



Numerical solution of compartmental models by meshless and finite difference methods



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ABSTRACT

In this paper, an operator splitting method based on meshless and finite difference procedures, is being considered for numerical solution of compartmental epidemiological population models with and without diffusion. A one step explicit meshless procedure is also applied for the numerical solution of the nonlinear model. The compartmental model contains susceptible, vaccinated, exposed, infected, and recovered (SVEIR) classes of the population. Effects of the diffusion on the simulation results of the model are being studied. Stability of endemic equilibrium point along with bifurcation analysis has also been investigated. Due to non-availability of the exact solution, the numerical results obtained are mutually compared and their correctness is being verified by the theoretical results as well.

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1. Introduction

Influenza, also known as flu, is a respiratory disease which is caused by orthomyxovirus, a virus. Millions of people are the victims of the disease and every year a considerable number of them lose their lives due to serious complications of the contagious disease. Recurrently a large chunk of resources are spent on the epidemic. Older people and children fall easy prey to this disease. Influenza viruses have been grouped in three categories naming influenza A; influenza B; and influenza C. Influenza A infection, usually, reaches to the peak during the Winter season and involve 10% or more of the population with the rate of 50%–70% in school going children. Influenza B accounts for only 3% of all flu cases in the United States [17,4,8]. The influenza A is the most complicated, severe and dangerous for human population. The Influenza A mostly specific HA and NA subtypes frequently caused the dangerous epidemic diseases which include all pandemics diseases of the last century [16,6]. This disease has taken more lives as well as suffered the health of the people than any other respiratory diseases. Every year, nearly 50,000 deaths occurs due to influenza. In 20th century, influenza pandemic outbreak many times – 1918, 1957 and 1968. During the period from 1918 to 1919, due to a flu pandemic, approximately one third of the world population were infected. The death rate was 2.3%–5% in the affected areas. During this period, in India 5% of population was deeply affected and about 17 millions people have lost their lives due to this epidemic disease. In Japan, round about 390,000 people have lost their lives and 23 millions were badly affected due to influenza. Likewise, 28% Americans were affected, and 500,000 to 675,000 people have lost their lives due to this disease. Similar situation was prevailed in Great Britain, where round about 250,000 people died due to the disease. The devastating effect of this disease had broaden its network to France and Canada

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where about 400,000 and 50,000 people have been died of this disease in the respective countries. Thousands of people lost their lives in the Fiji Islands and Western Samoa due to this disease [1].

Recently, in 2009 a widespread influenza pandemic was caused by a new virus named as H1N1/09 or "Swine Flu". It is thought that this virus spread in same pattern as that of a seasonal flu. Nearly 65 millions doses of vaccine had been administered in about 16 countries up to November 2009 to control this disease.

In this modern era, vaccination against infectious disease is considered to be an important weapon for controlling such infectious diseases. It is inevitable to safe guard the public health and to take sound measure for controlling influenza with the help of vaccination programs. Immunity of population is determined by decisions taken on individual level vaccination and thus help to determine the nature of an epidemic diseases too. It has been identified in [23,16,3,12,22] that mass vaccination strategies are inevitable for the prevention of epidemic diseases.

Due to devastating effects, experts in medical sciences have focused their attention on the eradication of the diseases because of high risk involved to human population. In order to devise effective strategies and control the devastating effects of the viruses, mathematical models were used effectively. Mathematical models help in understanding the disease dynamics, comparing and implementing different strategies, planning and assessing various aspects, optimizing various detection plans and prevention procedures, and effectively executing various control programs [11,24,8]. Different techniques are being used in order to devise a clear, realistic, and feasible model to look into different dynamics of the influenza and other diseases. These models are developed with a view to observe the epidemiological patterns. Similarly, these models also foretell the repercussion of the introduction of public health interference to overcome the spread of the diseases.

In this paper, our focus is on the numerical simulation of the SVEIR model by three types of numerical methods. They include meshless explicit method (MEM), meshless operator splitting method (MOSM) and finite difference operator splitting method (FDOSM). This helps us to analyze the disease dynamics in a better way. In this model the population is compartmentalized in susceptible, vaccinated, exposed, infected and recovered classes of the population. The susceptible population is considered to be vaccinated at a constant rate and some of the individuals get infected despite being vaccinated. It is supposed that susceptible individuals are entered into the exposed class by making contact with infected and exposed individuals but the effect of later one is less than the first one. To study the effects of vaccination as well as diffusion on the disease dynamics in the system, various cases discussed in [20] have been considered in present paper as well.

The rest of the paper is organized as follows: In Section 2, SVEIR model with diffusion is elaborated. In Section 3, three types of initial conditions are given. In Section 4, stability analysis is described. In Section 5, bifurcation analysis is discussed. In Section 6, time and space discretization is described. Numerical results and discussion are given in Section 7. Some conclusions are drawn in Section 8.

2. The SVEIR model in PDEs form

The purpose of this model is to study the long time behavior of five reaction–diffusion system stemmed from the SVEIR compartments of the population. The present model is basically the extension of the epidemic model [9]. The SVEIR model discussed in [20] is comprised of five classes (compartments) for a given population, namely: Susceptible ($S(x, t)$), Vaccinated ($V(x, t)$), Exposed ($E(x, t)$), Infected ($I(x, t)$) and Recovered ($R(x, t)$). The spatial distribution of total population is represented by $N(x, t)$ at time $t \geq 0$ in the one dimensional domain $[0, L]$, where $N(x, t) = S(x, t) + V(x, t) + E(x, t) + I(x, t) + R(x, t)$. The flow diagram of SVEIR model is shown in Fig. 3. The desired model can be derived easily with the help of the diagram shown in the Fig. 3. In the Fig. 3, the arrows represent the movement of the individuals between the compartments. The symbols above the arrow represent the rate at which the individuals move from one compartment to the other compartment. The term $\frac{ES}{N}$ indicates that when susceptible individuals do contact with exposed individuals in the whole population, they become exposed and enter into exposed class. Similarly the term $\frac{EI}{N}$ indicates that when susceptible individuals do contact with Infected individuals in the whole population, they become infected and enter into exposed class. The arrow towards compartment indicates that the individuals are entering into that compartment and the arrow away from the compartment indicates that the individual are going out from that compartment.

The interpretation of the parameters is given in Table 1 [20] and their values are given in Table (2). The following assumptions are being considered for construction of the PDEs compartmental model:

- The individuals of the classes S, V, I, E, R are free to diffuse along x -axis.
- The individuals of the class S are prone to get infection.
- The class S of the population is subject to variation. The class S is enhanced due to newborn and those individuals who lose either natural or vaccinated immunity.
- The class S is decreased by vaccination, infection and natural deaths.
- The class V is subject to variation as well. This class is enhanced due to vaccinating the susceptible population.
- The class V shrinks due to the spread of the infection among the population, erosion effects of vaccine based immunity and natural deaths.

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