Social influence, contagion, and the dynamics of large-scale community networks

PhD student: Klara Valentova

Supervisory team: Johan Koskinen, Termeh Shafie, András Vörös, David Schoch, Yoshihisa Kashima, Colin Hugh Gallagher

It is increasingly recognised that a number of social ills are contingent on how people are connected to each other in large-scale communities. For example, fake news spread in massive online and offline social circles ("echo-chambers"), sexual diseases spread through connections in large urban settings, and individuals' mental states may affect entire communities through social contacts. In the network literature, social influence and contagion are well-studied, including how information and social support spread through networks. This literature recognizes that people's networks also evolve over time ("social selection") and this may confound and lead to biased findings about influence. The stochastic actor-oriented model (SAOM) is currently the only method for longitudinal social network analysis (SNA) that allows the joint analysis of influence and selection processes. The application of SAOMs has been limited to traditional network data such as networks in small school classes or in small organisations. In contrast, network processes on the large-scale community and societal level have not been feasible to model in this approach. This project aims at extending and applying SAOMs to large-scale community networks in the context of a number of unique datasets: (a) a needle sharing network with hepatitis status; (b) support networks in bushfire affected areas with PTSD status; (c) a sexual network of young men who have sex with men. In the first stage, newly developed cross-sectional modelling approaches will be applied to these datasets: (i) Bayesian data-augmentation techniques for partial network modelling, (ii) Bayesian auto-logistic actor attribute models. In a second stage, a number of SAOM extensions will be explored, including (iii) the so-called settings model, (iv) treating non-sampled data as missing by design in a Bayesian framework, and (v) using a Bayesian Hierarchical SAOM for subsets of data. In addition to addressing domain-specific substantive research questions, the project will provide new methodological insights into studying the impact of large-scale network interventions when contagion and influence contaminate treatment effects.