

BIOLOGICAL AND SOCIAL NETWORKS (SYBN)

veranstaltet vom Arbeitskreis Physik Sozio-Ökonomischer Systeme (AKSOE)
 gemeinsam mit dem Arbeitskreis Biologische Physik (AKB),
 dem Fachverband Chemische Physik und Polymerphysik (CPP)
 und dem Fachverband Dynamik und Statistische Physik (DY)

Organisation

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The recent observation and study of complex network structures in the living world surrounding us, sparked an avalanche of research activity in the physics community. Examples are biological networks, spanning all scales from molecular communication networks in the genome, via neural networks to ecological food webs and species relationships. Other examples are the internet wiring and the World Wide Web, or social networks that range from email relationships to networks of sexual contacts. Methods from theoretical physics helped in understanding these systems, including new views on how epidemics spread on network structures, aspects of stability and robustness of communication networks, and are actively contributing to understanding the workings of our genome and complex diseases. The symposium presents a selected overview of this highly active field and sketches new perspectives for theoretical physics research in interdisciplinary applications.

ÜBERSICHT DER HAUPTVORTRÄGE UND FACHSITZUNGEN

(Hörsaal TU HE101)

Hauptvorträge

SYBN 1.1	Mo	09:45	(TU HE101)	Computation, evolution and tinkering in complex networks, <u>Ricard Sole</u>
SYBN 1.2	Mo	10:15	(TU HE101)	Properties of attractors and relevant nodes in random Boolean networks, <u>Barbara Drossel</u>
SYBN 1.3	Mo	10:45	(TU HE101)	Epidemic modeling: dealing with complex networks, <u>Alessandro Vespignani</u>
SYBN 1.4	Mo	11:15	(TU HE101)	Traffic and Computation in Genetic Regulation, <u>Kim Sneppen</u>

Fachsitzungen

SYBN 1	Biologische und Soziale Netzwerke I	Mo 09:45–11:45	TU HE101	SYBN 1.1–1.4
SYBN 2	Biologische und Soziale Netzwerke II	Mo 12:00–13:20	TU HE101	SYBN 2.1–2.4
SYBN 3	Biologische und Soziale Netzwerke, Postersitzung	Mo 14:00–15:30	Poster TU E	SYBN 3.1–3.34

Fachsitzungen

– Haupt-, Kurzvorträge und Posterbeiträge –

SYBN 1 Biologische und Soziale Netzwerke I

Zeit: Montag 09:45–11:45

Raum: TU HE101

Hauptvortrag

SYBN 1.1 Mo 09:45 TU HE101

Computation, evolution and tinkering in complex networks — ●RICARD SOLE — ICREA-Complex Systems Lab, Universitat Pompeu Fabra, Dr Aiguader 80, E-08003 Barcelona

Complex biological networks have very different origins than technological ones. The latter involve extensive design and, as engineered structures, include a high level of optimization. The former involve (in principle) contingency and structural constraints, with new structures being incorporated through tinkering with previously evolved modules or units. However, the observation of the topological features of different biological nets suggests that nature can have a limited repertoire of "attractors" suggesting some common principles of evolution beyond their specific nature. A relevant link in this context involves the presence of computation, which is known to be robust in biological systems and fragile within the technological universe. Surprisingly, many relevant features of complex natural networks (some shared by artificial ones) are a consequence of evolutionary rules with weak relation to functionality. Conversely, when evolving artificial systems using bio-inspired rules, robustness to failure and heterogeneous topology seem to emerge as a byproduct of the evolutionary rules. These observations will help understanding the evolution of complexity in nature and reinventing the way technology is being designed.

Hauptvortrag

SYBN 1.2 Mo 10:15 TU HE101

Properties of attractors and relevant nodes in random Boolean networks — ●BARBARA DROSSEL — TU Darmstadt, Institut für Festkörperphysik, Hochschulstraße 6, 64289 Darmstadt

This talk gives an overview of the properties of random Boolean networks, based on recent work by several groups, and including a java applet to illustrate the properties of these networks. The focus is on critical networks with connectivity 1 or 2. After a general introduction to these models, the talk deals first with the relevant nodes, which determine the number and lengths of attractors. It will be shown that the number of relevant nodes increases with system size N as $N^{1/2}$ and $N^{1/3}$ for connectivity 1 and 2. Then, the properties of the attractors will be investigated. It will be argued that their mean number and length increase faster than any power law. Finally, the robustness of these findings with respect to modifications of the model will be discussed.

Hauptvortrag

SYBN 1.3 Mo 10:45 TU HE101

Epidemic modeling: dealing with complex networks — ●ALESSANDRO VESPIGNANI — School of Informatics and Department of Physics, Indiana University — Lab. Physique Theorique, Universite Paris Sud, Paris

The systematic study of population networks and their social/spatial structure has shown the ubiquitous presence of complexity features mathematically encoded in heavy-tailed statistical distributions, diverging fluctuations and emerging properties. Despite a variety of approaches have been developed in order to take into account the many complications and heterogeneities observed in the spread of epidemics, complexity is not the same as the sum of the merely complicated elements accounted for in sophisticated epidemic modeling. Indeed complex properties generally correspond to the breakdown of standard models. For instance this is the case of epidemic spreading in scale-free networks in which the lack of any intrinsic epidemic threshold generates a peculiar scenario with implications in immunization and containment policies. In this perspective we will provide a discussion of epidemic modeling that accounts for the presence of the network's complexity at various levels: connectivity pattern, traffic intensity, population heterogeneity. Finally, we will discuss to which extent the protection of populations, defined in the context of immunization policies designed to effectively reduce or prevent the large scale spreading of epidemics, is affected by the system's complexity.

Hauptvortrag

SYBN 1.4 Mo 11:15 TU HE101

Traffic and Computation in Genetic Regulation — ●KIM SNEPPEN — Nordita/Niels Bohr Institute, Blegdamsvej 17, 2100 Copenhagen Ø

I will discuss physics of biological regulatory mechanism from simple recruitment, to traffic on DNA and to analysis of genetic regulatory networks. The talk will discuss design principles found in regulation of bacteriophages, using as examples the lambdaoid family versus the P2 family of temperate phages. We will use these to emphasize the parts of genetic regulative networks that deals with integrated computation, respectively the parts of the regulation that represents distributed signaling. We finally use the phage networks to teach us some basic lessons about how one can compare signaling networks of different organisms.

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-THALER¹, GREGORY GIANNONE¹, HARRY S. XENIAS¹, and MICHAEL P. SHEETZ¹ — ¹Department of Biology, Columbia University, New York, NY 10027 — ²Department 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, Zùlpicher 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.

SYBN 3 Biologische und Soziale Netzwerke, Postersitzung

Zeit: Montag 14:00–15:30

Raum: Poster TU E

SYBN 3.1 Mo 14:00 Poster TU E

The dynamics of Kauffman networks with connectivity two under stochastic asynchronous update — ●FLORIAN GREIL and BARBARA DROSSEL — Institut für Festkörperphysik, Technische Universität Darmstadt

We investigate critical random boolean networks, which are usually implemented with synchronous update. Biologically, this is highly improbable. For this reason, we study the influence of a stochastic updating scheme. We find that the number of attractors grows as a power law with the system size, while the size of the attractors increases exponentially. These results are compared with other updating schemes.

SYBN 3.2 Mo 14:00 Poster TU E

From simple Boolean networks to relevant critical networks — ●VIKTOR KAUFMAN und BARBARA DROSSEL — TU Darmstadt, Institut für Festkörperphysik, AG Drossel, Hochschulstraße 6, 64289 Darmstadt

Random Boolean networks (RBN) have now been studied for almost 40 years, but are still not fully understood. We first present results for the number and length of attractors in two types of simple Boolean networks and show that they share many features of critical RBN. The reason for this is that these simple networks occur also as components of the relevant part of critical RBN. We then focus on general properties of the relevant components of critical RBN, such as the component topology. Since direct computer simulations are unfeasible for large system sizes, we have to support them by analytical arguments.

SYBN 3.3 Mo 14:00 Poster TU E

Network topology from robustness of information processing — ●KONSTANTIN KLEMM¹ and STEFAN BORNHOLDT² — ¹Bioinformatik, Universität Leipzig, Kreuzstr. 7b, 04103 Leipzig — ²Theoretische Physik, Universität Bremen, Otto-Hahn-Allee, 28334 Bremen

In biological systems, highly robust information processing is crucial for fitness and survival. System output must be reproducible despite the intrinsic noise of the elements (genetic switches, neurons, etc.). Such noise poses severe stability problems to parallel information processing as it tends to desynchronize system dynamics (e.g. via fluctuating response or transmission time of the elements). We study the reliability of the output from networks of autonomous noisy elements. We find that the presence or absence of reliable dynamical attractors with self-sustained synchrony strongly depends on the underlying circuitry [1]. Our model suggests that the observed motif structure of biological signaling networks is shaped by the biological requirement for reproducibility of attractors.

[1] K. Klemm and S. Bornholdt, preprint q-bio/0409022

SYBN 3.4 Mo 14:00 Poster TU E

Dynamic Response Behavior of Random Networks — ●HAIJUN ZHOU and REINHARD LIPOWSKY — Max-Planck-Institute of Colloids and Interfaces, Potsdam 14424

A general class of dynamic models on random networks is studied by analytical methods and computer simulations. The networks differ in their connectivity and in their degree distribution, $P(k)$, which represents the probability that a vertex is connected to k nearest neighbors. Each vertex can attain two internal states described by binary variables or Ising-like spins which evolve in time according to local majority rules. Scale-free networks, for which the degree distribution has the power law tail $P(k) \sim k^{-\gamma}$, are shown to exhibit qualitatively different response behavior for $\gamma \leq 5/2$ and $\gamma > 5/2$. For $\gamma \leq 5/2$, even *infinite* networks recover from any perturbation within a *finite* response time. For $\gamma > 5/2$, this time diverges with the size of the network. This different response behavior sheds new light on the empirical observation that many real-world networks are scale-free with $2 < \gamma < 5/2$.

SYBN 3.5 Mo 14:00 Poster TU E

Spatially heterogeneous stimulation of networks of coupled oscillators — ●ANDREAS BOHN^{1,2} and JORDI GARCIA-OJALVO¹ — ¹Dept. de Física i Enginyeria Nuclear, Universitat Politècnica de Catalunya, Colom 11, 08222 Terrassa / Barcelona, Spain — ²FB Biologie - Graduiertenkolleg, TU Darmstadt, Schnittspahnstr. 10, 64287 Darmstadt, Germany

Heterogeneity, or non-uniformity, is a common feature in real-world networks, especially in spatially extended biological systems. In this work we investigate the effect of white noise with space-dependent intensity on the dynamics of a network of diffusively coupled FitzHugh-Nagumo oscillators in the excitable regime. The influence of coupling strength on the spatiotemporal coherence of the network dynamics is considered, as well as the possibilities of the an enhancement of the coherence through spatial non-uniformities in the excitability of the elements or the coupling strength. The influence of the network topology on the network coherence is investigated by cutting a single connection in various points of the network. The results are compared with similar investigations in networks of biologically motivated oscillators under spatially heterogeneous, periodic stimulation.

SYBN 3.6 Mo 14:00 Poster TU E

Robust Pattern Formation by Coupled Regulatory Networks — ●THIMO ROHLF¹ and STEFAN BORNHOLDT² — ¹Max-Planck-Institute for Mathematics in the Sciences, Inselstr. 22, D-04103 Leipzig, Germany — ²Institut für Theoretische Physik, Universität Bremen, Otto-Hahn-Allee, D-28334 Bremen, Germany

Based on a very general non-equilibrium mechanism for spatial pattern formation [1] we study how morphogenesis can be controlled by locally coupled discrete dynamical networks, similar to gene regulation networks of cells in a developing multicellular organism [2]. As an example we study the developmental problem of spatial domain formation and proportion regulation in the presence of noise and cell flow. We find that networks that solve this task exhibit a hierarchical structure of information processing and are of similar complexity as developmental circuits of living cells. A further focus of this study is a detailed analysis of noise-induced dynamics, which is a major ingredient of the control dynamics in the developmental network model. A master equation for domain boundary readjustments is formulated and solved for the continuum limit. Evidence for a discontinuity (similar to a first order phase transition) in equilibrium domain size at vanishing noise is given by finite size scaling. A second order phase transition at increased cell flow is studied in a mean field approximation. Finally, we discuss potential applications.

- [1] Rohlf, T. and Bornholdt, S. (2003). cond-mat/0312366, submitted.
 [2] Rohlf, T. and Bornholdt, S. (2004). qbio.MN/0401024, submitted.

SYBN 3.7 Mo 14:00 Poster TU E

Topology regulates pattern formation capacity of binary cellular automata on graphs — ●CARSTEN MARR and MARC-THORSTEN HÜTT — Bioinformatics Group, Department of Biology, Darmstadt University, Schnittspahnstr. 3-5, D-64287 Darmstadt

We study the effect of topology variation on the dynamic behavior of a system with local update rules. We implement one-dimensional binary cellular automata on graphs with various topologies by formulating two sets of degree-dependent rules, each containing a single parameter. We observe that changes in graph topology induce transitions between different dynamic domains without a formal change in the update rule. Along with topological variations, we study the pattern formation capacities of regular, random, small-world and scale-free graphs. Pattern formation capacity is quantified in terms of two entropy measures, which for standard cellular automata allow a qualitative distinction between the four Wolfram classes. We present a model which explains the differences in a mean-field manner. Implication for our understanding of information transport through complex, network-based systems are discussed.

By implementing these dynamics on protein interaction graphs we can assess the graph's capacity to produce complex (Wolfram class IV) patterns.

SYBN 3.8 Mo 14:00 Poster TU E

The role of loops in synchronization of networks — ●HILDEGARD MEYER-ORTMANN, FILIPPO RADICCHI, and SOON-HYUNG YOON — SES, International University Bremen, P.O.Box 750561, D-28725 Bremen

We derive conditions for synchronization in various ensembles of oscillators as a function of the network topology. In particular we study Kuramoto oscillators on linear chains, rings and Caley-trees. We also consider Rössler oscillators on scale-free (Barabasi-Albert) networks. As it turns out, the presence of loops facilitates synchronization in both type of ensembles if otherwise the parameters are unchanged.

SYBN 3.9 Mo 14:00 Poster TU E

Offdiagonal Complexity: A computationally quick complexity measure for graphs and networks — ●JENS CHRISTIAN CLAUSSEN — Theoretical Physics, University Kiel

A vast variety of biological, social, and economical networks shows topologies drastically differing from random graphs; yet the quantitative characterization remains unsatisfactory from a conceptual point of view. Motivated from the discussion of small scale-free networks, a biased link distribution entropy is defined, which takes an extremum for a power law distribution. This approach is extended to the node-node link cross-distribution, whose nondiagonal elements characterize the graph structure beyond link distribution, cluster coefficient and average path length. From here a simple (and computationally cheap) complexity measure can be defined. This Offdiagonal Complexity (OdC) [1] is proposed as a novel measure to characterize the complexity of an undirected graph, or network. While both for regular lattices and fully connected networks OdC

is zero, it takes a moderately low value for a random graph and shows high values for apparently complex structures as scale-free networks and hierarchical trees.

- [1] J. C. Clausen, arxiv.org q-bio/0410024

SYBN 3.10 Mo 14:00 Poster TU E

Networks with tunable clustering coefficient: Construction and Properties. — ●RAMON XULVI-BRUNET and IGOR M. SOKOLOV — Institut für Physik, Humboldt Universität zu Berlin, Newtonstr 15, D-12489, Berlin, Deutschland

To analyze the role of clustering in networks we introduce an algorithm which changes the clustering coefficient of a given network preserving exactly its degree distribution. Using it one can thus construct networks ranging from fully uncorrelated to maximally triangulated. We present some results related to topology and robustness of these strongly clustered networks.

SYBN 3.11 Mo 14:00 Poster TU E

Dynamics of scalefree networks: scaling behavior — ●CHRISTIAN VON FERBER, FLORIAN JASCH, and ALEXANDER BLUMEN — Theoretische Polymerphysik, Physikalisches Institut, Universität Freiburg

We characterize the dynamics of networks for problems ranging from the dynamics of randomly branched polymers and stress relaxation of near critical gels to diffusion and spreading (e.g. of viruses) on general networks. A basic property of a network is its degree distribution p_k , i.e. the probability that an arbitrary vertex is connected to k other vertices. If p_k exhibits a power law $p_k \sim k^{-\gamma}$ the network is called *scale-free*; scale-free networks differ from the classical random graphs, for which the distribution p_k is Poissonian. Recent work clarified that the properties of scale-free networks at the percolation threshold differ markedly from the classical case: for $\gamma < 4$ nontrivial γ -dependent critical exponents appear [1]. Many time and frequency-dependent observables can be written in terms of the spectrum $\rho(\lambda)$, the density of eigenvalues of the discrete Laplacian defined on the network. We develop and solve an integral equation for $\rho(\lambda)$ for random graphs with arbitrary degree distributions [2]. For scale-free networks close to percolation we find scaling forms for $\rho(\lambda)$. If p_k decays fast $\rho(\lambda)$ has a Lifshitz tail for $\lambda \rightarrow 0$ while for $p_k \sim k^{-\gamma}$ with $\gamma < 4$ a power law $\rho(\lambda) \sim \lambda^{d_s/2-1}$ with a γ -dependent spectral dimension d_s is found [2]. Extensive numerical diagonalizations of simulated ensembles of networks support our analytical findings.

- [1] R. Cohen et al. *Phys. Rev. E*, 66:036113, 2002.
 [2] F. Jasch, C. von Ferber, and A. Blumen. *Phys. Rev. E*, 68:051106, 2003; *Phys. Rev. E*, 70:016112, 2004

SYBN 3.12 Mo 14:00 Poster TU E

Community Structure of Complex Weighted Networks — ●SABINE TORNOW — Theoretische Physik III, Institut für Physik, Universität Augsburg, 86135 Augsburg, Germany

Complex networks arise in different contexts such as in biological systems (protein-protein interaction networks or in social systems, e.g., friendship networks). In addition to the complex topological structure these networks possess an intensity of their connection. It is therefore possible to assign a weight to each edge. One important property of many bio-molecular networks is the community structure which can be dependent on the network protein complexes, functional modules or co-expression clusters. We calculate the community structure of weighted bio-molecular networks with different methods including the superparamagnetic clustering and assess their results in the context of biological function.

SYBN 3.13 Mo 14:00 Poster TU E

Detecting fuzzy community structures in complex networks — ●JÖRG REICHARDT and STEFAN BORNHOLDT — Institute for Theoretical Physics, University of Bremen

Real world complex networks often show surprising modularity: nodes may be grouped into communities, the members of which are tightly linked among themselves but only loosely connected to the rest of the network. Often, these communities represent a higher organisational order or functional entities and are thus of special interest.

We present a recently developed community detection algorithm [1]. We map the problem of community detection onto finding the minima in the Hamiltonian of a Potts spin glass. By combining a short range ferromagnetic with an infinite range anti-ferromagnetic interaction in the Potts energy function, communities are found to coincide with the domains of equal spin value in these minima. Comparing global and local

minima of the Hamiltonian allows for the detection of hierarchies and overlapping ("fuzzy") communities and quantifying the association of nodes with multiple communities as well as the robustness of a community. No prior knowledge about the number of communities has to be assumed.

We show an exemplary application in biochemistry by detecting communities in a large protein folding network corresponding to stable and meta-stable conformations.

[1] J. Reichardt, S. Bornholdt, Phys. Rev. Lett. **93**, 218701, (2004)

SYBN 3.14 Mo 14:00 Poster TU E

Validation of community detection algorithms — ●STEFANIE MUFF, FRANCESCO RAO, and AMEDEO CAFLISCH — Biochemistry Department, University of Zurich, Switzerland

Several algorithms for the detection of community structure in complex networks have been proposed recently. Unless the grouping of the nodes into communities is already known, it is usually difficult to validate the performance of an algorithm and to compare the results of different clusterizations of the same network. Measures and algorithms for tackling this problem are introduced.

SYBN 3.15 Mo 14:00 Poster TU E

Complex networks for the description of energy landscapes — ●FRANCESCO RAO, STEFANIE MUFF, and AMEDEO CAFLISCH — Biochemistry Department, University of Zurich, Switzerland

The concept of energy landscapes is of great help for the understanding of dynamical systems. Many applications have emerged for the study of protein folding, clusters and supercooled liquids. Recently, an interesting analogy between complex networks and energy landscapes was shown [1,2]. Here, a method based on weighted network analysis is introduced for the quantitative characterization of free-energy basins. The method is applied in a study of folding for the description of the energy landscape of a 20-residue peptide. Although the method was developed for the analysis of energy landscapes its application can be extended to the study of weighted networks in general.

[1] J. Doye, PRL **88**, 238701 (2002) [2] F. Rao, A. Caflich, JMB **342**, 299-306 (2004)

SYBN 3.16 Mo 14:00 Poster TU E

Architecture of randomly evolving idiotypic networks — ●ULRICH BEHN¹ and MARKUS BREDE² — ¹Institut für Theoretische Physik, Universität Leipzig — ²CSIRO, Centre for Complex Systems Science, Canberra

B-Lymphocytes express on their surface receptors (antibodies) of a given specificity (idiotypic). Crosslinking these receptors by complementary structures (antigen or antibody) stimulates the lymphocyte. Thus a large functional network of interacting lymphocytes, the idiotypic network, emerges. Idiotypic networks conceived by Niels Jerne 30 years ago, experience a renewed interest, e.g. in the context of idiotypic vaccination and of autoimmune diseases.

In a minimalistic model [1] idiotypes are represented by bitstrings. We investigate the random evolution of the network towards a modularized functional architecture which is driven by the influx of new idiotypes, randomly generated in the bone marrow. The modules are clearly distinguished, e.g., by the mean life time of the occupied vertices. They include densely connected core groups and peripheral groups of isolated vertices, resembling central and peripheral part of the biological network.

[1] M. Brede, U. Behn, Phys. Rev. E (67), 031920 (2003).

SYBN 3.17 Mo 14:00 Poster TU E

Transition from an excitable to an oscillatory state in *Dictyostelium discoideum* — ●CHRISTIANE HILGARDT¹, ANDREY A. POLEZHAEV² und STEFAN C. MÜLLER¹ — ¹Otto-von-Guericke University Magdeburg, Universitätsplatz 2, 39106 Magdeburg, Germany — ²P.N. Lebedev Physical Institute, Leninsky prosp. 53, 119991 Moscow, Russia

Under conditions of starvation populations of the amoebae *Dictyostelium discoideum* aggregate mediated by chemical excitation waves of cAMP. Two types of waves can be observed, either spiral or circular-shaped ones. We investigate the transition of *Dictyostelium* patterns from the excitable to the oscillatory behaviour, in particular, the change from spiral waves to target patterns. In experiments a continuous transition from the spiral type pattern to target waves was observed at the later stages of aggregation. On the basis of a model for *Dictyostelium* aggregation we give a theoretical explanation for such transitions. It is shown that cell density can be an effective bifurcation parameter. Under certain

conditions the active medium is shifted from the excitable to the oscillatory state while the frequency of oscillations is proportional to the square root of the cell density. Thus the regions with the highest cell density, during the early stages of the spatial rearrangement of the cells, become pacemakers and produce target patterns. These analytic results were confirmed in numerical simulations of the model. We implement the model results into a biological context and discuss the role of experimental conditions and controlling factors for the type of the observed pattern.

SYBN 3.18 Mo 14:00 Poster TU E

Nonlinear Protein Degradation and the Function of Genetic Circuits — ●ULRICH GERLAND¹, NICOLAS BUCHLER², and TERENCE HWA³ — ¹Department Physik and CENS, LMU München, Germany — ²Center for Studies in Physics and Biology, The Rockefeller University, New York — ³Physics Department and Center for Theoretical Biological Physics, University of California at San Diego

The functions of genetic circuits require a sufficient degree of cooperativity in the circuit components. In this study, we examine a simple source of cooperativity that stems from the nonlinear degradation of multimeric proteins. Ample experimental evidence suggests that protein subunits degrade less rapidly when associated in multimeric complexes, an effect we refer to as 'cooperative stabilization'. For homodimers, this effect leads to a concentration dependence in the protein degradation rate, since monomers which are predominant at low protein concentrations are more rapidly degraded. For such proteins, cooperative stabilization can effectively widen the accessible range of protein levels *in vivo*. Such an increased range is important both for the robust operation of genetic circuits as well as their evolvability. Through theoretical analysis of two model gene circuits in bacteria, we show that a few-fold difference between the degradation rate of monomers and dimers can substantially enhance the operation of these circuits. Our results suggest that cooperative stabilization needs to be considered explicitly and characterized quantitatively in any systematic experimental or theoretical study of gene circuits.

SYBN 3.19 Mo 14:00 Poster TU E

Model selection and sampling properties of molecular networks — ●MICHAEL STUMPF¹, PIERS INGRAM¹, CARSTEN WIUF², and ROBERT MAY³ — ¹Department of Biological Sciences, Imperial College London, UK — ²Bioinformatics Research Center, University of Aarhus, 8000 Aarhus, Denmark — ³Department of Zoology, University of Oxford, UK

Most studies of molecular or cellular networks have only looked at small subsets of the true network. Applying formal statistical model selection methods to protein interaction and metabolic networks in 5 different organisms we find that simple scale-free network models do not adequately describe current data on such molecular networks. Only if the degree distributions of the network and randomly sampled subnets belong to the same family of probability distribution is it possible to extrapolate from subnet data to properties of the global network. We show that this is indeed the case for some important classes of networks, notably classical random graphs and exponential random graphs. For scale-free degree distributions, however, this is not the case.

We then apply the sampling formalism to several real data sets and discuss how it affects evolutionary inferences. Straightforward, and biologically realistic, extensions of scale-free models vastly improve qualitative and quantitative agreement between real data and theoretical models.

SYBN 3.20 Mo 14:00 Poster TU E

Primary Linguistic Units in Genomes — ●STEPHAN HEYMANN¹, PETER RIEGER¹, and ANDREAS SCHAAL² — ¹Humboldt-Universität zu Berlin; Institut für Informatik; Lehrstuhl für Datenbanken und Informationssysteme; Unter den Linden 6; 10099 Berlin — ²contraco Consulting and Software Ltd.; Diepenseestrasse 10; 15732 Waltersdorf

We will present a new method for decomposition of genetic information. This method give rise to primary linguistic units (PLU) along a chromosome (to not use words like 'syllables' or 'words'), which are derived without any extrinsic assumptions or artificial parameters. We will demonstrate that the proposed decomposition displays linguistic features. We find new information structures irrespective of the molecular service they convey. It turned out that PLU scissoring allows to clearly separate between static noise and information along the chromosomal base sequence. Moreover, we overcome the major dogmatic obstacle of current bioinformatics. This consists in the premature effort to capture semantic and topological organisation of genomes by application of non-metric

measures of similarity and distance. In the talk we will demonstrate the force of expression by various life science applications.

SYBN 3.21 Mo 14:00 Poster TU E

Entropic Forces between Biopolymers — ●AZAM GHOLAMI^{1,2} and ERWIN FREY^{3,2} — ¹Hahn-Meitner Institut, Glienickerstr 100,14109 Berlin, Germany — ²Freie Universität, Arnimallee 14, 14195 Berlin, Germany — ³Hahn-Meitner Institut, Glienickerstr 100, 14109 Berlin, Germany

The interaction between biopolymers in the cytoskeleton is characterized by the interplay of energy and entropy. There are electrostatic forces, interactions mediated by crosslinking proteins, and steric interactions induced by thermal fluctuations.

Our studies focus on steric interactions in various geometries. We have performed extensive Monte Carlo simulations, where the polymers are described by the wormlike chain model. The repulsive interaction obtained from the Monte-Carlo data is well explained in terms of analytical results obtained from scaling arguments.

We also study the thermal fluctuations of polymers in the presence of point-like and sheet-like obstacles by both analytical and Monte-Carlo methods. Finally, we have analyzed how the active polymerization of a biopolymer affects the repulsive interaction between the polymer and a fluctuating membrane.

SYBN 3.22 Mo 14:00 Poster TU E

Reversible Chemical Patterning On Stimuli Responsive Polymer Film - Environment Responsive Lithography — ●LEONID IONOV¹, SERGIY MINKO², MANFRED STAMM¹, JEAN-FRANCOIS GOHY³, ROBERT JEROME³, and ANDREAS SCHOLL⁴ — ¹Leibniz Institute of Polymer Research Dresden, Germany — ²Clarkson University, Chemistry Department, Potsdam, USA — ³Centre for Education and Research on Macromolecules (CERM), University of Liège, Sart-Tilman, Belgium — ⁴Lawrence Berkely National Laboratory, USA

This paper aims is reporting on a novel type of lithography based on thin stimuli responsive polymer films. The basic concept is the permanent storage of a pattern, which is reversibly developed and erased upon exposure to appropriate environments, e.g. solvent, pH and temperature. This technique is promising for the design of smart sensors and nanodevices, and in microfluidic technologies. The general concept of this novel type of environment-responsive lithography will be presented and discussed.

SYBN 3.23 Mo 14:00 Poster TU E

Morphology transformation of blood vessel networks during tumor-induced neo-vascularization — ●HEIKO RIEGER¹ and KATALIN BARTHA² — ¹Theoretische Physik, Universität des Saarlandes, 66041 Saarbrücken, Germany — ²Department of medical Biochemistry, Semmelweis University, Budapest, Hungary

During tumor growth the surrounding regular vascular network in normal tissue is transformed into a highly tumor specific capillary network with a characteristic morphology. In human melanoma for instance one observes the compartmentalization of the tumor/vasculature system into a highly vascularized peritumoral region, the tumor periphery with high vessel density and increased vessel diameter, and the tumor center with large necrotic regions, low vessel density and very thick vessels. We introduce a microscopic model incorporating tumor growth, vessel cooption, neo-vascularization, vessel collapse and cell death. We show that the plastic deformation of the network into the observed morphology depends crucially on the local response of the vessels on the global blood flow pattern determined by the current vessel network topology. Vessel density and vessel directions reflect for a broad range of parameters the characteristic features of human melanoma. It is predicted that microvascular density at or inside the tumor, regarded as an important diagnostic tool in cancer treatment, does not necessarily determine the tempo of tumor progression.

SYBN 3.24 Mo 14:00 Poster TU E

On an evolutionary food web model with foraging effect — ●SATOSHI UCHIDA and BARBARA DROSSEL — Institut für Festkörperphysik, TU Darmstadt, Hochschulstr. 6, D-64289 Darmstadt, Germany

We present numerical evidence that all food webs obtained by evolutionary models, that simply combine the population dynamics with conventional functional responses (Lotka-Volterra type, Holling type, Beddington type) and a long term change in the topology of the webs due to evolutionary changes of species, are unstable and collapse eventually.

We explain the findings first of all, and in order to get stable complex food webs, we propose a more realistic model in which the flexible behaviour of predators based on the foraging theory is taken into account. We show the evolution and the structure of webs obtained by computer simulations of the model in the poster.

SYBN 3.25 Mo 14:00 Poster TU E

Discrete Breathers in Neural Networks — ●HECKE SCHROBENDORFF, VINCENT DAVID, JOACHIM HASS, J. MICHAEL HERRMANN, and THEO GEISEL — MPI für Strömungsforschung und Institut für Nichtlineare Dynamik der Universität Göttingen, Bunsenstr. 10, D-37073 Göttingen

Localization in non-linear lattices of excitable elements is present in discrete breathers^[1], and forms an interesting counterpart to localization of activity in neural systems^[2]. We study the behavior of breather-like excitations in a system of locally interacting integrate-and-fire neurons. Both numerical and analytical results justify the notion of a neural breather, which may form an element of modeling working memory and attention.

In particular we consider formation and collapse of neural breathers in dependence of the structure of the underlying lattice, the oscillatory mechanisms in the units, the range of the interaction, delays, spike latency, refraction, and noise. We also discuss networks of spatially distributed breathers, which may model communication between prefrontal cortex and other brain regions.

^[1] Aubrey S (1997) *Physica D* 103:201-250.

^[2] Rubin J, Bose A (2004) *Network: Computation in Neural Systems* 15:133-158.

SYBN 3.26 Mo 14:00 Poster TU E

Aktivitätspropagation in nichtlokalen neuronalen Netzwerken mit verzögerter Rückkopplung — ●AXEL HUTT — Institut für Physik, Humboldt-Universität zu Berlin, Newtonstr.15, 12489 Berlin

Nichtlokale neuronale Netzwerke stellen realistische Modelle zur Beschreibung von raumzeitlicher Dynamik des Gehirns dar. Die vorgestellte Arbeit beschreibt ein Modell des Neocortex, der eine nichtlokale verzögerte Rückkopplung aufweist. Ein Beispiel für solch eine Rückkopplung ist die bekannte Schleife zwischen Neocortex und dem Thalamus. Das vorgestellte Modell berücksichtigt ebenfalls Laufzeitverzögerungen im neuronalen Gewebe, die durch endliche axonale Geschwindigkeiten entstehen. Wandernde Fronten und Wellen werden für allgemeine nichtlokale synaptische Konnektivitäten des Cortex beschrieben und ein neuer Effekt der verzögerten Rückkopplung auf die Form der laufenden Front wird gefunden.

Referenzen:

- 1) F.Atay and A.Hutt, *Stability and Bifurcations in Neural Fields with Finite Propagation Speed and General Connectivity*, SIAM J.Applied Mathematics, in press (2004)
- 2) A.Hutt, *Physical Review E*, *Effects of nonlocal feedback on traveling fronts in neural fields subject to transmission delay*, in press (2004)

SYBN 3.27 Mo 14:00 Poster TU E

Development and Robustness of Cortical Brain Networks — ●MARCUS KAISER and CLAUS C. HILGETAG — Intl. Univ. Bremen, Campus Ring 6, 28759 Bremen

Networks of connections among cortical areas in mammalian brains possess small-world and scale-free characteristics. However, previously suggested growth mechanisms for small-world or scale-free networks are inappropriate for neural systems as they overlook spatial constraints. We propose an alternative model for spatial network development that can generate various kinds of real-world networks, from cortical and metabolic to transportation networks. The model produces similar general network properties as found in cortical networks, such as multiple distributed clusters, and comparable clustering coefficients and all-pairs shortest paths (ASP).

The multi-cluster architecture of cortical networks has implications for their robustness against edge removal. While the loss of edges within clusters can be easily compensated, the loss of fibers between clusters is critical. Comparably, due to scale-free properties, node removal has little effect in most cases, but is critical for 'hubs'. Thus, network topology may account for the great robustness of the brain.

SYBN 3.28 Mo 14:00 Poster TU E

Organization of Cortical Brain Networks — ●CLAUS C. HILGETAG^{1,2} and MARCUS KAISER¹ — ¹Intl. Univ. Bremen, Campus Ring 6, 28759 Bremen — ²Boston University, Boston, USA

Networks of long-range projections in the cerebral cortex of mammalian brains possess an intricate, non-random organization. Specifically, connections are arranged in small-world networks, forming clusters of cortical areas, which are closely linked among each other, but less frequently with areas in other clusters. In order to delineate the structure of cortical clusters and to identify their members, we employed an evolutionary optimization approach. In different compilations of connectivity data for the cat and macaque monkey brain, the algorithm identified a small number of clusters, which broadly agreed with functional cortical subdivisions. The clustered, small-world organization of cortical networks, therefore, has implications for the efficient and flexible cooperation of different brain regions. This structural organization may also represent an optimal balance between different constraints on efficient design, flexible functioning as well as high robustness of the nervous system.

SYBN 3.29 Mo 14:00 Poster TU E

Pattern Formation in the Visual Cortex: A Numerical Study Based on Newton-Krylov Methods — ●D. HEIDE¹, M. KASCHUBE¹, S. LÖWEL², and F. WOLF¹ — ¹MPI für Strömungsforschung, Bunsenstrasse 10, 37073 Göttingen — ²Leibniz Institute for Neurobiology, Brenneckestr. 6, 39118 Magdeburg

In the visual cortex, neurons respond strongest to a visual stimulus of their preferred orientation. Parallel to the cortical surface, these preferred orientations form a complex pattern, called the orientation map. Orientation maps presumably emerge by activity-dependent self-organisation of the cortical network during development [1]. This process of dynamic pattern formation can be described by a phenomenological model based on biological plausible symmetry assumptions [2]. The dynamics of the orientation map is given by a Swift-Hohenberg type nonlinear integro-differential equation. Solving the model poses a substantial numerical challenge, because the equations of motion are stiff and one is interested in the asymptotic behaviour of large systems.

Here, we present a fully implicit parallel numerical integrator for this model. Discretisation in time is done using a Crank-Nicolson scheme. Spatially, the equation is discretised in real space, using finite difference stencils for the Swift-Hohenberg operator. The incomplete Newton-Krylov method is applied to solve the resulting nonlinear equation for every time step. We find that this fully implicit scheme is numerically much more stable than previous semi-implicit integrators.

[1] F. Wolf & T. Geisel. *Nature*, 395:73 (1998). [2] F. Wolf. In D. Hansel et al., *Methods and Models in Neurophysics*. Elsevier (in press).

SYBN 3.30 Mo 14:00 Poster TU E

Self-organized Critical Control — ●KLAUS PAWELZIK and CHRISTIAN EURICH — Universität Bremen, Institut für Theoretische Physik, Otto-Hahn-Allee 1, 28359 Bremen

In complex systems the distributions of global variables often obey power laws. These robust phenomena have been explained by self-organized criticality (SOC) of spatially extended systems which self-tune to critical points. Here we show that SOC may also arise in low-dimensional balance problems. We investigated the dynamics of feedback systems in which an intrinsically unstable sub-system becomes stabilized by a control system that employs optimal parameter estimation based on recent observations. We observe clear power-law fluctuations with exponents that depend only weakly on system parameters. This novel form of SOC generically emerges in control systems if controllers are very sensitive and have finite memory. Our mechanism might explain the movement statistics observed in human sensorimotor control systems and we suggest that also the power-law fluctuations of stock markets might originate from self-organized critical control.

SYBN 3.31 Mo 14:00 Poster TU E

Combinatorial auctions: A statistical physics approach — ●MARTIN WEIGT, MICHELE LEONE, and MAURO SELLITTO — Institute for Scientific Interchange, Viale S. Severo 65, I-10133 Torino, Italia

In combinatorial auctions, bidders are not only interested in bidding on single objects, but on combinations of goods. The auctioneer has to solve the problem of selecting a winning set of non-contradictory bids which maximizes his income, which is in general an NP-hard optimization problem. Using a mapping to a statistical-physics model on the network of conflicting interests between bidders, we can solve this problem analytical for the simplified case of random bidders, and we propose a message-passing algorithm to select a close-to-optimal winning set of bids also in single combinatorial auctions.

SYBN 3.32 Mo 14:00 Poster TU E

On thermodynamics of socio-economics networks — ●JÜRGEN MIMKES — Physics Department., Paderborn University

Data for traffic offenses indicate that social behaviour and misbehaviour is governed by the LeChatelier principle of least pressure. This principle corresponds to the Gibbs free energy of thermodynamics. Social networks correspond to the crystal structure of atomic systems, however, well organized societies have many different networks for water, food, waste, communication, energy, traffic etc. In homogeneous social systems we observe three phases: collective, inflexible structures, flexible nets and free individual systems. In traffic we find fixed railroad systems, flexible buses and individual cars, in air traffic we have air lines, charter and private planes. In communications we have fixed telephone networks, flexible mobile nets and independent walkie talkies. For energy we have the fixed electricity net, flexible local nets and individual generators or batteries. Like in atomic systems the state of a society and its networks depends on two parameters, social pressure p and social temperature or standard of living T . The network with the lowest free energy (costs) is observed.

SYBN 3.33 Mo 14:00 Poster TU E

Dynamic hierarchy in a network of chaotic maps with distributed sizes: application to epidemic outbreaks in city-networks — ●BERND BLASIUS — Institut f. Physik, Nichtlineare Dynamik, Universitaet Potsdam

We develop a theory for the dynamics of recurrent epidemic outbreaks and their synchronization in a network of coupled cities. The dynamics in each city is described by a one-dimensional map, which generates chaotic outbreak dynamics in excellent agreement with long-term data sets. To study the synchronization in a network of interacting cities we assume that the coupling topology is fully determined by the city-size distribution. In particular, we focus on the case where the interaction between two nodes depends on their size ratio. This gives rise to a network with dominance topology, where large nodes are able to influence smaller ones. To describe the network we calculate the degree distribution and clustering coefficient. In the coupled network we observe a dynamic hierarchy, i.e. by increasing a node's rank the dynamics follows a period doubling bifurcation. Thus, the mean field can show regular oscillations even though the uncoupled maps are in the range of fully developed chaos. Similar regular oscillations of the synchronization index are observed in real data.

SYBN 3.34 Mo 14:00 Poster TU E

A game-theoretical approach to network structure evolution — ●JAN SCHOLZ¹ and MARTIN GREINER² — ¹Institut für Theoretische Physik, Justus-Liebig-Universität, Heinrich-Buff-Ring 16, D-35392 Gießen — ²Corporate Technology, Information & Communications, Siemens AG, D-81730 München

Motivated by the possible application to technical communication networks, we study a game-theoretical approach to network structure formation. A short introduction to game theory with focus on the iterated prisoners dilemma and the concept of (network) Nash equilibria is given. Results on various generic couplings of the IPD game dynamics with network structure evolution are presented and shown to lead to various different selforganizing network topologies.