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Numerical study of an influenza epidemic model with diffusion

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ABSTRACT

A diffusive epidemic model is investigated with a view to describe the transmission of influenza as an epidemic. The equations are solved numerically using the splitting method under different initial distribution of population density. It is shown that the initial population distribution and diffusion play an important role for spread of disease. It is also shown that interventions (medical and nonmedical) significantly slow down the spread of disease. Stability of equilibria of the numerical solutions are also established.

1. Introduction

Epidemic models have long been of interest to mathematicians. In 1760, a mathematical model was formulated by Daniel Bernoulli in order to evaluate the effectiveness of variolation of healthy people with the smallpox virus [12]. In 1906, Hamer formulated a discrete time model to understand the recurrence of measles epidemics [1]. In 1911, Ross developed a deterministic model for malaria as a host-vector disease [12]. The recent models have involved aspects such as passive immunity, gradual loss of vaccine and disease-acquired immunity, stages of infection, vertical transmission, age structure, social and sexual mixing groups, spatial spread, vaccination, quarantine and chemotherapy. Special models have been formulated for diseases such as influenza, measles, rubella, chickenpox, whooping cough, diphtheria, smallpox, malaria, rabies, gonorrhea, syphilis and HIV/AIDS [12]. A variety of models have been formulated, analyzed and applied to different infectious diseases. Kermack and McKendrick are the pioneers in the field of mathematical epidemiology. Between 1927 and 1933, they published a series of papers [13–15] on the spread of infectious diseases.

Epidemic models have become important tools in studying a diverse range of infectious diseases. The model formulation process clarifies assumptions, variables and parameters estimation. Also models provide conceptual results such as thresholds, basic reproduction numbers, contact numbers and replacement numbers. The basic aim of modelling is to predict the spread of disease both in time and space and to gain a better understanding of transmission mechanisms which are the most influential in that spread. It helps to determine and evaluate control strategies. These days mathematical models have an important role to play in comparing, planning, implementing, evaluating, optimizing various detection, prevention, therapeutic and control programs. Mathematical models also contribute to the design and analysis of epidemiological surveys. Modelling also helps to identify the crucial data that should be collected in order to identify trends, make general forecasts and estimate the uncertainty in forecasts [12].

Infectious diseases are an important and often dramatic cause of human illness and mortality across the world. All infectious diseases have unique characteristics. Some of the diseases lead to permanent immunity and human are never infected by that disease again. On the other hand there are many diseases like influenza, where human get infected again and again. It is common conception that influenza is not a serious disease for our public heath system. Unfortunately, this is not true. In fact, influenza as a disease is an important issue for our health system. Influenza virus change dramatically and our immune

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system, in general, fails to recognize it quickly. That is why, one can get infected again and again with influenza. In view of that vaccine must be changed from time to time. Three important epidemiological factors in influenza are the latent period, incubation period and length of the infectious period. In general, researchers regard the latent period and incubation period in the same context and the average latent period is taken to be 1.9 days [8,20]. Another important factor is the length of the infectious period. This period is highly variable and has been estimated from 2 to 10 days [5,8,11,20].

Influenza has caused more morbidity and mortality than all other respiratory diseases. There are annual seasonal epidemics that cause about 500,000 deaths worldwide each year. During the twentieth century, there were influenza pandemic in 1918, 1957 and 1968. About one third of the world population was infected during the period 1918–1919 with flu pandemic. In most of the affected places the death rate was 2.3%–5%. During that period in India, almost 5% people were infected and about 17 million died. In Japan, 23 million were affected, and 390,000 died. In U.S., 28% of the population got affected, and 500,000 to 675,000 died. Almost 250,000 died in Britain. In France and Canada more than 400,000 and 50,000 died. About 12,000 people died in Fiji Islands and Western Samoa [27].

Spanish flu, is an airborne transmitted type virus which is positively correlated with low humidity and low rates of airflow. The main transmission route is by direct contact through contaminated hands or close contact with infective persons [20]. Unlike other places of the world the city of São Paulo, Brazil was also greatly affected with 1918 influenza pandemic. The total population was 523,194 in the city of São Paulo and 116,771 were infected by Spanish flu and 5331 died with an overall mortality rate 1% [20].

The analysis of the spread of influenza epidemics dates back to the 18th century. Since then different researchers developed these models on the basis of different type of anthropological parameters such as traffic patterns, contact patterns at work, in schools, at homes, at public places and the airline traffic. In 1977, Baroyan et al. [3] developed a model for the spread of influenza based on the transportation network. In 1981, Baroyan et al. [2] developed a mathematical model considering the global spread of influenza. Recently researchers [6,7,18] have investigated the spread of influenza in different cities around the globe. In 1982, Fine [10] classified these models into household studies, small community studies, large population studies and prediction and control studies. The models for influenza are in general concerned with household transmission studies for large as well as small population. Because of the limited size of households, it is easy to understand the factors that influence the likelihood of transmission of an infection from one person to another person [22].

In this paper, an influenza model (Massad et al. [20]) is considered with the inclusion of diffusion in the system. The main objective of this paper is to compare the different modes of disease transmission giving special emphasis to diffusion and different initial populations distribution. In order to observe the effect of interventions (medical and nonmedical) to the disease spread, different cases are taken into consideration.

2. The *SEIR* model

2.1. Equations

If the total population size is denoted by N, where $N = S + E + I + R$, the *SEIR* model (Massad et al. [20]) consists of the following equations

$$\frac{\partial S}{\partial t} = -\beta\frac{(E+I)}{N}S - \mu S + rN\left(1-\frac{N}{K}\right) + d_1\frac{\partial^2 S}{\partial x^2}, \tag{1}$$

$$\frac{\partial E}{\partial t} = \beta\frac{(E+I)}{N}S - (\mu+\sigma+\kappa)E + d_2\frac{\partial^2 E}{\partial x^2}, \tag{2}$$

$$\frac{\partial I}{\partial t} = \sigma E - (\mu+\alpha+\gamma)I + d_3\frac{\partial^2 I}{\partial x^2}, \tag{3}$$

$$\frac{\partial R}{\partial t} = \kappa E + \gamma I - \mu R + d_4\frac{\partial^2 R}{\partial x^2}, \tag{4}$$

where the variables S, E, I and R represent the proportion in the population of susceptible, exposed, infected and recovered individuals respectively. d_1, d_2, d_3 and d_4 are the diffusivity constants. The biological meaning of the parameters are specified

Table 1
Interpretation of parameters.

Parameter	Interpretation
β	Transmission coefficient
μ	Natural mortality rate
r	Birth rate
K	Carrying capacity
σ^{-1}	Duration of latency
κ	Recovery rate of latents
α	Flu induced mortality rate
γ	Recovery rate for clinically ill