Household Models for Endemic Diseases

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Contents

Signed Statement **ix**

Acknowledgements **xi**

Abstract **xiii**

1 Introduction **1**

1.1 Summary of chapters 9

2 Technical background **11**

2.1 Continuous-time Markov chains 11

2.1.1 Example of a CTMC 15

2.2 Methods for evaluating the dynamics of the model 17

2.2.1 Stochastic simulation 17

2.2.2 Deterministic approximation 19

2.2.3 Example on the evaluation methods 21

2.3 Linear stability analysis 23

3 Demography model **27**

3.1 Set-up 27

3.2 Preference function 34

3.3 Methods for evaluating the population dynamics 36

3.3.1 Stochastic simulation 36
3.3.2 Deterministic approximation 37
3.3.3 Numerical verification of evaluation methods 40
3.4 Parameterisation 44
3.4.1 Parameterising the stable model 46
3.4.2 Parameterising the growing model 49

4 Demography with disease model **53**
4.1 Events 56
4.1.1 Disease events 57
4.1.2 Demography events 61
4.2 Seasonal forcing 66
4.3 Analysis 67
4.3.1 Stochastic simulation 67
4.3.2 Deterministic approximation 69
4.4 Parametrisation 71

5 Results **76**
5.1 Periodicity 76
5.2 Outbreak of a flu-like disease 85
5.2.1 Increased mortality in children while infectious 86
5.2.2 Increased mortality in adults while infectious 89
5.2.3 Increased mortality in both children and adults while infectious 92
5.3 Epidemic fadeout 95
5.3.1 Non-forced model 95
5.3.2 Seasonally-forced model 98

6 Discussion **102**

6.1 Results and model discussion 103
6.2 Method discussion 111
6.3 Conclusion 114

A Demography deterministic matrices derivation 116

B Demography with disease deterministic matrices derivation 120

Bibliography 126

List of Tables

2.1 Summary of the SIR model with demography. 22

3.1 Summary of the demographic events. 33

3.2 A summary of the parameters and a brief description of the demography event to which it is associated. 34

3.3 Summary of the parameters associated with the stable population dynamics. 47

3.4 Summary of the parameters associated with the growing population dynamics. 50

4.1 The number of disease configurations for each different household type. 55

4.2 The dates of school terms in 2016. 66

4.3 Disease parameters for the non-seasonally forced model. 75

4.4 Transmission parameters for the seasonally forced model. 75

List of Figures

2.1 Ten realisations and the deterministic solution to an example CTMC. 21

3.1 Preference function for select parameters. 36
3.2 Comparison between the deterministic trajectory of the demographic dynamics and a single realisation. 42
3.3 Comparison between the deterministic trajectory of the demographic dynamics and the average of 50 realisations. 43
3.4 The number of each household type in South Australia, from the 2001, 2006, 2011 census data. 44
3.5 Comparison between the household compositional data and our model, for the stable population parameters. 48
3.6 Comparison between the household compositional data and our model, for the growing population parameters. 51

4.1 Deterministic trajectory of the number of infectious individuals in the population compared with a single realisation. 69

5.1 Eigenvalues of the Jacobian matrix associated with the deterministic household model. 77
5.2 A zoomed in look at the eigenvalues of the Jacobian matrix. . . . 78

5.3 Proportion of infectious in the seasonally forced model, varying transmission rate. 81
5.4 Proportion of infectious individuals recorded at the same time each year, varying transmission rate. 81
5.5 Proportion of infectious in the seasonally forced model, varying birth rate. 82
5.6 Proportion of infectious individuals recorded at the same time each year, varying birth rate. 82
5.7 Eight realisations of the number of infectious individuals, evaluating the seasonally-forced model. 83
5.8 Average of the seasonally-forced stochastic realisations. 84
5.9 Change in population and disease dynamics when children have an increased mortality rate during infectious period. 88
5.10 Change in population and disease dynamics when adults have an increased mortality rate during infectious period. 91
5.11 Change in population and disease dynamics when both children and adults have an increased mortality rate during infectious period. 94
5.12 Proportion of realisations where the number of infectious individuals reaches 0. 98
5.13 Proportion of realisations where the number of infectious individuals reaches 0, for the seasonally-forced model. 101

Signed Statement

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Signed: ..... Date: .....

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Abstract

The mathematical modelling of disease dynamics is now well-established, which allows us to better understand the processes affecting diseases in communities. Most of this work has focused on *epidemic* dynamics, in which we see a large outbreak of a disease but also its extinction within a short time-frame. Of interest in this thesis will be furthering the study of *endemic* diseases, which persist in populations over much longer time scales. This increased time scale means that it is important to account for demography, and in particular the replenishment of susceptible individuals through births and possibly waning immunity. Another feature that has been shown to be important for modelling disease dynamics is heterogeneity in the population, and in particular household structure. This is likely to be important for endemic diseases because of the close relationship between demography and household composition as these types of diseases persist in communities for periods long enough that assuming a static population structure is not realistic.

Hence we model both the disease and population dynamics as a continuous-time Markov chain, where the population of individuals is split into adults and children. These adults and children are assigned a household type, and within each household the number of adults is at most two, and the number of children is at most four. These households change through time as a consequence of demographic events such as births, deaths, children moving out of home, couples forming, separating, and migration. This demographic model is overlaid

with SEIR disease dynamics, where the rate of disease transmission is strongest within households, as opposed to between. We also develop a seasonally-forced model. The so-called Gillespie algorithm is used to simulate realisations of this process but simulation can be computationally expensive. Hence we also derive a deterministic approximation, valid in the limit of a large number of households. We use this deterministic approximation extensively to analyse the models dynamics.

For measles-like disease parameters, the period of the non-seasonally forced model is approximately two years, which agrees closely to the established biennial periodicity. In the model with seasonal forcing, the periodicity is more complicated, with annual periodicity in the deterministic approximation, and approximately 2-3 year periods for individual stochastic realisations.

The household model without seasonal forcing is used to investigate the case of a flu-like disease suddenly becoming fatal in children, adults, and both. We found that when the population has only a small proportion of susceptible individuals there is a higher chance of the disease being persistent when compared to the population with larger proportions of susceptible individuals. Significant change in household proportions are recorded initially during the first outbreak of the disease when the mortality rate increases during the infectious period of individuals.

In both the models with and without seasonal forcing, a measles-like disease fades out with higher probability in the household models compared to the homogeneous models. In each of the household models, within the first five years, we see periods of approximately 2-3 years where the proportion of realisations that fade out stay essentially constant for populations of greater than 225 thousand households in the seasonally-forced model, and above 250 thousand in the non-forced model. During these periods, the proportion of realisations that have not faded out is above 0.5, which is suggestive of a critical community size between 375-500

thousand individuals in both household models. However, the household model shows greater variability than the homogeneous models as a larger proportion of realisations fadeout over the course of 15 years.

The household models presented in this thesis allow a great deal of flexibility in parameterisation which means that many problems can be studied. However, as a consequence of the flexibility, the model's dynamics are evaluated at large computational expense, meaning approximations are necessary.