

## SOE 14: Networks: From Topology to Dynamics II (with BP, DY)

Time: Wednesday 10:45–13:15

Location: GÖR 226

SOE 14.1 Wed 10:45 GÖR 226

**Stem Diseases: Efficient Immunization Strategies** — •CHRISTIAN M. SCHNEIDER<sup>1</sup>, TAMARA MIHALJEV<sup>1</sup>, SHLOMO HAVLIN<sup>2</sup>, and HANS J. HERRMANN<sup>1,3</sup> — <sup>1</sup>Computational Physics, IfB, ETH Zurich, Schafmattstrasse 6, 8093 Zurich, Switzerland — <sup>2</sup>Minerva Center and Department of Physics, Bar-Ilan University, 52900 Ramat-Gan, Israel — <sup>3</sup>Departamento de Física, Universidade Federal do Ceara, 60451-970 Fortaleza, Ceara, Brazil

The spreading of diseases in social networks is crucial to the potential danger of the disease. We quantitatively analyze the effect of immunization strategies on the susceptibility to diseases. We introduce a novel immunization strategy and find for all studied networks that the spreading of diseases can be significantly suppressed compared to the known immunization strategies. As an example we show the results for the international airport network.

SOE 14.2 Wed 11:00 GÖR 226

**Vaccination Decisions with Limited Information** — •OLIVIA WOOLLEY MEZA, DANIEL GRADY, and DIRK BROCKMANN — Northwestern University, Evanston, USA

Widely practiced vaccination can eradicate a disease from a population. However, if rational, self-interested individuals believe there is any risk associated with the vaccine, their strategic vaccination decisions can lead to insufficient aggregate vaccination. In fact, recent work has shown that in a well-mixed population with perfect information the disease will not be eradicated. We consider a finite-size stochastic system, where each individual has both a contact neighborhood, the group of others who can contact the individual, and an information neighborhood, the group of others about whom the individual can obtain information. We find that in this setting strategic vaccination decisions can lead to disease eradication. We further investigate how the likelihood of eradication changes with the extent of information on which individuals base their decisions. We find that when information is very limited, increasing the extent of information helps to eradicate the disease. However, as more information becomes available we find a second regime where additional information reduces the effectiveness of vaccination. The information region with high disease extinction is larger when the underlying topology is highly clustered. The cause of suboptimal behavior as we approach global information also depends on the underlying topology. We use simulations and analytical models to explain this behavior.

SOE 14.3 Wed 11:15 GÖR 226

**Optimal vaccination strategies in metapopulation networks** — •VITALY BELIK — Massachusetts Institute of Technology, Cambridge, MA, USA — Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen, Germany

Human infectious diseases remain a profound challenge for the humankind. Recently a lot of attention is devoted to theoretical modeling of geographical epidemic spread taking into account human mobility patterns obtained from the ubiquitous real data. This considerably advances the design of effective preventive and containment strategies. We investigate a problem of optimal vaccine distribution in a metapopulation network employing game theoretical approaches. We answer such an important question, as to what extent different regions are interdependent and where vaccination need to be subsidized to minimize the overall impact of the epidemic. In our extensive numerical simulation we employ the real data on human mobility in the USA.

SOE 14.4 Wed 11:30 GÖR 226

**What is the front velocity in wave propagation without fronts? - Epidemics on complex networks provide an answer** — •RAFAEL BRUNE<sup>1,2</sup>, CHRISTIAN THIEMANN<sup>1,2</sup>, and DIRK BROCKMANN<sup>1</sup> — <sup>1</sup>Northwestern University, Evanston, USA — <sup>2</sup>Max-Planck-Institut für Dynamik und Selbstorganisation, Göttingen, Deutschland

The spatiotemporal patterns of infectious diseases that spread nowadays typically lack a well defined wave front as human mobility is multi-scale. The structure of emergent patterns is difficult to assess quantitatively, in particular spreading speeds are difficult to define and compare in different scenarios. We present a novel way to look at contagion phenomena on complex networks using the underlying topologi-

cal structure of the network. Shortest-path distances and arrival times are used to redefine the velocity of spreading patterns. We extend the idea of a wavefront that can be directly observed in simple networks like a regular lattice to the class of complex networks which in traditional views exhibit complicated patterns. This method substantially simplifies the way dynamics are analyzed and explains why patterns in complex modeling approaches share many similarities. Disease dynamics on various complex networks ranging from artificial to real human mobility networks show the benefit of representing the spatio-temporal patterns based on topological features of the network.

SOE 14.5 Wed 11:45 GÖR 226

**Limiting factors for the spread of infectious diseases in complex networks** — •HARTMUT H K LENTZ<sup>1,2</sup>, MARIO KONSCHAKE<sup>2</sup>, and IGOR M SOKOLOV<sup>1</sup> — <sup>1</sup>Department of Physics, Humboldt University, Newtonstr. 15, 12489 Berlin, Germany — <sup>2</sup>Friedrich-Loeffler-Institut, Institute of Epidemiology, Seestr. 55, 16868 Wusterhausen, Germany

Epidemics are expected to spread rapidly in networks with heavy-tail degree distributions. On the other hand, many real world networks comprise complex substructures like modules. Modules are subsets of nodes being densely interconnected. This yields subgraphs which are in the limiting case 'isolated' from each other. Furthermore the directed character of a network might play a role in disease spread. Most social and human networks can be treated as undirected. But many networks, e.g. trade networks, are inherently directed since there is an underlying economic/logistic process. In directed networks the number of possible ways for a pathogen is dramatically reduced. Our results show that direction and community structure are limiting factors for disease spread.

## 15 min. break

SOE 14.6 Wed 12:15 GÖR 226

**Are motifs a myth?** — •JÖRG REICHARDT<sup>1</sup>, ROBERTO ALAMINO<sup>2</sup>, and DAVID SAAD<sup>2</sup> — <sup>1</sup>Complexity Sciences Center, UC Davis and Würzburg University — <sup>2</sup>Aston University, Birmingham

Small subgraphs, called network motifs, have received considerable attention in network research over the last years and are suggested as simple building blocks of complex networks. Motifs are attributed functional significance due to their strong over- or underrepresentation when compared to random null models. However, the link randomized null models used for such comparisons generally match the observed networks only in terms of their microscopic structure, destroying all mesoscopic features and hence give biased estimates of the statistical significance of motif counts in real world networks.

We present a generative probabilistic model based on Exponential Random Graphs plus an algorithm to infer model parameters from a given network. This model allows to generate an ensemble of random null models that matches the observed network with respect to both its microscopic *and* mesoscopic structural features.

We show that such random null models may result in a much more conservative estimation of the statistical significance of motif counts in real world networks. Further, they maintain the parsimonious explanation of complex networks as a collection of conditionally independent edges.

SOE 14.7 Wed 12:30 GÖR 226

**Is there a bias in the generation of simple random graphs with the configuration model?** — •HENDRIKE KLEIN-HENNIG and ALEXANDER K. HARTMANN — Institute of Physics, University of Oldenburg

The configuration model is an often used and well known procedure to generate random graphs with an arbitrary degree sequence. The basic idea is to assign a fixed degree to each vertex, which create edges emerging from the vertex called stubs. In a second step random pairs of stubs are connected until there are no stubs left. This procedure generates every possible graph realization with the same probability. In this work two generation procedures are compared how to deal with self-loops and multiple edges (forbidden edges) to generate undirected simple graphs. In the first procedure the entire graph is disregarded and the generation process is restarted from the beginning as soon as

a forbidden edge is encountered. Another method, which is frequently applied [1], is to disregard only the forbidden edge, restoring the stubs and drawing a new pair, while keeping the rest of the graph. An analysis of small example graphs shows that for the second generation procedure the graphs are not necessarily created with equal probability. For large graph sizes the behavior is studied using statistical tests on computer generated graphs [2].

[1] M.Catanzaro, M.Boguñá and R. Pastor-Satorras, *Generation of uncorrelated random scale-free networks*, Phys. Rev. E 71 027103 (2005)

[2] A.K. Hartmann, *Practical Guide to Computer Simulations*, (World Scientific, 2009)

SOE 14.8 Wed 12:45 GÖR 226

**Surrogates and significance testing for spatially embedded complex networks** — •JONATHAN F. DONGES<sup>1,2</sup>, REIK V. DONNER<sup>1</sup>, NORBERT MARWAN<sup>1</sup>, and JÜRGEN KURTHS<sup>1,2</sup> — <sup>1</sup>Potsdam Institute for Climate Impact Research, P.O.Box 60 12 03, 14412 Potsdam, Germany — <sup>2</sup>Department of Physics, Humboldt University of Berlin, Newtonstr. 15, 12489 Berlin, Germany

The analysis of spatially embedded complex networks, i.e., networks with vertices embedded in a metric space, is of increasing interest in many fields of science. Examples are power grids in electrical engineering, the internet and world wide web in computer science or social networks in social science. In many cases, there is some degree of uncertainty about the network structure, e.g., edges might be missing in the network that exist in the system under study (the opposite may also be true). This is particularly relevant for networks constructed from multivariate data using the tools of time series analysis. Given this uncertainty, it is very important to evaluate the significance of measured network properties such as clustering coefficient, average path

length, degree distribution or various vertex centrality sequences with respect to a given null hypothesis. Here we present different types of surrogates for spatially embedded networks, i.e., random networks with prescribed spatial constraints such as fixed edge distance distribution or a fixed average edge distance sequence, and show how to use them for testing the associated null hypotheses. The method is illustrated using diverse example networks, e.g., the european power grid or a climate network representing correlation structure of the surface air temperature field.

SOE 14.9 Wed 13:00 GÖR 226

**Backbones and borders from shortest-path trees** — •DANIEL GRADY, CHRISTIAN THIEMANN, and DIRK BROCKMANN — Northwestern University, Evanston, IL, USA

One of the most important tasks in complex network research is to distinguish between vertices and edges that are topologically essential and those that are not. To this end, a variety of vertex and edge centrality measures have been introduced, ranging from measuring local properties (degree, strength) to quantities that depend on the global structure of the graph (betweenness). Here we introduce a novel technique based on the family of shortest-path trees, which is applicable to strongly heterogeneous networks. This approach can identify significant edges in the network, distinct from conventional edge betweenness, and these edges make up a network backbone relevant to dynamical processes that evolve on such networks. We will show that important network structures can be extracted by investigating the similarity and differences of shortest-path trees and show that tree dissimilarity in combination with hierarchical clustering can identify communities in heterogeneous networks more successfully than ordinary reciprocal-weight distance measures. We demonstrate the success of this technique on complex multi-scale mobility networks.