



A Numerical Study of SIR Epidemic Model

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Abstract

Epidemic and infectious disease fall into the category of time dependent dynamic system. The model under consideration is SIR-type (susceptible, infectious, recovered) which assumes that every individual has equally chances to be infected by the infectious individual in the case of contact except the pair formation or those who have a sufficient immunity for the disease. The model considered in this paper is non-fatal. If the portion of the immuned population exceeds the herd immunity level then the disease will no longer persist in the population. The model is solved with and without demographical effects. The vaccination effect is also discussed along with the physical parameters. The simulations have been performed for the non-linear coupled ordinary differential equations using Runge-Kutta 4th order method and MATLAB-SIMULINK software. The results obtained by both methods are in good agreement with the existing results in the literature.

Keywords: SIR Epidemic Model; Simulink; Runge-Kutta Method.

1. Introduction

Mathematical modeling of infectious diseases is an important area of mathematical biology. These models provide an explicit framework to understand biological systems and their infections. One of those models is the SIR model in which population is divided into disjoint components whose sizes change with the time.

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The infection status of any individual in a population can be susceptible(S) when the person is healthy and susceptible to the diseases, Infected (I) when the individual carries the disease and is infectious or removed (R) when the person has recovered. The interaction of these three classes leads to a coupled system of nonlinear ordinary differential equations.

Beretta and Takeuchi [1] investigated SIR models with constant and varying population size, respectively. Keeling and Grenfell [2] proposed a simple modification to the standard SIR models that vastly increased persistence by forcing the incubation and infectious periods to be closer to fixed intervals, rather than the standard exponential distribution that is commonly implemented. Work on SIR-type models has shown theoretically that constant periods destabilized disease dynamics.

Andersson et al [3] and Lloyd [4,5] observed that numerical simulations of Keeling & Grenfell [2] showed far greater persistence for constant periods. Trot tier and Philippe [6] presented a model which investigated measles cycles and the Role of Births and vaccination. Fadi Awawadeh et al [7] investigate the accuracy of the SIR epidemic model for the spread of non-fatal disease in the population using HAM. Many models have been developed in an attempt to reproduce this phenomenon. Recently, the use of constant infectious and incubation periods, rather than the more convenient exponential forms, has been presented as a simple means of obtaining realistic persistence levels. A key parameter for all these models was the basic reproductive number \mathfrak{R}_0 (the product of rate of transmission from an infectious individual and the infectious period). \mathfrak{R}_0 is thus the ratio between infection rate and the recovery rate. If infection rate is denoted by β and the recovery rate is denoted by γ then

$$\mathfrak{R}_0 = \beta \left(\frac{1}{\gamma} \right) = \frac{\beta}{\gamma}$$

The basic reproduction number has a threshold value one. If $\mathfrak{R}_0 > 1$, the global stability of the endemic equilibrium is proved. If $\mathfrak{R}_0 = 1$ then the disease will remain in the area and will present in the area in any condition with a constant proportion. If $\mathfrak{R}_0 < 1$, this case shows that the disease will not persist for a long time in the area and will be abolished very soon.

The paper is organized as such that in section 2 the non-linear coupled SIR model without demography is presented. Section 3 demonstrates the impact of important parameters present in the model. In section 4 the model with demographic effect is presented and discussed with respect to the different physical parameters. The impact of vaccination on the solution is given in section 5. Section 6 concludes the paper.

2. Mathematical formulation of SIR model without Demography

Epidemic modeling has three main aims. The first is to understand the spreading mechanism of the disease. For this, the essential part is a mathematical structure (equations give us threshold values and other constants which

we use to describe the behavior of the disease). The second aim is to predict the future course of the epidemic. The third is to understand how we may control the spread of the epidemic. In order to make a reliable model and predictions, to develop methods of control, we must be sure that our model describes the epidemic closely; it contains all its specific features. Without demography means the population remain constant with passage of time in this model we consider that there is no emigration and immigration during the required time and consider that there is no death occurred or increase in population by new birth. In SIR model the number of people remains dynamic within the population. There is only one chance for susceptible persons to enter in the infected group of the people and similarly infected persons can only enter in recovered group of the people. Recovered group of the people is the group of those people who have been infected and have recovered after getting sufficient immunity for that disease and will never infected again. In SIR model, if we denote the size of the population with “ N ” then

$$N(t) = S(t) + I(t) + R(t)$$

The system of non-linear coupled ordinary differential equations is

$$\begin{aligned} \frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned} \quad (2.1)$$

with the initial conditions:

$$S(0) = S_0, \quad I(0) = I_0 \text{ and } R(0) = R_0$$

Where $S(t)$ denote the susceptible class and $I(t)$ denote the infective class and $R(t)$ denote the recovered class, $\beta > 0$ is infective ratio in this model and $\gamma > 0$ is the recovery ratio in SIR model.

3. Numerical results of SIR Model without Demography

In order to solve the system (2.1) we need the numeric values of the physical parameters β and γ which in turn gives the reproductive number \mathfrak{R}_0 . The values of these physical parameters as well as the initial data are taken from [7]. The model is solved using the RK-4th order and MATLAB SIMULINK. We compare our results with the results given in [7] for $S(0) = 499, I(0) = 1, R(0) = 0$ and $\beta=0.001, \gamma=0.1$.

In Figure 3.1(a) Numerical solution of coupled nonlinear order ordinary differential equations with RK-4 for SIR model. Whereas Figure 3.1 (b) represents the graphical representation of results using Simulink. Both results are combined in Figure 3.2(a). The homotopy solutions given in the [7] are shown in Figure 3.2(b). The close

agreement in both the results confirms the validity of the solution.

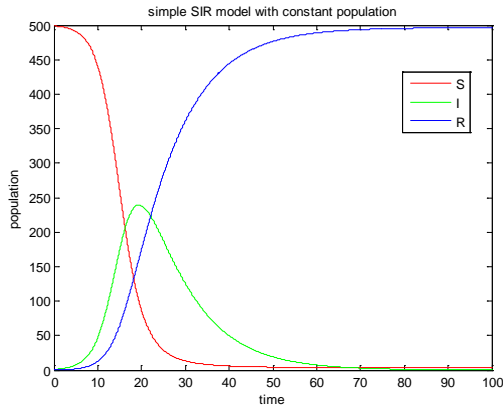


Figure 3.1(a):

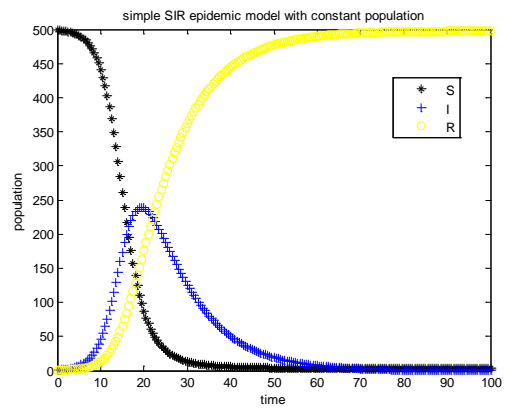


Figure 3.1(b):

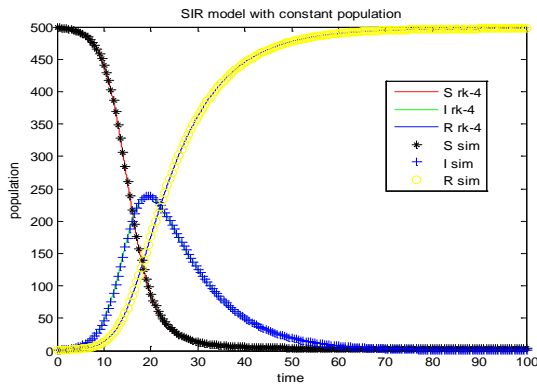


Figure 3.2(a):

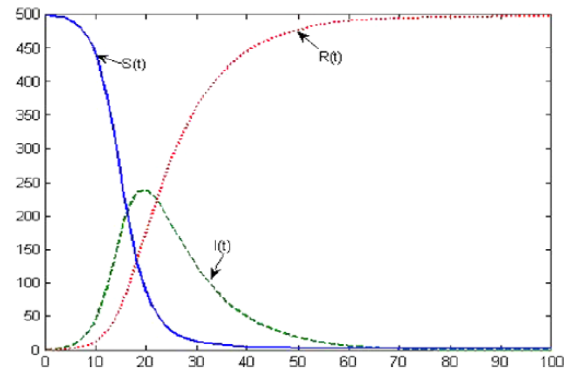


Figure 3.2(b):

Figure 3.2(a) Comparison of RK-4 method and Simulink results for SIR epidemic model with constant population with the initial conditions $S(0) = 499$, $I(0) = 1$, $R(0) = 0$ for $\beta = 0.001$, and $\gamma = 0.1$.

Figure 3.2(b) Homotopy solutions given in [7] for SIR epidemic model with constant population with the initial conditions $S(0) = 499$, $I(0) = 1$, $R(0) = 0$ for $\beta = 0.001$, and $\gamma = 0.1$

To see the effect of physical parameters and initial data on the results, we performed simulations using different values of parameters. Firstly, we fixed the values of $\beta = 0.001$ and $\gamma = 0.1$ as given in [7] and observed the

effect of initial data. It can be seen from the Figs. (3.3) – (3.5) that when $S_0 > \frac{\gamma}{\beta} = \frac{1}{\mathcal{R}_0}$, the number of infected

persons increased to a maximum before decreasing to zero which shows that there is a time period during which

the disease is epidemic. Where, if $S_0 < \frac{\gamma}{\beta} = \frac{1}{\mathcal{R}_0}$, the number of infected persons decreased from the start and

there is no epidemics as shown in the Figure (3.6), in that case $\frac{dI}{dt} < 0$ so infection dies out.

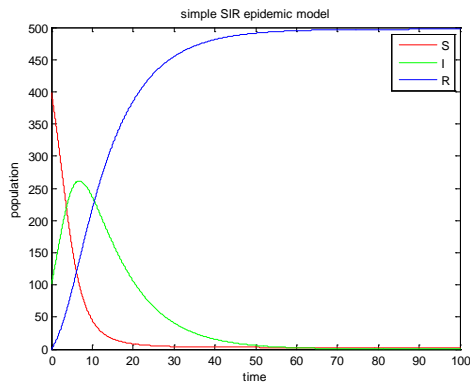


Figure (3.3): $S(0) = 399, I(0) = 101, R(0) = 0$

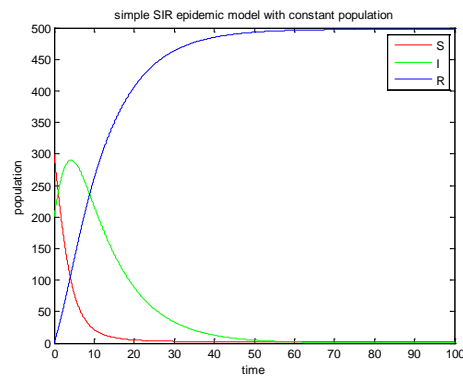


Figure (3.4): $S(0) = 299, I(0) = 201, R(0) = 0$

(0) = 0

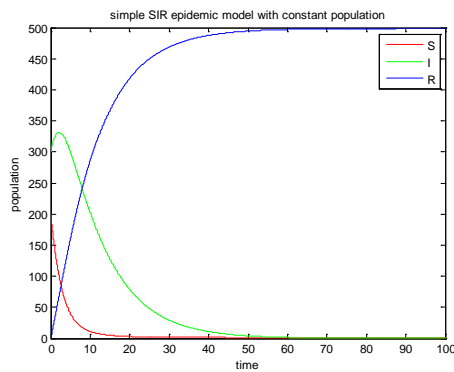


Figure (3.5): $S(0) = 199, I(0) = 301, R(0) = 0$

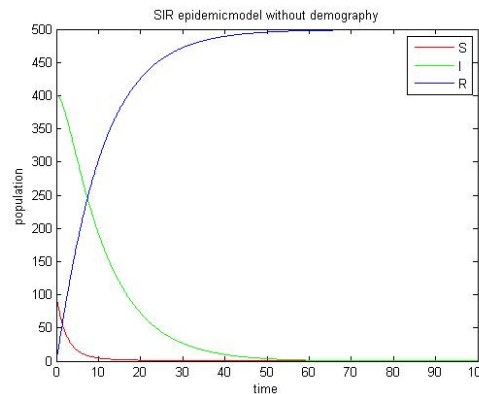


Figure (3.6): $S(0) = 99, I(0) = 401, R(0) = 0$

Secondly, we fix the initial data $S(0) = 499, I(0) = 1$ and $R(0) = 0$ and observed the effect of contact rate parameter β and recovery parameter γ on the population. From the system (2.1), it is clear that the contact rate β is directly proportional to the infected persons. The same behavior can be seen in the numerical results shown in the Figure (3.7). The impact of β on the class of recovered people can be seen in the Figure (3.8). We observed that an increase in the value of β results in a rapid increase in the $R(t)$ since in that case more population is infected to be recovered. On the other hand by increasing the contact rate β the time period decreases to become susceptible which can be easily observed from the Figure (3.9).

We also observed from the graphical results that if the recovery rate γ increases the threshold of susceptible class for endemic equilibrium increases as shown in the Figure (3.10) also the more of infected persons may fall in the class of susceptible persons by increasing recovery rate γ . On the other hand, as expected the threshold value of infected persons decreases as shown in the Figure (3.11). The Figure (3.12) depicts the impact of γ on

the recovered people, that is quite opposite. By increasing recovery parameter the $R(t)$ decreases because of less infected persons implies less recovered people.

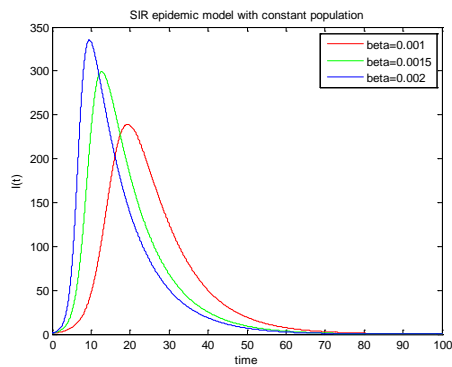


Figure (3.7): $S(0) = 499, I(0) = 1, R(0) = 0$

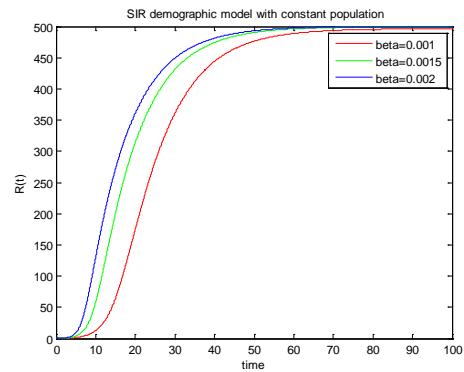


Figure (3.8): $S(0) = 499, I(0) = 1, R(0) = 0$

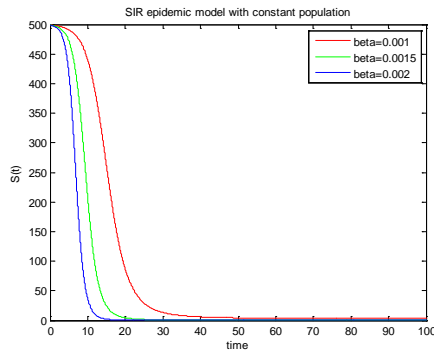


Figure (3.9): $S(0) = 499, I(0) = 1, R(0) = 0$

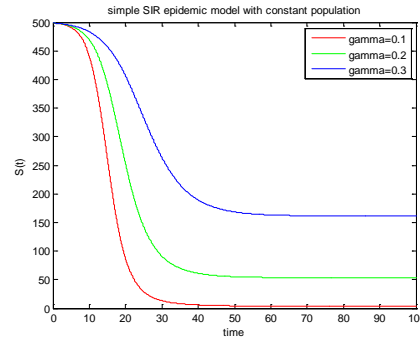


Figure (3.10): $S(0) = 499, I(0) = 1, R(0) = 0$

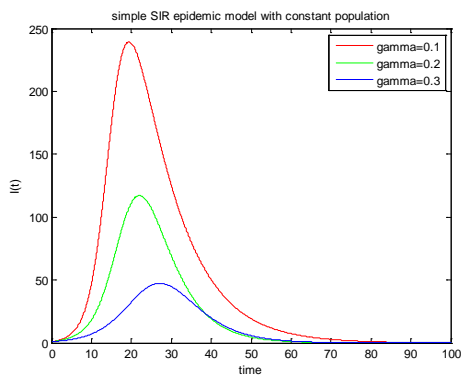


Figure (3.11): $S(0) = 499, I(0) = 1, R(0) = 0$

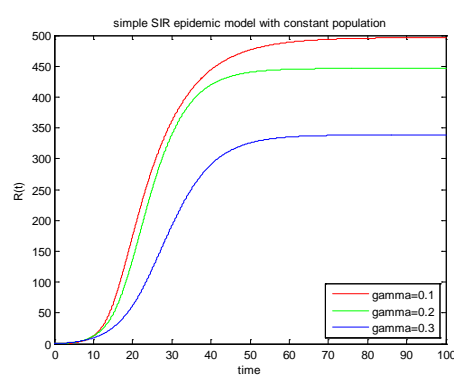


Figure (3.12): $S(0) = 499, I(0) = 1, R(0) = 0$

4. Solution of SIR model with Demography

The SIR model with demography means that the population is not constant. A simple way of introducing

demography into SIR model is to assume there is a natural host ‘ $\frac{1}{\mu}$ ’, years. Then, the rate at which the individual suffer natural mortality is given by μ . It is also assumed that μ also represents the population crude birth rate, thus ensuring that the total population size does not change through time. The governing equations for SIR model with demography are

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta SI - \mu S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\ \frac{dR}{dt} &= \gamma I - \mu R \end{aligned} \quad (4.1)$$

subject to initial conditions:

$$S(0) = S_0, \quad I(0) = I_0 \text{ and } R(0) = R_0$$

where μ is per capita birth and death rate.

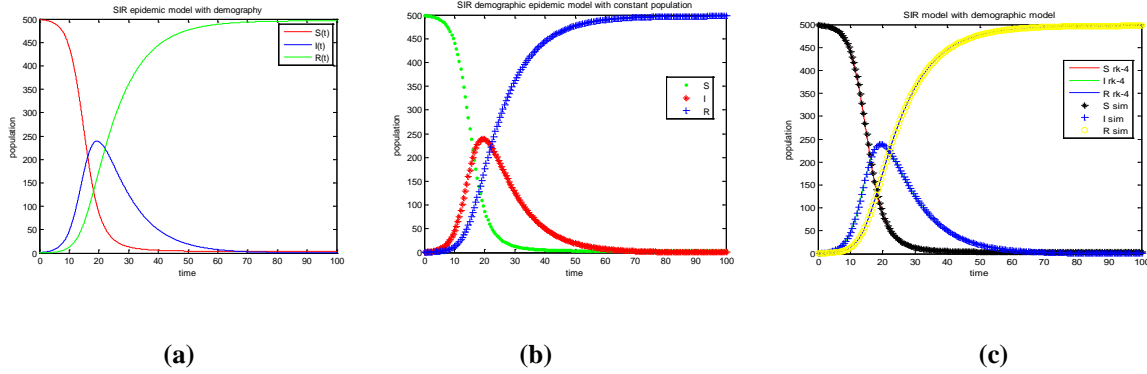
By introducing new parameter μ , the basic productive number will now depend on μ as well. Because if we observe the system (4.1), then in the second equation the parameter β represents the transmission rate per infective, while the negative terms in the equation tells us that each infectious individual spends an average $\frac{1}{\gamma + \mu}$ time units in this class. The infectious period is reduced due to individuals dying whilst infectious.

Therefore, if we assume the entire population is susceptible then the average number of new infections per infectious individual is determined by the transmission rate multiplied by the infectious period i.e. $\mathfrak{R}_0^* = \frac{\beta}{\gamma + \mu}$.

This value is generally similar to, but always smaller than basic productive number \mathfrak{R}_0 for a closed population as the natural mortality rate reduces the average time an individual is infectious. The system of nonlinear ODEs (4.1) is then solved numerically using RK-4th order and Matlab-Simulink. The results are presented graphically in the below figures.

Figure 4.1(a) Numerical results of SIR demographic epidemic model using RK-4, Figure 4.1(b) Matlab-Simulink solution for the SIR demographic epidemic model and Figure 4.1(c) Comparison of solutions of SIR demographic epidemic model using RK-4 and Matlab-Simulink; Lines: results using RK-4, Symbols: using Matlab-Simulink with $S(0) = 499, I(0) = 1,$

$$R(0) = 0 \text{ for } \beta = 0.001, \gamma = 0.1, \text{ and } \mu = 0.000003.$$



It is observed from the Figure (4.2c) that the as the value of μ increases by keeping the value of other parameters fixed the number of recovered person decreases. While the effect of μ on the susceptible and infected persons is quite opposite means the susceptible and infected decreases by increasing μ as shown in the Figure 4.2(a,b).

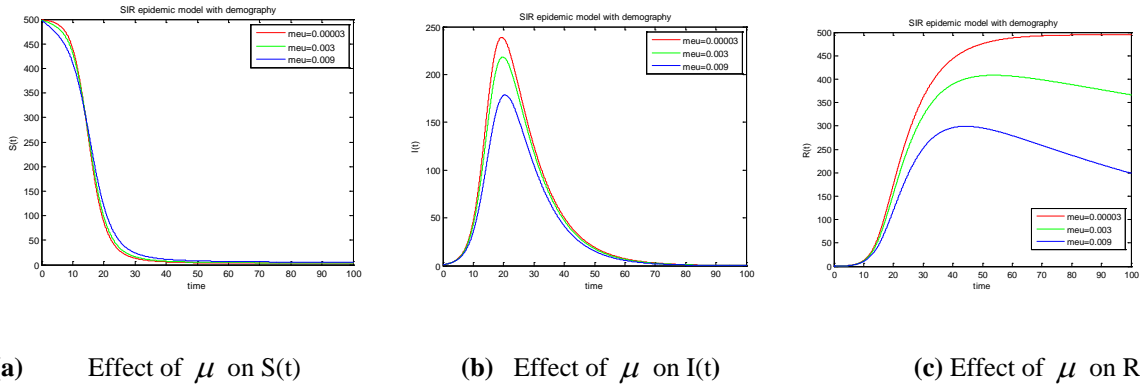


Figure 4.2 Effect of μ on $S(t)$, $I(t)$ and $R(t)$ using RK-4 with $S(0) = 499$, $I(0) = 1$, $R(0) = 0$ for $\beta = 0.001$, $\gamma = 0.1$

5. SIR demographic epidemic model with vaccination

In SIR model with vaccination some part of population is vaccinated. Vaccinated people become a part of recovered population after getting a sufficient immunity for the disease because of vaccination. The system of non-linear coupled differential equations with vaccination is

$$\begin{aligned}
 \frac{dS}{dt} &= \mu(1 - p) - \beta SI - \mu S \\
 \frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\
 \frac{dR}{dt} &= \mu p + \gamma I - \mu R
 \end{aligned}
 \tag{5.1}$$

subject to the initial conditions: $S(0) = S_0$, $I(0) = I_0$ and $R(0) = R_0$

Here, μ is the per capita birth / death rate, p is the vaccination parameter, β is contact rate parameter and γ is recovery rate parameter. Solution of the above coupled ODEs is presented graphically by using RK-4 method and Matlab-Simulink.

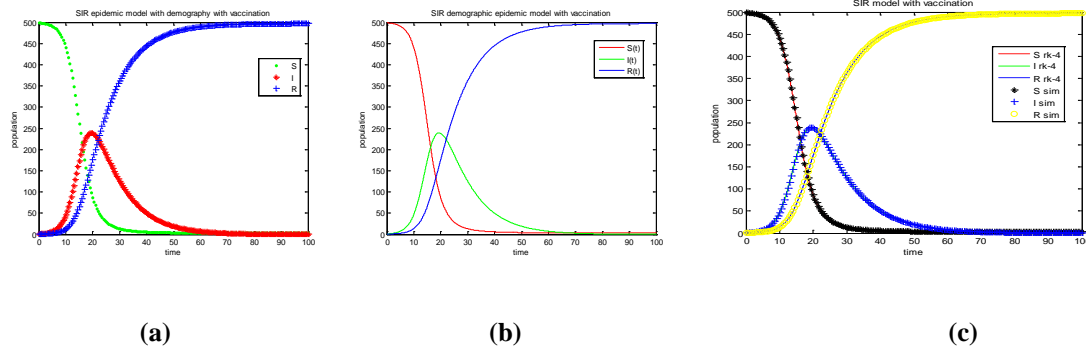


Figure 5.1(a) Numerical results of SIR demographic epidemic model with vaccination parameter using RK-4, Figure 5.1(b) Matlab-Simulink results and Figure 5.1(c) Comparison of both results: Lines: RK-4, Symbols: Matlab-Simulink with $S(0) = 499$, $I(0) = 1$, $R(0) = 0$ for $\beta = 0.001$, $\gamma = 0.1$, $p = 0.5$ and $\mu = 0.000003$.

6. Conclusion

In this paper, a well-known epidemic model namely Susceptible-Infected-Recovered (SIR) is considered with and without demographic effects. This model represents population dynamics during the disease as a set of non-linear coupled ordinary differential equations. There is no exact solution available in the literature for this model up to the best of author's knowledge. Therefore, the simulation tool, for instance Matlab-Simulink has been used to solve the model numerically. The model is also solved by using Runge-Kutta 4th order method and a good agreement is found with the Matlab-Simulink results. The effect of physical parameters like contact rate β , recovery rate γ , and per capita birth/death rate μ is discussed in detail. It is observed that the infection rate and reproductive numbers play a key role for an epidemic to occur and the epidemic can be controlled by vaccination. It is also observed that to eliminate the disease, it is not necessary to vaccinate whole of the population.

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