On the backward bifurcation of an $SEIRS$ epidemic model with nonlinear incidence rate

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Abstract: An $SEIRS$ epidemic model with a nonlinear incidence rate is investigated. Mathematical analysis reveals that the model has a locally asymptotically stable disease–free equilibrium (DFE) whenever a certain epidemiological threshold, known as the basic reproduction number R_0, is less than unity. Using the theory of centre manifold, the model exhibits the phenomenon of backward bifurcation, where the stable DFE coexists with a stable endemic equilibrium when $R_0 < 1$. The epidemiological consequence of this phenomenon is that the classical epidemiological requirement of the reproduction number being less than unity becomes only a necessary, but not sufficient, for disease elimination (hence, the presence of this phenomenon in the transmission dynamics of a disease makes its effective control in the community difficult).

Key–Words: SEIRS epidemic model, Nonlinear incidence rate, Backward bifurcation

1 Introduction

In modelling of communicable disease, the incidence rate (the rate of new infections) is considered to play a vital role in ensuring that the model can give a reasonable qualitative description of the disease dynamics [22]. Bilinear and standard incidence rate have been frequently used in classical epidemiological models [7, 18, 20, 23, 26, 32]. Such models always have only one endemic equilibrium when the basic reproduction number $R_0 > 1$, and the disease-free equilibrium is always stable when $R_0 < 1$ and unstable when $R_0 > 1$. So the bifurcation leading from a disease free equilibrium to an endemic equilibrium is forward. In recent years, actual data and evidences observed for many diseases show that dynamics of disease transmission are not always as simple as shown in these models. Thus, many researchers [4, 8, 9, 10, 13, 14, 15, 17, 19, 21, 30] have taken into account oscillations in many nonlinear incidence rates. For examples, Yorke and London [30] showed that an incidence rate $g(I)S = \beta(1 - cI)S$ with positive c and time dependent β is consistent with the results of the simulations for measles outbreaks. Capasso and his co-workers [9, 10], stressed the importance to consider nonlinear incidence rates for some specific disease: the case of study was a cholera epidemic spread. Liu et al. [25] studied the codimension-1 bifurcation for $SEIRS$ and $SIRS$ models with the incidence rate $\beta I^p S^q$ in [24]. Ruan and Wang [27] studied saddle-node bifurcation, Hopf bifurcation, BogdanovTakens bifurcation and the existence of none, one and two limit cycles of an $SIRS$ model with an incidence rate of $kI^2S/(1 + \alpha I^2)$, which was also proposed by Liu et al. [25]. van den Driessche and Watmough [13, 14] studied an incidence rate of the form

$$\beta I(1 + \nu I^{k-1}), \tag{1}$$

where $\beta > 0$, $\nu \geq 0$ and $k > 0$. When $v = 0$ this incidence rate is the bilinear incidence rate βIS [7]. In [4, 19], they studied an $SIRS$ and $SEIR$ models, respectively, with the incidence rate in (1) for $\nu > 0$ and $k = 2$, showing stability switches and backward bifurcations. The qualitative behavior of an epidemic system with a backward bifurcation differs from that of a system with a forward bifurcation in at least three important ways. If there is a forward bifurcation at $R_0 = 1$ it is not possible for a disease to invade a population if $R_0 < 1$ because the system will return to the disease–free equilibrium $I = 0$ if some infectives are introduced into the population. On the other hand, if there is a backward bifurcation at $R_0 = 1$ and enough infectives are introduced into the population to put the initial state of the system above the unstable endemic

equilibrium with $R_0 < 1$, the system will approach the asymptotically stable endemic equilibrium. Other differences are observed if the parameters of the system change to produce a change in R_0. With a forward bifurcation at $R_0 = 1$ the equilibrium infective population remains zero so long as $R_0 < 1$ and then increases continuously as R_0 increases. With a backward bifurcation at $R_0 = 1$, the equilibrium infective population size also remains zero so long as $R_0 < 1$ but then jumps to the positive endemic equilibrium as R_0 increases through unity. In the other direction, if a disease is being controlled by means which decrease R_0 it is sufficient to decrease R_0 to unity if there is a forward bifurcation at $R_0 = 1$ but it is necessary to bring R_0 well below unity if there is a backward bifurcation. Thus, it is important to identify backward bifurcations and establish thresholds for the control of diseases. Although, this phenomenon of the backward bifurcations has arisen the interests in epidemic models (see [2, 5, 16, 29, 31, 4, 19]and references therein), those reported have not been analyzed this phenomenon of $SEIES$ model with the nonlinear incidence rate in (1) for $\nu > 0$ and $k = 2$.

The objective of this paper is to derive conditions ensuring that an $SEIRS$ epidemic model with nonlinear incidence rate (given in (1) for $\nu > 0$ and $k = 2$) exhibits backward bifurcation and hence multiplicity of endemic equilibria. To this end,the four-dimensional model monitors the dynamics of the susceptible individuals, (S); exposed individuals but not yet infectious, (E); infectious individuals, (I), and recovered individuals, (R). The $SEIRS$ epidemic model with nonlinear incidence rate consists of the following equations:

$$\begin{aligned} \frac{dS}{dt} &= A - (\mu + \beta g(I))S + \delta R, \\ \frac{dE}{dt} &= \beta g(I)S - (\epsilon + \mu)E, \\ \frac{dI}{dt} &= \epsilon E - (\gamma + \mu)I, \\ \frac{dR}{dt} &= \gamma I - (\delta + \mu)R, \end{aligned} \tag{2}$$

with $g(I) = \beta I(1 + \nu I)$. The parameters (all positive constants) have the following meaning: A is the recruitment rate (either by birth or by immigration) into the population (assumed susceptible), β is the infection rate at which susceptible individuals become infected by those who are infectious, μ is the birth/death rate, ϵ is the rate at which the exposed individuals become infective (so that $1/\epsilon$ is the mean latent period), δ is the recovery rate and γ is the rate that recovered individuals lose immunity and return to the susceptible class. The nonlinear incidence $\beta SI(1 + \nu I)$ corresponds to an increased rate of infection due to two exposures over a short time period. The single contracts lead to infection at the rate βSI, whereas the new infective individuals arise from double exposure at a rate $\beta\nu I^2 S$ [14].

This paper is organized as follows. The existence of and threshold conditions for the onset of backward bifurcation are discussed in Section 2. Numerical simulations are carried out to investigate the influence of the key parameters on the phenomenon of in Section 3 and the conclusions is given in Section 4.

2 Qualitative analysis

2.1 Basic properties of the model

Consider the biologically-feasible region

$$\Omega = \{S, E, I, R) \in \mathbb{R}^4_+ | S + E + I + R \leq A/\mu\} \tag{3}$$

which is positively-invariant and attracting with respect to the model (2).

The rate of change of the total population, obtained by adding all the equations in the model (2) gives

$$\frac{dN}{dt} = A - \mu N. \tag{4}$$

It follows that $dN/dt \leq 0$ for $N \geq A/\mu$. Thus, a standard comparison theorem (see [**?**]) can be used to show that $N(t) \leq N(0)e^{-\mu t} + A/\mu(1 - e^{-\mu t})$. In particular, $N(t) \leq A/\mu$ if $N(0) \leq A/\mu$. Thus, Ω is positively-invariant set. Hence, it is sufficient to consider the dynamics of the flow generated by the model (2) in Ω. It is easy to see, by comparison theorem, that $\liminf_{t\to\infty} N(t) \leq A/\mu$. Thus, the omega limit sets of all solutions of the model (2) in $\mathbb{R}^4_+$ are contained in Ω. That is, solutions in Ω remain in Ω for all time, and those outside Ω (but in $\mathbb{R}^4_+$) are eventually attracted to Ω.

2.2 Disease-free equilibrium

The model (2) has the trivial, disease free equilibrium (DFE), namely, $P^0 = (A/\mu, 0, 0, 0)$. To find the conditions under which this equilibrium is locally asymptotically stable, the eigenvalues of Jacobian of the model (2) evaluated at P^0 are

$$\lambda = -\mu, \quad \lambda = -(\mu + \delta),$$

and the roots of quadratic equation

$$\lambda^2 + (2\mu + \epsilon + \gamma)\lambda + (\mu + \epsilon)(\mu + \gamma)(1 - R_0), \tag{5}$$

where

$$R_0 = \frac{\epsilon\beta A}{\mu(\mu + \epsilon)(\mu + \gamma)}. \tag{6}$$

It can be shown that the remaining two eigenvalues (the roots of (5)) have negative real parts if and only if $R_0 < 1$. Furthermore, it can be seen that at least one of these eigenvalues has a positive real part if $R_0 > 1$. Thus, the following result is established.

Lemma 1 *The disease–free equilibrium* (P^0) *of the model* (2) *is locally asymptotically stable* (LAS) *if* $R_0 < 1$ *and unstable if* $R_0 > 1$.

The threshold quantity R_0 in (6) is called the basic reproductive number of infection [1]. This number measures the average number of new infections generated by a single infected individual in a completely susceptible population. The epidemiological implication of Lemma 1 is that, in general, when R_0 is less than unity, a small influx of infected population into the community would not generate large outbreaks, and the disease dies out in time (since the DFE is LAS). However, we show in the next subsection that the disease may still persist even when $R_0 < 1$.

2.3 Existence of endemic equilibria and backward bifurcation

In order to find equilibria (endemic equilibria) of the model (2) where at least one of the infected components of the model (2) is non-zero, the following steps are taken. Let $P^* = (S^*, E^*, I^*, R^*)$ represents any arbitrary endemic equilibrium of the model (2). Setting the right-hand sides of the model (2) to zero and solve S, E, R from the last three equations of the model (2) gives

$$\begin{aligned} &S^* = \tfrac{(\epsilon+\mu)(\gamma+\mu)}{\epsilon\beta(1+\nu I^*)}, \quad E^* = \tfrac{(\gamma+\mu)I^*}{\epsilon}, \\ &R^* = \tfrac{\gamma I^*}{\delta+\mu}. \end{aligned} \tag{7}$$

Substituting (7) into the first equation of the model (2) yields

$$a_0 I^{*2} + b_0 I^* + c_0 = 0 \tag{8}$$

where

$$\begin{aligned} a_0 &= \nu\beta\mu\omega, \\ b_0 &= \beta(\mu\omega - \epsilon\nu A(\mu+\delta)), \\ c_0 &= \mu(\mu+\delta)(\mu+\gamma)(\mu+\epsilon)\,(1-R_0)\,, \\ \omega &= \gamma(\mu+\epsilon+\delta) + (\mu+\epsilon)(\mu+\gamma), \end{aligned} \tag{9}$$

Clearly, the coefficient a_0, in (9), is always positive and, c_0 is positive (negative) if R_0 is less than (greater than) unity, respectively. Since $a_0 > 0$, the existence of the positive solutions of (8) will depend on the signs of b and c. If $R_0 > 1$, then there are two roots of (8) of which one root is positive and thus there is a unique endemic equilibrium. If $R_0 = 1$, then $c_0 = 0$ and there is a unique nonzero solution of (8), $I = -b_0/a_0$, which is positive if and only if $b_0 < 0$. If $b_0 < 0$ there is a positive endemic equilibrium for $R_0 = 1$. Since equilibria depend continuously on R_0 which shows that there exists an interval to the left of R_0 on which there are two positive equilibria

$$I = \frac{-b_0 \pm \sqrt{b_0^2 - 4a_0c_0}}{2a_0}. \tag{10}$$

If $c_0 > 0$ and either $b \geq 0$ or $b_0^2 < 4a_0c_0$, there are no positive solutions of (8) and thus there are no endemic equilibria. For different range of these parameters the following results are established.

Theorem 2 *The model* (2) *has:*

(i) *a unique endemic equilibrium in* Ω *if* $c_0 < 0 \Rightarrow R_0 > 1$*;*

(ii) *a unique endemic equilibrium in* Ω *if* $b_0 < 0$*, and* $c_0 = 0$ *or* $b_0^2 - 4a_0c_0 = 0$*;*

(iii) *two endemic equilibria in* Ω *if* $c_0 > 0$*,* $b_0 < 0$ *and* $b_0^2 - 4a_0c_0 = 0$*;*

(iv) *no endemic equilibrium otherwise.*

It is clear from Theorem 2 Case (i) that the model has a unique endemic equilibrium whenever $R_0 > 1$. Further, Case (iii) indicates the possibility of backward bifurcation (where the locally-asymptotically stable DFE co-exists with a locally-asymptotically stable endemic equilibrium (see, for instance, [3, 6, 28]) in the model (2) when $R_0 < 1$. To find the bacward bifurcation, the discriminant $b_0^2 - 4a_0c_0$ is set to zero and solved for the critical value of R_0, denoted by R_c, given by

$$R_c = 1 - \frac{b_0^2}{4a_0\mu(\mu+\delta)(\mu+\epsilon)(\mu+\gamma)}. \tag{11}$$

Thus, $R_c < R_0$ is equivalent to $b_0^2 - 4a_0c_0 > 0$ and, therefore, backward bifurcation would occur for values of R_0 such that $R_c < R_0 < 1$. The associated bifurcation diagram is depicted in Figure 1. Thus, the following result is established.

Lemma 3 *The model* (2) *exhibits backward bifurcation when Case* (iii) *of Theorem* 2 *holds and* $R_c < R_0 < 1$.

The following result can be established using center manifold theory [11] (in particular, using Theorem 4.1 in [12].

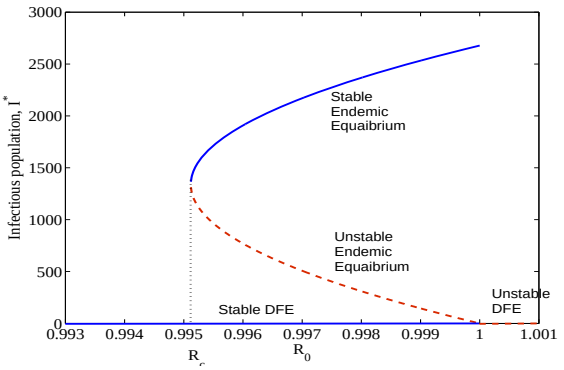


Figure 1: Bifurcation diagram for backward bifurcation in the plane (R_0, I^*) when $\nu = 0.000056 > \nu^*$. Parameter values used are: $A = 10$, $\mu = 3.65 \times 10^{-4}$, $\beta = 1.473197393 \times 10^{-6}$, $\epsilon = 0.3$, $\gamma = 0.04$, and $\delta = 0.2$. With this set of parameters, $R_c = 0.9951181087$ and $R_0 = 0.9987000002$ (so that, $R_c < R_0 < 1$).

Theorem 4 *Let*

$$\nu^* = \frac{\mu[\gamma(\mu+\epsilon+\delta)+(\mu+\epsilon)(\mu+\delta)]}{A\epsilon(\mu+\delta)}, \qquad (12)$$

the model (2) *undergoes backward bifurcation at* $R_0 = 1$ *if* $\nu > \nu^*$ *and forward bifurcation if* $\nu < \nu^*$.

Proof. The following simplification and change of variables are made on the model (2) first of all. Let $S = x_1$, $E = x_2$, $I = x_3$ and $R = x_4$, so that $N = x_1 + x_2 + x_3 + x_4$. Further, by using vector notation $X = (x_1, x_2, x_3, x_4)^T$, the model (2) can be written in the form $\frac{dX}{dt} = (f_1, f_2, f_3, f_4)^T$, as follows:

$$\begin{aligned}
\frac{dx_1}{dt} &:= f_1 = A - (\mu + \beta(1+\nu x_3)x_3)x_1 + \delta x_4,\\
\frac{dx_2}{dt} &= f_2 = \beta(1+\nu x_3)x_3 x_1 - (\epsilon+\mu)x_2,\\
\frac{dx_3}{dt} &= f_3 = \epsilon x_2 - (\gamma+\mu)x_3,\\
\frac{dx_4}{dt} &= f_4 = \gamma x_3 - (\delta+\mu)x_4
\end{aligned} \qquad (13)$$

Consider the case when $R_0 = 1$. Suppose, further, that $\beta = \beta^*$ is chosen as a bifurcation parameter. Solving for β from $R_0 = 1$ gives

$$\beta = \beta^* = \frac{\mu(\mu+\epsilon)(\mu+\gamma)}{A\epsilon}.$$

The eigenvalues of Jacobian of the system (13), evaluated at P^0 with $\beta = \beta^*$, are given by

$$\lambda_1 = -\mu,\ \lambda_2 = -(\mu+\delta),\ \lambda_3 = -(2\mu+\gamma+\epsilon),$$
$$\lambda_4 = 0.$$

Thus $\lambda_4 = 0$ is a simple zero eigenvalue and the other eigenvalues are real and negative. Hence, when $\beta = \beta^*$ (or equivalently when $R_0 = 1$), the disease-free equilibrium P^0 is a nonhyperbolic equilibrium, the assumption (A1) of Theorem 4.1 in [12], is then verified.

Now, a right eigenvector associated with the zero eigenvalue $\lambda_4 = 0$ are given by $w = (w_1, w_2, w_3, w_4)^T$, where

$$w_1 = -\frac{\gamma k_1 + (\mu+\epsilon)k_2}{\epsilon k_2} w_3,$$
$$w_2 = \frac{k_2}{\epsilon} w_3,\ w_3 = w_3 > 0, w_4 = \frac{\gamma}{k_2} w_3,$$

so that

$$w = \left(-\frac{k_1\gamma + (\mu+\epsilon)k_2}{\epsilon k_2}, \frac{k_2}{\epsilon}, 1, \frac{\gamma}{k_2}\right)^T, \qquad (14)$$

where $k_1 = \mu + \delta + \epsilon$ and $k_2 = \mu + \delta$.

Further, a left eigenvector associated with the zero eigenvalue $\lambda_4 = 0$ satisfying $v \cdot w = 1$ are given by $v = (v_1, v_2, v_3, v_4)^T$, where

$$v_1 = 0,\ v_2 = \frac{\epsilon}{\mu + k_3},\ v_3 = \frac{\mu+\epsilon}{\mu+k_3},\ v_4 = 0, \qquad (15)$$

where $k_3 = \mu + \gamma + \epsilon$. The coefficients a and b defined in Theorem 4.1 in [12] are computed as in the following.

For the system (13), the associated non-zero partial derivatives of the right hand side functions (f_i) are given by

$$\begin{aligned}
&\frac{\partial^2 f_1}{\partial x_1 \partial x_3} = \frac{\partial^2 f_1}{\partial x_3 \partial x_1} = -\beta^*,\ \frac{\partial^2 f_1}{\partial x_3^2} = -\frac{2\beta\nu A}{\mu},\\
&\frac{\partial^2 f_2}{\partial x_1 \partial x_3} = \frac{\partial^2 f_2}{\partial x_3 \partial x_1} = \beta^*,\ \frac{\partial^2 f_2}{\partial x_3^2} = \frac{2\beta\nu A}{\mu},\\
&\frac{\partial^2 f_1}{\partial x_3 \beta^*} = -A/\mu,\ \frac{\partial^2 f_2}{\partial x_3 \partial \beta^*} = A/\mu.
\end{aligned} \qquad (16)$$

Using the expressions (14)-(16), it follows that

$$\begin{aligned}
a &= \sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0)\\
&= \frac{2(\mu+\epsilon)(\mu+\gamma)}{\mu+k_3}\left(\nu - \frac{\mu\gamma k_1 + (\mu+\epsilon)k_2}{\epsilon A k_2}\right)\\
&= \frac{2(\mu+\epsilon)(\mu+\gamma)(\nu-\nu^*)}{\mu+k_3},
\end{aligned}$$

and

$$\begin{aligned}
b &= \sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \beta^*}(0,0)\\
&= \frac{\epsilon A}{\mu(\mu+k_3)}.
\end{aligned}$$

It is found that the coefficient b is always positive. The coefficient a is positive if $\nu > \nu^*$, and negative if $\nu < \nu^*$. Therefore, by Theorem A, the model (2) undergoes backward bifurcation if $\nu > \nu^*$ and forward bifurcation if $\nu < \nu^*$. The proof is complete.

It can be concluded that, from Lemma 3 and Theorem 4, when $R_c < R_o < 1$, the model (2) exhibits the phenomenon of backward bifurcation whenever $\nu > \nu^*$ and forward bifurcation whenever $\nu < \nu^*$. Although the phenomenon of backward bifurcation has been established in many epidemiological settings (see [2-6,18] and the references therein), to the authors knowledge, this is the first time such a phenomenon has been theoretically shown in the $SEIRS$ model (2). Further, as a consequence, it is instructive to try to determine the "cause" of the backward bifurcation phenomenon in the model (2). This is explored below by considering the mass action equivalent of the model (2). It is noted, from Theorem 4, that the backward bifurcation phenomenon will not occur if $\nu = 0$, since the right-hand side of the inequality in Theorem 4 is non-negative which is clarified the absence of backward bifurcation in the model (2) when the non-linear incidence rate of the form $\beta I(1+\nu I)S$ is the bilinear incidence rate βIS (i.e., $\nu = 0$)

3 Numerical Simulations

In this section aims to provide a numerical verification of the above theoretical results presented and to show their agreement with the endemic equilibria and their stability properties. The model (2) is simulated using the parameter values:

$$\begin{aligned} &A = 10,\ \mu = 3.65 \times 10^{-4},\ \epsilon = 0.3, \\ &\gamma = 0.04,\ \delta = 0.2. \end{aligned} \tag{17}$$

Using the parameter values in (17), the bifurcation parameters in (6) and (12) at $R_0 = 1$ take the values

$$\beta^* = 1.4751 \times 10^{-6} \quad \text{and} \quad \nu^* = 4.8698 \times 10^{-5}.$$

Then, in order to satisfy the conditions $R_0 < 1$, $R_0 > 0$, $\nu > \nu^*$ and $\nu < \nu^*$, the infection rate β and ν are chosen to be $\beta = 1.3575 \times 10^{-6}, 1.4732 \times 10^{-6}$, 2.9483×10^{-6}, $\nu = 5.6 \times 10^{-5}$ and $\nu = 3 \times 10^{-4}$, respectively. The four different relevant cases are discussed.

Case I For $\beta < \beta^*$ and $\nu > \nu^*$, choosing $\beta = 1.4732 \times 10^{-6}$ and $\nu = 5.6 \times 10^{-5}$ with the parameter values in (17) give $R_c = 0.9951$ and $R_0 = 0.9987$ (so that, $\nu > \nu^*$ and $R_c < R_0 < 1$). The simulation results using different initial conditions, depicted in Figure 2, show that the model has a disease free equilibrium (DFE) (corresponding to $I^* = 0$) and two endemic equilibria (corresponding to $I^* = 2485.6441$ and $I^* = 192.0313$, respectively). Further, Figure 2 shows that one of the endemic equilibria (corresponding to $I = 2485.6441$ is locally asymptotically stable (LAS), the other endemic equilibrium (corresponding to $I = 192.0314$ is unstable (saddle), and the DFE (corresponding to $I = 0$) is LAS. This clearly shows the co-existence of two locally-asymptotically stable equilibria when $R_c < R_0 < 1$, confirming that the model (2) undergoes the phenomenon of backward bifurcation if $\nu > \nu^*$ (as guaranteed by Lemma 3 and Theorem 4).

Case II For $\beta < \beta^*$ and $\nu < \nu^*$, choosing $\nu = 3 \times 10^{-5}$, $\beta = 1.4732 \times 10^{-6}$, 1.3575×10^{-6} with the parameter values in (17) give $R_c = 0.9403$ and $R_0 = 0.9987$, $R_c = 0.9449$ and $R_0 = 0.9203$ which imply that $R_c < R_0 < 1$ and $R_0 < R_c < 1$, respectively. It is found that the model (2) exhibits a forward bifurcation as shown in Figure 3. As a consequence, in the backward bifurcation scenario, these studies show that if $R_c < R_0 < 1$ and $\nu > \nu^*$, then the disease control strongly depends on the initial sizes of the various sub-populations of the models (see Figure 2). On the contrary, if $R_0 < 1$ (even $R_0 < R_c < 1$ or $R_c < R_0 < 1$), reducing $\nu < \nu^*$ may result in disease eradication, which is provided that the disease free equilibrium is locally asymptotically stable. Hence, determining the threshold value ν^* of nonlinear incidence function may have a crucial

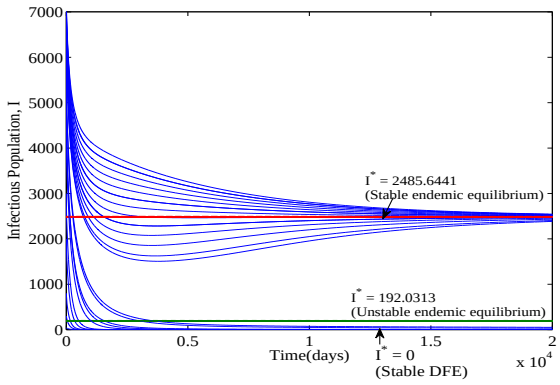


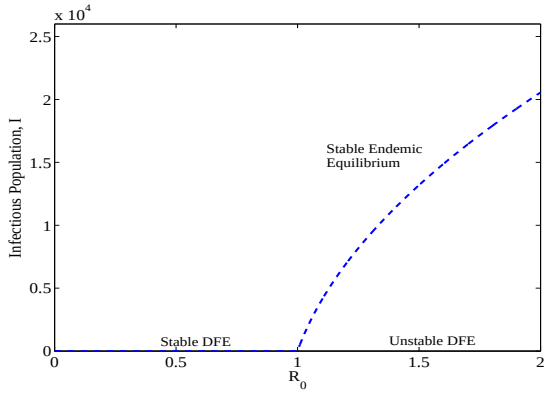
Figure 2: Time series plot using different initial conditions for the infectious population, I, of the model (2). Parameter values used are: $A = 10$, $\mu = 3.65 \times 10^{-4}$, $\beta = 1.473197393 \times 10^{-6}$, $\epsilon = 0.3$, $\gamma = 0.04$, $\delta = 0.2$, $\nu = 0.000056$. With this set of parameters, $R_c = 0.9951181087$ and $R_0 = 0.9987000002$ (so that, $R_c < R_0 < 1$ and $\nu > nu^*$).

importance in planning how to control a disease.

4 Conclusions

In this paper, an SEIRS epidemic model with a non-linear incidence rate $\beta I(1+\nu I)S$ is rigorously analysed to gain insights into its qualitative dynamics. The results are shown that the model with non-linear incidence rate undergoes backward bifurcation if $\nu > \nu^*$ and $R_c < R_0 < 1$, where the stable disease-free equilibrium co-exists with a stable endemic equilibrium. The backward bifurcation scenario may be qualitatively described as follows. In the neighborhood of unity, for $R_0 < 1$, a stable disease-free equilibrium coexists with two endemic equilibria: a smaller equilibrium (i.e., with a smaller number of infective individuals) which is unstable and a larger one (i.e., with a larger number of infective individuals) which is stable. These two endemic equilibria disappear if $\nu < \nu^*$ and $R_0 < 1$. Moreover, the epidemiological significance of the phenomenon of backward bifurcation is that the classical requirement of $R_0 < 1$ is, although necessary, no longer sufficient for disease elimination. In such a scenario, disease elimination would depend on the initial sizes of the sub-populations (state variables) of the model. That is, the presence of backward bifurcation in the $SEIRS$ model (2) suggests that the feasibility of controlling disease when $R_0 < 1$ could be dependent on the initial sizes of the sub-population of the model (2) as confirmed by numerical simulations (see Figure 2).

(a)



(b)

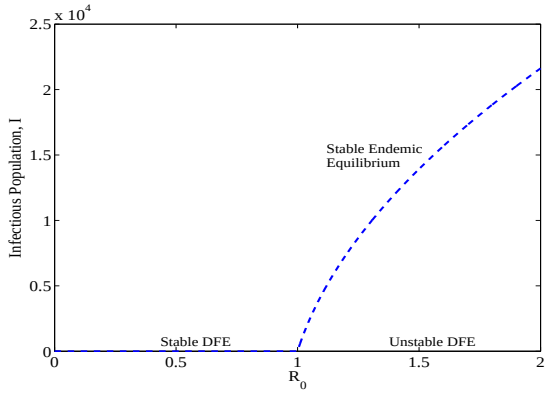


Figure 3: Bifurcation diagram for forward bifurcation in the plane (R_0, I^*) when $\nu = 0.00003 < \nu^*$. Parameter values used are: $A = 10$, $\mu = 3.65 \times 10^{-4}$, $\epsilon = 0.3$, $\gamma = 0.04$ and $\delta = 0.2$. With this set of parameters, (a) $\beta = 1.473197393 \times 10^{-6}$ gives $R_c = 0.9402518297$ and $R_0 = 0.9987000002$ (so that, $R_c < R_0 < 1$); (b) $\beta = 1.357474618 \times 10^{-6}$ gives $R_c = 0.9449451750$ and $R_0 = 0.9202500002$ (so that, $R_0 < R_c < 1$).

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