DY 33: Biologically Inspired Statistical Physics (joint session DY/BP)

Time: Wednesday 15:00–16:30 Location: ZEU 250

DY 33.1 Wed 15:00 ZEU 250

Comparison of fitting strategies to extract the diffusion coefficient in microrheological experiments — ●Sten Leipnitz, Christian Wagner, and Thomas John — Experimental Physics, Saarland University, Saarbrücken

Tracking of small particles undergoing a Brownian motion in liquids is a widespread method in passive microrheology to extract the diffusion coefficient D, the viscosity of the sample respectively. The mean-squared displacement (MSD) is determined from particle positions as a function of the timelag $MSD(\tau) = \sigma_0^2 + 2nD\tau + v_{\text{drift}}^2\tau^2$, where v_{drift} is a possible drift velocity and σ_0 is an offset due to position detection noise in experiments. We present: the extracted parameters depend strongly on the used number of fitting points in the MSD-relation. Surprisingly, considering only the beginning of the MSD-relation in the fitting procedure leads to the best expectation value of the diffusion coefficient. This is shown by numerical simulations of the Brownian motion as well as from experimental data.

DY 33.2 Wed 15:15 ZEU 250

Non-monotonic behavior of timescales of passage in heterogeneous media: Dependence on the nature of barriers — Moumita Dasgupta[1], ●Sougata Guha[2], Leon Armbruster[1], Dibyendu Das[2], and Mithun K. Mitra[2] — [1]Department of Physics, Augsburg University, USA — [2]Department of Physics, IIT Bombay, India

Usually time of passage across a region may be expected to increase with the number of barriers along the path. Can this intuition fail depending on the special nature of the barrier? We study experimentally the transport of a robotic bug which navigates through a spatially patterned array of obstacles. Depending on the nature of the obstacles we call them either entropic or energetic barriers. For energetic barriers we find that the timescales of first passage vary non-monotonically with the number of barriers, while for entropic barriers first passage times increase monotonically. We perform an exact analytic calculation to derive closed form solutions for the mean first passage time for different theoretical models of diffusion. Our analytic results capture this counter-intuitive non-monotonic behaviour for energetic barriers. We also show non-monotonic effective diffusivity in the case of energetic barriers. Finally, using numerical simulations, we show this non-monotonic behaviour for energetic barriers continues to hold true for super-diffusive transport. These results may be relevant for timescales of intra-cellular biological processes.

DY 33.3 Wed 15:30 ZEU 250

Phase behavior and finite-size effects in biology — ●Felix Herrmann, Burkhard Duenweg, and Martin Girard — Max-Planck Institut fuer Polymerforschung (MPI-P), Mainz, Germany

Phase behavior observed in biology remains puzzling. For instance, the plasma membrane of cells exhibits signs of criticality, as it is controlled to remain near a demixing point. This membrane contains thousand of components, and it is largely unclear how its composition is controlled. Beyond this, one can ask whether cells should obey the traditional thermodynamic picture, given their small size, large number of components and the presence of non-equilibrium processes.

Here, we study toy systems, lattice models containing many (>30) components. We show that these systems exhibit strong finite-size effects. These manifest as behavior that appears similar to traditional critical behavior, but vanish logarithmically with system size. We examine scaling laws, and whether traditional paradigms from macroscopic thermodynamics can be broken in such systems.

DY 33.4 Wed 15:45 ZEU 250

Hierarchical interactions in complex ecosystems — ●Lyle Poley[1], Joseph W. Baron[3], and Tobias Galla[1,2] — [1]Theoretical Physics, Department of Physics and Astronomy, School of Natural Sciences, The University of Manchester, Manchester M13 9PL, UK — [2]Instituto de Física Interdisciplinar y Sistemas Complejos IFISC (CSIC-UIB), 07122 Palma de Mallorca, Spain — [3]Laboratoire de Physique Statistique, École Normale Supérieure (ENS), Paris Sciences et Lettres (PSL) Research University, Sorbonne Université, 75005 Paris, France

In the analysis of complex ecosystems it is common to use random interaction coefficients, often assumed to be such that all species are statistically equivalent. We relax this assumption by imposing hierarchical inter-species interactions, which we incorporate into a generalised Lotka-Volterra dynamical system. These interactions impose a hierarchy in the community. Species benefit more, on average, from interactions with species below them in the hierarchy than from interactions with those above.

Using analytical tools from the theory of disordered systems, most notably path-integrals and dynamic mean-field theory, we demonstrate that a stronger hierarchy stabilises the community by reducing the number of species in the surviving community. We will also show that the probability of survival for a given species is dependent on its position in the hierarchy.

Reference: Poley L, Baron J W and Galla T Generalised Lotka-Volterra model with hierarchical interactions 2022 arXiv:2208.01569

DY 33.5 Wed 16:00 ZEU 250

Quantifying information content in continuous attractor networks — ●Tobias Kühn[1,2] and Rémi Monasson[1] — [1]Laboratoire de Physique de l'Ecole Normale Supérieure, ENS, Université PSL, CNRS, Sorbonne Université, Université Paris Cité, F-75005 Paris — [2]Institut de la Vision, Sorbonne Université, INSERM, CNRS, F-75012 Paris

Attractor networks are a theme with long tradition to model information storage in the brain. Continuous attractor neural networks (CANN), in particular, have been employed to describe the storage of information about space and orientation. However, it stays controversial how useful this paradigm really is to explain actual processes, for example the representation of space in grid and place cells in the entorhinal cortex and the hippocampus, respectively.

A common criticism is that the disorder present in the connections might deteriorate the system's capability to reliably preserve the information of a certain pattern. In order to investigate if this criticism is valid, a measure is needed to objectively quantify the information content of a given neural network. Using the replica-trick, we compute the Fisher information for a network receiving space-dependent input whose connections are composed of a distance-dependent and a disordered component. We observe that the decay of the Fisher information is slow for not too large disorder strength, indicating that CANNs have a regime in which the advantageous effects of connectivity on information storage outweigh the detrimental ones.

DY 33.6 Wed 16:15 ZEU 250

Gift of gab: Probing the limits of dynamic concentration-sensing across a network of communicating cells — ●Mohammadreza Bahadorian[1,2], Christoph Zechner[1,2,3], and Carl D. Modes[1,2,3] — [1]Max Planck Institut for Molecular Cell Biology and Genetics (MPI-CBG), 01307 Dresden, Germany — [2]Center for Systems Biology Dresden (CSBD), 01307 Dresden, Germany — [3]Cluster of Excellence Physics of Life, TU Dresden, 01069 Dresden, Germany

Many systems in biology and other sciences employ collaborative, collective communication strategies for improved efficiency and adaptive benefit. One such paradigm of particular interest is the community estimation of a dynamic signal, when, for example, an epithelial tissue of cells must decide whether to react to a given dynamic external concentration of stress-signaling molecules. At the level of dynamic cellular communication, however, it remains unknown what effect, if any, arises from communication beyond the mean field level. What are the limits and benefits to communication across a network of neighbor interactions? What is the role of Poissonian versus super-Poissonian dynamics in such a setting? How does the particular topology of connections impact the collective estimation and that of the individual participating cells? In this article we construct a robust and general framework of signal estimation over continuous-time Markov chains in order to address and answer these questions.