ABSTRACTS

of talks at the

Joint COPIRA/NTZ-Workshop on
Applications of Networks

ANet04

Institut für Theoretische Physik, Universität Leipzig, Germany

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http://www.physik.uni-leipzig.de/~janke/ANet04

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List of contributions

ANet04 Timetable

November 24, 2004 - Vor dem Hospitaltore 1, Large ("Grosser") Seminar Room 1L12/13

15:00-15:30		**- Welcome Coffee -**
15:30-16:00	**Philippe Blanchard**	Scale free graphs via the "Cameo principle": structure, function and processes
16:00-16:30	**Christian von Ferber**	Dynamics of scalefree networks: scaling behavior and spectral dimensions
16:30-17:00	**Changsong Zhou**	Complex network synchronization: a bridge from structure to function
17:00-17:30	**Piotr Bialas**	Random tree graphs
17:30-18:00		**- Coffee Break -**
18:00-18:30	**Konstantin Klemm**	Structure and dynamical robustness of biological networks
18:30-18:50	**Ulrich Behn**	Architecture of randomly evolving idiotypic networks
18:50-19:10	**Lev Shchur**	On the universality of rank distributions of website popularity
20:00		**- Dinner at "India Gate" -**

November 25, 2004 - Vor dem Hospitaltore 1, Large ("Grosser") Seminar Room 1L12/13

9:00- 9:30		**- Wake-up Coffee -**
9:30-10:00	**Peter Stadler**	Centrality measures in biological networks
10:00-10:30	**Johannes Berg**	Graph alignment in biological networks
10:30-11:00	**Pablo Kaluza**	Engineering of functional networks
11:00-11:30		**- Coffee Break -**
11:30-12:00	**Stefan Lämmer**	Synchronization and adaptive traffic light control in urban road networks
12:00-12:30	**Tyll Krüger**	Social networks, random set graphs and the epidemics of corruption
12:30-12:50	**Alexander Hartmann**	Hard core lattice gases on generalized 3D and mean-field graphs
12:50-14:00		**- Lunch at "Das Fass" -**
14:00-14:15		**- ANet04-Fare-Well & CompPhys04-Welcome Coffee -**
14:15		**- Start of CompPhys04 Workshop -** **(with network talks by Z. Burda and M. Brandau)**

Architecture of randomly evolving idiotypic networks

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B-Lymphocytes express on their surface receptors (antibodies) of a given specifity (idiotype). 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 deseases.

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.

References

[1] M. Brede and U. Behn, Phys. Rev. E67, 031920 (2003).

Graph alignment in biological networks

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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 entire biological networks across species.

Random tree graphs

Piotr Bialas

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Among graphs, trees constitute a small but important subclass. Its importance stems from the fact that on one hand many results on trees can be obtained analytically and on the other hand many classes of non-tree graphs are tree like at least locally. In my talk I will give an account of some exact results obtained for tree graphs.

Scale-free graphs via the “Cameo principle”: structure, function and processes

Philippe Blanchard

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We formulate a simple edge generation rule, called the ”Cameo principle” to explain the origin of scale-free graphs. We assume that each node has a property which attracts the others. We model the situation by assigning two random variables to each node, ω and α, where ω indicates some property of the node and α the affinity towards that property. The Cameo principle extends the concept of the random graph $\mathcal{G}(n, p)$ introduced by Erdös and Rényi which is obtained in the limit $\alpha \to 0$. We furthermore discuss and study some properties of Cameo graphs.

References

[1] Ph. Blanchard and T. Krüger, *The Cameo principle and the origin of scale-free graphs in social networks*, J. Stat. Phys. 114, 1399-1416 (2004).

[2] Ph. Blanchard, S. Fortunato, and T. Krüger, *Do extremists impose the structure of social networks?*, arXiv-preprint cond-mat/0407434v1.

Hard-core lattice gases on generalized 3D and mean-field graphs

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(with W. Barthel and M. Weigt)

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We introduce a simple hard-core lattice-gas model, equivalent to the NP-complete vertex-cover problem, on generalized graphs and investigate numerically its compaction behavior. If compactified slowly, the systems undergo a first-order crystallization transition. If compactified much faster, the systems stay in a meta-stable liquid state. For the mean-field graph, under further compaction, it undergoes a transition to a glassy state, which is not present in the 3D case. A glassy behavior for 3D has been found in the literature if longer ranged and more complicated interactions, or equivalently larger and less regular particles, are considered.

Engineering of functional networks

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(with A.S. Mikhailov)

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How natural networks evolve to develop a specific function? Such networks are not a product of human logical design and emerge instead as an outcome of an evolutionary optimization process. In our studies, we try to mimic this natural design procedure and explore artificial evolutionary algorithms for generation of chemical and biochemical networks specialized on certain functions. Two examples will be presented. In the first of them, a network of first-order chemical reactions is reconstructed from its relaxation data – a problem which is ultimately reduced to the reconstruction of a network from its Laplacian spectrum. In the second example, we engineer signal transduction networks which are functional and robust with respect to destructive mutations.

Structure and dynamical robustness of biological networks

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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. Our model suggests that the observed motif structure of biological signaling networks is shaped by the biological requirement for reproducibility of attractors.

Social networks, random set graphs and the epidemics of corruption

Tyll Krüger

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We study random set graphs as a model for certain classes of social networks. Set graphs can well reproduce essential features of the local clustering in real social networks. We further model the spread of corruption on such networks as a generalized epidemic process involving mean-field processes and voter-type dynamics. Special focus is on the role of clustering in corruption type processes and phase transitions.

Synchronization and adaptive traffic light control in urban road networks

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Urban traffic flow at intersections is traditionally organized in an oscillatory way by means of traffic lights. In order to develop an adaptive traffic light control, we have developed a mechanism producing efficient oscillations in a self-organized way. Moreover, we have designed strategies to synchronize neighboring traffic lights so that synchronization spreads over large parts of the system. The traffic flow is modeled as a dynamic queuing network. The network model treats traffic-light controlled intersections as nodes with dynamically changing service rates connected by links (road sections) of constant capacity. Interestingly, the traffic dynamics on the links can be eliminated, and it is possible to describe the complete dynamics of the system by coupled delay-differential equations for the traffic flows through the nodes (intersections), including the related travel times.

On the universality of rank distributions of website popularity

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We present an extensive analysis of long-term statistics of the queries to websites using logs collected on several web caches in Russian academic networks. We check sensitivity of the statistics to several parameters: (1) duration of data collection, (2) geographical location of the cache server collecting data, and (3) the year of data collection. We propose a two-parameter modification of the Zipf law and interpret the parameters. We find that the rank distribution of websites is stable when being approximated by the modified Zipf law.

Centrality measures in biological networks

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(with S. Wuchty)

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The central vertices in complex networks are of particular interest because they might play the role of organizational hubs. Metabolic networks, protein interaction networks, and protein domain networks will be used as examples. Three different geometric centrality measures (excentricity, status, and centroid value) will be discussed. These measures were originally used in the context of resource placement problems. These quantities lead to useful descriptions of the centers of biological networks which often, but not always, correlate with a purely local notion of centrality such as the vertex degree. Since centrality measures are defined for each vertex, they can be viewed as a "landscape" on a network. This view implies a natural definition of "local centers" in terms of local optima of a centrality value function.

References

[1] S. Wuchty and P.F. Stadler, J. Theor. Biol. 223, 45-53 (2003).

Dynamics of scale-free networks: scaling behavior and spectral dimensions

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(with F. Jasch and A. Blumen)

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We analytically determine dynamical properties of scalefree networks by analyzing the spectrum of the Laplacian defined on their graphs.

Recent studies of nets, ranging from social networks to power grids and the internet, revealed that in many cases the degree distribution p_k, i.e., the probability that an arbitrary vertex is connected to exactly k other vertices, often exhibits a power law, namely that $p_k \sim k^{-\gamma}$ holds. Networks for which this relation is fulfilled are called *scale-free*; scale-free networks differ from the classical random graphs, for which the distribution p_k is Poissonian, and from small-world-networks. In particular recent work clarified that the properties of scale-free networks, in particular percolation, differ markedly from the classical case: for $\gamma < 4$ nontrivial γ-dependent critical exponents appear [1].
Many problems ranging from the dynamics of randomly branched polymers [2] and the stress relaxation of near critical gels [3], over random resistor-capacitor networks to glassy relaxation dynamics, depend on the discrete Laplacian $\mathbf{A}$ defined on the network. Based on the Laplacian, many time and frequency-dependent observables can be written in terms of $\rho(\lambda)$, the density of eigenvalues of $\mathbf{A}$. Following the ideas used in the analysis of gel dynamics [3] and hyperbranched polymers [2], we develop and solve an integral equation for $\rho(\lambda)$ for a class of random graphs with arbitrary degree distributions. Specializing to scalefree networks with degree distributions $p_k \sim k^{-\gamma}$ we find characteristic changes in the spectrum $\rho(\lambda)$ when lowering γ to $\gamma < 4$. Close to the percolation threshold we find scaling functions for the spectrum $\rho(\lambda)$. While for fast decaying distributions we find a Lifshitz tail behavior (I) for $\lambda \to 0$ the spectrum of the percolation ensemble of networks with a fat tail distribution $\gamma < 4$ follows a power law (II) [2, 4]:

$$\text{(I)}\ \rho(\lambda) \sim \exp(-\Delta^{3/2}/\lambda^{1/2})\ , \qquad \text{(II)}\ \rho(\lambda) \sim c(\Delta)\lambda^{\alpha},$$

with $\alpha = 2\gamma - 5$ valid below and $\alpha = (4-\gamma)/(2\gamma-5)$ valid at the percolation threshold ($\Delta = 0$). α is related to the spectral dimension of the percolation system by $d_s' = 2\alpha + 2$ which is different from d_s of the percolating cluster alone.
Extensive numerical diagonalizations of simulated ensembles of networks support our analytical findings.

References

[1] R. Cohen, D. ben Avraham, and S. Havlin. Phys. Rev. E66, 036113 (2002).

[2] F. Jasch, C. von Ferber, and A. Blumen. Phys. Rev. E68, 051106 (2003).

[3] K. Broderix, T. Aspelmeier, A. K. Hartmann, and A. Zippelius. Phys. Rev. E64, 021404 (2001).

[4] F. Jasch, C. von Ferber, and A. Blumen. Phys. Rev. E70, 016112 (2004).

Complex network synchronization: a bridge from structure to function

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Many real-world systems display complicated interaction structures among their sub-units, forming complex networks. Examples of complex networks in neuro- and cognitive sciences include neural networks, cortical and functional connectivity of brain and language, etc. Recent research has revealed general organization principles in the structure of complex networks. A problem of fundamental importance is to understand the impact of network structure on its dynamical properties. Here we study phase synchronization of generic nonlinear oscillators on the nodes of complex networks. We have identified an important ingredient in the complex structure of random networks that governs universally the synchronization properties of complex networks. The results based on the network of cat cortical connectivity may shed some light into the relationship between the cortical connectivity and the functional connectivity of brain.