



**Dong Yao**  
PhD Thesis

SI and SIR models are useful mathematical models for understanding the process of information diffusion, species evolution and epidemics spreading. In the standard SIR model, each individual is in one of the three states; state S (susceptible), I (infected) or R (recovered). An individual  $x$  in state S will become in state I at a rate equal to the infection rate  $A$  multiplied by the number of friends of  $x$  that are in state I. An individual in state I recovers from the disease at rate  $\lambda$ . In the SI model there is no recovery. In the real world when a person becomes infected, other people may try to reduce their contact with him or her. Hence it is meaningful to study the epidemic spreading process on a social network with an evolving structure.

## Epidemics on evolving graphs

The evoSIR model is one such model where S-I connections are broken at rate  $B$  and the S connects to a uniformly chosen individual. The evoSI model is the same as evoSIR but recovery is impossible. In a paper by three Duke undergraduates the critical value for evoSIR was computed and simulations showed that when the network is given an Erdős-Rényi graph with mean degree 5 the system has a discontinuous phase transition, i.e., as the infection rate decreases to the critical rate, the final fraction of once infected individuals does not converge to 0. In my thesis I study evoSI dynamics on graphs generated by the configuration model. We show that there is a quantity  $\Delta$  determined by the first three moments of the degree distribution, so that the transition is discontinuous if  $\Delta > 0$  and continuous if  $\Delta < 0$ .

