SOE 12: Networks: From Topology to Dynamics (joint session SOE/BP/DY)

Time: Wednesday 10:15–12:45   Location: H11

SOE 12.1   Wed 10:15   H11

Modeling tumor disease and sepsis by networks of adaptively coupled phase oscillators — •Eckehard Schöll[1,2,3], Jakub Sawicki[2], Rico Berner[1,4], and Thomas Löser[5] — [1]Institut für Theoretische Physik, TU Berlin, Germany — [2]Potsdam Institute for Climate Impact Research — [3]Bernstein Center for Computational Neuroscience Berlin — [4]Institut für Physik, HU Berlin — [5]Institut LOESER, Wettiner Straße 6, 04105 Leipzig

In this study, we provide a dynamical systems perspective to the modelling of pathological states induced by tumors or infection. A unified disease model is established using the innate immune system as the reference point. We propose a two-layer network model for carcinogenesis and sepsis based upon the interaction of parenchymal cells (organ tissue) and immune cells via cytokines, and the co-evolutionary dynamics of parenchymal, immune cells, and cytokines [1]. Our aim is to show that the complex cellular cooperation between parenchyma and stroma (immune layer) in the physiological and pathological case can be functionally described by a simple paradigmatic model of phase oscillators. By this, we explain carcinogenesis, tumor progression, and sepsis by destabilization of the healthy state (frequency synchronized), and emergence of a pathological state (multifrequency cluster). The coupled dynamics of parenchymal cells (metabolism) and nonspecific immune cells (reaction of innate immune system) are represented by nodes of a duplex layer. The cytokine interaction is modeled by adaptive coupling weights. [1] Sawicki, J., Berner, R., Löser, T., and Schöll, E., Frontiers Netw. Physiology 1,730385 (2022), arXiv:2106.13325v2.

SOE 12.2   Wed 10:45   H11

Analysis of the Football Transfer Market Network — •Tobias Wand — WWU Münster — CeNoS Münster

Football clubs buy and sell players for millions of Euros and until Covid, their combined transfer values were growing steadily at an impressive rate. Instead of analysing their aggregated transfer activities, one can take a look at the topology of the network of player transfers: complex networks have already been used in various sciences [1] including research on sports [2] and provide a novel approach to investigate the football transfer market network and in particular the impact of Covid on football clubs.

[1] G. Caldarelli and A. Vespignani, "Large Scale Structure and Dynamics of Complex Networks". World Scientific Publishing, 2007.

[2] Arriaza-Ardiles et al. "Applying graphs and complex networks to football metric interpretation". Human Movement Science 57, 2018.

SOE 12.3   Wed 11:00   H11

Variability in mesoscale structure inference using stochastic blockmodels — •Lena Mangold and Camille Roth — CNRS (Paris) / Centre Marc Bloch (Berlin)

Characterising the mesoscale structure of networks, in terms of patterns variously called communities, blocks, or clusters, has represented both a central issue and a key instrument in the study of complex systems. Clearly, distinct methods designed to detect different types of patterns may provide a variety of answers to the mesoscale structure. Yet, even multiple runs of a given method can sometimes yield diverse and conflicting results, posing challenges of model and partition selection. As an alternative to forcing a global consensus from a distribution of partitions (i.e. choosing one among many by maximising some objective), recent work has emphasised the importance of exploring the variability of partitions. Here we examine how a specific type of mesoscale structure (e.g. assortative communities or core-periphery) may be linked with more or less inconsistency in resulting partitions. We focus on Stochastic blockmodels (SBMs), initially proposed in mathematical sociology and increasingly used to infer mesoscale structure with a relatively general definition of similarity between nodes in the same group, and whose stochastic nature lends itself to the exploration of disagreement within populations of partitions. In particular, we generate families of synthetic networks in which we plant different types of mesoscale structures and explore the transitions between consensus and dissensus in the landscape of partitions over multiple SBM runs.

SOE 12.4   Wed 11:15   H11

Extracting signed relations from interaction data — •Georges Andres, Giona Casiraghi, Giacomo Vaccario, and Frank Schweitzer — ETH Zürich, Chair of Systems Design, Switzerland

Social relations influence human interactions and hence, help to explain individual behaviours. Moreover, humans perceive patterns of signed relations, either positive (e.g., friendship) or negative (e.g., enmity), and adapt to them. Data about signed relations are rare, despite their importance for understanding phenomena at the community level. Interaction data is, however, more abundantly available, for example, about proximity or communication events. Interactions and relations change on different time scales; interactions are more volatile and evolve faster than relations. Using this, I will present an ensemble-based approach to infer pair-wise signed relations from interaction data and consequently construct a signed network from them. By studying different datasets on interactions and relations, e.g. between students, I will further evaluate the quality of the inferred networks. Subsequently, I will study the presence of structural balance in the studied communities, describing the cognitive dissonance ensuing from particular triadic constellations of signed relations. Bearing similarities to frustrations in spin systems, structural balance can now be analysed solely from interaction data thanks to the presented method, a task which was previously out of reach.

SOE 12.5   Wed 11:45   H11

Disentangling homophily, community structure and triadic closure in networks — •Tiago Peixoto — Central European University, Vienna, Austria

Network homophily, the tendency of similar nodes to be connected, and transitivity, the tendency of two nodes being connected if they share a common neighbor, are conflated properties in network analysis, since one mechanism can drive the other. Here we present a generative model and corresponding inference procedure that is capable of distinguishing between both mechanisms. Our approach is based on a variation of the stochastic block model (SBM) with the addition of a triadic closure dynamics, and its inference can identify the most plausible mechanism responsible for the existence of every edge in the network, in addition to the underlying community structure itself, based only on the final observation of the network. We show how the method can evade the detection of spurious communities caused solely by the formation of triangles in the network, and how it can improve the performance of link prediction when compared to the pure version of the SBM without triadic closure.

[1] Tiago P. Peixoto, Disentangling homophily, community structure and triadic closure in networks, Phys. Rev. X 12, 011004 (2022)

SOE 12.6   Wed 12:15   H11

Evolving networks towards complexity: an evolutionary optimization approach — Archan Mukhopadhyay and •Jens Christian Claussen — University of Birmingham, UK

Complexity measures for graphs have been proposed and compared [1,2] widely, but the question how to mathematically define complexity is less clear as for text strings where Lempel-Ziv and Kolmogorov complexity provide clear approaches. In complexity science, the notion of complexity implies distinction from regular structures (lattices) as well as from random structures (here: random graphs). This however has not lead to any constructive definition. Complexity measures therefore typically assess artefacts of complexity (in some cases quite successfully). Here we present a complementary computational approach: we utilize each complexity measure as a fitness function of an evolutionary algorithm, and investigate the properties of the resulting networks. The goal is a better understanding of the existing complexity measures, and to shed some light on (artificial) network evolution: what evolutionary goals lead to complexity?