BP 22: Statistical Physics of Biological Systems III (with DY)

Time: Thursday 15:00–17:30 Location: H 1058

BP 22.1 Thu 15:00 H 1058

Predicting the evolution of the transport network of *Physarum polycephalum* — •Werner Baumgarten and Marcus Hauser — Abteilung Biophysik, Institut für Experimentelle Physik, Otto-von-Guericke-Universität Magdeburg, Germany

The plasmodium of the unicellular slime mould *Physarum polycephalum* forms a characteristic two-dimensional vein network, which extends in search of food. Protoplasm is transported periodically back and forth through the tubular network. With time, the network coarsens by deletion of the least efficient pathways.

The vein network of *P. polycephalum* is a weighted, undirected, regular graph where the veins form the edges and the branching points the nodes [1,2]. The weight is given by the local drag through each vein segment and the efficiency of the transport pathways is calculated using Dijkstra's algorithm [3] and the edge betweenness. This provides for a predictive tool to identify the least effective veins, and to predict the evolution of the network.

[1] W. Baumgarten, M.J.B. Hauser, Phys. Rev. E 82, 046113 (2010).

[2] W. Baumgarten, M.J.B. Hauser, J. Comp. Interdisc. Sci. 1, 241 (2010).

[3] E.W. Dijkstra, Num. Math. 1, 269 (1959).

BP 22.2 Thu 15:15 H 1058

Universal Network Percolation in the Slime Mold *Physarum polycephalum* — •Adrian Fessel[1,2], Christina Oettmeier[1,2], Erik Bernitt[1,2], and Hans-Günther Döbereiner[1,2] — [1]Institut für Biophysik, Universität Bremen, 28334 Bremen, Germany — [2]Mechanobiology Institute, National University of Singapore, 117411 Singapore, Singapore

The tubular vein network formed by the true slime mold *Physarum polycephalum* during its plasmodial phase has been subject to various recent studies. However, only the late stages of network growth have been thoroughly investigated. We analyze fusion-driven early morphogenesis of the plasmodial network via advanced digital image processing, revealing a prominent percolation transition universally present in biological networks. Physarum networks are grown from scattered microplasmodia on an agar-covered petri dish. Images are taken every minute over multiple days using a high-resolution digital camera. We found an exact solution to the percolation transition for small link degree which predicts the percentage of nodes observed in the largest component without an adjustable parameter.

BP 22.3 Thu 15:30 H 1058

Mutual Repression enhances Gene Boundary Precision by Steepening — •Thomas R. Sokolowski[1], Thorsten Erdmann[2], and Pieter Rein ten Wolde[1] — [1]FOM Institute AMOLF, Science Park 104, 1098XG Amsterdam, The Netherlands — [2]University of Heidelberg, Institute for Theoretical Physics, Philosophenweg 19, 69120 Heidelberg, Germany

Embryonic development is driven by spatial patterns of gene expression that determine the fate of each cell in the embryo. While gene expression is often highly erratic, embryo development is usually exceedingly precise. How development is robust against intra- and inter-embryonic variations is not understood. To assess the role of mutual repression in the robust formation of gene expression patterns, we have performed spatially resolved large-scale stochastic simulations of two gap genes in Drosophila melanogaster, hunchback (hb) and knirps (kni), which are activated by their morphogens Bicoid (Bcd) and Caudal (Cad), respectively, and mutually repress each other. Our analysis shows that mutual repression can markedly increase the steepness and precision of the gap gene expression boundaries. Moreover, it dramatically enhances their robustness against embryo-to-embryo variations in the morphogen levels. Finally, our simulations reveal that diffusion of the gap proteins plays a critical role not only in reducing the width of the gap gene expression boundaries via the mechanism of spatial averaging, but also in repairing patterning errors that could arise because of the bistability induced by mutual repression.

BP 22.4 Thu 15:45 H 1058

Buffering of the intracellular ribosome pool and protein production by ribosomal queues — •Philip Greulich[1], Luca Ciandrini[2], Mamen C. Romano[2], and Rosalind J. Allen[1] — [1]ICMCS, School of Physics and Astronomy, University of Edinburgh, Edinburgh, United Kingdom — [2]Institute for Complex Systems and Mathematical Biology, King's College, University of Aberdeen, Aberdeen, United Kingdom

In cells, mRNAs compete for a finite number of ribosomes when producing proteins. Thus, high production of one protein can lower the expression of others, since many ribosomes are bound on mRNAs of the former one and are not available for others. This effect is also known as "protein burden".

mRNA sequences can contain "slow" codons where ribosomes proceed much slower than on other parts of mRNA. These slow codons act as bottlenecks to protein synthesis, which can lead to ribosome queues on the mRNA molecules. We present a stochastic model for the traffic of ribosomes on many mRNAs competing for a finite pool of particles. Using realistic sequences of fast and slow codons, we show that ribosomal queues can effectively buffer the free ribosome pool, making it independent of fluctuations in mRNA-number and total amount of ribosomes. The effect can reduce the protein burden due to high expressions of a single gene. This mechanism works instantaneously and does not require explicit regulation of the ribosome pool.

Our results may have significant implications for cells' ability to respond independently to multiple demands on the ribosome pool.

BP 22.5 Thu 16:00 H 1058

Modeling a Circadian Clock's Slave Oscillator in *Arabidopsis thaliana* — •Christoph Schmal[1,2], Dorothee Staiger[1], and Peter Reimann[2] — [1]Molecular Cell Physiology, Faculty of Biology — [2]Condensed Matter Theory, Faculty of Physics, Bielefeld University

Circadian clocks, generating self-sustained or slowly damped oscillations with a period of approximately 24 hours are usually described as transcriptional-translational feedback loops and can be found in nearly all eukaryotes and some prokaryotes. Entrainment by environmental signals, e.g., light, synchronizes the clock to the period of the Earth's rotation.

It still remains unclear how the rhythmicity of the clock is transmitted to its output pathways. Slave oscillators could be candidates. The RNA binding proteins *At*GRP7 and *At*GRP8 may represent such a slave oscillator. The transcription of both genes is rhythmically repressed by the partially redundant core oscillator genes LHY/CCA1 and they further shape their oscillatory profile via auto- and cross-regulating each other using an alternative splicing mechanism.

We model the system in terms of ordinary differential equations and estimate the barely known parameters with a cost function that quantifies the overlap between our model and key experimental features. Properties such as the waveform, the period and the phase of the oscillations, the mRNA and protein half-life and the response to varying photoperiods found in our simulations are compared with experimental findings. We make also suggestions and predictions for further experiments.

BP 22.6 Thu 16:15 H 1058

Investigating intrinsic fluctuations in biochemical systems — •Joseph Challenger[1], Jürgen Pahle[2], Alan McKane[1], and Pedro Mendes[2] — [1]School of Physics and Astronomy, The University of Manchester, Manchester, UK — [2]Manchester Interdisciplinary Biocentre, The University of Manchester, Manchester, UK

In many biochemical reaction systems it is important to be able to quantify the stochastic fluctuations that are present. Deterministic rate equations, which are often used to describe these systems mathematically, do not allow for these fluctuations. An alternative, probabilistic, formalism is available, using the master equation. An approximate solution to this equation can be found using the van Kampen expansion, which provides leading order corrections to the rate equations. The terms in the expansion relate to objects in the rate equations in a very general way. We show how this approach can be generalised to biochemical systems which involve many neighbouring compartments.

We have incorporated this technique into COPASI, a software package designed to study biochemical reaction systems. This allows the procedure to be automated. Given a particular reaction system, COPASI calculates the fluctuations around the system's steady state. This analysis can be performed in tandem with the other tasks available in

COPASI e.g. parameter scanning or optimisation. This is useful if there is uncertainty associated with numerical values of some of the reaction parameters. If the fluctuations are calculated via numerical simulation, these tasks can be computationally expensive. In contrast, these calculations can be done quickly using our approach.

BP 22.7 Thu 16:30 H 1058

Brownian dynamics simulation with hydrodynamic interactions of crowded protein solutions — •Paolo Mereghetti[1,2] and Rebecca Wade[1] — [1]Heidelberg Institute for Theoretical Studies (HITS) gGmbH, Schloß-Wolfsbrunnenweg 35, 69118 Heidelberg, Germany — [2]Interdisciplinary Center for Scientific Computing (IWR), University of Heidelberg, Im Neuenheimer Feld 368, 69120 Heidelberg, Germany

The study of solutions of biomacromolecules provides an important basis for understanding the behavior of many fundamental cellular processes, such as protein folding, self-assembly, and signal transduction. We have developed the SDAMM Brownian dynamics simulation software to investigate the dynamic and structural properties of dilute protein solutions. In the model used, the proteins are treated as atomically detailed rigid bodies moving in a continuum solvent. The method showed good agreement with experimental data for proteins of concentrations up to 60 g/L even though hydrodynamic interactions were neglected. We here describe new developments of the simulation model to extend the range of applicability to protein solutions as concentrated as cell-like environments where the effect of hydrodynamic interactions cannot be neglected. To take hydrodynamic interactions into account, we use a mean field model and we apply the method to investigate the behaviour of concentrated solutions (up to 40% volume fraction) of normal and sickle cell hemoglobin, and of myoglobin. From these simulations, we assessed the effects of hydrodynamic interactions, short-range interactions and excluded volume effects on diffusion.

BP 22.8 Thu 16:45 H 1058

Implicit Electrohydrodynamics of Polyelectrolytes Using Lattice-Boltzmann — •Owen A. Hickey and Christian Holm — Institut für Computerphysik, Universität Stuttgart, Deutschland

We make use of an implicit method to simulate the electrohydrodynamics of a polyelectrolyte to an external electric field. The method uses a new coupling of Lennard-Jones beads to a lattice-Boltzmann fluid which forces the difference between the velocity of a bead and the local fluid velocity to be the Smoluchowski slip velocity. The method is validated by first simulating the free solution electrophoresis of polymers. The technique is then used to verify the surprising result that the force necessary to hold a charged polymer at rest in an electric field is proportional to the hydrodynamic radius, and not the total charge on the polymer. Further results show other surprising effects, like how heterogeneously charged objects with no net charge can have non-zero mobilities and that they can even move perpendicular to the applied electric field.

BP 22.9 Thu 17:00 H 1058

Using Branching Processes to Model Critical Neuronal Networks — •Anna Levina[1,2], J. Michael Herrmann[3], and Theo Geisel[1,4] — [1]BCCN Göttingen, Germany — [2]MPI MIS, Leipzig, Germany — [3]University of Edinburgh, UK — [4]MPI DS, Göttingen, Germany

Many authors use branching processes (BPs) formalism to model critical neuronal networks. It is indeed very tempting, because BP are a well studied mathematical concept, where it is easy to define what is critical and what is not. Additionally, for BPs it is proved, that a distribution of avalanche sizes follows a power-law with an exponent -3/2. However, only in very few cases does the approximation of activity propagation in a neuronal network by BPs have a rigorous basis. Moreover, a straightforward BPs approximation fails in the presence of delays in the network. Nevertheless, this approach is still used unrestricted to argue about a critical network even for the small system sizes, where the discrepancies are very large.

Here we present analytical and numerical results illustrating reservations in using BPs approximation and ways to overcome them. We show analytically that in the case of a simple neuronal network with a probabilistic synaptic transmission BPs can be used as a valid model in the large network limit. However, for small networks the finite-size corrections are required. We derive these corrections and also discuss how to modify them in the presence of delays. This topic is especially interesting for a growing field of self-organized critical neuronal networks, where branching approximation is used ubiquitously.

BP 22.10 Thu 17:15 H 1058

Solution of the Fokker-Planck equation for neurons with adaptation — •Tilo Schwalger and Benjamin Lindner — Institute of Physics, Humboldt-University at Berlin; Bernstein Center of Computational Neuroscience, Berlin, Philippstr. 13,10115 Berlin

Firing rate adaptation is an ubiquitous features of neurons throughout the nervous system. Slow adaptation currents that act as a negative feedback give rise to an intricate neuron dynamics leading to a characteristic spiking statistics already in the spontaneous firing activity. A prominent example are negative correlations between interspike intervals, which have been frequently measured in experiments. We have recently derived an analytical expression of the correlation coefficient of a perfect integrate-and-fire neuron with an adaptation current [1]. This result holds in the deterministic limit, where the white-noise driving is infinitesimally small. To extend the result to stronger noise driving, it is necessary to determine self-consistently the stationary distribution of the adaptation current sampled at the spike times. To this end, we solve the associated two-dimensional Fokker-Planck equation about the deterministic limit distribution: this amounts to a WKB approximation for weak noise. Our approximations of the solution are compared with extensive simulations of the adapting neuron model.

[1] Schwalger T, Fisch K, Benda J, Lindner B, Plos Comp Biol., 2010