IJST (2013) 37A4: 483-489
Iranian Journal of Science & Technology

http://ijsts.shirazu.ac.ir

Global analysis of a delay SVEIR epidemiological model

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Abstract

This paper is concerned with global analysis of a delay SVEIR epidemiological model in a population of varying size. By using Lyapunov stability method and LaSalle's invariance principle for delay systems, we prove that when there is no endemic equilibrium, the disease free equilibrium is globally asymptotically stable, otherwise the endemic equilibrium is globally stable.

Keywords: SVEIR epidemiological model; delay differential equation; disease free equilibrium; endemic equilibrium; lyapunov functional

1. Introduction

Compartmental models for infectious diseases separate a population into various classes based on the stages of infection [1]. Most of the authors assume that the latent period of diseases is negligible, i.e. once infected, each susceptible individual ($\boldsymbol{S}$) instantaneously becomes infectious ($\boldsymbol{I}$), and later recovers ($\boldsymbol{R}$) with a permanent or temporary acquired immunity. These epidemic models are customarily called SIR (susceptible, infectious, recovered) models, [2-5]. Actually, vaccination is the most common method to control the spread of diseases**.** There are two different ways to consider vaccination in epidemiological models based on two different strategies, continuous vaccination and pulse vaccination. It is known that for some diseases, such as influenza and tuberculosis, on adequate contact with an infectious individual, a susceptible becomes exposed for a while; that is, infected but not yet infectious. Thus it is realistic to introduce a latent compartment (usually denoted by $\boldsymbol{E}$) leading to an SEIR and SVEIR model [4, 6-9]. Such type of models, with or without time delays, has been widely discussed in recent decades. Local and global stability analysis of the disease-free and endemic equilibria have been carried out using different assumptions, contact rates and sometimes by introducing reproduction number $\boldsymbol{R_0}$, (see [4-14]).

For instance, for an SVEIR model with pulse vaccination, the global behavior of an 'infection-free' equilibrium when $\boldsymbol{R_0 < 1}$, and the permanence of the disease when $\boldsymbol{R_0 > 1}$ have been proved in [8]. Recently, Wang et al. [13] have shown that the global stability of disease-free and endemic equilibria is governed by the basic reproduction number.

Motivated by the models in [8] and [13], we consider a delay SVEIR epidemiological model with continuous vaccination in a varying population. We assume that both susceptible and vaccinated individuals are capable of being infected through a mass action contact with infectious individuals. Actually, each time only susceptible and vaccinated individuals that have had contacted with infectious individuals $\boldsymbol{\tau}$ time units ago, become infectious, provided that they have survived the period of $\boldsymbol{\tau}$ units, as in [8]. Our vaccination model is suitable for the diseases with partial immunity just after the vaccination. As soon as the susceptible individuals enter the vaccination process, they are different from susceptible and recovered individuals. When the vaccinees gain complete immunity, they would enter the recovered group**.** We prove that for our model the disease-free equilibrium is globally stable when $\boldsymbol{R_0 \leq 1}$, and there is a unique endemic equilibrium, which is globally stable, when $\boldsymbol{R_0 > 1}$. The rest of the paper is organized as follows. In the next section, SVEIR epidemic model and its reduction to an SVI model are introduced. The existence of disease-free and endemic equilibria and the basic reproduction

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Received: 29 October 2012 / Accepted: 24 March 2013

number $\boldsymbol{R_0}$, are presented in section 3. Moreover, local stability of disease-free equilibrium and also global behavior of disease-free and endemic equilibria by constructing suitable Lynapunov functional are analyzed in this section. Finally, we show that similar results are valid for general model. In section 4, we provide some numerical simulations of the system.

2. SVEIR epidemic model and preliminary information

In this section we introduce an SVEIR [4, 8] epidemic model with time delay. The population is divided into five groups: susceptible (those who are capable of contracting the disease); vaccinated (those who receive vaccination to defeat disease); exposed (those who are infected but not yet infectious); infectious (those who are infected and capable of transmitting the disease); and recovered (those who are permanently immune), denoted by $\boldsymbol{S(t), V(t), E(t), I(t)}$, **and** $\boldsymbol{R(t)}$ respectively. We introduce the following model in which all the parameters are assumed to be nonnegative:

$$\begin{aligned}
\dot{S} &= b - dS(t) - \beta S(t)I(t) - \gamma S(t),\\
\dot{V} &= \gamma S(t) - \beta_1 V(t)I(t) - dV(t) - \alpha V(t),\\
\dot{E} &= \beta S(t)I(t) + \beta_1 V(t)I(t)\\
&\quad - \beta e^{-\mu\tau} S(t-\tau)I(t-\tau)\\
&\quad -\beta e^{-\mu\tau} V(t-\tau)I(t-\tau) - \mu E(t),\\
\dot{I} &= \beta e^{-\mu\tau} S(t-\tau)I(t-\tau)\\
&\quad + \beta_1 e^{-\mu\tau} V(t-\tau)I(t-\tau)\\
&\quad -(\delta_1 + \delta_2)I(t),\\
\dot{R} &= \alpha V(t) + \delta_1 I(t) - dR(t). \qquad (1)
\end{aligned}$$

The following parameters have been considered in the above system**:**

(i) b, d, μ and δ_2 are respectively per capita rate of birth, natural death, total death for exposed and infectious individuals including natural death and the disease induced mortality.

(ii) Let γ be the rate for susceptibles who receive vaccination.

(iii) Let β be the transmission rate of disease when susceptible individuals contact with infected individuals. The vaccinated contact with infected individuals before obtaining immunity has the possibility of infection with a disease transmission rate β_1.

(iv) The recovery rate of infected the individual is δ_1. The recovered individuals are assumed to have immunity (so called natural immunity) against the disease.

(v) Let α be the average rate for vaccinated to obtain immunity and move into recovered population.

(vi) τ is a nonnegative constant and shows the time delay.

The time delay is introduced in the system as follows. At time t only susceptible and vaccinated individuals that have contact with infected individuals τ time units ago, that is at time $-\tau$, become infectious, provided that they have survived the incubation period of τ units, given that they were alive at time $t-\tau$ when they had contact with infected individuals. Thus the incidence of newly infected individuals is given by the mass action term $\beta e^{-\mu\tau} S(t-\tau) I(t-\tau)$ and $\beta e^{-\mu\tau} V(t-\tau) I(t-\tau)$, [11, 15].

A special case of the above model ($b = d = \mu$ and $\gamma = 0$) has been investigated in [8]. The existence and global behavior of the 'infection-free' equilibrium and the permanence of the disease in the presence of the endemic equilibrium are analyzed. Here we give a complete global analysis of the above general model. In order to analyze (1) we reduce it to a three dimensional system**.** Since the equations for E and R are independent of other equations, we can rewrite the equations as follows:

$$\begin{aligned}
\dot{S} &= b - (d+\gamma)S(t) - \beta S(t)I(t),\\
\dot{V} &= \gamma S(t) - \beta_1 V(t)I(t) - (d+\alpha)V(t),\\
\dot{I} &= \beta e^{-\mu\tau} S(t-\tau)I(t-\tau) + \beta_1 e^{-\mu\tau} V(t-\tau)I(t-\tau) - \delta I(t), \qquad (2)
\end{aligned}$$

where $\delta = \delta_1 + \delta_2$.

The initial conditions of (2) are given by

$$S(\theta) = \varphi_1(\theta), V(\theta) = \varphi_2(\theta), I(\theta) = \varphi_3(\theta), -\tau \le \theta \le 0,$$

where $\varphi = (\varphi_1, \varphi_2, \varphi_3)^T \in C$, such that $\varphi_i(\theta) \ge 0$ $(i = 1,2,3)$, for all $-\tau \le \theta \le 0$, and C is the Banach space $C([-\tau, 0], \mathbb{R}^3)$ of continuous functions, and $\|\varphi\|$ denotes the norm on C and is defined by

$$\|\varphi\| = \sup_{-\tau \le \theta \le 0} \{|\varphi_1(\theta)|, |\varphi_2(\theta)|, |\varphi_3(\theta)|\}.$$

From the first equation of (2), we obtain $\dot{S} \le b - (d+\gamma)S$. Hence, $limsup_{t\to\infty} S(t) \le \frac{b}{d+\gamma}$. Moreover, from the second equation of (.2), we obtain $\dot{S} + \dot{V} \le b - d(S+V)$. Thus, $limsup_{t\to\infty}(S+V)(t) \le \frac{b}{d}$. Since $e^{-\mu\tau}(S(t-\tau) + V(t-\tau)) + I(t) \le b - d(e^{-\mu\tau}(S(t-\tau) + V(t-\tau)) + I(t))$, we can say $limsup_{t\to\infty} e^{-\mu\tau}(S(t-\tau) + V(t-\tau)) + I(t) \le \frac{b}{d}$. Since $S(t)$ and V(t) are bounded we conclude that I(t) is bounded as well.

Moreover, the following set is positively invariant for the system (2),

$$\begin{aligned}
\Theta = \{(\varphi_1(t), \varphi_2(t), \varphi_3(t)) \mid & 0 \le \varphi_1(0) \le \tfrac{b}{d+\gamma},\\
& 0 \le \varphi_1(0) + \varphi_2(0) \le \tfrac{b}{d},\\
& 0 \le e^{-\mu\tau}(\varphi_1(-\tau) + \varphi_2(-\tau) + \varphi_3(0)) \le \frac{b}{d}\}.
\end{aligned}$$

3. The Equilibrium Points

In delay differential equations the equilibrium points are constant functions. The equilibrium points of (2) are the solutions of the system:

$$\begin{aligned} & b - (d + \gamma)S(t) - \beta S(t)I(t) = 0, \\ & \gamma S(t) - \beta_1 V(t)I(t) - (d + \alpha)V(t) = 0, \\ & \beta e^{-\mu\tau} S(t-\tau)I(t-\tau) + \beta_1 e^{-\mu\tau} V(t-\tau)I(t-\tau) \\ & - \delta I(t) = 0. \end{aligned} \quad (3)$$

It is easy to check that the disease-free equilibrium (DFE) is $P_0 = (\frac{b}{(d+\gamma)}, \frac{b\gamma}{(d+\alpha)(d+\gamma)}, 0)$. Also, we can derive endemic equilibria of the system (2), $P^* = (S^*, V^*, I^*)$, from the two first equations of (3):

$$S^* = \frac{b}{d+\beta I^*+\gamma} \;\&\; V^* = \frac{b\gamma}{(d+\beta_1 I^*+\alpha)(d+\beta I^*+\gamma)} \quad (4)$$

We put the above relations in the third equation of (3), which leads to:

$$\begin{aligned} & \beta e^{-\mu\tau} \frac{b}{d+\beta I^*+\gamma} \\ & + \beta_1 e^{-\mu\tau} \frac{b\gamma}{(d+\beta_1 I^*+\alpha)(d+\beta I^*+\gamma)} - \delta = 0. \end{aligned}$$

and rewrite it as,

$$\begin{aligned} -\delta\beta_1\beta {I^*}^2 + (& \beta_1\beta e^{-\mu\tau} b - \delta(d\beta + d\beta_1 \\ & + \gamma\beta_1 + \alpha\beta)) I^* \\ & + e^{-\mu\tau} b(\beta d + \gamma\beta_1 + \alpha\beta) \\ & - \delta(d+\alpha)(d+\gamma) = 0. \end{aligned} \quad (5)$$

The coefficients of the above quadratic equation are denoted by:

$$\begin{aligned} & a_0 = -\delta\beta_1\beta, \\ & b_0 = be^{-\mu\tau}\beta\beta_1 - \delta(d\beta + d\beta_1 + \gamma\beta_1 + \alpha\beta), \\ & c_0 = be^{-\mu\tau}(\beta d + \gamma\beta_1 + \alpha\beta) - \delta(d + \\ & \alpha)(d + \gamma). \end{aligned} \quad (6)$$

In order to determine the existence of endemic equilibria in the phase space, we should discuss the sign of c_0 and b_0. By considering c_0 let us define the basic reproduction number R_0 as follows:

$$R_0 = \frac{be^{-\mu\tau}(\beta d+\gamma\beta_1+\alpha\beta)}{\delta(d+\alpha)(d+\gamma)} \quad (7)$$

which is known as the number of secondary infections produced by one primary infection in a wholly susceptible population. The existence of endemic equilibrium is determined by the basic reproduction number as the following proposition [13].

Proposition 3.1. If $R_0 \leq 1$, then the DFE is the only equilibrium of the system. When $R_0 > 1$, the system has a unique endemic equilibrium.

Proof: The condition $R_0 < 1$, is equivalent to $\frac{c_0}{a_0} > 0$.

In order to determine the sign of $-\frac{b_0}{a_0}$, let us define R_1 by

$$R_1 = \frac{be^{-\mu\tau}\beta\beta_1}{\delta(d\beta + d\beta_1 + \gamma\beta_1 + \alpha\beta)}$$

According to the definition of R_0 and R_1, we have

$$\begin{aligned} R_0 &= R_1 \frac{(\beta d + \gamma\beta_1 + \alpha\beta)(d\beta + d\beta_1 + \gamma\beta_1 + \alpha\beta)}{\beta\beta_1(d+\gamma)(d+\alpha)} \\ &= R_1(\frac{d+\alpha}{\beta_1} + \frac{\gamma}{\beta})(\frac{\beta_1}{d+\alpha} + \frac{\beta}{d+\gamma}). \end{aligned} \quad (8)$$

Since all parameters are positive, it provides that $(\frac{d+\alpha}{\beta_1} + \frac{\gamma}{\beta})(\frac{\beta_1}{d+\alpha} + \frac{\beta}{d+\gamma}) > 1$, which implies $R_0 > R_1$.

Now assume that $R_0 < 1$. According to the above relation, $R_1 < 1$ which is equivalent to $-\frac{b_0}{a_0} < 0$, hence (5) has no positive root. When R0 = 1, we have $\frac{c_0}{a_0} = 0$ and $R_1 < 1$, hence (5) has one zero and one negative roots. All in all, we found that when $R_0 \leq 1$ there is no endemic equilibrium, and the DFE is the only equilibrium of the system. When $R_0 > 1$, it is equivalent to $\frac{c_0}{a_0} < 0$. Thus (5) has two roots; one positive and one negative. Since only positive equilibria are meaningful in our system, we conclude that the system has a unique endemic equilibrium when $R_0 > 1$.

3.1. The Stability of the DFE

In this section we show that the basic reproduction number, R_0, governs the stability of P_0. First, in Theorem 3.1, we prove local stability of DFE and then in Theorem 3.2 by introducing a Lyapunov functional, the global stability of P_0 is shown when $R_0 \leq 1$.

Theorem 3.1. The DFE is locally asymptotically stable if $R_0 < 1$ and it is unstable if $R_0 > 1$.

Proof: We apply linear stability technique for delay differential equations [16]. The characteristic equation of the system at P_0 is of the following form:

$$\begin{aligned} & (\lambda + d + \alpha)(\lambda + d + \gamma)(\beta e^{-(\mu+\lambda)\tau} S(t-\tau) \\ & + \beta_1 e^{-(\mu+\lambda)\tau} V(t-\tau) - (\delta + \lambda)) = 0. \end{aligned} \quad (9)$$

Since the roots of the first two phrases are negative, in order to study the stability of P_0 we should determine the roots of the third phrase:

$$\beta e^{-(\mu+\lambda)\tau} S(t-\tau) + \beta 1 e^{-(\mu+\lambda)\tau} V(t-\tau) - (\delta+\lambda) = 0.$$

We can multiply the above equation by τ and let $x = -\lambda\tau$, the result is:

$$x + e^{x-\mu\tau}\frac{b\tau}{(d+\gamma)}(\beta + \beta_1\frac{\gamma}{(d+\alpha)}) - \delta\tau = 0.$$

Rewrite it as $x - qe^x + p = 0$ where $p = -\delta\tau$ and $q = \frac{\tau b e^{-\mu\tau}}{(d+\alpha)(d+\gamma)}((d+\alpha)\beta + \beta_1\gamma)$. Hayes in [17] showed that all roots of the equation $x - qe^x + p = 0$, where p and q are real numbers, have negative real parts if and only if $p < 1$ and $p < q < \sqrt{a_1^2 + p^2}$, where a_1 is a root of $a = p(tan(a)), 0 < a < \pi$. Since $-\delta < 0$ and $p - q = -\delta + \frac{be^{-\mu\tau}}{(d+\alpha)(d+\gamma)}((d+\alpha)\beta + \beta_1\gamma) = \delta(R_0 - 1) < 0$, thus P_0 is locally stable if $R_0 < 1$, and unstable if $R_0 > 1$.

Now we prove the global asymptotic stability of the DFE using a Lyapunov functional, and Lyapunov-LaSalle theorem.

Theorem (Lyapunov-LaSalle). If V is a Lyapunov functional on G and $x_t(\Phi)$ is a bounded solution of a delay differential equation that stays in G, then $x_t(\Phi)$ converges to the maximal invariant set in $\{\Phi \in ClG : V(\Phi) = 0\}$ as $t \to +\infty$. The following result indicates that the disease dies out in the host population if $R_0 \leq 1$.

Theorem 3.2. The DFE is globally asymptotically stable, if $\mathbf{R_0} \leq \mathbf{1}$.

Proof: For all $\boldsymbol{\varepsilon} \geq \mathbf{0}$, let $\Omega_\varepsilon = \{(\boldsymbol{\varphi_1(t)}, \boldsymbol{\varphi_2(t)}, \boldsymbol{\varphi_3(t)}) : \boldsymbol{\varphi_1(0)} \leq \frac{b}{d+\gamma} + \boldsymbol{\varepsilon}\}$. Since $\boldsymbol{S} < \mathbf{0}$, the ω−limit set of any orbit lies in Ω_ε, and since ε is arbitrary, it lies in $\Omega_\mathbf{0}$. Therefore, we should focus on the dynamics of $\Omega_\mathbf{0}$. We should notice that the solutions in $\Omega_\mathbf{0}$ are bounded, because $\boldsymbol{S^\tau} + \boldsymbol{V^\tau} + \boldsymbol{I}$ is bounded in Ω. We consider the following Lyapunov functional in $\Omega_\mathbf{0}$:

$$\boldsymbol{\phi(t)} = \boldsymbol{I(t)} + \boldsymbol{\beta e^{-\mu\tau}} \int_{t-\tau}^{t} \boldsymbol{S(t)\, I(t) dt} + \boldsymbol{\beta_1 e^{-\mu\tau}} \int_{t-\tau}^{t} \mathbf{V(t)\, I(t) dt}. \quad (10)$$

One can check that,

$$\dot{\boldsymbol{\phi}} = \boldsymbol{I(t)}(\boldsymbol{\beta e^{-\mu\tau} S(t) + \beta_1 e^{-\mu\tau} V(t) - \delta}).$$

Since $\boldsymbol{S} \leq \frac{\boldsymbol{b}}{\boldsymbol{d+\gamma}}$ in $\Omega_\mathbf{0}$, we can apply this to the second equation of (2), which gives $\boldsymbol{V} \leq \frac{\boldsymbol{b\gamma}}{\boldsymbol{(d+\alpha)(d+\gamma)}}$. Therefore, when $\boldsymbol{R_0} \leq \mathbf{1}$ for the solutions in $\Omega_\mathbf{0}$ we have

$$\dot{\boldsymbol{\phi}} \leq \boldsymbol{I(t)}\left(\boldsymbol{\beta e^{-\mu\tau}}\frac{\boldsymbol{b}}{\boldsymbol{d+\gamma}} + \boldsymbol{\beta_1 e^{-\mu\tau}}\frac{\boldsymbol{b\gamma}}{\boldsymbol{(d+\alpha)(d+\gamma)}} - \boldsymbol{\delta}\right) = \boldsymbol{I\delta(R_0 - 1) \leq 0}.$$

By Lyapunov-LaSalle asymptotic stability Theorem (see Hale [16] and Kuang [18]) it remains to find the maximal invariant set in $\{\dot{\boldsymbol{\phi}} = \mathbf{0}\}$, which in this case is equivalent to $\boldsymbol{\varphi_3(0)} = \mathbf{0}$. In addition, notice that the points in maximal invariant set should satisfy $\boldsymbol{\varphi_3(-\tau)} = \mathbf{0}$. Therefore, in $\Omega_\mathbf{0}$ the system becomes:

$$\dot{\boldsymbol{S}} = \boldsymbol{b} - \boldsymbol{dS(t)} - \boldsymbol{\gamma S(t)},$$
$$\dot{\boldsymbol{V}} = \boldsymbol{\gamma S(t)} - \boldsymbol{dV(t)} - \boldsymbol{\alpha V(t)}. \quad (11)$$

By applying the Bendixson criteria we conclude that the system does not have any limit cycle. Hence, according to the Poincare´-Bendixson Theorem, all solutions tend to the unique equilibrium of the system that is $\boldsymbol{P_0}$. In addition, for $\boldsymbol{M} = \{\boldsymbol{\Phi} \in \Omega : \dot{\boldsymbol{\Phi}} = \mathbf{0}\}$, we have $\boldsymbol{M} \subseteq \Omega_\mathbf{0}$, and the largest invariant set in M is $\{\boldsymbol{P_0}\}$.

Now, when $\boldsymbol{R_0 = 1}, \dot{\boldsymbol{\phi}} = \mathbf{0}$ is equivalent to $\boldsymbol{\varphi_3(0) = 0}$ or $\boldsymbol{\beta e^{-\mu\tau} S(t) + \beta_1 e^{-\mu\tau} V(t) - \delta = 0}$. Since $\boldsymbol{\beta e^{-\mu\tau} S(t) + \beta_1 e^{-\mu\tau} V(t) - \delta \leq \delta(R_0 - 1) = 0}$, the equality occurs when $\boldsymbol{\varphi_1} \equiv \frac{\boldsymbol{b}}{\boldsymbol{d+\gamma}}$ and $\boldsymbol{\varphi_2} \equiv \frac{\boldsymbol{b\gamma}}{\boldsymbol{(d+\alpha)(d+\gamma)}}$. Thus, the points in invariant set should satisfy $\dot{\boldsymbol{S}} = \mathbf{0}$ and $\dot{\boldsymbol{V}} = \mathbf{0}$. In this situation, by considering the first equation of (3), we conclude that $\boldsymbol{I(t)} = \mathbf{0}$, when $\boldsymbol{\varphi_1} \equiv \frac{\boldsymbol{b}}{\boldsymbol{d+\gamma}}$. Therefore, when $\boldsymbol{R_0} = \mathbf{1}$ the maximal invariant set is again M. Therefore, by applying Lyapunov-LaSalle asymptotic stability theorem, $\boldsymbol{P_0}$ is globally stable.

3.2. Global stability of the endemic point

The stability analysis of the endemic equilibria is more challenging, and many authors examine it through numerical simulation, [5, 8]. In this section, we will establish the global stability of the endemic equilibrium.

Before introducing the Lyapunov functional we need to define the function $\boldsymbol{h(x)} = \boldsymbol{x - 1 - ln(x)}$, for $\boldsymbol{x(t)} > \mathbf{0}$. We can see that it is a non-negative function, and $\boldsymbol{h(x)} = \mathbf{0}$ if and only if, $\boldsymbol{x} = \mathbf{1}$. Moreover, note that $\boldsymbol{S^* h(\frac{S(t-\tau)}{S^*})} \geq \mathbf{0}$, $\boldsymbol{V^* h(\frac{V(t-\tau)}{V^*})} \geq \mathbf{0}$ and $\boldsymbol{I^* h(\frac{I(t)}{I^*})} \geq \mathbf{0}$. From now on we will use $\boldsymbol{S^\tau}$, $\boldsymbol{V^\tau}$ and $\boldsymbol{I^\tau}$ instead of $\boldsymbol{S(t-\tau), V(t-\tau), I(t-\tau)}$.

Theorem 3.3. If $\mathbf{R_0} > \mathbf{1}$, then the endemic equilibrium, $\mathbf{P}^*$, is globally asymptotically stable.

Proof: We define a Lyapunov functional for $\boldsymbol{P}^*$ by

$$\boldsymbol{U = U_1 + U_2},\tag{12}$$

where

$$\boldsymbol{U_1 = \left(S^* h\left(\frac{S^\tau}{S^*}\right) + V^* h\left(\frac{V^\tau}{V^*}\right)\right) + e^{\mu\tau} I^* h\left(\frac{I(t)}{I^*}\right)},$$

$$\boldsymbol{U_2 = (\beta S^* I^* + \beta_1 V^* I^*) \int_{t-\tau}^{t} h\left(\frac{I(t)}{I^*}\right) dt}.\tag{13}$$

The time derivative of $\boldsymbol{U_1}$ along the solution of system (3) satisfies**:**

$$\begin{aligned}\dot{U}_1 = {} & b - dS^\tau - \beta S^\tau I^\tau - \gamma S^\tau - b\frac{S^*}{S^\tau} + dS^* + \beta I^\tau S^* \\ & + \gamma S^* + \gamma S^\tau - \beta_1 V^\tau I^\tau - dV^\tau - \alpha V^\tau - \gamma S^\tau \frac{V^*}{V^\tau} \\ & + \beta_1 I^\tau V^* + dV^* + \alpha V^* + \beta S^\tau I^\tau + \beta_1 V^\tau I^\tau \\ & - e^{\mu\tau}\delta I(t) - \beta S^\tau I^\tau \frac{I^*}{I(t)} - \beta_1 V^\tau I^\tau \frac{I^*}{I(t)} + e^{\mu\tau}\delta I^* \\ & = dS^*\left(2 - \frac{S^*}{S^\tau} - \frac{S^\tau}{S^*}\right) \\ & + \gamma S^*\left(3 - \frac{S^*}{S^\tau} - \frac{S^\tau V^*}{V^\tau S^*} - \frac{V^\tau}{V^*}\right) \\ & + \beta S^* I^*\left(2 - \frac{S^*}{S^\tau} - \frac{S^\tau I^\tau}{S^* I(t)}\right) \\ & + \beta_1 V^* I^*\left(\frac{V^\tau}{V^*} - \frac{V^\tau I^\tau}{V^* I(t)}\right) + \beta S^* I^\tau + \beta_1 V^* I^\tau \\ & + \beta S^* I(t) - \beta_1 V^* I(t).\end{aligned}\tag{14}$$

Similarly the time derivative of $\boldsymbol{U_2}$ along the solution of system (3) satisfies:

$$\begin{aligned}\dot{U}_2 = {} & \beta S^* I(t) - \beta S^* I^\tau - \beta S^* I^* \ln\left(\frac{I(t)}{I^*}\right) \\ & + \beta S^* I^* \ln\left(\frac{I(t)}{I^*}\right) \\ & + \beta_1 V^* I(t) - \beta_1 V^* I^\tau \\ & - \beta_1 V^* I^* \ln\left(\frac{I(t)}{I^*}\right) + \beta_1 V^* I^* \ln\left(\frac{I^\tau}{I^*}\right).\end{aligned}\tag{15}$$

Combining 14 and 15, we obtain:

$$\begin{aligned}\dot{U} = {} & dS^*\left(2 - \frac{S^*}{S^\tau} - \frac{S^\tau}{S^*}\right) + dV^*\left(3 - \frac{S^*}{S^\tau} - \frac{S^\tau V^*}{V^\tau S^*} - \frac{V^\tau}{V^*}\right) \\ & + \beta_1 V^* I^*\left(1 - \frac{V^\tau I^\tau}{V^* I(t)} + \ln\left(\frac{V^\tau I^\tau}{V^* I(t)}\right)\right) \\ & + \beta S^* I^*\left(1 - \frac{S^\tau I^\tau}{S^* I(t)} + \ln\left(\frac{S^\tau I^\tau}{S^* I(t)}\right)\right) \\ & + \beta_1 V^* I^*\left(1 - \frac{S^\tau V^*}{V^\tau S^*} + \ln\left(\frac{S^\tau V^*}{V^\tau S^*}\right)\right) \\ & + (\beta_1 V^* I^* + \beta S^* I^*)\left(1 - \frac{S^*}{S^\tau} + \ln\left(\frac{S^*}{S^\tau}\right)\right).\end{aligned}$$

By inequality of arithmetic and geometric means, it is clear that

$$\boldsymbol{2 - \frac{S^*}{S^\tau} - \frac{S^\tau}{S^*} \le 0}, \text{ and } \boldsymbol{3 - \frac{S^*}{S^\tau} - \frac{S^\tau V^*}{V^\tau S^*} - \frac{V^\tau}{V^*} \le 0}.\tag{16}$$

Recall that $\boldsymbol{h(x) \ge 0}$ for $\boldsymbol{x \ge 0}$ and $\boldsymbol{h(x) = 0}$ if and only if, $\boldsymbol{x = 0}$, therefore, $\boldsymbol{\dot{U} \le 0}$ and the equality occurs when $\boldsymbol{\varphi_1 \equiv S^*, \varphi_2 \equiv V^*}$ and $\boldsymbol{\varphi_3(0) = \varphi_3(-\tau)}$. By applying Lyapunov-LaSalle asymptotic stability Theorem (see Hale [16] and Kuang [18]), solutions tend to the largest invariant subset of $\boldsymbol{M = \{\dot{U} = 0\}}$. From the third equation of (2), we can say that in all points of $\boldsymbol{M}$, $\boldsymbol{\dot{I}}$ satisfies**:**

$$\boldsymbol{\dot{I} = \beta e^{-\mu\tau} S^* I^\tau + \beta_1 e^{-\mu\tau} V^* I^\tau - \delta I^\tau = 0}$$

It implies that $\boldsymbol{\varphi_3}$ is a constant function in M. Since $\boldsymbol{\dot{S} = 0}$ for each point of $\boldsymbol{M}$, we obtain that $\boldsymbol{I(t) = I^*}$ for all t, hence we have $\boldsymbol{M = \{(S^*, V^*, I^*)\}}$. Now since the solutions are bounded in $\boldsymbol{\theta}$, by the LaSalle's invariant principle, the global asymptotic stability of $\boldsymbol{P^*}$ follows.

3.3. Dynamics of general model

The above analysis resolves the global stability of the system (2)**,** which is a subsystem of (1). Now we show that the above mentioned results are valid for the original system (1) too**.** Both $\boldsymbol{E(t)}$ and $\boldsymbol{R(t)}$ satisfy equations of the following form

$$\boldsymbol{\dot{x} = f(t) - ax}.$$

It is easy to see that if $\boldsymbol{\lim_{t\to\infty} f(t) = M}$, then $\boldsymbol{\lim_{t\to\infty} x(t) = \frac{M}{a}}$.

Now consider the equation for exposed and recovered individuals

$$\begin{aligned}\dot{E} = {} & \beta S(t) I(t) + \beta_1 V(t) I(t) - \beta e^{-\mu\tau} S(t - \tau) I(t - \tau) \\ & - \beta_1 e^{-\mu\tau} V(t - \tau) I(t - \tau) - \mu E(t), \\ \dot{R} = {} & \alpha V(t) + \delta_1 I(t) - dR(t).\end{aligned}$$

When $\boldsymbol{R_0 > 1}$, by Theorem 3.3, we know that I(t) and $\boldsymbol{I(t-\tau), S(t)}$ and $\boldsymbol{S(t-\tau)}$, and $\boldsymbol{V(t)}$ and $\boldsymbol{V(t-\tau)}$ converge to positive constants $\boldsymbol{I^*}$, $\boldsymbol{S^*}$ and $\boldsymbol{V^*}$, respectively. Thus

$$\begin{aligned}\lim_{t\to\infty} E(t) = E^* = \frac{1}{\mu}(\beta(1 - e^{-\mu\tau}) S^* I^* \\ + (1 - e^{-\mu\tau})\beta_1 V^* I^*), \\ \lim_{t\to\infty} R(t) = R^* = \frac{1}{d}(\alpha V^* + \delta_1 I^*).\end{aligned}$$

When $\boldsymbol{R_0 \le 1}$, similar argument leads to $\boldsymbol{\lim_{t\to\infty} E(t) = 0}$ and $\boldsymbol{\lim_{t\to\infty} R(t) = \frac{\alpha V_0}{d}}$. Therefore, the following theorem has been proved**.**

Theorem 3.4. (i) When $\mathbf{R_0 \le 1}$, the DFE of the system (1) is globally stable.
(ii) When $\mathbf{R_0 > 1}$, the endemic equilibrium of the system (1) is globally asymptotically stable.

4. Conclusion and some numerical simulation

Throughout this paper, we considered an SVEIR epidemic model with time delay and obtained global stability results in terms of the basic

reproduction number, $\boldsymbol{R_0}$. More specifically, when $\boldsymbol{R_0 \leq 1}$, the disease will die out, and when $\boldsymbol{R_0 > 1}$, the endemic equilibrium of the system is globally asymptotically stable, and the disease will always exist.

In this section, we provide some numerical simulations of the system to visualize the dynamical behavior of the model. In Fig. 1, the parameters are chosen such that $\boldsymbol{R_0 < 1}$. Hence $\boldsymbol{P_0}$ is globally stable, and the disease extinct, ($\boldsymbol{R_0 = 0.52}$). In Fig. 2, the parameters are chosen such that $\boldsymbol{R_0 > 1}$. Hence $\boldsymbol{P^*}$ is globally stable and the disease persists, ($\boldsymbol{R_0 = 1.32}$).

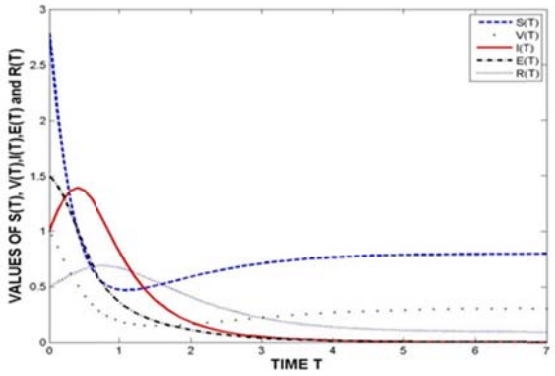

Fig. 1. Movement paths of *S; V; I; E* and *R* as functions of time *t*. Here, b = $\boldsymbol{1.2}$, $\boldsymbol{\beta = 105}$, $\boldsymbol{\beta_1 = 1.2}$, $\boldsymbol{\mu = 1.015}$, $\boldsymbol{\gamma = 0.5}$, $\boldsymbol{\tau = 0.2}$, $\boldsymbol{\alpha = 0.3}$ and $\boldsymbol{\delta_1 = 0.55}$

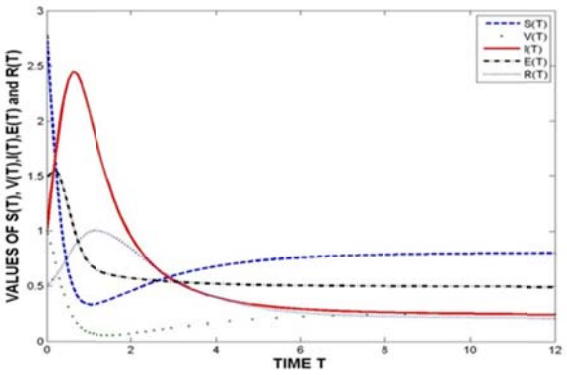

Fig. 2. Movement paths of *S; V; I; E* and *R* as functions of time *t*. Here, $\boldsymbol{b = 1.5}$, $\boldsymbol{\beta = 1.5}$, $\boldsymbol{\beta_1 = 1.2}$, $\boldsymbol{\mu = 0.0015}$, $\boldsymbol{\delta = 1.5115}$, $\boldsymbol{d = 1}$, $\boldsymbol{\gamma = 0.\tau = 0.2}$, $\boldsymbol{\alpha = 0.3}$ and $\boldsymbol{\delta_1 = 0.55}$

In Fig. 3 the parameters are chosen such that $\boldsymbol{R_0 = 1}$. Hence P_0 is globally stable and the disease extinct. The basic reproduction number also governs the convergence rate of the solutions to the DFE, when $\boldsymbol{R_0 \leq 1}$. More specifically, the closer $\boldsymbol{R_0}$ to one, the slower the extinction of the disease. Thus, it is more efficient to decrease $\boldsymbol{R_0}$ for a short time, in order to decrease the number of infected individuals more rapidly. To illustrate let $\boldsymbol{b = 2, \beta = 10}$, $\boldsymbol{\beta 1 = 8}$, $\mu = \boldsymbol{1.5, \delta = 2.55}$, $\boldsymbol{d = 1}$, $\boldsymbol{\tau = 0.5}$, $\boldsymbol{\alpha = 4.15}$ and $\boldsymbol{\delta 1 = 0.5}$, and $\boldsymbol{\gamma}$ be the control parameter. When $\boldsymbol{\gamma = 8}$ the basic reproduction number is $\boldsymbol{R0 = 0.92}$, and the graph of I(t) is depicted in Fig. 4. Now we assume that $\boldsymbol{\gamma}$ varies as follows

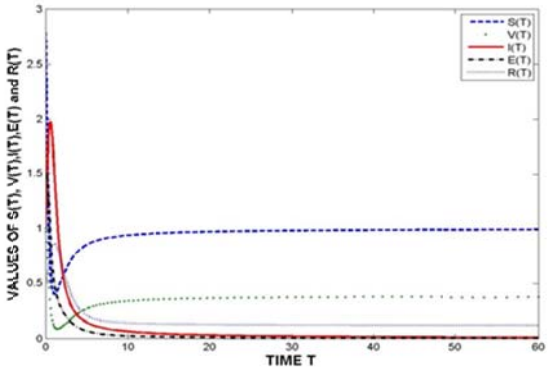

Fig. 3. Movement paths of S; V; I; E and R as functions of time t. Here, $\boldsymbol{b = 1.5}$, $\boldsymbol{\beta = 1.5345}$, $\boldsymbol{\beta_1 = 1.2}$, $\boldsymbol{\mu = 0.615}$, $\boldsymbol{\delta = 1.765}$, $\boldsymbol{d = 1}$, $\boldsymbol{\gamma = 0.5}$, $\boldsymbol{\tau = 0.2}$, $\boldsymbol{\alpha = 0.3}$, and $\boldsymbol{\delta_1 = 0.55}$

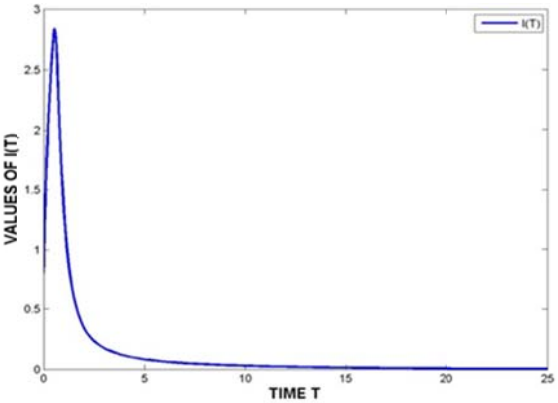

Fig. 4. Movement path of *I* as a function of time *t*. Here, $\boldsymbol{b = 2}$, $\boldsymbol{\beta = 10}$, $\boldsymbol{\beta_1 = 8}$, $\boldsymbol{\mu = 1.5}$, $\boldsymbol{\delta = 2.55}$, $\boldsymbol{d = 1}$, $\boldsymbol{\gamma = 8}$, $\boldsymbol{\tau = 0.5}$, $\boldsymbol{\alpha = 4.15}$ and $\boldsymbol{\delta_1 = 0.5}$

$$\boldsymbol{\gamma = -20000(|t - 0.501| - |t - 0.5| + |t - 7| - |t - 7.001|) + 8.}$$

Figure 5 shows that the disease eliminates about three times faster when $\boldsymbol{\gamma}$ varies as above, in comparison with the case $\boldsymbol{\gamma = 8}$. The movement path of $\boldsymbol{\gamma}$ is depicted in Fig. 6. According to the definition of $\boldsymbol{\gamma}$ as a function of time, for $\boldsymbol{5.001 < t < 7}$, we have $\boldsymbol{\gamma = 48}$ and $\boldsymbol{R_0 = 0.63}$.

Figure 4, shows that when $\boldsymbol{\gamma = 8}$ the disease becomes extinct at about 20. In comparison, Fig. 5 shows that when $\boldsymbol{\gamma}$ varies, the disease becomes extinct at about 8.

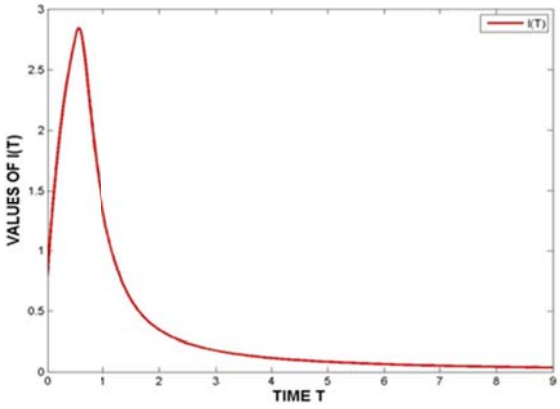

Fig. 5. Movement path of I as a function of time t. Here, $\boldsymbol{b = 2}$, $\boldsymbol{\beta = 10}$, $\boldsymbol{\beta_1 = 8}$, $\boldsymbol{\mu = 1.5}$, $\boldsymbol{\delta = 2.55}$, $\boldsymbol{d = 1}$, $\boldsymbol{\tau = 0.5}$, $\boldsymbol{\alpha = 4.15}$ and $\boldsymbol{\delta_1 = 0.5}$

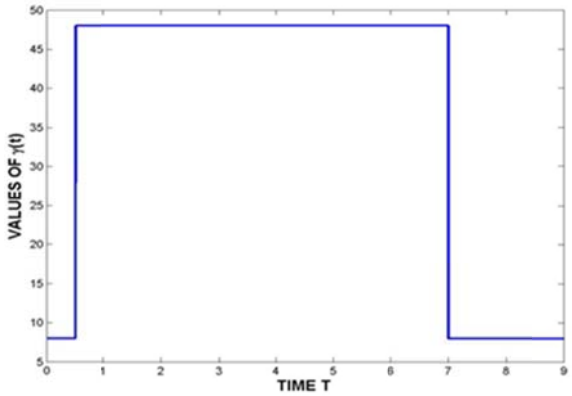

Fig. 6. Movement path of $\boldsymbol{\gamma}$ as a function of time t

Acknowledgments

This research was supported in part by a grant from the Institute for Research in Fundamental Sciences (IPM) (No 91920127).

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