

#30 Topic: A model for the co-evolution of dynamic social networks and infectious disease dynamics

Leading researcher: [Hendrik Nunner](#)

In an increasingly globalized world, we face risks of outbreaks of infectious diseases, such as AIDS, Ebola, or new strains of influenza. Human behavior is known to have strong influence on infectious disease dynamics. A number of studies show that avoidant behaviors (e.g., avoiding public places during waves of influenza) affect social contact patterns and thus transmission pathways. It remains however unclear how avoidant behaviors shape the co-evolution of social networks and infectious diseases.

In recent years we see a growing interest in the interplay of social networks and infectious diseases. However, most studies either neglect health behavior or consider networks to be static, despite empirical evidence that people seek to distance themselves from diseases in social networks. In our current work, we propose an adaptable steppingstone model that integrates theories of social network formation from sociology, risk perception from health psychology, and infectious diseases from epidemiology. We argue that social networking in the context of infectious diseases can be described as a trade-off between the benefits, efforts, and potential harm a connection creates.

Agent-based simulations using a generic model implementation show that: (i) high (perceived) health risks create strong social distancing, thus resulting in low epidemic sizes, (ii) large numbers of ties provide more opportunities for disease spread, thus creating higher attack rates and shorter epidemics, and (iii) minor changes in health behavior can be decisive for whether the outbreak of a disease turns into an epidemic or not. These findings suggest a complex interplay between social network, health behavior, and infectious disease dynamics. Furthermore, they contribute to solving the issue that neglect of health behavior in models of disease spread may create mismatches between observed transmissibility and epidemic sizes of model predictions. Finally, we discuss possible modifications of the model that allow to capture a large variety of infectious diseases and social scenarios.