

**BP 30: Focus Session: Complex Contagion Phenomena I (joint session SOE/DY/BP)**

Contagion processes are stochastic dynamical systems that are ubiquitous in natural and engineered systems and their fundamental understanding is of crucial importance for prediction and control of large-scale system behavior. A classical example of a contagion process is the spread of infectious diseases. In addition, in recent years, there has been also an increased scientific interest in so-called social contagion phenomena, which is largely fueled by the rise of digital communication in online social platforms. New challenges that arise due to the digital transformation of communication can be addressed by developing new concepts like collective risk perception.

(Session organizers and chairs: Philipp Hövel, Pawel Romanczuk, and Jonathan Dongs)

Time: Thursday 9:30–13:15

Location: MA 001

**Invited Talk** BP 30.1 Thu 9:30 MA 001  
**Epidemic threshold on temporal networks** — ●VITTORIA COL-  
IZZA — Inserm, Paris, France

Our understanding of communicable diseases prevention and control is rooted in the theory of host population transmission dynamics. The network of host-to-host contacts along which transmission can occur drives the epidemiology of communicable diseases, determining how quickly they spread and who gets infected. A large body of epidemiological, mathematical and computational studies has provided a number of insights into the understanding of the process and the identification of efficient control strategies. The explosion of time resolved contact data has however opened the stage to new challenges. What are the structural and temporal aspects, and possibly their non-trivial interplay, that are critical for disease spread? To answer this question, I will introduce the infection propagator approach, a theoretical framework for the assessment of the degree of vulnerability of a host population to disease epidemics, once we account for the time variation of its contact pattern. By reinterpreting the tensor formalism of multi-layer networks, this approach allows the analytical computation of the epidemic threshold for an arbitrary time-varying network of host contacts, i.e. the critical pathogen transmissibility above which large-scale propagation occurs. I will apply this framework to a set of empirical time-varying contact networks and show how it can be used to test different intervention strategies for infection prevention and control in realistic settings.

**Invited Talk** BP 30.2 Thu 10:00 MA 001  
**Critical regimes driven by recurrent mobility patterns of reaction-diffusion processes in networks** — ●JESUS GOMEZ-  
GARDENES — University of Zaragoza, Spain

Reaction-diffusion processes have been widely used to study dynamical processes in epidemics and ecology on networked metapopulations. In the context of epidemics, reaction processes are understood as contagions within each subpopulation (patch), while diffusion represents the mobility of individuals between patches. Recently, the characteristics of human mobility, such as its recurrent nature, have been proven crucial to understand the phase transition to endemic epidemic states. Here, by developing a framework able to cope with the elementary epidemic processes, the spatial distribution of populations and the commuting mobility patterns, we uncover three different critical regimes of the epidemic incidence as a function of these parameters. Interestingly, we show a regime of the reaction\*diffusion process in which, counter-intuitively, mobility detracts the spreading of the disease. We analytically determine the precise conditions for the emergence of any of the three possible critical regimes in real and synthetic networks.

**Invited Talk** BP 30.3 Thu 10:30 MA 001  
**Phase Transitions in Cooperative Coinfections** — ●PETER  
GRASSBERGER<sup>1</sup>, LI CHEN<sup>2</sup>, FAKHTEH GHANBARNEJAD<sup>3</sup>, and WEIRAN  
CAI<sup>4</sup> — <sup>1</sup>Juelich Research Center, Juelich, Germany — <sup>2</sup>Northwestern  
Polytechnical University, Xi'an, Shaanxi, China — <sup>3</sup>Technische Uni-  
versität Berlin, Berlin, Germany — <sup>4</sup>Technische Universität Dresden,  
Dresden, Germany

We study the spreading of two mutually cooperative diseases on different network topologies, with two stochastic versions of an SIR type model. Cooperativity can lead to hybrid spreading/extinction transitions, which show at the same time typical signatures both of first order (discontinuous) and second order (continuous) phase transitions. Details depend strongly on the underlying network(s), but also on some details of the algorithms.

As a rule, first order and hybrid transitions occur on networks with

few short but many long loops, while continuous transitions are found when there are either many short or few long loops. The latter happens on 2-d lattices, while the former is typical for high-dimensional regular lattices or Erdős-Rényi networks. In three dimensions, the behavior is most rich, and a zoo of different first order / second order mixtures are observed.

**15 min. break**

**Invited Talk** BP 30.4 Thu 11:15 MA 001  
**Linear and nonlinear scenarios of societal change** — ●ANDRZEJ  
NOWAK — University of Warsaw, Poland

We argue that is that rapid social changes occur rapidly in an abrupt and nonlinear manner resembling a phase transition. Societies in the midst of rapid change are characterized by dual realities corresponding to the new and the old, and the change occurs as the islands of the new expand at the expense of the islands of the old. The central notion is that social influence processes play a pivotal role in promoting social change. Dynamic Theory of Social Impact, which is based on numerous experiments, describes social influence of a group of sources on the target. The findings are based on computer simulations of the theory and confirmed by empirical data collected during the societal transitions that occurred in Poland in the late 1980s and early 1990s. We discuss the dynamics associated with rapid transitions in a society\*s norms and attitudes, potential for rapid reversals and role of history in social dynamics.

**Invited Talk** BP 30.5 Thu 11:45 MA 001  
**Collective Sensing and Decision-Making in Animal Groups: From Fish Schools to Primate Societies** — ●IAIN COUZIN —  
Dept. of Collective Behaviour, Max Planck Institute for Ornithology & Chair of Biodiversity and Collective Behaviour, University of Konstanz, Konstanz, Germany

Understanding how social interactions shape biological processes is a central challenge in contemporary science. Using an integrated experimental and theoretical approach I will address how, and why, animals exhibit highly-coordinated collective behavior. I will demonstrate new imaging technology that allows us to reconstruct (automatically) the dynamic, time-varying networks that correspond to the visual cues employed by organisms when making movement decisions. Sensory networks are shown to provide a much more accurate representation of how social influence propagates in groups, and their analysis allows us to identify, for any instant in time, the most socially-influential individuals within groups, and to predict the magnitude of complex behavioral cascades before they actually occur. I will also introduce a new fully-immersive Virtual Reality environment for freely-moving animals, and investigate the coupling between spatial and information dynamics in groups. Finally I will reveal the critical role uninformed, or unbiased, individuals play in social networks effecting fast and democratic consensus decision-making in collectives, including with experiments involving schooling fish and wild baboons.

**Invited Talk** BP 30.6 Thu 12:15 MA 001  
**Quantitative assessment of import risks for emergent infectious disease outbreaks** — ●OLGA BARANOV<sup>1</sup> and DIRK  
BROCKMANN<sup>1,2</sup> — <sup>1</sup>Robert Koch-Institut, Berlin, Germany — <sup>2</sup>Humboldt-Universität zu Berlin, Germany

During the last decade outbreaks of emergent pathogens that potentially pose a risk of global dissemination have increased in number and magnitude. When new outbreaks occur, one of the key challenges is a quantitative assessment of the situation, especially concerning global

spread. To this end, sophisticated computational models have been developed incorporating exact situation details, disease parameters and demographics. One of the key problems is that highly detailed models are difficult to gauge, because of the initial lack of parameters, substantially impacting the applicability of even the most sophisticated models. We propose an alternative approach for estimating relative import risk from network topology and outbreak origin. It is based on the assumption that during the initial outbreak phase, global import risk is determined by a low dispersal count regime. In this regime disease specific data play only a minor role. Using world aviation network, we demonstrate how import risk at any location can be inferred. We show that this method can be used to compute an airports dissemination profile as a function of outbreak location and how outbreaks in different regions lead to a different subset of key airports. Our method is fast and not limited to a particular type of infectious disease. It can be used as an initial risk assessment tool for public health researchers and policy makers that need to address a real world scenario.

BP 30.7 Thu 12:30 MA 001

**How to compete in a multi-pathogen system?** — FRANCESCO PINOTTI<sup>1</sup>, ●FAKHTEH GHANBARNEJAD<sup>2</sup>, PHILIPP HÖVEL<sup>2</sup>, and CHIARA POLETTI<sup>1</sup> — <sup>1</sup>Sorbonne Universités, UPMC, INSERM, IPLESP UMRS 1136, Paris, France — <sup>2</sup>Institute of Theoretical Physics, TU Berlin, Berlin, Germany

In an ecological system pathogens often need to share their host with other pathogens, and therefore compete for the resources with different spreading strategies. Both cooperative and competitive interactions in bacterial infections have been observed. These two mechanisms have been studied separately in the majority of cases and non-trivial dynamical effects can be expected to arise from their combination. In this work, we study two strains competing with each other for host resources in the presence of a third pathogen cooperating with both of them. We first treat dynamics in a homogeneously mixed population by means of mean-field theory and stability analysis. We study the impact of cooperation on the outcome of the two-pathogen competition, which can be quantified in terms of dominance of one competing pathogen or the co-circulation of both of them. We show that the presence of a third cooperating pathogen can alter the outcome of competition as it may favor the more cooperative pathogen over the more infectious one. We then consider more complex contact structures among hosts and perform computer simulations to study the evolution of the diseases.

BP 30.8 Thu 12:45 MA 001

**Defining the scope: A context specific approach to identify-**

**ing key airports during a pandemic** — ●CLARA JONGEN<sup>1,2</sup>, OLGA BARANOV<sup>2</sup>, and DIRK BROCKMANN<sup>1,2</sup> — <sup>1</sup>Humboldt-Universität zu Berlin, Germany — <sup>2</sup>Robert Koch-Institut Berlin, Germany

Human transportation and mobility networks play an important role in the global spread of infectious diseases. Network theory is one of the key methods to understand the nature of these phenomena. In this context, a family of node and link centrality measures has been devised to identify network elements that facilitate the spread and thus require particular attention in the development of containment strategies. However, most centrality measures are not context sensitive, e.g. they do not account for the location of an outbreak. Using the example of disease dynamics on the global air-transportation network we introduce the concepts of node *scope* and *confluence*. These quantities are context dependent centrality measures that are designed to account for the initial outbreak location. We show that scope and confluence can strongly depend on regional aspects of an outbreak and can therefore be adapted to specific outbreak scenarios. We show that each airport is characterized by a node specific scope and confluence profile as outbreak locations are varied. Scope and confluence also permit to address what outbreak locations are particularly threatening to specific nodes in the network. Our method can be used as an assessment tool for understanding global disease dynamics and permit a fast yet specific assessment of an airport's role in global disease dynamics.

BP 30.9 Thu 13:00 MA 001

**Comparison of Control Strategies for the Spread of Bovine Viral Diarrhea: A Stochastic Agent-Based Model** — ●JASON BASSETT<sup>1</sup>, PASCAL BLUNK<sup>1</sup>, THOMAS M. ISELE<sup>1</sup>, HARTMUT H. K. LENTZ<sup>2</sup>, JÖRN GETHMANN<sup>2</sup>, PHILIPP HÖVEL<sup>1,3</sup>, and FRANZ J. CONRATHS<sup>2</sup> — <sup>1</sup>TU Berlin, Berlin, Germany — <sup>2</sup>Friedrich Loeffler Institute, Greifswald, Germany — <sup>3</sup>BCCN, Berlin, Germany

*Bovine Viral Diarrhea* (BVD) is an important cattle disease due to its global prevalence and its economic implications [1]. In this work we have developed a stochastic agent-based model to describe the spread of BVD in Thuringia through trade mediated contacts of animals. The agents act at the level of the animal, the herd or the farm on a network of farms connected according to a supply and demand managing system, while the BVD dynamics are based on a model by [2]. We initialise the simulation according to a realistic farm size distribution for Germany and the state of Thuringia, and compare the results of the simulation with demographic and endemic data solely for the state of Thuringia. We also run the simulation for different parameter settings (scenarios) including vaccination strategies and currently implemented or considered regulations. Finally, we present and discuss some network analysis results on the simulated network [3].