
JUNLING MA, University of Victoria

Modeling SIS disease dynamics on random contact networks

Contact networks represent persons by nodes and contacts by edges. It is a more realistic model of disease related human contacts than the random mixing model, which assumes that every pair of individuals have identical contact rate. An effective degree SIS epidemic model was developed before, and was shown to have different disease thresholds than an SIR model. This contradicts with the prediction of classic disease models that SIR and SIS models should have the same disease threshold. But this effective degree model is too complex to derive a closed formula for the disease threshold. In this talk, I will introduce a simplified SIS model on random contact networks, which agrees with stochastic simulations and is mathematically tractable. The model yields a disease threshold formula that bears a clear biological meaning: for the disease to spread, the average number of transmissible neighbours times the average number of times a neighbour can be infected must be greater than unity. The threshold converges to that of the SIR model under the homogeneous mixing limit.