## BP 19: Focus Session: Dynamics of Adaptive Networks (joint with SOE and DY)

Adaptive Networks attracted recent interest through their dynamical properties that emerge from the interaction of two classes of processes (which may include stochasticity): (i) Growth and restructuring of the network topology itself, and (ii) Coupled dynamical systems defined on the network nodes. In this session, an introduction and overview into adaptive networks and their analytical and numerical investigation is complemented by their recent application to socio-economic, biological and epidemologic systems. (Session compiled by Eckehard Schöll, TU Berlin and Jens Christian Claussen, U Lübeck.)

Time: Wednesday 9:30–12:30 Location: H37

Topical Talk BP 19.1 Wed 9:30 H37

Adaptive Networks: Of social interactions and mathematical tools — •Anne-Ly Do — Max-Planck-Institut für Physik komplexer Systeme, Dresden

Adaptive networks are characterized by the co-evolution of local and topological degrees of freedom. Prime examples are networks of social interactions: Individuals are altered and shaped through interaction with others. On the other hand, they can often decide with whom to interact. Adaptive network models of social systems have attracted keen interest as they promise to provide the key to a number of prominently discussed phenomena such as fragmentation of groups into like-minded subgroups, evolution or break-down of social structures promoting cooperation, and emergence of fairness and leadership. In this talk, I review recent studies that link emergent phenomena in social systems to adaptive feedback in the respective interaction nets. Moreover, I discuss the analytical techniques used, thus aiming to outline both, findings and tools.

BP 19.2 Wed 10:00 H37

Controlling cluster synchronization by adaptive network topology — ●JUDITH LEHNERT¹, ANTON SELIVANOV², ALEXANDER FRADKOV²,³, and ECKEHARD SCHÖLL¹ — ¹Institut für Theoretische Physik,TU-Berlin, Hardenbergstr 36, 10623 Berlin, Germany, — ²SPb State University, Universitetskii pr.28, St.Petersburg, 198504 Russia — ³Institute for Problems of Mechanical Engineering, Russian Academy of Sciences, Bolshoy Ave, 61, V. O., St. Petersburg, 199178 Russia

Adaptive networks are characterized by a complicated interplay between the dynamics on the nodes and a changing topology: The topology evolves according to the state of the system, while at the same time the dynamics on the network and thus its state is influenced by that topology. Here, we present an algorithm for a changing topology that allows us to control the dynamics on the network. In particular, we control zero-lag and cluster synchronization in delay-coupled networks of Stuart-Landau oscillators. Our method is robust towards different initial conditions. Furthermore, it is not necessary to adapt the network as a whole but it is sufficient to apply the method to a subset of the links to control the dynamics of all nodes. Finally, we discuss the topological characteristics of the network after successful control.

BP 19.3 Wed 10:15 H37

Resilience of collective dynamics in fluctuating network environments — • ALEXANDER GRIMM — ETH Zürich, Chair of Systems Design, Switzerland

Do totalitarian networks perform better than democratic networks? What is the most appropriate hierarchy level for networks embedded in volatile environments? We use agent-based models to discover the effect of hierarchy on performance in networks located in highly fluctuating environments. We investigate the emergence of collective dynamics of many units embedded in complex network environments which change boundary conditions constantly. The agents have to adopt their behavior due to these constantly changing conditions. Although the individual node properties do not change, the network shows permanently changing structure with enormously differing properties. The fluctuating environments come into force via three different dynamics which happen on different time scales in adiabatic approximations. We show that a synchronization process is a good approach to model information transfer. The information transfer in the model interlinks the three dynamics. First, the link formation process is the most fundamental process. It is driven by centrality. Second, the a synchronization process describes the information transfer among the nodes. And third, an endogenized node churn removes those nodes which deviate from the networks' common culture. In differing hierarchy values we find a phase transition in centrality. Hysteresis effects and trade-off properties make it possible to determine the most appropriate topology of the network, given its operation area.

BP 19.4 Wed 10:30 H37

Absence of epidemic thresholds in a growing adaptive network —  $\bullet$ GÜVEN DEMIREL<sup>1</sup> and Thilo Gross<sup>2</sup> — <sup>1</sup>Max-Planck-Institute for the Physics of Complex Systems, Dresden, Germany — <sup>2</sup>University of Bristol, Bristol, United Kingdom

In epidemics on network, a central role is played by the degree distribution, i.e. the distribution of the number of neighbors of nodes. In particular in scale-free networks, where the variance of the degree distribution diverges, no epidemic thresholds exist, such that even diseases with arbitrary low infectiousness can percolate. By contrast, in networks where the variance of the degree distribution is finite, diseases generally need to surpass a threshold infectiousness to persist. In the real world the degree distribution is not independent of epidemics, but is shaped through disease induced behavioral changes and mortality in a complex interplay. Here, we consider the growth of a network from which nodes are simultaneously removed due to disease-induced mortality. We show analytically and numerically that in this system no epidemic thresholds exists, although the interplay between network growth and epidemic spreading leads to networks in which the degree distribution has a finite variance.

BP 19.5 Wed 10:45 H37

Hierarchical transport structures in the network of *Physarum polycephalum* — •Werner Baumgarten and Marcus J. B. Hauser — Abteilung Biophysik, Otto-von-Guericke-Universität Magdeburg, Magdeburg, Germany

The plasmodium of the slime mould *Physarum polycephalum* consists of a single multinucleate giant amoeboid cell that forms a characteristic two-dimensional vein network. Through the entire tubular network protoplasm is transported periodically back and fro. During evolution this transportation network is optimized for efficiency [1].

The vein network of P. polycephalum is considered a weighted undirected graph, with veins as edges and branching points as nodes, the weight is given by the local drag of each vein [2]. A graph analysis is performed on the network of P. polycephalum based on the conjecture of laminar flow in the veins. Experiments to quantify the structure were carried out on multiple scales. We demonstrate that the network posses a self-similar hierarchic structure which consists of nested loops of veins of decreasing transport efficiency. These results are used to describe the network evolution.

A. Tero, S. Takagi, T. Saigusa, K. Ito, D. P. Bebber, M. Fricker,
 K. Yumiki, R. Kobayashi, T. Nakagaki, 2010, Science, 327, 439

[2] W.Baumgarten, T. Ueda, M.J.B. Hauser, Phys. Rev. E 2010, 82, 046113

BP  $19.6 \mod 11:00 \mod 37$ 

Natural emergence of clusters and bursts in network evolution —  $\bullet$ James Bagrow and Dirk Brockmann — Northwestern University

Network models with preferential attachment, where new nodes are injected into the network and form links with existing nodes proportional to their current connectivity, have been well studied for some time. Extensions have been introduced where nodes attach proportional to arbitrary fitness functions. However, in these models attaching to a node increases the ability of that node to gain more links in the future. We study network growth where nodes attach proportional to the clustering coefficients, or local densities of triangles, of existing nodes. Attaching to a node typically lowers its clustering coefficient, in contrast to preferential attachment or rich-get-richer models. This simple modification naturally leads to a variety of rich phenomena, including aging, non-poissonian bursty dynamics, and community for-

mation. This shows that complex network structure can be modeled without artificially imposing multiple dynamical mechanisms.

BP 19.7 Wed 11:15 H37

Evolution of Cooperation on Stochastic Dynamical Networks — •BIN Wu and ARNE TRAULSEN — Research Group for Evolutionary Theory, Max-Planck-Institute for Evolutionary Biology, Plön, Germany

Cooperative behavior that increases the fitness of others at a cost to oneself can be promoted by natural selection only in the presence of an additional mechanism. One such mechanism is based on population structure, which can lead to clustering of cooperating agents. Recently, the focus has turned to complex dynamical population structures such as social networks, where the nodes represent individuals and links represent social relationships. We investigate how the dynamics of a social network can change the level of cooperation in the network. Individuals either update their strategies by imitating their partners or adjust their social ties. For the dynamics of the network structure, a random link is selected and breaks with a probability determined by the adjacent individuals. Once it is broken, a new one is established. This linking dynamics can be conveniently characterized by a Markov chain in the configuration space of an ever-changing network of interacting agents. Our model can be analytically solved provided the dynamics of links proceeds much faster than the dynamics of strategies. This leads to a simple rule for the evolution of cooperation: The more fragile links between cooperating players and non-cooperating players are (or the more robust links between cooperators are), the more likely cooperation prevails. Our approach may pave the way for analytically investigating coevolution of strategy and structure.

Topical Talk BP 19.8 Wed 11:30 H37 Bio-molecular Networks: Structure, Function, Evolution —

•Michael Lässig — Institut für theoretische Physik, Universität zu

Köln

In biological systems, networks exist at multiple levels. One is structure: components of a system are linked because they are close in space. An example is the adjacency of amino acids in a protein. Another level is function: components are linked because they do something together, such as the genes in a regulatory or metabolic network. In this talk, I discuss how structure and function networks shape the evolutionary dynamics of organisms and species - and conversely, how evolutionary observations can uncover underlying functional networks. I use two examples: the evolutionary properties of gene regulatory networks and the evolution of the human influenza virus.

Topical Talk BP 19.9 Wed 12:00 H37 Adaptive networks and critical dynamics — ◆STEFAN BORNHOLDT — Institut für Theoretische Physik, Universität Bremen

Dynamical networks have been studied from the perspective of statistical physics, motivated by questions of information processing in neural networks and genetic networks. In both applications, hypotheses have been discussed that relate optimality of information processing to dynamical criticality in the networks. Consequently, toy models for adaptive networks have been constructed that robustly establish criticality in the network. Here I review a particularly simple model class based on models from physics and discuss its application to the phenomenon of criticality in biological neural networks.

- [1] M. Rybarsch and S. Bornholdt, Self-organized criticality in neural network models, in: "Criticality in Neural Systems", Niebur E, Plenz D, Schuster HG (eds.) 2013 (in press); arXiv:1212.3106.
- [2] M. Rybarsch and S. Bornholdt, Binary threshold networks as a natural null model for biological networks, Phys. Rev. E 86 (2012) 026114.
- [3] M. Rybarsch and S. Bornholdt, Self-organization to criticality in neural networks: A minimal model with binary threshold nodes, arXiv:1206.0166.