Mathematical Modelling of Measles Dynamics in Sri Lanka

by

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ABSTRACT

Infection diseases and epidemics fall in to the category of time-dependent dynamical systems. In this thesis we considers a mode for measles dynamics involving three coupled nonlinear ordinary differential equations.

This system of ODE's cannot be solved analytically. But number of qualitative properties can be derived. The model is judged on how accurate it simulates the biological properties of measles epidemics. A number of possible refinements are pointed out.

Special emphasize is focused on the basic reproduction rate, because that is the key term of eradicating an epidemic from a society. Various numerical experiments are conducted for the model for various basic reproduction rates.

Finally, with the help of available data, suggestions are made, using regression analysis, about the vaccination programme.

Chapter 1

Introduction

1.1 Continuous Population Models

The increasing study of realistic and practically useful mathematical models in population biology, whether we are dealing with a human population with or without its age distribution, population of an endangered species, bacterial or viral growth and so on, is a reflection of their use in helping to understand the dynamic processes involved and in practical predictions. [7]

Mathematical epidemiology is one of the major areas in population biology, which uses mathematical modelling in their studies. Many different models have been used in epidemiology. These includes descriptive growth curves, epidemic simulations and to recently, models more in line with those developed in theoretical epidemiology for viral or bacterial diseases directly

transmitted from one person to another or transmitted by an intermediate host like mosquitos.

The growth curve most widely used to describe and compare epidemic progress is the logistic model

$$\frac{dY}{dt} = rY\left[1 - \left(\frac{Y}{K}\right)\right]$$

where Y represents the quantity of disease, r is a disease rate parameter, and K is the maximum quantity of disease or "carrying capacity". When Y is measured as a proportion in disease assessments, $K = 1$. From a disease dynamic perspective, it is preferable to represent diseases as the amount of infectious individuals.

Epidemic infectious diseases have accompanied mankind since the beginnings of history and are still of major concern. The discovery of penicillin and other antibiotics and the rise of vaccination programmes have not always succeeded in the extinction of infectious diseases while new ones are ever appearing, like AIDS to name just one. Thus, the modelling of epidemic processes is as important as ever, not only to understand the nature of diseases but also to help formulating appropriate vaccination strategies to fight the illnesses.

Measles is among the best documented human diseases, as far as popula-

tion dynamics are concerned, and thus ideally suited to the testing of mathematical models. Furthermore, measles is still a relevant illness, not only in developing countries, where a large number of children die after measles infection, usually due to reduced immunity and attracted secondary diseases, but also in developed nations.

The modelling of epidemics was among the first cases of mathematics entering the fields of biology and medicine. The differential equations involved in the models, how ever, usually cannot be solved analytically and thus one has to rely on numerical methods.

The model investigated in this thesis, called the SEIR Model, is far too simplified to simulate the dynamics of measles adequately. Nevertheless, it captures the essence of microparasitic interaction that builds the foundation of the disease. More sophisticated models are readily formulated but will usually still have the simple SEIR Model at their core. Hence it makes sense to understand the dynamics of this model before turning to more complicated and, hopefully, more realistic approaches. Furthermore, since a lot of the qualitative properties of the SEIR Model can be derived analytically, the numerical methods can be tested quite easily on how good they approximate the true behaviour of the system. It may then be estimated that a method which performs well on the simple model does so on a more sophisticated approach.

Chapter 2

Epidemiological Models

2.1 Simple Epidemic Models and Practical Applications

In the classical, but still highly relevant models we consider here the total population is taken into be constant. If a small group of infected individuals is introduced into a large population, a basic problem is to describe spread of the infection within the population as a function of time. Of course this depends on a variety of circumstances, including the actual disease involved, but as a first attempt at modelling directly transmitted diseases we make some not unrealistic general assumptions.

Consider a disease which, after recovery, confers immunity which, if lethal,

includes deaths: dead individuals are still counted. Suppose the disease is such that the population can be divided into three distinct classes: the susceptible, S, who can catch the disease, the infective, I, who have the disease and can transmit it, and the removed class, R, namely, those who have either had the disease, or are recovered, immune or isolating until recovered. The progress of individuals is schematically represented by

$$S \rightarrow I \rightarrow R.$$

Such models are often called SIR models. The number of classes depend on the disease. SI models, for example, have only susceptible and infected classes while $SEIR$ models have a susceptible class, S, a class in which the disease is latent, E, an infectious class, I, and a recovered or dead class, R. This kind of models are sometimes called *compartment models* and can be used to model effectively some epidemics, such as Measles, Mumps, Chicken pox, Smallpox.[4]

Today the theoretical framework most commonly used to mimic the dynamics of viral and bacterial infections is one based on the division of the human population into categories containing susceptible, infected who are not yet infectious(latent), infectious individuals and those who are recovered and immune. Models based on this type of framework do not explicitely de-

scribe changes in parasite population size. They simply mirror the dynamics of the number of infected people without reference to the abundance of organisms within each individual.

It is conventional to assume that the size(or density) of the human population, N, remains roughly constant, or at least changes on a time scale that is long compared to all other time scales of interest in an epidemiological context.

This model also assumes that individuals mix at random within the population, age and sex are not crucial variables. Obviously, these assumptions are unrealistic; notwithstanding, the model is able to rescue the familiar cycle of population childhood infections.

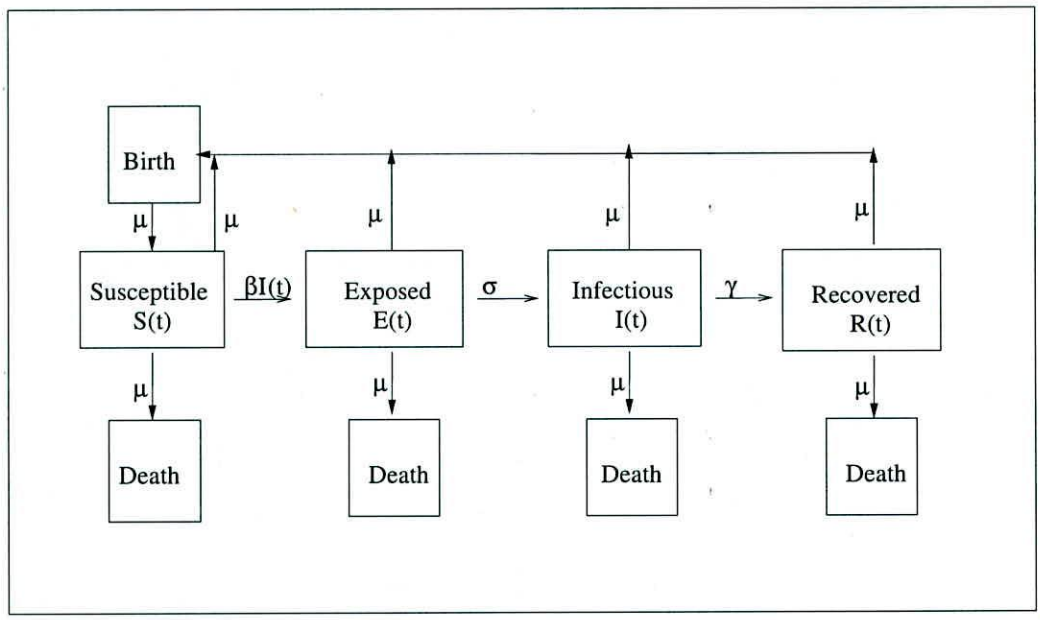

Figure 2.1: Schematic representation of the flow of hosts through the compartments.

Note that hosts both die and reproduce at the per capita rate μ. It is assumed that nobody dies of measles, therefore the infected hosts do not experience a higher mortality rate. Recovered individuals do not flow back into the susceptible compartment, as life- long immunity is supposed.

2.1.1 The SEIR Model

The SEIR Model is obtained by 'translating' the compartmental model proposed above into mathematical terms. It consists of three coupled, non-linear, ordinary differential equations