

### **3 Problems in Network Epidemiology**

#### **Background**

The science of networks has had a profound impact on epidemiology due to the intimate link between contacts and networks. This has led to a wealth of publication in the area, ranging from highly theoretical studies to applied simulation modelling to statistical analysis of data. The problem areas are also equally wide-ranging, from the study of human contacts and age-dependent transmission to the movement of livestock (and hence infections) between farms.

In this proposal I outline three potential distinct projects that aim to address outstanding questions in network epidemiology. The projects call for different skill sets, from largely theoretical to mostly computational.

#### **Problem 1: Correlations between stochastic epidemics in populations with network coupling.**

One under-explored issue is how network connections between populations affects the correlations between the epidemics that they experience. The stochastic dynamics around the endemic disease equilibrium can generally be found using diffusion-approximation methods. An open question is how such stochastic dynamics in multiple populations are correlated if there is movement of infection between them. A simple case is two weakly coupled populations, but this can be extended to a network of coupled populations. This can be applied to human or animal populations, with the network structure coming from commuter movement or the movement of cattle respectively. A much larger challenge is understanding the dynamics if the infection can go extinct in the sub-populations.

#### **Problem 2: Dynamics of SIS-type diseases on networks.**

For diseases that obey the SIR paradigm, we know that many approximation methods for calculating the mean number of cases on a network over time are exact (as long as the network is unclustered). However, when the disease has SIS-type dynamics predicting the behaviour is far more complicated. In essence this is the same problem as the contact-process, but we are often interested in more complex network constructions. On-going work within the WIDER group has shed some light into the transmission dynamics, but multiple questions remain. One of the most tractable is understanding the dynamics when there is a fixed (or non-exponential) duration infectious period, potentially followed by a short resistant period during treatment.

#### **Problem 3: Vaccination on network-based models.**

Most decisions to vaccinate human populations are based on the results of model predictions. However, these models are invariably mean-field (random-mixing) models, which ignore network structure. An important applied question is to understand (and estimate) the effects of this omission. A simple approach would be to develop an SIR simulation on a network (allowing for birth and death in the population); the output from such a network can then be fitted with a standard (mean-field) SIR model. Using this approach we can calculate the expected

impact vaccination has in the mean-field model and compare this with the effects in the simulation.

**Suitable Literature.**

Danon, L. et al., 2011. Networks and the epidemiology of infectious disease. *Interdisciplinary perspectives on infectious diseases*, 2011, p.284909. provides an introduction to the subject area.