SOE 8: Networks, From Topology to Dynamics (joint session SOE/BP/DY)

Time: Wednesday 15:00–17:30 Location: H45

SOE 8.1 Wed 15:00 H45

Self-organized transport in noisy dynamic networks — •Frederic Folz[1], Joshua Rainer Ganz[1], Kurt Mehlhorn[2], and Giovanna Morigi[1] — [1]Theoretische Physik, Universität des Saarlandes, 66123 Saarbrücken, Germany — [2]Algorithms and Complexity Group, Max-Planck-Institut für Informatik, Saarland Informatics Campus, 66123 Saarbrücken, Germany

We present a numerical study of multicommodity transport in a noisy, nonlinear network. The nonlinearity determines the dynamics of the edge capacities, which can be amplified or suppressed depending on the local current flowing across an edge. We consider network self-organization for three different nonlinear functions: For all three we identify parameter regimes where noise leads to self-organization into more robust topologies, that are not found by the sole noiseless dynamics. Moreover, the interplay between noise and specific functional behavior of the nonlinearity gives rise to different features, such as (i) continuous or discontinuous responses to the demand strength and (ii) either single or multistable solutions. Our study shows the crucial role of the activation function on noise-assisted phenomena.

SOE 8.2 Wed 15:15 H45

Critical properties of Heider balance on multiplex networks — •Krishnadas Mohandas, Krzysztof Suchecki, and Janusz Hołyst — Faculty of Physics, Warsaw University of Technology, Koszykowa 75, PL-00-662 Warsaw, Poland

Heider's structural balance theory has proven invaluable in comprehending the dynamics of social groups characterized by both friendly and hostile relationships. Extending this understanding to multiplex networks, we investigate Heider balance dynamics in systems where agents exhibit correlated relations across multiple layers. In our model, intralayer interactions adhere to Heider dynamics, while interlayer correlations are governed by Ising interactions, using heat bath dynamics for link signs. This framework reveals a multifaceted equilibrium landscape, with distinct phases coexisting across layers. Starting from a paradise state with positive links in all layers, increasing temperature induces a discontinuous transition to disorder, similar to single-layer scenarios but with a higher critical temperature, as verified through extended mean-field analysis and agent-based simulations.

We extend this analysis to Erdös-Rényi random graphs in noisy environments. We predict a first-order transition with a critical temperature scaling as p^2 for monolayers and follow a more complex behavior for bilayers. To replicate dynamics observed in complete graphs, intralayer Heider interaction strengths must scale as p^{-2}, while interlayer interaction strengths scale as p^{-1} in random graphs. Numerical simulations confirm these analytical predictions for dense graphs.

SOE 8.3 Wed 15:30 H45

Functional Motifs in Food Webs and Networks — •Melanie Habermann[1,2,3], Ashkaan Fahimipour[4], Justin Yeakel[5,6], and Thilo Gross[1,2,3] — [1]Helmholtz Institute for Functional Marine Biodiversity (HIFMB), Oldenburg, GER — [2]Alfred-Wegener Institute (AWI), Helmholtz Center for Polar and Marine Research, Bremerhaven, GER — [3]Carl-von-Ossietzky University, Institute for Chemistry and Biology of the Marine Environment (ICBM), Oldenburg, GER — [4]Florida Atlantic University, Boca Raton, FL, USA — [5]University of California Merced, Merced, CA, USA — [6]The Santa Fe Institute, Santa Fe, NM, USA

It is interesting to ask when the presence of a small subgraph in a complex network is sufficient to impose constraints on system dynamics that are independent of the broader network structure. We refer to these subgraphs as functional motifs. A classic example can be found in ecology with the competitive exclusion motif in food webs, where two species compete for the same resource without regulation. The presence of this motif precludes any stable equilibrium for the entire system. However, examples of other motifs with similarly definitive implications for system stability are rare. But our usual notion of asymptotic stability is just one among many different concepts of stability. Another one, reactivity, captures a system's immediate response to small perturbations. In this talk, we explain why functional stability motifs are rare and show that every subgraph is a functional reactivity motif. This highlights reactivity as a promising concept for exploring a vast range of networked phenomena.

SOE 8.4 Wed 15:45 H45

Infecting Apex Predators Could Lead to Their Extinction — •Fakhteh Ghanbarnejad[1] and Hooman Saveh[2] — [1]SRH University of Applied Sciences, Leipzig, Germany — [2]Sharif University of Technology, Tehran, Iran

Food webs have been extensively studied from both ecological and mathematical aspects. However, most of the models studied in this area do not capture the effects of infectious diseases simultaneously. Recently, the idea of including an infectious disease in a food web model has been investigated. We study and simulate a small food chain consisting of only prey, predators, and apex predators governed by the generalized Lotka-Volterra equations and we implement the Susceptible-Infected-Recovered (SIR) model on only one of the species at a time in the food chain. To study the effects of an infectious disease on the food chain, we introduce a new parameter that increases predation rate by a factor of w and decreases hunting rate by a factor of $1/w$ for infected species. When the infectious disease is in our predators we observe that predators do not extinct under any set of parameters, however, an oscillation in its population size occurs under some circumstances which we do not observe in ordinary SIR or the generalized Lotka-Volterra equations alone. When an infectious disease is present in apex predators, oscillations in the population size do not happen; but if the set of parameters is in a specific range the apex predators may extinct. Furthermore, the chance of survival of the community, known as community persistence, increases for the predators and decreases for the apex predators.

15 min. break

SOE 8.5 Wed 16:15 H45

Behavioral Heterogeneity in Disease Spread: Contrasting Effects of Prevention Strategies and Social Mixing — •Fabio Sartori[1,2] and Michael Maes[1] — [1]Chair of Sociology and Computational Social Science, Karlsruhe Institute of Technology, Karlsruhe — [2]Max Planck Institute for Dynamics and Self Organisation, Göttingen, Germany

Despite mounting evidence of behavioral heterogeneity in response to disease threats, the majority of epidemiological models assume uniform behavior across populations for mathematical tractability. We analyze three distinct mechanisms of behavioral response to disease threat: susceptibility reduction (e.g., mask-wearing), active testing, and vaccination propensity. Through extensive numerical analysis, we demonstrate that the impact of behavioral heterogeneity strongly depends on the specific mechanism involved. While heterogeneous susceptibility-reducing behaviors generally decrease disease spread, heterogeneity in testing rates and vaccination propensity typically amplifies epidemic severity. Furthermore, we show that non-homogeneous mixing patterns, particularly when correlated with behavioral traits, exacerbate disease spread across all three mechanisms. These findings reveal fundamental principles about the interplay between behavioral heterogeneity and epidemic dynamics, challenging the conventional homogeneous assumption and providing important implications for public health interventions and policy design.

SOE 8.6 Wed 16:30 H45

Modelling retweet cascades using multivariate Hawkes processes on sparse networks — Alexander Kreiss[1] and •Eckehard Olbrich[2] — [1]Leipzig University, Germany — [2]Max Planck Institute for Mathematics in the Sciences, Leipzig, Germany

We apply a model that considers vertices in a network who are able to cast events, e.g. users of the online social media platform Twitter. Furthermore, there is a directed edge from vertex A to vertex B if A takes note of the events cast by B and changes its own behavior accordingly. More precisely, the model assumes that the activity of B increases the activity of A and likewise its other neighbors. This is called peer effects. However, there might also be other information, which also influences the activity of the vertices, e.g. the time of the day for social media posts. This is called global effects. We use a Hawkes model that incorporates, both, peer and global effects. This allows for the estimation of the network, that is, the influence structure while controlling for network effects or the estimation of the global effects while controlling for peer effects. The estimation is based on a LASSO strategy, which respects sparsity in the network. We apply this model to retweets on Twitter in order to reconstruct potential retweet cascades and identify accounts that are influential in sharing information.

SOE 8.7 Wed 16:45 H45

Influence, Incidence, Imitators and Individualists: Comparing social influence models of protective behavior in an epidemic — •Andreas Reitenbach — Karlsruhe Institute of Technology, Karlsruhe, Germany

To manage a pandemic, it is critical that citizens voluntarily engage in protective behavior (e.g. masking or vaccinating). Voluntary behavior is subject to complex dynamics of social influence, however. While various models couple social influence dynamics with disease spreading, assumptions about how individuals influence each other differ markedly. Models assuming herding implement that agents imitate their peers. On the contrary, rational agents (individualists) engage in protective behavior when their peers are not and vice versa, potentially free-riding on others' contributions to herd immunity.

Here, I study whether and why these competing behavior models translate into different disease dynamics. Following a recent call to abstract from psychological mechanisms underlying social influence, I translate the behavior theories into influence-response functions.

I find that individualists self-coordinate on a moderate level of protection and experience long-lasting but flat incidence curves. Herding, in contrast can result in rapid cycling through waves of high incidence and strong collective efforts to mitigate. Whether herders or individualists navigate an epidemic better can depend on the population's hospital capacity and disease parameters.

SOE 8.8 Wed 17:00 H45

Formalism and Physical Principles of Human Mobility and Routine — •Marlli Zambrano[1], Ashish Thampi[2], Alejandra Rincon[2], Andrzej Jarynowski[1], Steven Schulz[2], and Vitaly Belik[1] — [1]Freie Universität Berlin, Germany — [2]Machine Learning Unit, NET CHECK GmbH, Berlin, Germany

The physical principles underlying human mobility have been extensively studied in recent years, enabled by the availability of large-scale mobile phone data. While significant progress has been made in understanding general mobility patterns, capturing the dynamics of individual trajectories, specifically how mobility varies from person to person and day to day, remains challenging due to the need for highly detailed and persistent data. This study addresses this challenge by examining sequences of individual daily mobility motifs, as defined by Schneider et al., from a stochastic process perspective. The analysis uses a persistent mobile phone user panel in Berlin, with high-frequency GPS data collected over four years. Twenty motifs were identified, covering 96% of all observations. The extent of inter- and intra individual variability is explored, focusing on how motifs change within individuals over time and differ between individuals in various contexts (e.g., weekends, seasons). Additionally, sequences of motifs are modeled as a stochastic process, and properties such as transition probabilities are analyzed. These findings provide deeper insights into the variability and structure of human mobility, contributing to a better understanding of individual mobility dynamics.

SOE 8.9 Wed 17:15 H45

The world air transportation network: import risk of diseases, pandemic potentials and passenger routes — •Pascal Klamser[1,2], Adrian Zachariae[1,2], Benjamin Maier[3], Olga Baranov[4], and Dirk Brockmann[1,2] — [1]Technische Universität Dresden, Dresden, Germany — [2]Robert Koch-Institute, Berlin, Germany — [3]University of Copenhagen, Copenhagen, Denmark — [4]LMU München, München, Germany

Disease propagation between countries strongly depends on their effective distance, a measure derived from the world air transportation network. It reduces the complex spreading patterns of a pandemic to a wave-like propagation from the outbreak country, establishing a linear relationship to the arrival time of the unmitigated spread of a disease. However, in the early stages of an outbreak, what concerns decision-makers in countries is understanding the relative risk of active cases arriving in their country*essentially, the likelihood that an active case boarding an airplane at the outbreak location will reach them. While there are data-fitted models available to estimate these risks, accurate mechanistic, parameter-free models are still lacking.

We (i) introduce the "import risk" model, which defines import probabilities using the effective-distance framework, (ii) show its application to estimate the pandemic potential of emerging variants of COVID-19 and (iii) show that the effective distance shortest path tree, on which the "import risk" model is based on, is an extremely accurate representation of true passenger routes.