BP 45: Statistical Physics in Biological Systems III (Joint Session with DY)

Time: Wednesday 15:30–16:15 Location: H46

BP 45.1 Wed 15:30 H46

Bursting noise in gene regulation networks: exact and numerical results for stationary distributions and first passage times — •Yen Ting Lin[1], Charles Doering[2], and Tobias Galla[1] — [1]The University of Manchester, Manchester, UK — [2]University of Michigan, Ann Arbor, USA

Understanding how effects of noise propagate from one level of modelling to another is key in a number of applications in physiological or biological systems. Including short-lived mRNA populations in models of gene regulation networks introduces bursting noise, and understanding the effects of this in higher-level models is an open task. In this talk, I will present a coarse-graining method to construct mesoscopic models for such type of dynamical systems, which fully accounts for the bursting noise. We systematically compare different levels of modeling, ranging from individual-molecule-based models including mRNA populations, over protein-only individual-based models to mesoscopic models such as diffusion-type models and our proposed model. We show that the proposed mesoscopic model outperforms conventional diffusion-type models. In a one-dimensional autoregulated network, we present closed-form analytic solutions for both the stationary distribution of protein expression as well as first-passage times of the dynamical system. We present numerical solutions for higher-dimensional gene regulation networks, in which case we also carry out analysis in the weak-noise limit. References: arXiv:1508.02945, arXiv:1508.00608 (*J. R. Soc. Interface* in press)

BP 45.2 Wed 15:45 H46

Population dynamics in switching environments — •Peter Hufton, Yen Ting Lin, Tobias Galla, and Alan McKane — School of Physics and Astronomy, The University of Manchester, Manchester, UK

In gene regulatory networks, the binary state of a single gene can have drastic effects on the dynamics of a population of proteins. Similarly, switches between environmental states are important in bacterial populations and in models of epidemic spread. The mathematical treatment of problems of this type—populations in switching environments—is an open challenge. We present a systematic approach to computing stationary states of these problems. We identify two sources of randomness: the stochasticity from environmental switches, and the intrinsic noise from fluctuations in the population. By extending the linear-noise approximation and utilising a piecewise-deterministic Markov process, we develop a method which incorporates both these effects.

BP 45.3 Wed 16:00 H46

Geometry Dependence of the Diffusion Coefficient in Molecular Dynamics Simulations with Periodic Boundary Conditions — •Martin Vögele and Gerhard Hummer — Max-Planck-Institut für Biophysik, Frankfurt am Main

We investigate the dependence of the diffusion coefficient on the box geometry and its application to lipid membrane simulations.

For this purpose, we compare predictions from a simple analytic correction based on hydrodynamic arguments to molecular dynamics simulations of liquid argon. Increasing the box size in two dimensions, we find a logarithmic dependence on the system size. Increasing the box size in only one dimension, we find a linear dependence. In both cases, diffusion is anisotropic. Additionally, we observe an upper limit for the diffusion coefficient in the limit of infinite systems.

We also test the effect of box geometry on the diffusion in lipid membranes, which are usually simulated in very flat periodic boxes. There we find the predicted logarithmic increase with growing edge lengths.