SYBN 2 Biologische und Soziale Netzwerke II

Zeit: Montag 12:00–13:20 Raum: TU HE101

SYBN 2.1 Mo 12:00 TU HE101

Regulation of Cell Motility via Functional Phases and Modules — •Hans-Günther Döbereiner[1,2], Benjamin J. Dubin-Thaler[1], Gregory Giannone[1], Harry S. Xenias[1], and Michael P. Sheetz[1] — [1]Department of Biology, Columbia University, New York, NY 10027 — [2]Department of Physics, Columbia University, New York, NY 10027

We have observed the existence of distinct phases [1] and dynamic phase transitions [2] in the motile behavior of mouse embryonic fibroblasts. The main phase exhibits periodic contractions of the actomyosin cytoskeleton. These periodic contractions are used by the cell to probe the elasticity of the substrate via integrin linkages [3]. We suggest a hierarchical classification of proteins into modules linked to phase structure, phase regulation parameters, and pure signaling components controlling these parameters. A tentative phase diagram is presented. A phase model of motility could serve as a paradigmatic example for a powerful general ordering principle in quantitative systems biology.

[1] B. Dubin-Thaler, G. Giannone, H.-G. Döbereiner, and M. P. Sheetz, Biophys. J. **86**, 1794 (2004).

[2] H.-G. Döbereiner B. Dubin-Thaler, G. Giannone, H. S. Xenias, and M. P. Sheetz, Phys. Rev. Lett. **93**, 108105 (2004).

[3] G. Giannone, B. Dubin-Thaler, H.-G. Döbereiner, N. Kieffer, A. R. Bresnick, and M. P. Sheetz, Cell **116**, 431 (2004).

SYBN 2.2 Mo 12:20 TU HE101

Network Topology Induces Speed Limits to Coordinating Spikes — An Approach Using Random Matrix Theory — •Marc Timme, Fred Wolf, and Theo Geisel — Max-Planck-Institut für Strömungsforschung, 37073 Göttingen, Germany

When a neural network processes information, a number of specific neurons need to coordinate their activity, e.g. synchronize their spikes. Given that neurons are typically interconnected to a large network of complicated topology the question arises: How fast can neurons in such a network coordinate their spikes?

Here we analyze the dynamics of large random networks of integrate-and-fire neurons. In such networks, a balanced state of irregular activity coexists with a regular synchronous state [1]. Using a random matrix approach, introduced by Wigner in the 1950s to characterize energy spectra of atomic nuclei, we predict the characteristic time of synchronization in dependence of neuron and network properties [2]. We find that the speed of synchronization is limited by the network topology and remains finite, even if the coupling strengths between neurons become infinite.

[1] M. Timme et al., Phys. Rev. Lett., **89**, 258701 (2002).
[2] M. Timme et al., Phys. Rev. Lett., **92**, 074101 (2004).

SYBN 2.3 Mo 12:40 TU HE101

Graph Alignment in Biological Networks — •Johannes Berg — Institut für Theoretische Physik, Universität zu Köln, Zülpicher Str.77, 50937 Köln

Interaction networks are of central importance in post-genomic molecular biology, with increasing amounts of data becoming available by high-throughput methods. Examples are gene regulatory networks or protein interaction maps. It is clear that the arrival of large-scale data in the form of networks also brings the need for new concepts and tools for its analysis.

Topological motifs, i.e., patterns occurring repeatedly at different positions in the network have recently been identified as basic modules of molecular information processing, implementing simple computations, such as filtering, on a molecular level. Using concepts from sequence alignment and from the statistical mechanics of networks, I discuss a scoring function and alignment algorithm for network motifs. The algorithm is applied to the regulatory network of E. coli. I also discuss global graph alignment in order to compare biological networks across species.

SYBN 2.4 Mo 13:00 TU HE101

Structural and game-theoretical analysis of biochemical networks — •Stefan Schuster — Universität Jena, Lehrstuhl für Bioinformatik, Ernst-Abbe-Platz 2, 07743 Jena

A major challenge in biology is to clarify the relationship between structure and function in complex intracellular networks. Dynamic mathematical modelling of large-scale metabolic and regulatory networks meets difficulties as the necessary mechanistic detail is rarely available. In contrast, structure-oriented methods such as metabolic pathway analysis only require network topology. One of the central concepts in this analysis is that of elementary flux modes. Here, we explain that concept and an algorithm for calculating all elementary modes. We show that it is well-suited for determining routes enabling maximum yields of bioconversions and for analysing redundancy and robustness properties of living cells. For understanding the characteristics of metabolic pathways, evolutionary game theory is a promising approach. Two species of micro-organisms that use the same nutrient, but may choose between two different pathways of ATP production, can be considered as players in the sense of game theory. The pathways are regarded as distinct strategies to which payoffs can be assigned. The payoffs are assumed to be proportional to the steady-state number of individuals sustainable on the basis of these strategies. For each species (or strain), this number does not only depend on the strategy chosen by that species but also on the strategy of the other species. In a certain parameter range, the payoffs fulfil the conditions for the prisoner's dilemma.