SOE 16: Networks (joint session SOE / DY / BP)

Time: Thursday 9:30–13:00   Location: GÖR 226

SOE 16.1   Thu 9:30   GÖR 226

Structure and dynamics of multiplex networks: beyond degree correlations — •Kaj-Kolja Kleineberg — Computational Social Science, ETH Zurich, Clausiusstrasse 50, CH-8092 Zurich, Switzerland

The organization of constituent network layers to multiplex networks has recently attracted a lot of attention. Here, we show empirical evidence for the existence of relations between the layers of real multiplex networks that go beyond degree correlations. These relations consist of correlations in hidden metric spaces that underlie the observed topology. We discuss the impact and applications of these relations for trans-layer link prediction, community detection, navigation, game theory, and especially for the robustness of multiplex networks against random failures and targeted attacks. We show that these relations lead to fundamentally new behaviors, which emphasizes the importance to consider organizational principles of multiplex networks beyond degree correlations in future research.

SOE 16.2   Thu 10:00   GÖR 226

Large-deviation properties of the stochastic block model — •Stephan Adolf[1], Tiago P. Peixoto[2], and Alexander K. Hartmann[1] — [1]Institut of Physics, University of Oldenburg — [2]Department of Mathematical Sciences, University of Bath

In this contribution we study the distribution of the size of the largest components for the stochastic block model. The stochastic block model is a generative model for graphs, which can be used to model social relationships [1, 2]. Suppose $N \in \mathbb{N}$ vertices which can partioned into at least two groups (also called blocks). For generating a graph in the stochastic block model ensemble one inserts edges between pairs of vertices with different probabilities depending on whether the vertices are in the same group or not [1]. To obtain the distribution of the size of the largest component over the full support we use a large-deviation method [3] to determine even small probabilities (like for example 10^{-100}). We compare the results to those obtained for Erdős-Rhényi random graphs.

[1] A. Decelle and F. Krzakala and C. Moore and L. Zdeborová, Phys. Rev. E **84**, 066106 (2011)
[2] P.W. Holland and K.B. Laskey and S. Leinhardt, Social networks **5**, 109-137 (1983)
[3] A.K. Hartmann, Eur. Phys. J. B **84**, 627-634 (2011)

SOE 16.3   Thu 10:15   GÖR 226

Improving Causal Gaussian Bayesian Network Inference using Parallel Tempering — •Pascal Fieth[1], Gilles Monneret[2,3], Andrea Rau[3], Florence Jaffrézic[3], Alexander K. Hartmann[1], and Gregory Nuel[2] — [1]IfP, University of Oldenburg, Germany — [2]LPMA, CNRS 7599, UPMC, Paris, France — [3]GABI, INRA, Jouy-en-Josas, Paris, France

Gene regulatory networks describe causal relationships in biological processes like signal transduction or disease mechanisms. A considerable interest exists in supporting experimental network inference by developing computational methods to infer gene regulatory networks from available gene expression data.

To infer causality within those networks from mixed, observational and intervention, data, we make use of causal orderings and Gaussian Bayesian networks. An introduction to the necessary foundations is given. In the presented framework, for a given causal ordering, the likelihood of the model network can be maximized analytically. The space of causal orderings, growing as $n!$ for n genes, can be reliably explored via a simple Markov Chain Monte Carlo algorithm[1] for 10-20 genes only.

We show that parallel tempering helps in finding the orderings with highest maximum likelihood estimators as well as in exploring the set of alternative orderings with comparable maximum likelihood estimators for networks with > 50 genes.

[1] A. Rau, F. Jaffrézic, G. Nuel, BMC Sys. Biol., **7**(1):111 (2013)

SOE 16.4   Thu 10:30   GÖR 226

Phase transition in detecting causal relationships from obervationaland interventional data — •Alexander K. Hartmann[1] and Gregory Nuel[2] — [1]Institut for Physics, University of Oldenburg, Germany — [2]Laboratory of Probability and Stochastic Models (LPMA), Université Pierre et Marie Curie, Paris, France

Analysing data of, e.g., gene-expression experiments, and modelling it via network-based approaches is one of the main data analysis tasks in modern science. If one is interested in modelling *correlations*, approaches like the inverse Ising model can be used, which is already algorithmically challenging. If one wants to analyse even *causal relationships*, i.e., beyond correlations, it becomes even harder.

One way out is to include interventions to the system, e.g., by knocking out genes when studying gene expression. This allows, in principle, to get a grip on the causal structure of a system. Here, we model the data using Gaussian Bayesian networks defined on directed acyclic graphs (DAGs). Our approach [1] allows for multiple interventions in each single experiment and calculating joint maximum likelihoods (MLs) for the complete network. Furthermore, we have to sample different causal orderings, which induce different DAGs. The sampling is efficient because we approximate the full ML by probabilities of orderings of triplets. This allows us to study the quality of the causality detection as a function of the fraction of interventional experiments. We observe an information phase transition between phases where the causal structure cannot be detected and where it can be detected.
[1] A. Rau, F. Jaffrézic, and G. Nuel, BMC Sys. Biol. **7**:111 (2013)

SOE 16.5   Thu 10:45   GÖR 226

Surveillance for outbreak detection in livestock-trade networks — •Philipp Hövel[1], Frederik Schirdewahn[1], Andreas Koher[1], Vitaly Belik[2], Hartmut H. K. Lentz[3], and Vittoria Colizza[4] — [1]TU Berlin — [2]FU Berlin — [3]Friedrich-Loeffler-Institut — [4]INSERM Paris

We analyze a temporal network of livestock trade and present results of numerical simulations of epidemiological dynamics. The considered network is the backbone of the pig trade in Germany [1], which forms a major route of disease spreading between agricultural premises. The network is comprised of farms connected by a link, if animals are traded between them. We propose a concept for epidemic surveillance generally performed on a subset of the system due to limited resources. The goal is to identify agricultural holdings that are more likely to be infected during the early phase of an epidemic outbreak. These farms, which we call *sentinels* [2], are excellent candidates to monitor the whole network. To identify potential sentinel nodes, we determine most probable transmission routes by calculating functional clusters. These clusters are formed by nodes that have similar invasion paths. Then, we select sentinels by choosing nodes out of every cluster. We show that any epidemic outbreak can be reliably detected at an early stage by monitoring a small number of those sentinels.

[1] H. H. K. Lentz, A. Koher, P. Hövel, J. Gethmann, C. Sauter-Louis, T. Selhorst, and F. Conraths, PLoS ONE, **11**, e0155196 (2016).
[2] P. Bajardi, A. Barrat, L. Savini, V. Colizza, J. Roy. Soc. Interface **9**, 2814 (2012).

SOE 16.6   Thu 11:00   GÖR 226

Outbreaks of interacting dynamics — •Fakhteh Ghanbarnejad — Institut für Theoretische Physik, Technische Universität Berlin

Susceptible-Infective-Susceptible (SIS) and Susceptible-Infective-Recovered (SIR) are two successful idealized and simplified models for understanding the dynamics of infectious diseases. Nevertheless deadly records of some cases like tuberculosis during the 1918-1919 Spanish Flu and unexpected HIV cases in presence of hepatitis B and C, TB and Malaria, and vice versa, showed us that interaction between two spreading dynamics can dramatically change the epidemic dynamics. Here we investigate some microscopic mechanisms which might lead to the unexpected macroscopic outbreaks; In this work, we study spreading of two diseases: either cooperative or competitive interacting as a SIS or/and a SIR dynamics and address similarities and differences in comparison to other minimal cooperative models, i.e. SIR-SIR [1] and SIS-SIS [2]. We build up an idealized and simplified model and treat it in mean field approximations as well as stochastic agent based models. We find out in presence of cooperation an emerging region in the parameter space where the stable endemic and stable free-disease states co-exist. Interestingly this region appears differently in comparison to the SIR-SIR and SIS-SIS models. Also We track the dynamics on random generated networks; And argue how topological features can facilitate or neutralize the cooperation/competition effects.

[1] EPL 104 (2013) 50001; Nature Physics 11, 936-940 (2015); Rev. E 93, 042316. [2] arXiv:1603.09082v1.

15 min. break

SOE 16.7   Thu 11:30   GÖR 226

Collective navigation of complex networks: Participatory greedy routing — •Kaj-Kolja Kleineberg and Dirk Helbing — Computational Social Science, ETH Zurich, Clausiusstrasse 50, CH-8092 Zurich, Switzerland

Many networks are used to transfer information or goods, in other words, they are navigated. The larger the network, the more difficult it is to navigate efficiently. Indeed, information routing in the Internet faces serious scalability problems due to its rapid growth, recently accelerated by the rise of the Internet of Things. Large networks like the Internet can be navigated efficiently if nodes, or agents, actively forward information based on hidden maps underlying these systems. However, in reality most agents will deny to forward messages, which has a cost, and navigation is impossible. Can we design appropriate incentives that lead to participation and global navigability? Here, we present an evolutionary game where agents share the value generated by successful delivery of information or goods. We show that global navigability can emerge, but its complete breakdown is possible as well. Furthermore, we show that the system tends to self-organize into local clusters of agents who participate in the navigation. This organizational principle can be exploited to favor the emergence of global navigability in the system.

SOE 16.8   Thu 11:45   GÖR 226

Epidemic threshold in temporally-switching networks — Leo Speidel[1], •Konstantin Klemm[2,3], Victor M. Eguiluz[2], and Naoki Masuda[4] — [1]University of Oxford, UK — [2]IFISC, Palma, Spain — [3]Nazarbayev University, Astana, Kazakhstan — [4]University of Bristol, UK

Data of physical contacts and face-to-face communications suggest temporally varying networks as the media on which infections take place among humans and animals. Epidemic processes on temporal networks are complicated by complexity of both network structure and temporal dimensions. We develop a theory to understand the susceptible-infected-susceptible epidemic model on arbitrary temporal networks, where each contact is used for a finite duration. We show that temporality of networks always lessens the epidemic threshold such that infections persist more easily in temporal networks than in their static counterparts [1]. The effect of temporality on the epidemic threshold, which depends on a data set, is approximately predicted by the magnitude of a commutator norm.

[1] Speidel, Klemm, Eguíluz & Masuda, New J Phys 18, 073013 (2016).

SOE 16.9   Thu 12:00   GÖR 226

Correlations in sectoral value added growth in the global economic network — •Julian Maluck and Reik V. Donner — Potsdam Institute for Climate Impact Research, Germany

Complex supply chains have resulted in increasing interconnectedness within the International Trade Network (ITN). In this context the question arises how industries adapt to changes in the demand and supply of their trading partners. We address this problem by empirically analyzing both positive and negative correlations of value added growth between industries and construct the World Economic Performance Network (WEPN). By comparing topological characteristics of the WEPN and the ITN we obtain insights into the interconnection between trade relations and correlations in economic performance. We observe that trade relations of higher orders are particularly important for assessing performance correlations on an international level. Our results contribute to a better understanding of the consequences from demand and supply changes within the ITN from a model-independent analysis.

SOE 16.10   Thu 12:15   GÖR 226

Timescale of reaching stable state with relation to different ranking strategies in the stable marriage problem. — •Piotr Nyczka — Jacobs University Bremen, Germany

Stable marriage problem is wery well known topic. However there is still plenty of room for further investigation. In my presentation I will discuss process of reaching the stable state in the system consisting of two different types of agents.

Agents from two sets (eg. men and women) undergo random encounters and then decide whether they want to be together or not. They want to form a new couple only in the case where, as a result of this change, both of them will end up with "better" partner than actual one.

Each agent have its personal ranking list with "attraciveness" scores for potential partners of opposite sex and it's possible to make network out of these lists. In my presentation I will focus on relation between structure of this network, and timescale of process of reaching stable state. There is very strong and interesting relation between them, definitely worth of further investigation.

SOE 16.11   Thu 12:30   GÖR 226

Identifying the driving processes of coupled friendship and enmity dynamics in a two-layer network model — •Maximilian Sadilek[1] and Stefan Thurner[1,2,3] — [1]Section for Science of Complex Systems, Medical University of Vienna, Spitalgasse 23, A-1090, Austria — [2]Santa Fe Institute, 1399 Hyde Park Road, Santa Fe, NM 87501, USA — [3]International Institute for Applied Systems Analysis, Schlossplatz 1, A-2361 Laxenburg, Austria

With the advent of social media it has become possible to study human social relations in a quantitative way. However, in most cases only data on positive relations (like friendship) are available while social balance theory states that in a social network positive and negative relations strongly depend on each other.

In the massive multiplayer online game PARDUS players can mark each other not only as friends but also as enemies, leading to a two-layer multiplex network structure.

We discuss the dynamics of friendship and enmity relations between thousands of players in PARDUS. We identify and quantify the driving processes of the associated two-layer social network formation. Well known sociological hypotheses like "The enemy of my enemy is my friend" turn out to be important building blocks of understanding the dynamics of the coupled formation of friendly and hostile interactions within a society.

SOE 16.12   Thu 12:45   GÖR 226

Master Stability Functions reveal Turing Instabilities in Multi-layer Foodwebs — Andreas Brechtel[2], Philipp Gramlich[2], Daniel Ritterskamp[1], Barbara Drossel[2], and •Thilo Gross[1] — [1]University of Bristol, UK — [2]Technische Universität Darmstadt

Many systems in science and technology can be described as multilayer networks, which are known to exhibit phenomena such as catastrophic failure cascades and pattern-forming instabilities.

A particular class of multilayer networks describes systems where different interacting copies of a local network exist in different spatial locations, including for instance regulatory and metabolic networks of identical cells and interacting habitats of ecological populations.

Here, we show that such systems can be analyzed by a master stability function (MSF) approach, which reveals conditions for diffusion-driven instabilities (DDIs).

We demonstrate the methodology on the example of state-of-the-art meta-foodweb models, where it reveals diffusion-driven instabilities that lead to localized dynamics and spatial patterns.

This type of approach can be applied to a variety of systems from nature, science and engineering to aid the understanding and design of complex self-organizing systems.