DY 21: Statistical Physics in Biological Systems (joint session DY/ BP/CPP)

Time: Tuesday 14:00–16:00 Location: ZEU 118

DY 21.1 Tue 14:00 ZEU 118

Epidemic spread in heterogeneous populations - Propagation of uncertainty and linear-noise approximation — •Francisco Herrerías-Azcué and Tobias Galla — School of Physics and Astronomy, The University of Manchester, Manchester, UK

The assumption of homogeneity in classic epidemic models is known to be far from realistic; Different susceptibilities may arise from gene expression and strain mutation. We explore the effects of heterogeneity in susceptibility and infectivity on the stochastic susceptible-infective-recovered (SIR) model of epidemic spread. Our focus is on understanding how these heterogeneities and uncertainties propagate to long-term periodic outbreaks. To do so, we study a structured population consisting of sub-classes with different susceptibilities and infectivities. These are assigned at birth, drawn from underlying fixed distributions.

We show how the system can be reduced to a four dimensional set of equations at the fixed point in the deterministic limit, independent of the number of sub-classes, and we derive the Langevin dynamics characterising fluctuations about this fixed point. To characterise the resulting noise-induced cycles we calculate the power spectra of fluctuations, and determine the features of the distributions of susceptibilities and infectivities shaping the quasi-cycles. In particular we explore how the mean or spread of susceptibilities affect the magnitude of the epidemic, and the period of outbreak cycles. We also investigate the dynamic behaviour and relative phase lag of different sub-populations during the outbreaks.

DY 21.2 Tue 14:15 ZEU 118

Impact of stochastic migration on species diversity in metafoodwebs consisting of several patches — •Tatjana Thiel and Barbara Drossel — Technische Universität Darmstadt, Germany

The structure of space has an appreciable influence on the diversity of ecosystems. So far, there are only few theoretical studies investigating the population dynamics of foodwebs consisting of many species that can migrate between several patches, and in most of these models migration is a continuous, deterministic process. However, when migration events are rare (for instance because the patches are far apart), migration is a stochastic process and should be modelled accordingly.

For this purpose, we place a foodweb model consisting of many species on a spatial network of several patches and evaluate the stable configurations and long-time patterns that arise due to the population dynamics. This dynamics has a deterministic contribution from the processes within a patch, and a stochastic contribution due to migration events, which are implemented using the Gillespie algorithm.

We will discuss how the frequency of migration events impacts species diversity on local and regional scales. Furthermore, we investigate in particular the adiabatic limit in which population dynamics always reaches an equilibrium before the next migration event and we will discuss which long-term scenarios are possible.

DY 21.3 Tue 14:30 ZEU 118

The Evolution of Network Structure and Species Diversity in an Evolutionary Meta-Foodweb Model — •Tobias Rogge[1], Korinna T. Allhoff[2], and Barbara Drossel[1] — [1]Technische Universität Darmstadt, Germany — [2]Université Pierre et Marie Curie, Paris, France

Evolutionary foodweb models provide important insights into the stability and the functioning of ecosystems on long time scales, since the network structure is a highly nontrivial outcome of the ongoing processes of species addition and species deletion. Here, we present and investigate an evolutionary food web model that includes no population dynamics but generates nevertheless a large variety of complex, multi-trophic networks. In this model, species are characterized by a few traits that are based on their body mass and that determine the connections to other species in the network. The system evolves due to the addition of new species, which are modifications of existing species. Species survival depends on the predators, the prey, and the competitors of the new species. We investigate this model on one habitat as well as on many habitats coupled by migration. Depending on the parameters, the long-term dynamics of the network can show layered structures, highly dynamical configurations with frequent extinctions, or frozen configurations that allow no mutant to survive. We identify the conditions under which the different types of dynamical and structural patterns emerge. Furthermore, we evaluate local and regional species diversities in the spatial model as well as species lifetime distributions, and we discuss them in an ecological context.

DY 21.4 Tue 14:45 ZEU 118

Mixed Percolation as a Model for Intra-Cellular Transport — •Andreas Koher[1], Patrick Hu[1], Igor M. Sokolov[2], and Philipp Hövel[1] — [1]TU Berlin — [2]HU Berlin

Intra-cellular diffusion is driven by a complex interplay between passively moving particles and a highly disordered, time-varying environment. To understand transport properties on a microscopical scale we propose a (mixed) percolation model that allows to reproduce a wide range of experimental observations analytically. The novel approach places a random walker on a lattice with *dynamic and static bonds*, i.e. parts of the lattice fluctuate with a given relaxation rate. Similar to static percolation problems, we find that the mean squared displacement undergoes a phase transition from a locally confined to a globally diffusing phase. However, unlike previous models the relaxation rate allows to fit short- and long-term transport properties to experimental observations. Finally, we validate our analytical results with Monte-Carlo simulations.

DY 21.5 Tue 15:00 ZEU 118

Entanglement of knotted DNA ring and an entwined DNA loop — •Saeed Najafi and Raffaello Potestio — MPIP, Mainz, Germany

Self-entanglement and knotting can play a crucial role in the mechanical and functional properties of bio-polymers such as DNA and RNA strands and fibers. By means of computer simulations of model DNA systems, we demonstrate that the crossing pattern of a braid of entwined DNA rings has a large impact on its structural and dynamical properties. In particular, we identify under which conditions the braid crossing pattern enforces a positive and stronger correlation between the entangled rings.

DY 21.6 Tue 15:15 ZEU 118

Chirality-mediated interaction between knots on tensioned polymers — •Raffaello Potestio — Max Planck Institute for Polymer Research, Mainz, Germany

Knots appear frequently in semiflexible (bio)polymers, including double-stranded DNA, and their presence can affect the polymers' physical and functional properties. It is possible and indeed often the case that multiple knots appear on a single chain, with effects which are under scrutiny since only a few years. In this talk I will discuss the equilibrium properties of two knots on a stretched semiflexible polymer, an idealization of a typical optical tweezer experiment. Specifically, I will focus on how the knots' relative chirality affects their interaction, rationalizing some of their pertinent features by means of simple effective models. The implications of the chirality-dependent knot-knot interaction will be discussed, in particular with respect to their consequences for the characterization and manipulation of these systems -be they artificial or of biological origin- and for their technological application.

DY 21.7 Tue 15:30 ZEU 118

Phenotypic switching as a strategy for persistence in stochastic environments — •Peter Hufton, Yen Ting Lin, and Tobias Galla — School of Physics and Astronomy, The University of Manchester, Manchester, UK

Bet-hedging constitutes a strategy for life to survive in demanding, fluctuating environments. The ideal example is found in bacterial populations: switching stochastically between phenotypes conveys a fitness advantage when exposed to episodes of antibiotics. But what does the optimum switching strategy look like when, as in nature, the environment is itself unpredictable? Here, we present a theoretical study of the dynamics of growing populations subject to stochastic environmental switching, and provide a general framework for the analytic study of the fitness of such populations. Our original approach utilises the piecewise-deterministic Markov process, a technique which has seen increasing use in modelling biochemical process. Our results reveal significantly different behaviours to those found in periodic environmental conditions. We report that stochastic environments produce globally fitter populations, and that the optimum switching regimes in

each case are markedly different.

DY 21.8 Tue 15:45 ZEU 118

Effect of slow-switching genetic states in gene regulatory network governing stem cell pluripotency — •Yen Ting Lin[1], Peter Hufton[2], Esther Lee[3], and Davit Potoyan[4] — [1]T-6 and CNLS, Los Alamos National Laboratory, USA — [2]School of Physics and Astronomy, The University of Manchester, UK — [3]Department of Bioengineering, Rice University, USA — [4]Center for Theoretical Biological Physics, Rice University, USA

Construction of the gene regulatory network (GRN) from experimental data requires a post-experimental analysis which established the pairwise correlations between the measured dynamical quantities. Then as a coarse description, each gene controls and/or is controlled by another gene(s), forming a network (GRN). Form another perspective of a single gene, the expression mechanism is encapsulated by the central dogma: the mRNA transcribes the sequence, and then the mRNA left the chromatin and synthesize proteins.

We present a detailed model combining these two approaches. Utilizing an analytic approximation we previously proposed, we show that the computational efficiency is dramatically increased on a GRN governing stem-cell differentiation. At different switching rates between the genetic states we inferred a unique parameter space which reproduces experimental results. Moreover, we found a unique space for the switching rates reproducing features from single-molecule experiments. Interestingly, the information entropy was maximized in this space. We argue that the consequence may be utilized to cell differentiations as an maximal information is encoded in the dynamics.