

## BP 6: Statistical Physics of Biological Systems I (joint session BP/DY)

Time: Monday 15:00–17:15

Location: SCH A251

BP 6.1 Mon 15:00 SCH A251

**Stability and diversity in random Lotka-Volterra systems with non-linear feedback** — ●LAURA SIDHOM and TOBIAS GALLA — The University of Manchester, Oxford Road, Manchester, M13 9PL

Ecosystem stability is important for maintaining a healthy microbiome, so understanding the factors that contribute to stability is of great relevance. In this talk I will discuss an ecosystem of many interacting species, that evolve according to Lotka-Volterra dynamics, with interaction coefficients drawn from a random distribution. We investigate the effects of sigmoidal nonlinear feedback on the stability of the ecosystem, and on its diversity. We find that nonlinear feedback causes species growth to be bounded, increasing ecosystem stability. In the talk I will illustrate the model parameters, using examples of interactions found in nature. We also investigate how pairwise interactions, and the introduction of higher-order interactions affect ecosystem stability, and how this relates to ecosystems in nature. I will briefly discuss the generating-functional path integral approach and the linear stability analysis, and discuss these results in terms of the human microbiome and explain how attributes of the host can influence its stability.

BP 6.2 Mon 15:15 SCH A251

**Towards a grammar of probabilistic models for large biological networks** — ●PHILIPP FLEIG<sup>1</sup> and ILYA M. NEMENMAN<sup>2</sup> — <sup>1</sup>University of Pennsylvania, Philadelphia, USA — <sup>2</sup>Emory University, Atlanta, USA

Biological interaction networks such as biological neural networks, amino acid sequences in proteins, etc. are critical to the functioning of any living system. The trend of modern experiments is to record data with a rapidly increasing number of simultaneously measured network variables. Inferring models for such complex data is becoming increasingly more difficult, since one is confronted with a combinatorial explosion in the number of possible interactions between variables. Here we present first steps of an approach to overcome this obstacle. We investigate the question whether a small set of carefully chosen statistical models suffices to describe rich phenomenology in data of biological networks. As candidate models for this grammar we consider low-rank approximation, clustering, sparsity, etc.. We discuss the distribution of eigenvalues and pairwise correlations characteristic for each model, working under the assumption that they serve as key indicators for the phenomenology described by a model. We provide examples of modelling data of Ising spin systems and outline a vision for how combinations of models in the grammar cover a large part of model space occupied by biological networks.

BP 6.3 Mon 15:30 SCH A251

**Kauffman NK models interpolated between  $K=2$  and  $K=3$**  — JAMES E. SULLIVAN, DMITRY NERUKH, and ●JENS CHRISTIAN CLAUSSEN — Department of Mathematics, Aston University, Birmingham B4 7ET, U.K.

The NK model was introduced by Stuart Kauffman and coworkers [1] as a model for fitness landscapes with tunable ruggedness, to understand epistasis and pleiotropy in evolutionary biology. In the original formulation, fitness is defined as a sum of fitness functions for each locus, each depending on the locus itself and  $K$  other loci. Varying  $K$  from  $K = 0$  to  $K = N - 1$  leads to different ruggedness of the landscape. In previous work we introduced a generalization that allows to interpolate between integer values of  $K$  by allowing  $K_i$  to assume different values for each locus. We focus on the interpolation between the most widely studied cases of  $K = 2$  and  $K = 3$  and characterize the landscapes by study of their local minima. Here we transfer this approach to Random Boolean Networks and investigate attractor basins and limit cycles where the average  $K$  assumes integer and noninteger values. Relaxing the assumption of degree-homogeneity is an important step towards more realistic boolean network models, relevant to a broad range of applications in the dynamics of social systems and in systems biology.

[1] Kauffman, S.; Levin, S., *Journal of Theoretical Biology.* 128, 11 (1987); Kauffman, S.; Weinberger, E., *Journal of Theoretical Biology.* 141, 211 (1989).

Invited Talk

BP 6.4 Mon 15:45 SCH A251

**Density waves, jamming and dynamic arrest in growing microbial communities** — ●OSKAR HALLATSCHKEK — University of California, Berkeley, USA

Microbes often colonize spatially-constrained habitats, such as pores in the skin or crypts in the colon. The resulting micro-communities are often stable and contribute to the genetic diversity and function of our microbiomes. It is, however, unclear how spatial constraints influence microbial community assembly. By monitoring and modeling microbial populations under controlled microfluidic confinement, we find a rich spectrum of dynamical patterns that are controlled by the competition between density-dependent outflow and population growth. Our results show that density-dependent passive diffusion can drive a reproducing populations to a jamming threshold, which entails a total loss of mixing and intra-species competition.

15 min. coffee break

BP 6.5 Mon 16:30 SCH A251

**Effect of alternating between sexual and asexual reproduction on the number of expected mating types in isogamous species** — ●ERNESTO BERRÍOS-CARO<sup>1</sup>, GEORGE W. A. CONSTABLE<sup>2</sup>, and TOBIAS GALLA<sup>1</sup> — <sup>1</sup>The University of Manchester — <sup>2</sup>University of York

The number of mating types of sexually reproducing isogamous species can range from two to thousands. The latter case is highly unusual and contradicts the argument that new types are sexually advantaged, which would imply a consistent growth of the number of types. Recent works based on a Moran-type individual-based model seem to suggest that the rate of sexual reproduction plays a crucial role in the low number of mating types observed in nature. Motivated by species that alternate between sexual and asexual reproduction, we subject the reproduction events to a switching environment of both states. We explore how the distribution of the number of mating types is affected by different switching regimes. When the environments switch slowly, we find that the distribution of mating types can become bimodal if the population size is large enough and the time spent in both environments (on average) is similar. When the switching is fast, we find that the system behaves as if it were in an effective single-fixed environment, where the sex is facultative. Also, we investigate the transition from slow to fast switching environments by calculating the distributions of the number of types in each environment based on the Kolmogorov equations of the system.

BP 6.6 Mon 16:45 SCH A251

**Specialisation and plasticity in a primitive social insect** — ●ADOLFO ALSINA<sup>1</sup>, SOLENN PATALANO<sup>2</sup>, MARTIN BACHMAN<sup>3</sup>, IRENE GONZALEZ-NAVARRETE<sup>4</sup>, STEPHANIE DREIER<sup>5</sup>, SHANKAR BALASUBRAMANIAN<sup>3</sup>, SEIRIAN SUMNER<sup>5</sup>, CARLOS GREGORIO-RODRIGUEZ<sup>6</sup>, WOLF REIK<sup>2</sup>, and STEFFEN RULANDS<sup>1</sup> — <sup>1</sup>Max Planck Institute for the Physics of Complex Systems, Dresden, Germany — <sup>2</sup>The Babraham Institute, Cambridge, UK — <sup>3</sup>University of Cambridge, Cambridge, UK — <sup>4</sup>Centre for Genomic Regulation (CRG), Barcelona, Spain — <sup>5</sup>Institute of Zoology, London, UK — <sup>6</sup>Universidad Complutense de Madrid (UCM), Madrid, Spain

Biological systems not only have the remarkable capacity to build and maintain complex spatio-temporal structures in noisy environments, they can also rapidly break up and rebuild such structures. How can such systems can simultaneously achieve both robust specialisation and plasticity is poorly understood. Here we use primitive societies of *Polistes* wasps as a model system where we experimentally perturb the social structure by removing the queen and follow the relaxation dynamics back to the social steady state over time. We combine a unique experimental strategy correlating measurements across vastly different spatial scales with a theoretical approach. We show that *Polistes* integrates antagonistic processes on multiple scales to distinguish between extrinsic and intrinsic perturbations and thereby achieve both robust specialisation and rapid plasticity. Such dynamics provide a general principle of how both specialization and plasticity can be achieved in biological systems.

BP 6.7 Mon 17:00 SCH A251

**Coarse graining of biochemical systems described by discrete**

**stochastic dynamics** — •DAVID SEIFERTH and STEFAN KLUMPP —  
Institute for the Dynamics of Complex Systems, University of Göttingen,  
Friedrich Hund Platz 1, 37077 Göttingen, Germany

Many biological systems can be described by finite Markov models. A general method for simplifying master equations will be presented by merging two adjacent states. The method preserves the steady-

state probability distribution and all steady-state fluxes disregarding the one between the merged states. As the order of merging states is not important, different levels of coarse-grained models of the underlying microscopic dynamics can be obtained. Different criteria for the level of coarse graining or the resolution of the process will be proposed. The application of the method will be discussed for specific biochemical examples.