabolic costs to predict that adaptive costs matter more for smaller organisms. Taken together, we predict stabilizing niche construction will evolve when environments are volatile and niches are separable, possibly enriching the behavioral repertoire of social organisms.

DY 53.11 Fri 12:30 H 2032

Interfaces as a probe for interactions in biological systems — •Nirvana Caballero — University of Geneva

Controlling cells, either individually or as a proliferating cell front, remains elusive because the plethora of interactions at widely varying lengthscales present in these systems leads to highly complex dynamical and geometrical properties. Interfaces separating regions of heterogeneous composition, or domains, can encode critical information about these systems' underlying physics. I will show how physical theories describing interfaces can be used to capture the microscopic interactions dominating a system. I will give examples at different scales from cell membranes [1], where the heterogeneous domain composition is key to biological function, to migrating colonies of cells, where interfaces reveal the main interactions present in a colony [2].

[1] NC, K. Kruse, T. Giamarchi. Phase separation on surfaces in the presence of matter exchange. Phys. Rev. E 108, L012801 (2023)

[2] Roughness and dynamics of proliferating cell fronts as a probe of cell-cell interactions. G. Rapin*, NC*, I. Gaponenko, B. Ziegler, A. Rawleight, E. Moriggi, T. Giamarchi, S. A. Brown, and P. Pruch, Sci. Rep. 11, 8869 (2021)

DY 53.12 Fri 12:45 H 2032

Heterogenity in Mucus by statistical analysis from particle tracking — •Thomas John, Sten Leipnitz, Enkeleda Meziu, and Christian Wagner — Campus, University Saarland, Saarbrücken, Germany

In the respiratory tract, cells constantly produce mucus that transports tiny dust particles out of the lungs. It's a protein solution that consists of more than 95% water. It's believed that the proteins form a heterogeneous network, but this cannot be resolved with light microscopy. We are investigating the diffusion behavior of nanoparticles (multi-particle tracking) in mucus and comparing it to glycerol-water mixtures with comparable viscosity. We show that the probability density function of individual particle diffusion coefficients D_i in mucus is significantly broader than expected from a homogeneous solution. The spatial autocorrelation of D_i also declines more slowly in mucus compared to glycerol-water mixtures. Experiments are compared with numerical simulations of Brownian motion. With these statistical analysis methods, we can support the model of a heterogeneous structure of mucus.