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Mathematical modelling of infectious diseases: A Review

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ABSTRACT

Mathematical modeling of infectious diseases using compartmental models have been surging huge importance since the middle of the 20th century. In this review article, we discuss the advantages of studying disease transmission of the infectious disease using mathematical models. Some important factors that play a key role in predicting the dynamics and controlling the disease are also discussed.

INTRODUCTION

Infectious diseases have been one of the main causes of mortality in the develop-ing countries. Infectious agents adapt and evolve so that new infectious diseases emerge and reemerge. Some newly identified infectious are Lyme disease (1975), Legionnaire's disease (1976), toxic-shock syndrome (1978), hepatitis C (1989), hepatitis E (1990), and hantavirus (1993). Antibiotic-resistant strains of tuber-culosis, pneumonia, and gonorrhea have evolved. Malaria, dengue, and yellow fever have reemerged and are spreading into new regions as climate changes oc-cur. Diseases such as plague, cholera, and hemorrhagic fevers (Bolivian, Ebola, Lassa, Marburg, etc.) continue to erupt occasionally. Emerging and reemerging diseases have restored the interest in infectious diseases.

LITERATURE REVIEW

Mathematical models have been studied to analyze and control the spread of infectious diseases. Formulation of a mathematical model is based on the under-lying assumptions, dependent variables and parameters. Mathematical models provide vital information e.g., reproduction numbers, threshold values of the infection parameters, contact rates etc. Mathematical analysis and computer simulations of the model help to answer specific questions and to prove the already existing conjectures [1]. In particular, mathematical analysis of the model provides qualitative insight into the spread of the infection whereas com-puter simulations help to understand the long-term behaviour of the model and also enable to deal with the data available.

Understanding the transmission characteristics of a specific disease can help in taking the preventive measures. Epidemiological models have been very beneficial in providing forecasts and treatment strategies for infectious diseases.The first epidemiological model was formulated in 1906 by Hamer. The model was analyzed to understand the recurrence of measles epidemics [2]. This was the first model to assume that the incidence(number of new cases per unit time) depends on the product of the densities of the susceptibles and infectives. Later in 1911, Ross presented a host-vector differential equation model of malaria to understand the incident and the control of the disease [3]. Subsequently, other mathematical models were presented in [4, 5, 11]. In 1926, Kermack and McKendrick presented model that depict that for a dis-ease outbreak to take place, the density of susceptible individuals must be greater than a critical value [4, 7, 8]. Starting in the middle of the 20th cen-tury, studies based on mathematical epidemiology have grown exponentially [9, 10, 5, 11, 12, 13, 14, 15].

The complexity of models have been increased recently by incorporating various factors such as vertical transmission, age struc-ture, social and sexual mixing groups, immunity, vaccination,spatial spread, chemotherapy etc. The death of the epidemiological modeling is shown in [16, 17, 18, 4, 19, 20, 21, 22, 23, 10, 24, 25, , 27].

Compartmental models have been primarily used in epidemiology and the se-lection of the compartments depend on the characteristics of the disease, aspect of disease been studied, and purpose of the study. The basic compartmental model is an SIR model where S represents the individuals who can become infected, I represents the individuals who are infected and R represents the in-dividuals who are recovered or removed because of death. It is assumed that the individuals move from the S compartment to I compartment after they be-come infected and then to R compartment if they get recovered or they die. The passively immune class M and the latent period class E are often omitted, because they are not crucial for the susceptible-infective interaction. Acronyms for models are usually based on how the population moves from one compart-ment to the other e.g., MSEIR, MSEIRS, SEIR, SEIRS, SIR, SIRS, SEI, SEIS, SI, and SIS.

The threshold for many epidemiology models is the basic reproduction num-ber R0, which is defined as the average number of secondary infections produced when one infected individual is introduced into a host population where every one is susceptible [28]. For many deterministic epidemiology models, an infec-tion can get started in a fully susceptible population if and only if R0> 1. Thus the basic reproduction number R0 is often considered as the threshold quantity that determines when an infection can invade and persist in a new host pop-ulation. The contact number σ is defined as the average number of adequate contacts of a typical infective during the infectious period [29, 30] The replacement number R is defined to be the average number of secondary infections produced by a typical infective during the entire period of infectiousness [29]

CONCLUSION

Mathematical epidemiology has now evolved into a separate area of population dynamics that is parallel to mathematical ecology. Epidemiology models are now used to combine complex data from various sources in order to study equally complex outcomes. In this paper we have given a brief overview of the existing literature and discussed the types of compartmental models that are generally used in epidemiology.

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