Berlin 2018 – BP Friday

## BP 39: Focus Session: Complex Contagion Phenomena II (joint session SOE/DY/BP)

Session organizers and chairs: Philipp Hövel, Pawel Romanczuk, and Jonathan Donges. See part I of the session for a synopsis.

Time: Friday 9:30–13:15 Location: MA 001

Topical Talk BP 39.1 Fri 9:30 MA 001

Network reconstruction for the prediction of spreading processes — •Diego Garlaschelli — Lorentz Institute for Theoretical Physics, University of Leiden, The Netherlands

Financial contagion is an epidemic-like phenomenon whereby financial distress can propagate across a network of banks connected by credit relationships, possibly leading to the collapse of the entire system. In order to estimate the systemic risk of financial contagion, the knowledge of the entire interbank network is required. However, due to confidentiality issues, banks only disclose their total exposure towards the aggregate of all other banks, and not their individual exposures towards each bank. A similar problem is encountered in epidemiology. Is it possible to statistically reconstruct the hidden structure of a network in such a way that privacy is protected, but at the same time higher-order properties are correctly predicted? In this talk, I will present a general maximum-entropy approach to the problem of network reconstruction and systemic risk estimation. I will illustrate the power of the method when applied to various economic, social, and biological systems. Then, as a counter-example, I will show how the Dutch interbank network started to depart from its reconstructed counterpart in the three years preceding the 2008 crisis. Over this period, many topological properties of the network showed a gradual transition to the crisis, suggesting their usefulness as early-warning signals. By definition, these signals are undetectable if the network is reconstructed from partial bank-specific information.

BP 39.2 Fri 10:00 MA 001

Agent-based modeling of innovation spreading in ancient times — •Natasa Djurdjevac Conrad¹, Luzie Helfmann¹,², Johannes Zonker¹,², Stefanie Winkelmann¹, and Christof Schuette¹,² — ¹Zuse Institute Berlin — ²Freie Universitaet Berlin

Modeling of spreading processes has gained a lot of attention in the last decades, since these processes play a crucial role in understanding a wide range of real-world systems that span biological, technical, economical and social sciences. However, very little is known about processes/systems that have happened in ancient times, available data is sparse and we can not observe these systems again.

In this talk, we will present an agent-based model for the spreading of the wool-bearing sheep in a population of herders in the Near East and Europe, between 6200 and 4200 BC. In our model, the herders are represented by agents moving diffusively in a geophysical landscape and simultaneously interacting with other agents. The diffusion of the innovation is thus happening on a spatial network that is changing in time, as the connections between the agents are changing in time due to their movements. We will use our model to explore the dynamical properties of the spreading process and to study the qualitative effect of different aspects affecting the speed and spatial evolution of this spreading process.

BP 39.3 Fri 10:15 MA 001

Identifying the source of large-scale outbreaks of infectious disease — Abigail Horn¹ and •Hanno Friedrich² — ¹Bundesinstitut für Risikobewertung, Berlin, Germany — ²Kühne Logistics University, Hamburg, Germany

We study the problem of identifying the source of emerging large-scale disease outbreaks: given a model of the underlying network and reports of illness, determine the outbreak source location. Existing work on the network source identification problem has focused on studying this problem in trees and extending to general network structures in an ad hoc manner; this is to assume the contamination travels along a specific set known paths through a network, which may be an unrealistic approximation. In this work we develop a novel, computationally tractable solution that accounts for all possible contagion transmission paths through the network. We formulate a probabilistic model of the contamination transmission process as a random walk on a network and derive the maximum likelihood estimator for the source location. If the temporal dimension of the spreading process is well understood, we also estimate the epidemic start time. We demonstrate the benefits of this approach to source detection through application to var-

ious real network and outbreak contexts, including the 2011 STEC outbreak in Germany spread through the food supply network and ongoing outbreaks of cholera in Mozambique spread through human travel, showing significant improvements in accuracy and robustness compared with the relevant state-of-the-art methods.

BP 39.4 Fri 10:30 MA 001

Spreading of multiple pathogens and their evolutionary stable strategies —  $\bullet$ Kai Seegers<sup>1</sup>, Fakhteh Ghanbarnejad<sup>1</sup>, Alessio Cardillo<sup>2</sup>, and Philipp Hövel<sup>1</sup> — <sup>1</sup>Institut für Theoretische Physik, TU Berlin — <sup>2</sup>Institut Catalá de Paleoecologia Humana i Evolució Social (IPHES)

Different pathogens usually spread simultaneously in a host population and thus often influence each other. They can either be competitive, e.g. due to cross immunity, or cooperative, e.g. by suppressing the immune system of the host. The latter can lead to unexpectedly large outbreaks [EPL 104, 50001 (2013), Nature Physics 11, 936-940 (2015)] as it has been seen in the Spanish Flu pandemic in the early 20th century and it has been recently on serious warning alarm for co-infection of HIV and tuberculosis or hepatitis, for instance. However cooperation might not always be the best strategy for pathogens to survive, due to death of the host population or enforced countermeasures. Therefore we combine in a novel approach spreading dynamics of different strains of multiple pathogens with evolutionary game theory. We show bistability of strategies in the parameter space and finally discuss the emergence of competition and cooperation of pathogens.

BP 39.5 Fri 10:45 MA 001

Complex Social Contagion of Structural Discrimination — •GORM GRUNER JENSEN and STEFAN BORNHOLDT — Institute for Theoretical Physics University of Bremen Otto-Hahn-Allee D-28359 Bremen Germany

One approach within evolutionary game theory study the spreading of contagious behaviors in populations of agents distributed on a graphs. Typically the agents interact in well defined games with their nearest neighbors, and the evolutionary dynamics are implemented by letting agents copying the behavior of their neighbors. Here we demonstrate that this modelling approach can be applied in studying the complex social contagion of structural discrimination. Starting from established models designed to study the evolution of behaviors like cooperation and altruism, we split the agents into groups distinguished only by an observable labels. This generally entails an increased strategy-spaces, as strategies may now be discriminating, ie. imply different behaviors towards agents from different groups. Our model approach is fundamentally different from previous theories of the emergence and persistence of discrimination, which usually rely on on an intrinsic preference for helping your own kind, on games with asymmetric Nash equilibria like the Hawk-Dove Game, or on self-fulfilling prophecies. We do, however, find a strong connection between the evolutionary stability of discriminating strategies and the strength of the evolution pressure, which indicates that an evolutionary perspective coul be an important compliment to the existing theories.

BP 39.6 Fri 11:00 MA 001

Making rare events happen: prediction and control of network extinction, switching, and other extreme processes. — •JASON HINDES — U.S. Naval Research Lab, Washington D.C., United States of America

Many complex networks must operate in uncertain and dynamic environments. Over long time scales, combinations of random internal interactions and dynamical perturbations can organize to drive a network from one collective state to another. Such noise-induced large fluctuations may be associated with desirable outcomes, such as epidemic extinctions, or undesirable ones, such as switching in collective order, or loss of network synchrony. In this talk I will discuss a general formalism for predicting rare events in networks with internal and external noise, the role of topology in facilitating the most extreme network events, techniques for optimal network control that leverage uncertainty, and numerical solutions for the aforementioned when ex-

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plicit formulas are unknown. Along the way, I will consider many examples: from epidemic dynamics to opinion formation and synchronization of coupled oscillators.

## 15 min. break

BP 39.7 Fri 11:30 MA 001

Complex contagion in social media — •Philipp Lorenz<sup>1</sup>, Jonas Braun<sup>2</sup>, and Philipp Hövel<sup>1</sup> — <sup>1</sup>Institute of Theoretical Physics, Technische Universität Berlin, Hardenbergstraße 36, 10623 Berlin, Germany — <sup>2</sup>Department of Physics, Humboldt-Universität zu Berlin, Newtonstraße 15, 12489 Berlin, Germany

Spreading processes on a network of individuals can be described either under the assumption of independent interaction with equal transmission rates, like the classic SIS/SIR models (simple contagion) or one can take the structure of an individual's neighborhood into account (complex contagion). A very interesting model is sociologically inspired and includes the relative threshold of a node's surrounding required to change its state to infected (convinced). For the online world, especially social platforms, which became the stage of opinion spreading, these models have to be extended. We propose two extensions of the classical threshold model:

- Reposting, the state of a node can be multiple infected (convinced) changing the binary state variable to an integer.
- Recovery, a saturation of exposure, introducing a second threshold that turns nodes into a recovered (immune) state.

We investigate the interplay of these ingredients, separated and in combination with respect to the spreading dynamics and the role of initiators by the quantitative comparison of various scenarios.

BP 39.8 Fri 11:45 MA 001

Flockworks: A class of dynamic network models for face-to-face interactions — ◆Benjamin F. Maier<sup>1,2</sup> and Dirk Brockmann<sup>1,3</sup> — ¹Robert Koch-Institut, Nordufer 20, 13353 Berlin — ²Institut für Physik, Humboldt-Universität zu Berlin, Newtonstraße 15, 12489 Berlin — ³Institut für Theoretische Biologie, Humboldt-Universität zu Berlin, Philippstr. 13, 10115 Berlin

Studying the dynamics of face-to-face interaction networks is essential for a better understanding of contact mediated processes, contagion processes, and disease spreading. In many studies regarding social systems, networks are reconstructed using time averages in which links reflect an interaction likelihood, although this measures serves as a qualitative feature from which network properties are computed. During the last years a significant effort was made to resolve this issue by developing algorithms to analyze dynamic processes on the actual time-dependent contact patterns of social systems. However, there is still a lack of simple dynamic network models generating temporal networks of typical behaviour observed in real systems.

We introduce a class of minimal dynamic network models that naturally yield group formation and are easy to control with a small number of parameters. We discuss a variety of properties of those models and show that they reflect the character of real-world temporal data as well as the properties of dynamic processes on this data remarkably well, up to the prediction of epidemic curves.

BP 39.9 Fri 12:00 MA 001

Cooperation vs. defection in an evolutionary ecological framework — •Felix Köster and Fakhteh Ghanbarnejad — Technische Universität Berlin, Hardenbergstraße 36, 10623 Berlin, Germany

In this work, we first extend the CGB model [1] by considering each pathogen has two different strategies: cooperation or defection. Then we analyse the fundamental properties of the interacting contagious processes in a well-mixed population, i.e. homogeneous mean field approximation. Altering parameters we discover new discontinuous phase transitions for which we investigate the multi-stability shift in the phase diagram. We show also qualitatively same results by stochastic simulations. Furthermore, an evolutionary game is introduced to mimic conditions, which force agents to adept their strategies by minimizing their payoff. This study improves our understanding of the natural dynamics of species populations in an evolutionary ecological framework

[1] L. Chen, F. Ghanbarnejad, D. Brockmann "Fundamental properties of cooperative contagion processes"; New J. Phys. 19, 103041(2017)

key words; SIS, interacting dynamics, co-infection, complex contagions, discontinuous transitions

BP 39.10 Fri 12:15 MA 001

Effective Distances for Epidemic Spreading — ◆Andreas Koher¹, Flavio Iannelli², Igor M. Sokolov², and Philipp Hövel¹ — ¹Technische Universität Berlin — ²Humboldt Universität zu Berlin

The analysis of global epidemics revealed that physical distances can hardly be used to forecast the arrival time of the first infected person. Instead, recent results on the global air traffic network suggest that network based measures, so called effective distances correlate well with actual detection times.

We compare numerical simulations on the global air traffic network with different measures that are based on shortest distances, parallel paths and the recently proposed random walk effective distance [1]. Furthermore, we extend the latter and propose an effective distance that is based on non-backtracking walks. This simple diffusion model allows to consider the directed nature of epidemic spreading and relates the hitting probability to the infection arrival time.

[1] F. Iannelli, A. Koher, D. Brockmann, P. Hövel, and I.M. Sokolov, Effective distances for epidemics spreading on complex networks, Phys. Rev. E 95, 012313 (2017).

BP 39.11 Fri 12:30 MA 001

Modeling of Behavioral Cascades in Fish Schools — ◆Pawel Romanczuk<sup>1,2</sup>, Matt Grobis<sup>3</sup>, Bryan Daniels<sup>4</sup>, Winnie Poel<sup>1,2</sup>, Colin Twomey<sup>5</sup>, and Iain Couzin<sup>6,7</sup> — ¹Institute for Theoretical Biology, Dept of Biology, Humboldt Universität zu Berlin, Germany — ²Bernstein Center for Computational Neuroscience, Berlin, Germany — ³Dept. of Ecology and Evol. Biology, Princeton University, USA — ⁴ASU-SFI Center for Biosocial Complex Systems, Arizona State University, USA — ⁵Dept. of Biology, University of Pennsylvania — ⁶Dept. of Collective Behavior, MPIORN, Konstanz, Germany — ¹Dept. of Biology, University of Konstanz, Germany

Recently, it was shown that the spreading of stereotypical escape behavior (startle) in fish schools corresponds to a complex contagion process [1]. Here, we will discuss the modeling of such behavioral cascades using an extension of the generalized contagion model proposed by Dodds & Watts [2]. In particular, using networks extracted from experimental data, we will identify and discuss parameter regions providing best agreement with experimentally observed cascades. Furthermore, we will apply our modeling ansatz to new experiments on the impact of different risk perception on the behavioral contagion dynamics in fish schools.

- [1] Rosenthal, S.B., et al., PNAS 112, 15, 4690-4695 (2015)
- [2] Dodds, P. & Watts, D.J., Phys Rev Lett, 92, 218701 (2004)

BP 39.12 Fri 12:45 MA 001

The effect of compatibility and heterogeneous adoptability in contagion processes — •BYUNGJOON MIN and MAXI SAN MIGUEL — Instituto de Fisica Interdisciplinar y Sistemas Complejos (CSIC-UIB), Campus Universitat Illes Balears, E-07122 Palma de Mallorca, Spain

While competition and compatibility of multiple contagious entities and heterogeneous adoptability of agents are omnipresent in social contagions, so far these factors are overlooked in traditional models of contagion processes. Here, we study generalized contagion processes in two directions: i) unifying simple and complex contagions reflecting heterogeneous adoptability and ii) considering competition and compatibility among multiple transmittable entities. For a generalized contagion model unifying simple and complex contagion processes, we find a rich variety of phase transitions such as continuous and discontinuous phase transitions, criticality, tricriticality, and double transition. We also examine the role of dual users who possess multiple contagious technologies simultaneously, and find that the compatibility induced by the dual user facilitates spread of innovation and extinction of pre-existing technology.

BP 39.13 Fri 13:00 MA 001

Modeling of startling cascades and information transfer in fish —  $\bullet \rm HAIDER~KLENZ^1$  and PAWEL ROMANCZUK $^{1,2}$  —  $^1 \rm Department$  of Biology, Humboldt-Universität zu Berlin, Berlin 10115, Germany —  $^2 \rm Bernstein$  Center for Computational Neuroscience, Humboldt-Universität zu Berlin, Berlin 10099, Germany

Animals come together in groups, e.g. school of bird or swarms of

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fish, in which information is processed collectively. Especially in situation where the collective is exposed to a threat, this information and the speed with which it propagates through the collective is of great importance to the individual.

This work focuses on shoals of *Poecilia Sulphuraria* and their reaction to danger. Through environmental dependencies the fish can only swim at the surface and therefore forms a 2D-system. When attacked by preying birds the fish dive down. This diving behavior then spreads

through the swarm in a wave like fashion and is repeated for several minutes without further triggers.

We explored the mechanism behind wave spreading with agent-based modeling. We propose a stochastic contagion process and show that the speed of the wave depends on the underlying information network. Furthermore we study different possible explanations for repeated waves.