DY 27: Posters - Statistical Physics Biological Systems

Time: Tuesday 18:15–21:00 Location: P3

DY 27.1 Tue 18:15 P3

Effects of migration on an evolutionary food-web model without explicit population dynamics — •David Jones, Tobias Rogge, and Barbara Drossel — Hochschulstraße 6, 62489 Darmstadt

Given the complexity of the structure of ecosystems and the interactions of the multitude of species therein, modeling of food-webs can prove to be a crucial tool in understanding the patterns that can be observed in nature. Here we present an evolutionary model to generate a network of complex, multi-trophic food-webs on a grid of habitats without a need for population dynamics. The individual species are defined by a small number of body mass based traits. These traits in turn define the links between the species within the food-web. After the initiation of a simple food-web on each node of the grid, mutations of existing species lead to the addition of species to a food-web, whereas migration allows a species to invade a neighboring food-web on the grid. Random extinction events are additionally implemented to prevent frozen configurations of the food-web network. After each mutation, migration or extinction event, the survival criterion is evaluated for the altered food-web structure. Species that do not fulfill the survival criterion within a food-web die out of the respective food-web. We explore the effect of migration on the network of food-webs and evaluate quantities that are of ecological interest, in particular species area laws.

DY 27.2 Tue 18:15 P3

Thermodynamic bounds on the ultra- and infra-affinity of Hsp70 for its substrates — •Basile Nguyen[1,2], David Hartich[1], Paolo De Los Rios[2], and Udo Seifert[1] — [1]II. Institut für Theoretische Physik, Universität Stuttgart, Stuttgart, Germany — [2]Laboratory of Statistical Biophysics, École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland

Heat shock proteins 70 (Hsp70s) have essential functions in living systems, such as protecting proteins against aggregation and assisting protein folding. They are ATP-driven machines which rely on allosteric regulation to optimally tune their affinity to specific substrates (e.g., misfolded or partially folded proteins). Hsp70s use the chemical free energy from an ATP hydrolysis to show affinity to their substrates beyond the equilibrium bounds, these regimes are called ultra- and infra-affinity. We derive a thermodynamic relation which quantifies how far the affinity can be tuned using the finite energy budget of hydrolysing one ATP. We find that an optimal tuning requires fast hydrolysis and nucleotide exchange reactions with respect to substrate binding and unbinding. Most remarkably, Hsp70s work with cofactors which are observed to catalyze these key reactions. Therefore, we show that the Hsp70 system is optimally tuned to achieve ultra-affinity, thus explaining how it prevents aggregation and refolds efficiently. Finally, we consider small GTPases which can benefit from infra-affinity to optimize intracellular signal transduction.

DY 27.3 Tue 18:15 P3

Giant Acceleration of Diffusion for Molecular Motors — •Lukas P. Fischer, Patrick Pietzonka, and Udo Seifert — II. Institut für Theoretische Physik, Universität Stuttgart, Germany

Recent experimental studies have shown the existence of giant acceleration of diffusion for molecular motors [1]. Typically, such an effect is observed for driven continuous motion in a periodic potential [2]. The existence of giant acceleration for molecular motors gives rise to new characteristics for probing the underlying molecular mechanism. We examine the hybrid model, consisting of a bead harmonically coupled to a discretely jumping motor, under the effect of an external force [3]. We present the force-dependence of the velocity and the diffusion coefficient which is comparable to the diffusion in periodic potentials. This allows us generalize the giant diffusion to more complex models. By considering different system parameters we reveal a rich structure of the dependence of the velocity and diffusion coefficient. For very large jump rates of the motor the hybrid system can be effectively mapped to a probe particle diffusing in a periodic potential. The general behavior, however, depends crucially on the complete set of parameters.

[1] R. Hayashi *et al.*, Phys. Rev. Lett. **114**, 248101 (2015)
[2] P. Reimann *et al.*, Phys. Rev. Lett. **87**, 010602 (2001)
[3] E. Zimmermann *et al.*, Neq J. Phys. **14**, 103023 (2012)

DY 27.4 Tue 18:15 P3

Can one hear the length of an axon? — •Frederic Folz[1], Lukas Wettmann[1], Karsten Kruse[2], and Giovanna Morigi[1] — [1]Department of Theoretical Physics, Saarland University, Saarbrücken, Germany — [2]NCCR Chemical Biology, Department of Biochemistry, Department of Theoretical Physics, University of Geneva, Geneva, Switzerland

Axons are linear processes of nerve cells that can range from a few tens of micrometers up to meters in length. In addition to external cues, the length of an axon is also regulated by unknown internal mechanisms. Molecular motors have been suggested to generate oscillations with a length-dependent frequency that could be used to measure an axon's extension. Here, we present a mechanism that uses the oscillatory signal to regulate the axon length. We show that in addition to the frequency also the form of the oscillations contribute significantly to determining the steady state length.

DY 27.5 Tue 18:15 P3

Receptor activation — •Cheng-Yu Sun[1] and Hsuan-Yi Chen[1,2] — [1]Department of Physics, Nation Central University, Taoyuan 32001, Taiwan — [2]Institute of Physics, Academia Sinica, Taipei 11520, Taiwan

To effectively detect external environment, receptors in biological cells have to be sensitive and efficient. In this study, we consider a general receptor activation model. In our model, a binding site can bind to a ligand, it can also be activated by an activator. Depending on its binding and activation state, a binding site has four states. We allow couplings between sites through their binding states and activation states. The equilibrium study reveals that strong switch-like behavior can be achieved by strong coupling of the activation states between the sites, while the additional coupling of the binding state helps to strengthen this effect. We also study the dynamics of coupled sites. The results show the important role played by the ratio between binding rate and activation rate. The regions where the behavior of this system becomes similar to classical MWC and Pauling models are discussed.

DY 27.6 Tue 18:15 P3

A minimal spatial cell lineage model of epithelium exhibits tissue stratification and multi-stability — Wei-Ting Yeh[1] and •Hsuan-Yi Chen[1,2] — [1]Department of Physics, National Central University, Jhongli, 32001, Taiwan — [2]Institute of Physics, Academia Sinica, Taipei, 11529, Taiwan

In this work, we consider stratified epithelium, which is a multi-layered self-renewal tissue, and build up a minimal model which includes the spatial information and cell lineage dynamics. We numerically and analytically solve the steady state and discuss how different differentiation models can lead to different tissue functionality and stratification. Thus, we provide a possible way to deduce the unknown cell differentiation mechanism by fitting the observed degree of stratification with our model.

The minimal model also shows other properties. For example, we find that there is no stratified steady state if there is only short-range interaction between cells. In other word, we need long-range interaction like coupling with morphogen dynamics to avoid the trivial homogeneous state. Interestingly, our model in general permits the existence of multiple steady states if both long- and short-range interaction between cells are present, and the degree of functionality and stratification is different for each steady state. In the future, it is possible to study the transition between these states and discuss its biological relevance to tissue morphogenesis and cancer invasion.