

**BP 22: Networks, From Topology to Dynamics I (joint SOE/DY/BP)**

Time: Tuesday 15:00–16:00

Location: GÖR 226

BP 22.1 Tue 15:00 GÖR 226

**The Hidden Geometry of Complex, Network-Driven Contagion Phenomena** — ●DIRK BROCKMANN<sup>1,2</sup> and DIRK HELBING<sup>3</sup> — <sup>1</sup>Humboldt University, Berlin — <sup>2</sup>Robert Koch Institute, Berlin — <sup>3</sup>ETH Zurich

The global spread of epidemics, rumors, opinions, and innovations are complex, network-driven dynamic processes. The combined multiscale nature and intrinsic heterogeneity of the underlying networks make it difficult to develop an intuitive understanding of these processes, to distinguish relevant from peripheral factors, to predict their time course, and to locate their origin. We show that complex spatiotemporal patterns can be reduced to surprisingly simple, homogeneous wave propagation patterns, if conventional geographic distance is replaced by a probabilistically motivated effective distance[1]. In the context of global, air-traffic-mediated epidemics, we show that effective distance reliably predicts disease arrival times. Even if epidemiological parameters are unknown, the method can still deliver relative arrival times. The approach can also identify the spatial origin of spreading processes. We validate the approach by application to data on the worldwide 2009 H1N1 influenza pandemic, the 2003 SARS epidemics and the 2011 outbreak of EHEC/HUS in Germany.

D. Brockmann, D. Helbing, Science (2013)

BP 22.2 Tue 15:15 GÖR 226

**Spread of Infectious Diseases with Finite Infectious Period on Temporal Networks** — ●ANDREAS KOHER, LUCIAN WILLARETH, HARTMUT LENTZ, and IGOR M. SOKOLOV — Institut für Physik, Humboldt-Universität zu Berlin, Newtonstr. 15, 12489 Berlin, Germany

Traversal in temporal networks is only possible, if paths are formed by a causal sequence of edges. Recently, a matrix formalism has been introduced in order to compute the causal path structure of temporal networks [1]. This formalism describes the spread of infectious diseases that can traverse the network even after arbitrary waiting times, i.e. a SI-model (susceptible-infected-model). Many infectious diseases however possess a finite infectious period, i.e. the time period after which the infection dies out, if it is not passed on. This can be implemented as an SIS or SIR (susceptible-infected-recovered) model, respectively. In this work, we introduce a novel matrix formalism that allows for an explicit consideration of finite infectious periods, which gives a more realistic model of outbreak scenarios. As a central result, we compute

the critical infectious period necessary in order to allow for percolation on a given temporal network. The introduced methods can be implemented efficiently and we demonstrate their capability on different datasets.

[1] Lentz et al., Unfolding Accessibility Provides a Macroscopic Approach to Temporal Networks, Phys. Rev. Lett. (2013)

BP 22.3 Tue 15:30 GÖR 226

**Dynamics of Manufacturing Supply Networks** — ●THILO GROSS — University of Bristol

High-value manufacturing builds on increasingly complex supply networks. In contrast to classical supply chains these networks have a high connectivity and can contain loops and hubs. Failure of the supply network can cause business disruptions associated with high financial losses. Presently, already more than 30% of such losses are caused by cascading effects that propagate through the system. In the face of this threat mathematical tools are needed to assess the robustness and resilience of supply networks and identify vulnerabilities. In this talk I present modelling approaches and results on the stability of dynamical manufacturing supply networks. In particular, I identify potential bifurcations of the network and propose a method to identify the most critical suppliers in large networks.

BP 22.4 Tue 15:45 GÖR 226

**Automatic discovery of plausible network models** — TELMO MENEZES<sup>1,2</sup> and ●CAMILLE ROTH<sup>1</sup> — <sup>1</sup>Centre Marc Bloch Berlin, CNRS — <sup>2</sup>Centre d'Analyse et de Mathématique Sociales, CNRS/EHESS

A methodology is proposed to discover plausible network generators for complex networks. Generators are defined as computer programs that define local morphogenetic behaviors. We employ a machine learning technique inspired by biological Darwinism to look for generators that produce synthetic networks which match a number of metrics on target real networks. We use a number of metrics that capture both global and fine-grained structural characteristics of networks. Remarkably, when applied on networks stemming from prototypical models of the Erdős-Rényi or Barabási-Albert sort, our approach generally discovers the exact original generator. Empirical validation of our methodology is then presented in the form of a number of plausible generators for a series of five real networks, including a simple brain and a social network.