BP 13: Statistical Physics of Biological Systems I (joint session DY/BP)

Time: Tuesday 9:30–13:00 Location: BH-N 334

Invited Talk BP 13.1 Tue 9:30 BH-N 334

Dynamics of genome replication — •Simone Pigolotti — Okinawa Institute of Science and Technology

The DNA replication program of an organism determines the timing at which different genomic regions are replicated, with fundamental consequences for cell homeostasis and genome stability. I will present a method to infer the DNA replication program, by combining stochastic modeling and deep sequencing experiments. Our approach can be applied to a vast range of organisms from bacteria to eukaryotes. Applied to E. coli, our method reveals regular variations of replication speed, that correlate with previously measured variations of the mutation rate. In budding yeast, our method is able to infer the location of replication origins with remarkable accuracy.

BP 13.2 Tue 10:00 BH-N 334

Theory for Adaptive Systems: Collective Robustness of Genotype-Phenotype Evolution — •Tuan Pham and Kunihiko Kaneko — Niels Bohr Institute, University of Copenhagen

Biological and neural networks are adaptive - their connections slowly change in response to the state of the coupled elements making up the systems. The dynamics of such adaptive networks are intriguingly complex, rendering it extremely difficult to answer the fundamental question of how the resulting collective states of biological and neural systems are functionally robust against environmental stochasticity. We tackle this problem by developing a new framework based on the path-integral formalism of non-equilibrium statistical physics. We demonstrate the wide applicability of our framework to various very high-dimensional dynamical systems on multiple timescales, often encountered in biological evolution and neural network learning. As a specific example of our theory, we apply it to biological evolution, where phenotypes are shaped by gene-expression fast dynamics that are subjected to an external noise while genotypes are encoded by the configurations of a network of gene regulations. This network slowly evolves under natural selection with a mutation rate, depending on how adapted the shaped phenotypes are. Here we find phenotypes with a robust high-valued mean gene-expression level within an intermediate level of noise. The emergence of such robustness can be characterised analytically within our framework as the onset of instability of the attractor state with zero gene-expression levels.

BP 13.3 Tue 10:15 BH-N 334

Modelling antibiotic killing and tolerance dynamics in tuberculosis treatment — •Miriam Clincy[1], Vijay Srinivasan[2], Rosalind J Allen[2], and Martin R Evans[3] — [1]Hochschule Esslingen, Esslingen, Germany — [2]Friedrich-Schiller-Universität, Jena, Germany — [3]University of Edinburgh, Edinburgh, UK

The bacterium Mycobacterium tuberculosis (Mtb), which causes tuberculosis, is the leading global cause of deaths from infectious disease. The antibiotic treatment regime for tuberculosis is very long, because Mtb can switch into tolerant physiological states that are only slowly killed by antibiotic. Here we introduce a stochastic two-species birth-death model for antibiotic treatment of an Mtb infection accounting for this switching.

Solving analytically for the probability generating function describing the treatment phase in which neither state proliferates allows 1) to recover the mean subpopulation dynamics from which numerical estimates for the birth, death and switching rates specifically for Mtb can be derived, and 2) the calculation of the extinction probability as a function of time. From the latter, a numerical measure for the extinction time of the bacterial population is defined. Studying this extinction time reveals distinct regimes in which the required treatment time is limited by either the rate of killing of tolerant bacteria, or the rate of switching out of the tolerant state.

BP 13.4 Tue 10:30 BH-N 334

Information theory of chemotactic agents using both spatial and temporal comparison — Julian Rode[1], Maja Novak[2], and •Benjamin M. Friedrich[1] — [1]Physics of Life, TU Dresden, Germany — [2]University of Zagreb, Croatia

Biological system process information despite noise-corrupted input, often operating at physical limits. A prime example is chemotaxis, i.e., active navigation of biological cells in spatial fields of chemical cues. Intriguingly, cells of different size use two different chemotaxis strategies, comparing concentrations in either space or time. Only heuristic arguments exist to explain this evolutionary choice. We present an information theory of an ideal agent that combines both strategies to quantify 'chemotaxis in bits' [1]. This enables us to predict when each strategy provides more information as function of a new powerlaw that combines agent size, motility noise and sensing noise. We demonstrate our theory with a bio-inspired search robot. [1] https://www.biorxiv.org/content/10.1101/2023.10.14.562229v1

BP 13.5 Tue 10:45 BH-N 334

Relaxation and first passage properties of boundary driven run and tumble particle — •Pritha Dolai[1,2] and Arghya Das[3] — [1]Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany — [2]Max-Planck-Zentrum für Physik und Medizin, Erlangen, Germany — [3]TIFR Centre for Interdisciplinary Sciences, Tata Institute of Fundamental Research, Gopanpally, Hyderabad, 500046, India

We study the spatio-temporal properties of boundary-driven noninteracting Run and tumble particles (RTPs) in one-dimension. We found exact results for the steady state density and current. The spatial and internal degrees of freedom, combined together, possess a symmetry, using which we have analytically obtained the full eigen-spectrum. The eigenvalues are arranged in bands around 0 and -2ω where ω is the tumble rate of the RTP. In the large system size limit, the steady state and dynamical properties are closely approximated by an effective passive-like dynamics with an effective diffusivity. Interestingly, we found that the genuine signatures of activity in the dynamics appear only as subleading correction in system size. Further, there is a crossover from the system size independent relaxation rate to the diffusive relaxation as the system size is increased. Along the lines of equilibrium, we explored the possibility of defining an effective temperature in the single active particle case. It turns out that the effective temperature not only depends on the details of the system parameters, but on the quantities through which it is defined as well as the boundary conditions. We also studied the first passage properties of an RTP in the presence of absorbing boundaries.

BP 13.6 Tue 11:00 BH-N 334

Single particle analysis of sorbing tracers — •Timo Doerries[1], Aleksei Chechkin[1,2,3], and Ralf Metzler[1,4] — [1]Institute of Physics & Astronomy, University of Potsdam, 14476 Potsdam, Germany — [2]Faculty of Pure and Applied Mathematics, Hugo Steinhaus Center, Wrocław University of Science and Technology, Wyspianskiego 27, 50-370 Wrocław, Poland — [3]Akhizer Institute for Theoretical Physics National Science Center "Kharkiv Institute of Physics and Technology", 61108 Kharkiv, Ukraine — [4]Asia Pacific Center for Theoretical Physics, Pohang 37673, Republic of Korea

Based on a simple switching diffusion process we describe tau proteins changing between a mobile (diffusive) and an immobile state, leading to strong non-Gaussian displacements. For long but finite observation times the time averaged mean squared displacements have a significant spread, of which we obtain the exact distribution. This behaviour is similar to the well known continuous time random walk, which has instantaneous jumps in contrast to our model. We discuss the role of the non-zero mobile duration in our model compared to the instantaneous jumps in the continuous time random walk.

15 min. break

BP 13.7 Tue 11:30 BH-N 334

Furutsu-Novikov theorem for shot-noise driven systems — •Jakob Stubenrauch[1,2] and Benjamin Lindner[1,2] — [1]Physics Department of Humboldt University Berlin, Newtonstraße 15, 12489 Berlin, Germany — [2]Bernstein Center for Computational Neuroscience Berlin, Philippstraße 13, Haus 2, 10115 Berlin, Germany

We consider an arbitrary system (later exemplified by a spiking neuron) that is driven by an intensity-modulated Poisson process with intensity $\lambda(t) = \lambda_0 + \varepsilon s(t)$. We derive an exact relation between the input-output cross-correlation in the spontaneous state ($\varepsilon = 0$) and the response function for a weak time-dependent modulation of the input intensity ($\varepsilon > 0$). This can be regarded as a variant of the famous Furutsu-Novikov theorem (FNT) for the case of shot noise. Neu-

rons in networks fluctuate spontaneously and respond if stimulated. Spontaneous fluctuations and response properties are linked, in correspondence to the fluctuation-dissipation theorem, as has recently been shown (Lindner, 2022). Such relations constrain the signal-to-noise ratio, they can be used to fit models, and to advance theories. However, for the biologically relevant case of shot-noise driven neurons, such relations have not been reported yet. As we demonstrate, we can use the new FNT to obtain a fluctuation-response-relation between the spontaneous fluctuations of a neuron's output and its systematic response to a time-dependent stimulus, extending the approach of (Lindner, 2022) from Gaussian noise to shot noise. The relations are numerically tested and their limitation to Poissonian input exemplified for the important example of a leaky integrate-and-fire neuron with alpha synapses.

BP 13.8 Tue 11:45 BH-N 334

Mesoscopic dynamics of spiking neuron population with quenched randomness — •Nils Erik Greven[1,2], Jonas Ranft[3], and Tilo Schwalger[1,2] — [1]TU Berlin — [2]BCCN Berlin — [3]IBENS, Ecole Normale Supérieure & CNRS

To understand the neural mechanisms underlying the response and variability dynamics of neuronal populations in the brain, simple mean-field models at the mesoscopic scale are required that faithfully describe the fluctuations of population activities and recurrent synaptic inputs in network of spiking neurons. We derive a nonlinear stochastic mean-field model for a network of spiking Poisson neurons with random connectivity. The quenched disorder of the connectivity is treated by an annealing approximation leading to a simpler fully connected network with additional noise in the neurons. This annealed network enables a reduction to a mesoscopic model as a two-dimensional closed system of coupled Langevin equations for the mean and variance of the neuronal membrane potentials. Compared to microscopic simulations, the mesoscopic model well describes the fluctuations and nonlinearities of finite-size neuronal populations and outperforms previous mesoscopic models that neglected the recurrent noise effect caused by quenched disorder. This effect can be analytically understood as a softening of the effective nonlinearity. The mesoscopic theory also shows that, in the presence of synaptic transmission delays, quenched disorder can stabilize the asynchronous state. Furthermore, our theory correctly predicts the effect of connection probability and stimulus strength on the variance of the population firing rate.

BP 13.9 Tue 12:00 BH-N 334

Low-dimensional stochastic dynamics of finite-size, spiking-neuron populations via eigenmode expansion — •Tilo Schwalger[1,2] and Bastian Pietras[3] — [1]Technical University Berlin, 10623 Berlin, Germany — [2]Bernstein Center for Computational Neuroscience Berlin, 10115 Berlin, Germany — [3]Universitat Pompeu Fabra, Barcelona, Spain

Low-dimensional neural population models in the form of nonlinear Langevin equations provide an effective description of the collective stochastic dynamics of neural networks in the brain. However, existing population models are largely heuristic without a clear link to the underlying neuronal and synaptic mechanisms. Here, we derive a system of Langevin equations at the mesoscopic scale from a microscopic model of a finite-size, fully-connected network of integrate-and-fire neurons with escape noise. The theory is based on a stochastic integral equation for the mesoscopic dynamics of the neural network (Schwalger et al. PloS Comput Biol. 2017) and an eigenmode expansion of the corresponding refractory-density equation (Pietras at al., Phys. Rev. E 2020). Truncating the hierarchy of coupled spectral modes after the first M modes yields a $2M$-dimensional Langevin equation, permitting a systematic model reduction. Retaining only the dominant spectral mode, $M = 1$, already captures well oscillatory transients and finite-size fluctuations when compared to microscopic simulations. Our bottom-up theory thus connects biologically plausible spiking neural networks to the efficient firing-rate models often used in applcations.

BP 13.10 Tue 12:15 BH-N 334

The Effect of Temperature on Large Biochemical Networks — •Julian Voits[1] and Ulrich S. Schwarz[1,2] — [1]Institute for Theoretical Physics, University of Heidelberg, Heidelberg, Germany — [2]BioQuant-Center for Quantitative Biology, University of Heidelberg, Heidelberg, Germany

An increase of temperature of a few Kelvin might seem modest on the absolute temperature scale, but it can have a dramatic impact on complex biosystems. Instructive examples are fever, when a rise in body temperature of 2-3K has strong effects on our immune system, or climate change, when even smaller temperature changes lead to dramatic shifts in ecosystems. From the physics point of view, the main effect of increased temperature should be the exponential acceleration of biochemical reactions (Arrhenius equation). However, it is unclear how this law plays out in the large biochemical networks of complex systems. We have developed a universal theory that describes the effect of temperature on large biochemical networks. We approach this problem with a graph theoretical interpretation of the mean first passage times of a biochemical master equation. We show that in the limit of large networks, one obtains quadratic forms of the Arrhenius plots, in excellent agreement with experimental data on developmental rates of Drosophila.

BP 13.11 Tue 12:30 BH-N 334

Tensile elasticity of multi-state flexible chains and loops — •Geunho Noh and Panayotis Benetatos — Department of Physics, Kyungpook National University, Daegu, Republic of Korea

Polymer loop structure commonly appears in biological phenomena, such as DNA looping and DNA denaturation. When a chain forms a loop, its elastic behavior differs from that of an open chain due to the loss of entropy. In the case of reversible loop formation, interesting behavior emerges related to the multi-state nature of the conformations. In this study, we model a multi-state reversible loop as a looping Gaussian chain which can bind to form a loop, or a zipping Gaussian loop which can zip to form a double-stranded chain. For each model, we calculate the force-extension relations in the fixed-force (Gibbs) and the fixed-extension (Helmholtz) statistical ensembles. Unlike the single Gaussian chain or loop, the multi-level systems demonstrate qualitatively distinct tensile elasticity and ensemble inequivalence. In addition, we investigate a Gaussian necklace consisting of reversible alternating blocks of the chain and loop, and obtain the temperature-force phase diagram. The phase diagram implies a force-induced phase transition from a completely looped (denatured) state to a mixed (chains and loops) state.

BP 13.12 Tue 12:45 BH-N 334

Manifestation of hidden degrees of freedom in dissipative self-assembly — •Seeralan Sarvaharman and Aljaz Godec — Max Planck Institute for Multidisciplinary Sciences, Göttingen 37077, Germany

Dissipative self-assembly is crucial for the development and healthy functioning of biological systems. By breaking time-reversal symmetry in either the binding or unbinding process of at least one of the components, living organisms are able to assemble structures with much more diverse compositions in a robust fashion. One such example that is of fundamental biological relevance are microtubules. Through a process called "dynamic instability" these microtubules, which are made up of several filaments, grow and shrink depending on the instantaneous compositions of the filaments. The observable that is often used to quantify such dynamic instability is the length of the assembled microtubule. However, the ability to infer the many-body effects underlying this instability from the projected length observable has remained elusive. Here we address this challenge by considering a stochastic Ising-type model of microtubule assembly with thermodynamically consistent driving. Using a mixture of analytical techniques and computational methods we uncover the manifestation of many-body physics encoded the time-ordering of the length of the assembly.