BP 6: Networks: From Topology to Dynamics I (Joint Session SOE/DY/BP)

Time: Monday 10:00–11:30   Location: H36

BP 6.1   Mon 10:00   H36

Revealing physical interaction networks from nonlinear dynamics — Jose Casadiego[1], Dimitra Maoutsa[1], Hauke Hähne[1], Mor Nitzan[2], and •Marc Timme[1] — [1]Network Dynamics, MPI for Dynamics and Self-Organization, Göttingen, Germany — [2]Racah Institute of Physics, The Hebrew University of Jerusalem, Israel

Structural connectivity of networks reflects the direct physical interactions between pairs of dynamical units, as opposed to effective, functional or other statistical measures of connectivity. How to uncover physical interaction structure from measured time series of networked systems remains an open question. Here we present a dynamical systems' view on collective network dynamics, thereby proposing an approach to reveal physical interaction networks from the nonlinear dynamics they generate. Introducing the notion of *explicit dependency matrices*, we present two examples: one, where the time series consists of the full network states as a function of time, the other, where the time series exhibits only partial information about the full states. We apply the latter to neural circuit dynamics where the observables are spike timing data, i.e. only a discrete, state-dependent output of the neurons. These results may help revealing network structure for systems where direct access to dynamics is simpler than to connectivity.
   For an introductory review of the state of the art, see
J. Phys. A: Math. Theor. 47 343001 (2014)
http://dx.doi.org/10.1088/1751-8113/47/34/343001

BP 6.2   Mon 10:15   H36

Theory and experiments on anomalous critical and supercritical connectivity transitions — •Jan Nagler — ETH Zurich

The emergence of large-scale connectivity on an underlying network or lattice, the so-called percolation transition, has a profound impact on the system's macroscopic behaviours. There is thus great interest in controlling the location of the percolation transition to either enhance or delay its onset and, more generally, in understanding the consequences of such control interventions. Here we report on the sudden emergence of large-scale connectivity that results from repeated, small interventions designed to delay the percolation transition. These transitions exhibit drastic, unanticipated and sometimes exciting consequences in complex networked systems but also pose experimental challenges. In particular, I will report on both theoretical and experimental progress (D'Souza & Nagler, Nature Physics 11:531, 2015; Nagler et al., unpublished).

BP 6.3   Mon 10:30   H36

What does Big Data tell? Sampling the social network by communication channels — •János Török[1,2], Yohsuke Murase[3], Hang-Hyun Jo[4,5], János Kertész[2,1,5], and Kimmo Kaski[5] — [1]Department of Theoretical Physics, Budapest University of Technology and Economics, Budapest H-1111, Hungary — [2]Center for Network Science, Central European University, Budapest H-1051, Hungary — [3]RIKEN Advanced Institute for Computational Science, Kobe, Hyogo 650-0047, Japan — [4]BK21plus Physics Division and Department of Physics, Pohang University of Science and Technology, Pohang 37673, Republic of Korea — [5]Department of Computer Science, Aalto University School of Science, P.O. Box 15500, Espoo, Finland

Big Data has become the primary source of understanding the structure and dynamics of the society at large scale. However, usually one has information only about one of the channels, which should be considered as a sample of the whole. We show by simulations and analytical methods that this sampling may lead to bias. For example, while it is expected that the degree distribution of the whole social network has a maximum at a value larger than one, we get with reasonable assumptions about the sampling process a monotonously decreasing distribution as observed in empirical studies of single channel data. Also we find, that assortativity may occur or get strengthened due to the sampling process. We analyze the far-reaching consequences of our findings.

BP 6.4   Mon 10:45   H36

Effective Distances in Complex Networks — Flavio Iannelli[1],

•Andreas Koher[2], Philipp Hövel[2], and Igor M. Sokolov[1] — [1]Humboldt Universität zu Berlin, Germany — [2]Technische Universität Berlin, Germany

The analysis of global epidemics revealed that physical distances can hardly be used to forecast the outbreak dynamics. Instead, a network-based measure which has been introduced recently [1] allows to predict infection arrival times with a surprisingly high accuracy. The so-called effective distances are solely based on the (weighted) network topology.
   We present an alternative approach, which is motivated by a fundamental property from the theory of random walks: The distribution of first passage times. This random walk based distance allows to forecast disease dynamics on various topologies. For the special case of highly heterogeneous networks it reduces to the previously introduced effective distance.
[1] Brockmann D, Helbing D "The hidden geometry of complex, network-driven contagion phenomena." Science. 2013;342(6164):1337–1342

BP 6.5   Mon 11:00   H36

A Geometrical Approach to Infection Dynamics on Temporal Networks — •Felix Herrmann[1], Philipp Hövel[1], Vitaly Belik[1], Andreas Koher[1], Hartmut H. K. Lentz[2], and Dirk Brockmann[3,4] — [1]Institut für Theoretische Physik, Technische Universität Berlin — [2]Friedrich-Loeffler-Institut, Greifswald — [3]Institut für Theoretische Biologie, Humboldt-Universität zu Berlin — [4]Robert Koch-Institut, Berlin

We investigate the extension of a recently introduced geometrical approach for the description of spreading processes on static undirected networks [1] to directed temporal networks. Its key quantity is a probabilistically motivated "effective distance" between nodes, which is based on the weights of the links and allows reliable predictions of disease arrival times and the identification of the origin of spreading processes. The approach has already been successfully applied to study infection dynamics on a static undirected air traffic network [1].
   By demonstrating how this approach can be generalized, we contribute to a framework for the investigation of spreading dynamics on temporal networks. Specifically, we consider an empirical livestock trade network in Germany, consisting of 97,980 nodes (agricultural holdings) and 6,359,697 temporal edges (trade events) [2], and use a SIR model to simulate the local dynamics of the nodes. Strong fluctuations in the activity of the nodes render the application of the geometrical approach particularly challenging.
[1] D. Brockmann and D. Helbing, Science 342, 1337 (2013).
[2] H. H. K. Lentz et al., Phys. Rev. Lett. 110, 118701 (2013).

BP 6.6   Mon 11:15   H36

Controlling recurrent epidemics on temporal networks — •Vitaly Belik[1,2], Florian Fiebig[1], Hartmut H K Lentz[3], and Philipp Hövel[1,4] — [1]Institut für Theoretische Physik, Technische Universität Berlin — [2]Helmholtz Zentrum für Infektionsforschung, Braunschweig — [3]Institute of Epidemiology, Friedrich-Loeffler-Institute, Greifswald — [4]Bernstein Center for Computational Neuroscience Berlin, Humboldt Universität zu Berlin

We consider a rucurrent epidemic on a temporal network. The goal of the control is to reduce the prevalence or make the epidemic extinct, respectively. To this end we propose a protocol based on rewiring the edges away from infected nodes, after they are detected as those: instead of an infected node, we randomly choose a healthy one (or perceived as such). In contrast to coevolutionary adaptive networks, the intrinsic dynamics of the network is taken into account by our approach alongside with the adaptive rewiring. The proposed control scheme significantly expands the range of a disease-free parameter region. For example, on the network of German pig trade, diseases with detection times up to 10 days and infectious periods up to 3 months could be efficiently controlled by our method [1]. Thus changing the behaviour of trading partners could have significant impact on the epidemic outcome.
[1]V Belik, F Fiebig, HHK Lentz, P Hövel arXiv preprint arXiv:1509.04054