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# Modelling Infectious Disease Epidemiology and Vaccination Impact

A thesis presented in partial fulfilment of the requirements for the degree of  
Doctor of Philosophy  
in  
Mathematics  
at Massey University, Albany,  
New Zealand.

by

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2009



## Abstract

This thesis presents mathematical models for the dynamics of vaccine preventable diseases, specifically looking at the New Zealand situation. Through the use of integral and differential equations, we develop models and compare the results of these to known data.

Using game theory analysis we determine and compare the proportion of the population that needs to be vaccinated in order to minimise the expected costs to the individuals in the population and to the community. Two different scenarios and methods are considered, where the effects of vaccination last only one epidemic cycle (using an integral equation method) and where vaccination is effective over an entire lifetime (using a differential equation method). For both scenarios, we find that the minimum cost for the individuals is reached when a lower proportion of the population is vaccinated than needed for the minimum cost to the community.

We then elaborate on the integral equation method to produce a model for repeated epidemics of measles in a population, where a discrete mapping is used to include the year to year demographics of the population. The results of this model show a different epidemic pattern than that produced from a differential equation model, with numerical problems encountered. From here on, we use differential equation models in our analysis.

A critique and extension to an existing model for the dynamics of the hepatitis B virus is presented, with discussion on the appropriateness of the model's construct for predicting the incidence of infection. Alternative differential equation models for hepatitis B virus and immunisation that include splitting the population into age groups with non-homogeneous mixing are presented. The results of these models are compared with the known data on incidence of infection and carriage in New Zealand, showing how affective different immunisation schedules may have been.

Differential equation models are then presented for meningococcal B virus epidemiology in New Zealand, with the models incorporating different features of the virus until the best model is found that fits the New Zealand data. Each model is compared with the known incidence of infection, with the population being either treated as a whole or split into age groups with non-homogeneous mixing. The effect of vaccination is included in this model so that we can explore the future of the infection in the population, and how best to tackle any future epidemics. The model shows that the current vaccination campaign was the best solution for controlling the epidemic, but there will be epidemics in the future that will need subsequent vaccination campaigns to limit the number of infections.



# Acknowledgements

This work was carried out at the Institute of Information and Mathematical Sciences at Massey University in Albany. My PhD programme was funded by a Massey University Doctoral Scholarship, and supported by the Institute of Information and Mathematical Sciences, for which I am extremely grateful.

I express my gratitude to my two supervisors, Professors Mick Roberts and Graeme Wake, for their help and guidance over the course of my studies. To Mick, I thank you for our weekly meetings and your continual encouragement and belief in me. Your patience and understanding over the years is very much appreciated, and my work would have been a much harder and longer road without your help.

To all the staff and other post graduate students in IIMS, your companionship and encouragement over the years has made my stay at Massey very enjoyable. Many thanks to both Mick Roberts and Nancy Simpson for proof reading this thesis.

Lastly, my thanks to my family for seeing me through to the end of my studies, to Mum and Kenny for their love and support each day.

Dedicated to Ian Mann, 1942–2005.



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