An Analytical Approach to Modelling Epidemics on Networks.

A thesis presented in partial fulfilment of the requirements for the degree of

Doctor of Philosophy
in
Applied Mathematics

at Massey University, Albany,
New Zealand.

Karen McCulloch

December 21, 2016

Abstract

A significant amount of effort has been directed at understanding how the structure of a contact network can impact the spread of an infection through a population. This thesis is focused on obtaining tractable analytic results to aid our understanding of how infections spread through contact networks and to contribute to the existing body of research that is aimed at determining exact epidemic results on finite networks. We use SIR (Susceptible-Infected-Recovered) and SIS (Susceptible-Infected-Susceptible) models to investigate the impact network topology has on the spread of an infection through a population.

For an SIR model, the probability mass functions of the final epidemic size are derived for eight small networks of different topological structure. Results from the small networks are used to illustrate how it is possible to describe how an infection spreads through a larger network, namely a line of triangles network. The key here is to correctly decompose the larger network into an appropriate assemblage of small networks so that the results are exact.

We use Markov Chain theory to derive results for an SIS model on eight small networks such as the expected time to absorption, the expected number of times each individual is infected and the cumulative incidence of the epidemic. An algorithm to derive the transition matrix for any small network structure is presented, from which, in theory, all other results for the SIS model can be obtained using Markov Chain theory. In theory, this algorithm is applicable to networks of any size, however in practice it is too computationally intensive to be practical for larger networks than those presented in this thesis.

We give examples for both types of model and illustrate how to parameterise the small networks to investigate the spread of influenza, measles, rabies and chlamydia through a small community or population.

Acknowledgements

I would like to thank my supervisor, Professor Mick Roberts; for his guidance, support and patience throughout this project; without which this research would not have been possible.

I would also like to thank my co-supervisor, Associate Professor Carlo Laing, for his guidance, support and patience throughout this project.

Thirdly, I would like to thank all my colleagues whom I have met and had inspirational discussions with over the past few years. In particular, I would like to thank Dr Roslyn Hickson for her help with the Gillespie algorithm code.

Lastly, I would like to thank my partner, family and friends who have supported me throughout this endeavour; for that I am very grateful.

A paper based on the work presented in Chapter 2 and Appendix A of this thesis has been published in the following.

K. McCulloch, M.G. Roberts and C. R. Laing, Exact analytical expressions for the final epidemic size of an SIR model on small networks, *ANZIAM Journal*, 2016, 57 (4), p429-444.

Contents

List of Figures

List of Tables