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Analysis of an Epidemic Model with Vaccination and Non-monotonic Incidence Rate

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ABSTRACT

In this paper, an epidemic model with vaccination and non-monotonic incidence rate is considered. It also incorporated the roll of temporary immunity. The model exhibits the disease free and the endemic equilibria. Threshold R_0 determines the outcome of the disease. If $R_0 < 1$, the infection disappears and the disease-free equilibrium of the system is globally asymptotically stable. If $R_0 > 1$, the infection persists and the endemic equilibrium of the system is globally asymptotically stable under certain conditions. The global stability of endemic equilibrium is proved by using a geometric approach, based on generalization of Bendixson's criterion. Finally numerical simulations are provided in support of analytical results.

KEYWORDS: Endemic, incidence, basic reproduction number, stability, equilibrium.

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1. INTRODUCTION

Epidemic models have become important tools in analyzing the spread and control of infectious diseases. The most commonly used effective methods to control the spread of disease are quarantine, treatment and vaccination. Vaccination is a potentially reasonable approach and is usually used to control and prevent the spread of infectious disease[1, 2]. Many infectious diseases like measles, mumps, rubella, hepatitis B, influenza, tetanus are greatly reduced by the use of vaccination. Many clinical results[3] show that the vaccination does not give long time immunity to the disease. Thus, once a vaccine wanes from the body, the vaccinated person again becomes susceptible to the disease. Therefore, in order to prevent the infection and eradication of the disease, the optimal level of population should be vaccinated. In[4], a mathematical study of a model for childhood diseases with non-permanent immunity is presented and shown that the disease will persist within the population if the vaccination coverage level is below a certain threshold value. In[5], an SEIV epidemic model with a nonlinear incidence rate and a waning preventive vaccination is formulated and shown that there is always a backward bifurcation for increasing the rate at which infected individuals are treated. An epidemic model incorporating partial temporary immunity and saturated incidence rate is discussed in[6] and obtained the threshold vaccination coverage required to eradicate the disease.

In epidemic models, the incidence is the rate at which susceptible become infectious. Various incidence rates have been investigated and studied by researchers. Bilinear, nonlinear, standard, saturated, specific nonlinear, general incidence rates have been used in epidemic models and presented a detailed qualitative analysis of the models[7-12].

Motivated from the work of[6], we proposed an epidemic model with vaccination and non-monotonic incidence rate $\beta SI/(1+aI^2)$, which increases with small I and decreases with large I. In this incidence rate, βI measures the infection force of the disease and $1/(1+aI^2)$ measures the psychological effect from the behavioral change of the susceptibles when the number of infectives becomes large. This is important because the number of effective contacts between infectives and susceptible decreases at high infective levels due to the quarantine of infectives or the protective measures taken by the susceptible[12].

The organization of this paper is as follows: In the next section, we formulate the mathematical model. In section 3, we study the equilibrium states of model and derive the disease-free and endemic equilibrium. Also, we find the basic reproduction number by next generation matrix. In section 4, the

local stability analysis of equilibria is carried out. In section 5, the global analysis is discussed. Some numerical simulations with a brief discussion are provided in concluding section.

2. MATHEMATICAL MODEL

The proposed model is given by the following system of equations:

$$\left.\begin{aligned}
\frac{dS}{dt} &= (1-p)A - \frac{\beta SI}{1+aI^2} - \mu S + \theta V + (1-q)\gamma I \\
\frac{dE}{dt} &= \frac{\beta SI}{1+aI^2} - \mu E - \sigma E \\
\frac{dI}{dt} &= \sigma E - \mu I - \gamma I \\
\frac{dV}{dt} &= pA - \theta V - \mu V + q\gamma I
\end{aligned}\right\} \qquad (1)$$

with initial conditions $S(0), E(0), I(0), V(0) > 0$; where S, E, I and V denotes susceptible, exposed, infectious and vaccinated individuals. The total population at time t is given by $N = S + E + I + V$.

All the parameters A, β, θ, μ, γ, σ, p, q and a are positive constants. The constant A is the recruitment rate (including births and immigrations) of susceptible individuals, μ is the per capita natural death rate, β is the average number of adequate contacts of a person per unit time, θ is the rate at which vaccine wanes, γ is the rate at which infected individuals are treated or recovered, σ is the rate at which exposed individuals become infectious, p is the fraction of recruited individuals who are vaccinated ($0 \le p \le 1$), q is the fraction of recovered individuals getting disease acquired immunity ($0 \le q \le 1$) and a is the parameter measures the psychological or inhibitory effect of disease on the population when the number of infectives become larger.

3. EQUILIBRIUM POINTS AND BASIC REPRODUCTION NUMBER

In this section, we determine all equilibrium points and basic reproduction number. Here total population size $N = S + E + I + V$ and hence $N'(t) = A - \mu N$. As $t \to \infty$, N approaches to the carrying capacity A/μ . It follows that the solutions of the system (1) remains in the biologically meaningful region, defined by $\Omega = \left\{(S,E,I,V) \in R_4^+ : S,E,I,V \ge 0, S+E+I+V \le A/\mu\right\}$. Since solutions remain bounded in the positively invariant region Ω , the maximal interval is [0, ∞). Thus the initial value problem is well posed. The disease-free equilibrium of the system (1) is $P_0 = (S_0, 0, 0, V_0)$ and is given by

$$S_0 = \frac{A}{\mu}\left\{\frac{(1-p)\mu + \theta}{\mu + \theta}\right\}, \quad V_0 = \frac{Ap}{\mu + \theta} \qquad (2)$$

The basic reproduction number R_0 has been defined as the average number of secondary infections when one infective is entered into totally susceptible population[13]. It is one of the most useful parameters which determine whether or not an infection will spread through the population. We compute R_0 as described in[13]. Let $x=(E,I)$, then from (1), we have $x'=F-\overline{V}$, where

$$F=\begin{bmatrix}\beta SI/(1+aI^2)\\0\end{bmatrix}\quad,\quad \overline{V}=\begin{bmatrix}(\mu+\sigma)E\\-\sigma E+(\mu+\gamma)I\end{bmatrix}.$$

At disease-free equilibrium P_0 Jacobians of F and $\overline{V}$ are given by

$$F_0=\begin{bmatrix}0 & \beta S_0\\0 & 0\end{bmatrix}\quad,\quad \overline{V_0}=\begin{bmatrix}\mu+\sigma & 0\\-\sigma & \mu+\gamma\end{bmatrix}$$

The next generation matrix for the model (1) is

$$F_0\overline{V_0}^{-1}=\begin{bmatrix}\dfrac{\beta S_0\sigma}{(\mu+\gamma)(\mu+\sigma)} & \dfrac{\beta S_0}{(\mu+\gamma)}\\0 & 0\end{bmatrix}$$

The basic reproduction number of the model (1) is the spectral radius of $F_0\overline{V_0}^{-1}$, i.e., $R_0=\rho(F_0\overline{V_0}^{-1})$, i.e.

$$R_0=\frac{\beta\sigma S_0}{(\mu+\gamma)(\mu+\sigma)}=\frac{A\beta\sigma[(1-p)\mu+\theta]}{\mu(\mu+\gamma)(\mu+\sigma)(\mu+\theta)} \tag{3}$$

Now solving (1) for positive equilibria, we get $S=\frac{S_0}{R_0}(1+aI^2)$, $V=\frac{pA+q\gamma I}{\mu+\theta}$, $E=\left(\frac{\mu+\gamma}{\sigma}\right)I$ and I is given by the quadratic equation,

$$a_1I^2+a_2I+a_3=0 \tag{4}$$

Where, $a_1=a\mu(\mu+\theta)(\mu+\gamma)(\mu+\sigma)$

$a_2=\beta[(\mu+\theta)(\mu+\gamma)(\mu+\sigma)-\sigma\gamma\{(1-q)\mu+\theta\}]$

$a_3=\mu(\mu+\theta)(\mu+\gamma)(\mu+\sigma)(1-R_0)$

Here $a_1>0$ and $a_2>0$. Thus from equation (4) we can see that

(i) If $R_0\le 1$, then there is no positive equilibrium.

(ii) If $R_0>1$, then there is a unique positive equilibrium $P_*=(S_*,E_*,I_*,V_*)$, called the endemic equilibrium and is given by

$$S_* = \frac{S_0}{R_0}(1+aI_*^2)\,,\; V_* = \frac{pA+q\gamma I_*}{\mu+\theta}\,,\; E_* = \left(\frac{\mu+\gamma}{\sigma}\right)I_* \tag{5}$$

and $$I_* = \frac{-\beta[(\mu+\theta)(\mu+\gamma)(\mu+\sigma)-\sigma\gamma\{(1-q)\mu+\theta\}]+\sqrt{\Delta}}{2a\mu(\mu+\theta)(\mu+\gamma)(\mu+\sigma)} \tag{6}$$

where, $\Delta = \beta^2[(\mu+\theta)(\mu+\gamma)(\mu+\sigma)-\sigma\gamma\{(1-q)\mu+\theta\}]^2 - 4a\{\mu(\mu+\theta)(\mu+\gamma)(\mu+\sigma)\}^2(1-R_0)$

4. LOCAL STABILITY OF EQUILIBRIA

The original system (1) can be reduced to the three dimensional limiting system by using $S+E+I+V=A/\mu$. Thus, we focus on the reduced limiting system,

$$\left.\begin{aligned}
\frac{dS}{dt} &= \frac{A}{\mu}\{(1-p)\mu+\theta\} - \frac{\beta SI}{1+aI^2} - (\mu+\theta)S - \theta E + \{(1-q)\gamma-\theta\}I \\
\frac{dE}{dt} &= \frac{\beta SI}{1+aI^2} - (\mu+\sigma)E \\
\frac{dI}{dt} &= \sigma E - (\mu+\gamma)I
\end{aligned}\right\} \tag{7}$$

with initial conditions $S(0),E(0),I(0)>0$. Now we discuss the local stability for disease-free and endemic equilibrium.

Theorem 4.1. The disease-free equilibrium P_0 is locally asymptotically stable when $R_0<1$ and is unstable when $R_0>1$.

Proof . The Jacobian matrix of the reduced system (7) is given by

$$J = \begin{pmatrix}
-\frac{\beta I}{1+aI^2} - (\mu+\theta) & -\theta & -\frac{\beta S(1-aI^2)}{(1+aI^2)^2} + (1-q)\gamma - \theta \\
\frac{\beta I}{1+aI^2} & -(\mu+\sigma) & \frac{\beta S(1-aI^2)}{(1+aI^2)^2} \\
0 & \sigma & -(\mu+\gamma)
\end{pmatrix} \tag{8}$$

At disease-free equilibrium P_0, we have

$$J_0 = \begin{pmatrix}
-(\mu+\theta) & -\theta & -\beta S_0 + (1-q)\gamma - \theta \\
0 & -(\mu+\sigma) & -\beta S_0 \\
0 & \sigma & -(\mu+\gamma)
\end{pmatrix}$$

The characteristic equation of J_0 is

$$\{\lambda+(\mu+\theta)\}[\lambda^2+(2\mu+\sigma+\gamma)\lambda+(\mu+\sigma)(\mu+\gamma)(1-R_0)]=0 \tag{9}$$

It is obvious from (9) that, all the three eigen values of J_0 have negative real parts, if $R_0 < 1$. Hence disease-free equilibrium is locally asymptotically stable, if $R_0 < 1$. Also two eigen values of J_0 have negative real parts and one eigen value has positive real part, if $R_0 > 1$. Hence disease-free equilibrium is unstable in this case.

Theorem 4.2. If $R_0 > 1$, then the endemic equilibrium point P_* is locally asymptotically stable.

Proof. The Jacobian matrix of system (7) at the endemic equilibrium point P_* is given by

$$J_* = \begin{pmatrix} -\frac{\beta I_*}{1+aI_*^2} - (\mu+\theta) & -\theta & -\frac{\beta S_*(1-aI_*^2)}{(1+aI_*^2)^2} + (1-q)\gamma - \theta \\ \frac{\beta I_*}{1+aI_*^2} & -(\mu+\sigma) & \frac{\beta S_*(1-aI_*^2)}{(1+aI_*^2)^2} \\ 0 & \sigma & -(\mu+\gamma) \end{pmatrix}$$

The characteristic equation of J_* is $\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3 = 0$, where

$$A_1 = 3\mu + \sigma + \gamma + \theta + \frac{\beta I_*}{(1+aI_*^2)} ,$$

$$A_2 = 2a(\mu+\gamma)(\mu+\sigma)\frac{I_*^2}{(1+aI_*^2)} + (2\mu+\sigma+\gamma)\left(\mu+\theta+\frac{\beta I_*}{(1+aI_*^2)}\right) + \frac{\beta\theta I_*}{(1+aI_*^2)} ,$$

$$A_3 = \left[2a(\mu+\theta)(\mu+\gamma)(\mu+\sigma)I_* + \beta\{\theta(\mu+\gamma) + \sigma(q\gamma+\theta) + \mu(\mu+\sigma+\gamma)\}\right]\frac{I_*}{(1+aI_*^2)}$$

Also,

$$\begin{aligned} A_1A_2 - A_3 = {} & (3\mu+\theta+\gamma+\sigma)(2\mu+\sigma+\gamma)(\mu+\theta) \\ & + \{2a(\mu+\gamma)(\mu+\sigma)I_* + \beta(2\mu+\sigma+\gamma+\theta)\}\frac{\beta I_*^2}{(1+aI_*^2)^2} \\ & + [2a(\mu+\gamma)(\mu+\sigma)(2\mu+\sigma+\gamma)I_* \\ & + \beta\{7\mu^2+\sigma^2+\gamma^2+\theta^2+(5\mu+2\theta)(\sigma+\gamma)+6\mu\theta+\sigma\gamma(2-q)\}]\frac{I_*}{(1+aI_*^2)} \end{aligned}$$

Clearly $A_1 > 0, A_2 > 0, A_3 > 0$ and $A_1A_2 - A_3 > 0$. Then by the theorem of Routh-Hurwitz the endemic equilibrium point P_* is locally asymptotically stable.

5. GLOBAL STABILITY OF EQUILIBRIA

In this section, we examine the global stability of the disease-free and endemic equilibrium. To study the global stability of disease-free equilibrium, we use the method given in[14]. Rewrite the system (7) as

$$\left.\begin{aligned} \frac{dX}{dt} &= F(X,Z), \\ \frac{dZ}{dt} &= G(X,Z), \quad G(X,0)=0 \end{aligned}\right\}$$

where, $X=(S)\in R$ denotes the number of uninfected individuals and $Z=(E,I)\in R^2$ denotes the number of infected individuals including the exposed and the infectious. We denote the disease-free equilibrium by $Q_0=(X_0,0)$. The following conditions $(H1)$ and $(H2)$ are essential for the existence of global stability:

$(H1)$ For $\frac{dX}{dt}=F(X,0)$, X_0 is globally asymptotically stable,

$(H2)$ $G(X,Z)=BZ-\bar{G}(X,Z)$, where $\bar{G}(X,Z)\geq 0$, for $(X,Z)\in\Omega$,

where $B=D_zG(X_0,0)$ is an M-matrix (the off-diagonal elements of B are non-negative) and Ω is the biologically feasible region for the model. Then the following lemma holds:

Lemma 5.1. If $R_0<1$ and the assumptions $(H1)$ and $(H2)$ are satisfied, then the fixed point $Q_0=(X_0,0)$ is globally asymptotically stable.

Now we prove the following theorem:

Theorem 5.2. Suppose $R_0<1$, then the disease-free equilibrium P_0 is globally asymptotically stable.

Proof. Let $X=(S)$, $Z=(E,I)$ and $Q_0=(X_0,0)$, where $X_0=\frac{A\{(1-p)\mu+\theta\}}{\mu(\mu+\theta)}$. Then

$$\frac{dX}{dt}=F(X,Z)=\frac{A\{(1-p)\mu+\theta\}}{\mu}-\frac{\beta SI}{1+aI^2}-(\mu+\theta)S-\theta E+\{(1-q)\gamma-\theta\}I.$$

At $S=S_0$, $F(X,0)=0$ and $\frac{dX}{dt}=F(X,0)=\frac{A}{\mu}\{(1-p)\mu+\theta\}-(\mu+\theta)X$.

As $t\to\infty, X\to X_0$. Thus, $X=X_0(=S_0)$ is globally asymptotically stable. Now

$$G(X,Z)=\begin{bmatrix}-(\mu+\sigma) & \beta S_0\\ \sigma & -(\mu+\gamma)\end{bmatrix}\begin{bmatrix}E\\ I\end{bmatrix}-\begin{bmatrix}\beta S_0 I-\frac{\beta SI}{1+aI^2}\\ 0\end{bmatrix}=BZ-\bar{G}(X,Z),$$

Where, $B=\begin{bmatrix}-(\mu+\sigma) & \beta S_0\\ \sigma & -(\mu+\gamma)\end{bmatrix}$, $Z=\begin{bmatrix}E\\ I\end{bmatrix}$ and $\bar{G}(X,Z)=\begin{bmatrix}\beta S_0 I-\frac{\beta SI}{1+aI^2}\\ 0\end{bmatrix}$.

In the reduced system (7), total population is bounded by $(N_1)_0\to\frac{A\{(1-p)\mu+\theta\}}{\mu(\mu+\theta)}$, i.e. $S,E,I\leq(N_1)_0$.

Since $S_0\geq(N_1)_0$, we have $S_0\geq(N_1)_0\geq S\geq S/(1+aI^2)$, and hence $\bar{G}(X,Z)\geq 0$. Obviously, B represents an

M-matrix, so conditions $(H1)$ and $(H2)$ hold good and by Lemma 5.1 the disease-free equilibrium P_0 is globally asymptotically stable provided $R_0 < 1$. □

Next we investigate the global stability of the endemic equilibrium by using a geometrical approach developed in[15]. We will find simple sufficient conditions that the endemic equilibrium is globally asymptotically stable. Firstly we will briefly explain the geometrical approach method. Consider the autonomous system:

$$x' = f(x) \tag{10}$$

where $x \mapsto f(x) \in R^n$ is a C^1 function about x in $D \subset R^n$. Let $x(t, x_0)$ be the solution of (10) such that $x(0, x_0) = x_0$ and x^* be an equilibrium of (10), i.e. $f(x^*) = 0$. Assume that the following hypotheses hold:

$(H3)$ There is a compact absorbing set $K \subset D$.

$(H4)$ Differential equation (10) has a unique equilibrium x^* in D.

Let $x \to P(x)$ be a $\binom{n}{2} \times \binom{n}{2}$ matrix-valued function that is C^1 for $x \in D$. Assume that $P^{-1}(x)$ exists and is continuous for $x \in K$, the compact absorbing set. We define a quantity $\bar{q}$ as

$$\bar{q} = \limsup_{t \to \infty} \sup_{x \in K} \frac{1}{t} \int_0^t \eta(B(x(s, x_0)))ds, \tag{11}$$

where $B = P_f P^{-1} + PJ^{[2]}P^{-1}$, the matrix P_f is obtain by replacing each entry P_{ij} of P by its derivative in the direction of f and the matrix $J^{[2]}$ represents the second additive compound matrix of the Jacobian matrix J. The quantity $\eta(B)$ is the Lozinskiĭ measure of B with respect to a vector norm $|.|$ in R^N, $N = \binom{n}{2}$, defined by $\eta(B) = \lim_{h \to 0^+} \frac{|I + hB| - 1}{h}$.

The following global stability result is proved in Theorem 3.5 of [15].

Lemma 5.3. Suppose that D is simply connected and that assumptions $(H3)$ - $(H4)$ hold, then the unique equilibrium x^* of (10) is stable in D if $\bar{q} < 0$.

Now, we apply the theory given in[15], in particular Lemma 5.3, to prove the global stability of P_*.

Theorem 5.4. If $R_0 > 1, \sigma > \theta$ and $(1-q)\gamma \geq \theta$, then the endemic equilibrium P_* of the system (7) is globally stable in Ω.

Proof. It is clear from Theorem 4.2 that $R_0 > 1$ implies the existence and uniqueness (as an interior equilibrium) of the endemic equilibrium P_*, which is also locally asymptotically stable. From theorem

4.1 when $R_0 > 1$, P_0 is unstable. The instability of P_0, together with $P_0 \in \partial\Omega$ (boundary of Ω), implies the uniform persistence[16], i.e., there exists a constant $c > 0$ such that

$$\liminf_{t\to\infty} x(t) > c, \qquad x = S, E, I .$$

As Ω is bounded, the uniform persistence is equivalent to the existence of a compact set in the interior of Ω which is absorbing for the system (7)[17]. Hence, the condition $(H3)$ is satisfied. Now, the second additive compound matrix $J^{[2]}$ of the Jacobian matrix (8) is given by

$$J^{[2]} = \begin{pmatrix} -\frac{\beta I}{1+aI^2} - 2\mu - \theta - \sigma & \frac{\beta S(1-aI^2)}{(1+aI^2)^2} & \frac{\beta S(1-aI^2)}{(1+aI^2)^2} - (1-q)\gamma + \theta \\ \sigma & -\frac{\beta I}{1+aI^2} - 2\mu - \theta - \gamma & -\theta \\ 0 & \frac{\beta I}{1+aI^2} & -2\mu - \sigma - \gamma \end{pmatrix}$$

Choose the function $P = P(S,E,I) = \text{diag}\left\{1, \frac{E}{I}, \frac{E}{I}\right\}$. This shows that $P^{-1} = \text{diag}\left\{1, \frac{I}{E}, \frac{I}{E}\right\}$.

Also we have $P_f = \text{diag}\left\{0, \frac{E'I - EI'}{I^2}, \frac{E'I - EI'}{I^2}\right\}$. So that $P_f P^{-1} = diag\left\{0, \frac{E'}{E} - \frac{I'}{I}, \frac{E'}{E} - \frac{I'}{I}\right\}$. Then

$$B = P_f P^{-1} + PJ^{[2]}P^{-1}$$

$$= \begin{pmatrix} -\left(\frac{\beta I}{1+aI^2} + 2\mu + \theta + \sigma\right) & \frac{\beta S(1-aI^2)I}{(1+aI^2)^2 E} & \left\{\frac{\beta S(1-aI^2)}{(1+aI^2)^2} - (1-q)\gamma + \theta\right\}\frac{I}{E} \\ \sigma\frac{E}{I} & -\left(\frac{\beta I}{1+aI^2} + 2\mu + \theta + \gamma\right) + \frac{E'}{E} - \frac{I'}{I} & -\theta \\ 0 & \frac{\beta I}{1+aI^2} & -(2\mu + \sigma + \gamma) + \frac{E'}{E} - \frac{I'}{I} \end{pmatrix}$$

The matrix B can be written in block form as $B = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix}$, Where

$$B_{11} = -\left(\frac{\beta I}{1+aI^2} + 2\mu + \theta + \sigma\right), \quad B_{12} = \left[\frac{\beta S(1-aI^2)I}{(1+aI^2)^2 E}, \left\{\frac{\beta S(1-aI^2)}{(1+aI^2)^2} - (1-q)\gamma + \theta\right\}\frac{I}{E}\right],$$

and $B_{21} = \left[\frac{\sigma E}{I}, 0\right]^T$, $B_{22} = \begin{bmatrix} -\left(\frac{\beta I}{1+aI^2} + 2\mu + \theta + \gamma\right) + \frac{E'}{E} - \frac{I'}{I} & -\theta \\ \frac{\beta I}{1+aI^2} & -(2\mu + \sigma + \gamma) + \frac{E'}{E} - \frac{I'}{I} \end{bmatrix}$

Let (u,v,w) be a vector in R^3. We define a norm in R^3 as $|(u,v,w)|=\max\{|u|,|v|+|w|\}$ and let η be the Lozinskiĭ measure with respect to this norm. We have $\eta(B)\le Sup\{g_1,g_2\}$, where $g_1=\eta_1(B_{11})+|B_{12}|, g_2=\eta_1(B_{22})+|B_{21}|$ and $|B_{12}|,|B_{21}|$ are matrix norms with respect to the L^1 vector norm and η_1 denote the Lozinskiĭ measure with respect to the L^1 norm[18]. Then,

$$g_1=\eta_1(B_{11})+|B_{12}|$$

$$=-\left(\frac{\beta I}{1+aI^2}+2\mu+\theta+\sigma\right)+\max\left\{\frac{\beta S(1-aI^2)I}{(1+aI^2)^2E},\frac{\beta S(1-aI^2)I}{(1+aI^2)^2E}-\{(1-q)\gamma-\theta\}\frac{I}{E}\right\}$$

$$=-\left(\frac{\beta I}{1+aI^2}+2\mu+\theta+\sigma\right)+\frac{\beta S(1-aI^2)I}{(1+aI^2)^2E} \qquad [\text{when}\,(1-q)\gamma\ge\theta]$$

$$\le-\left(\frac{\beta I}{1+aI^2}+2\mu+\theta+\sigma\right)+\frac{\beta SI}{(1+aI^2)E}$$

$$\le\frac{E'}{E}-\mu-\theta-\frac{\beta I}{1+aI^2} \qquad [\text{from}\,(7)]$$

$$\le\frac{E'}{E}-\mu$$

To calculate $\eta_1(B_{22})$ we add the absolute value of the off-diagonal elements to the diagonal one in each column of B_{22}, and then take the maximum of two sums. Thus

$$g_2=\eta_1(B_{22})+|B_{21}|$$

$$=\max\left\{\frac{E'}{E}-\frac{I'}{I}-2\mu-\theta-\gamma,\frac{E'}{E}-\frac{I'}{I}-2\mu-\sigma-\gamma+\theta\right\}+\sigma\frac{E}{I}$$

$$=\frac{E'}{E}-\frac{I'}{I}-2\mu-\gamma+\max(-\theta,\theta-\sigma)+\sigma\frac{E}{I}$$

$$=\frac{E'}{E}-\mu+\max(-\theta,\theta-\sigma) \qquad [\text{from}\,(7)]$$

$$\le\frac{E'}{E}-\mu \qquad [\text{when}\,\sigma>\theta]$$

Therefore, $\eta(B)\le Sup\{g_1,g_2\}=\frac{E'}{E}-\mu$. Integrating both sides at the same time, we get

$$\frac{1}{t}\int_0^t\eta(B)ds\le\frac{1}{t}\log\frac{E(t)}{E(0)}-\mu,$$

which shows that $\bar{q} = \limsup_{t\to\infty} \sup_{x_0\in\Omega} \frac{1}{t}\int_0^t \eta(B(x(s,x_0)))ds \le -\mu < 0$. □

6. NUMERICAL SIMULATION AND CONCLUDING REMARKS

In this paper an SEIV model with non-monotonic incidence rate and partial temporary immunity is investigated. The basic reproduction number R_0 is given by (3). We have proved that if $R_0 < 1$, the disease-free equilibrium is globally asymptotically stable and if $R_0 > 1$, the endemic equilibrium is globally asymptotically stable under certain conditions. If $R_0 = 1$, then from the definition of R_0 we obtain the threshold vaccination coverage $p_v = (\mu+\theta)[\sigma\beta A - \mu(\mu+\sigma)(\mu+\gamma)]/\sigma\beta\mu A$. Clearly, if $p > p_v$, then $R_0 < 1$ and if $p < p_v$, then $R_0 > 1$. Thus the disease will be eradicated from the population if $p > p_v$, i.e., the vaccinated number must be greater than the threshold vaccination coverage; otherwise the disease will persist in the population.

Now we provide some numerical simulations by using MATLAB in support of the analytical findings of previous sections.

(i) Disease-free equilibrium: Considering the parameters in system (1) as A=4, μ=0.1, a=2, γ=0.2, θ=0.2, σ=0.1, β=0.01, q=0.5, p=0.2 , we get basic reproduction number $R_0 = 0.622 < 1$. Thus the conditions of the Theorem 4.1 and 5.2 are satisfied and the system (1) has a disease-free equilibrium $E_0 = (S_0, E_0, I_0, V_0) = (37.2, 0, 0, 2.67)$ and is globally asymptotically stable. In this case the disease disappears and dies out (see fig. 1).

(ii) Endemic equilibrium: Considering the parameters in system (1) as A=4, μ=0.2, a=2, γ=0.2, θ=0.1, σ=0.2, β=0.2, q=0.5, p=0.2 , we get basic reproduction number $R_0 = 4.3333 > 1$. Thus the conditions of the Theorem 4.2 and 5.4 are satisfied and the system (1) has an endemic equilibrium $E_* = (S_*, E_*, I_*, V_*) = (13.6688, 2.1987, 1.0994, , 3.03312)$ and is globally asymptotically stable. Thus the disease becomes endemic and persists in the population (see fig. 2).

(iii) Keeping all parameters fixed of endemic equilibrium and taking different initial conditions in limiting system (7), the phase portrait in SEI-space is displayed. This phase diagram shows that $\lim_{t\to\infty}(S(t), E(t), I(t)) = (S_*, E_*, I_*)$ for $R_0 = 4.3333 > 1$ (see fig. 3).

(iv) Taking all parameters of endemic equilibrium and varying the values of p, we see that increase in the values of p decreases the infected population. At $p = 0, \theta = 0$ i.e. without vaccination the size of infected population is high and at $p = 0.2, \theta = 0.1$ and $p = 0.4, \theta = 0.1$ i.e. increasing the

vaccination coverage, the size of infected population get decreases. This shows the effect of vaccination coverage on size of infected population with and without vaccination (see fig. 4).

(v) Though the basic reproduction number R_0 and p_v does not depend on q, numerical results show that when the disease is endemic, the steady-state value S_* of the susceptible population decreases as q increases. This indicates that q affects the size of the susceptible population and hence the dynamics of the system (see fig. 5).

(vi) On keeping all parameters fixed in endemic equilibrium and changing the values of a, we see that the steady-state values of I_* of the infectives decreases as a increases. This shows that the spread of disease decreases as the protective measures for the susceptible individuals increases (see fig. 6).

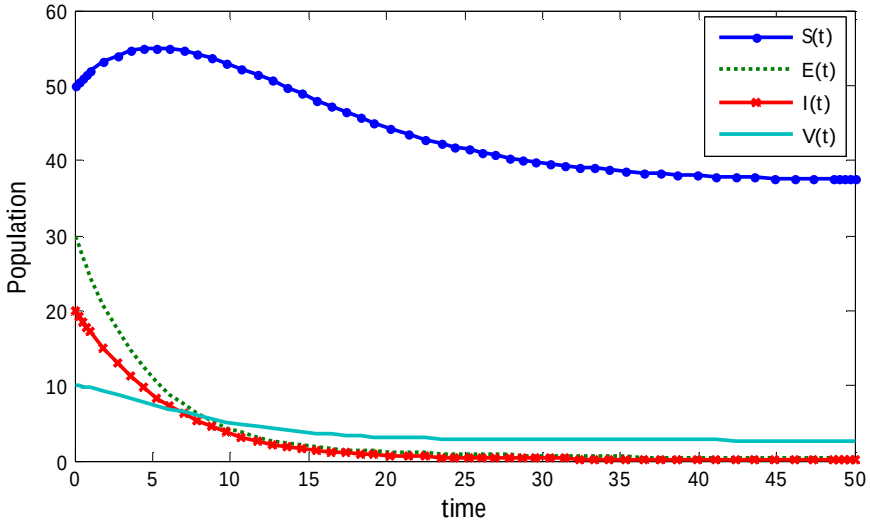

Figure 1: Disease-free equilibrium P_0 is globally asymptotically stable and disease dies out

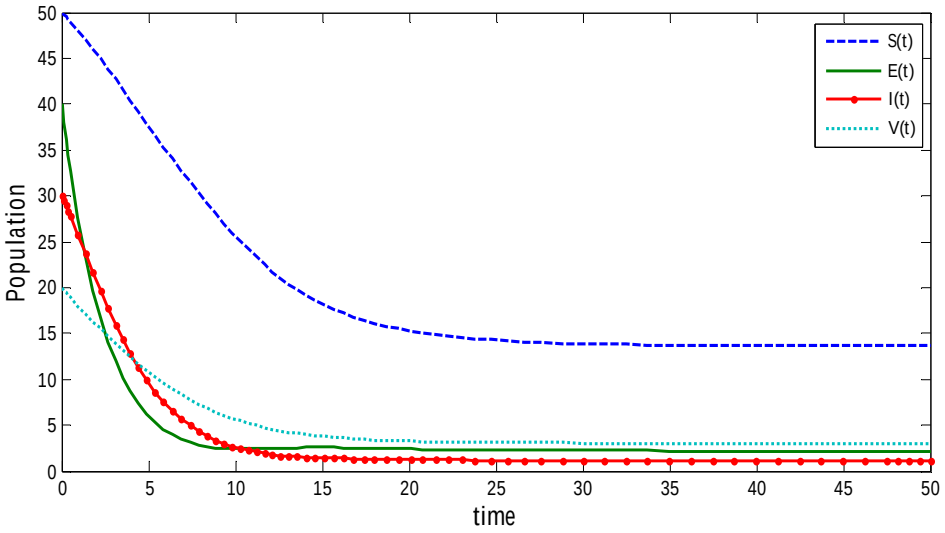

Figure 2: Endemic equilibrium P_* is globally asymptotically stable and disease persists

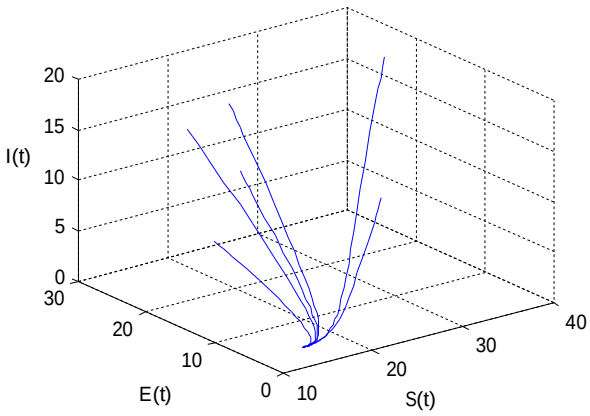

Figure 3: Phase portrait in SEI-space for endemic equilibrium.

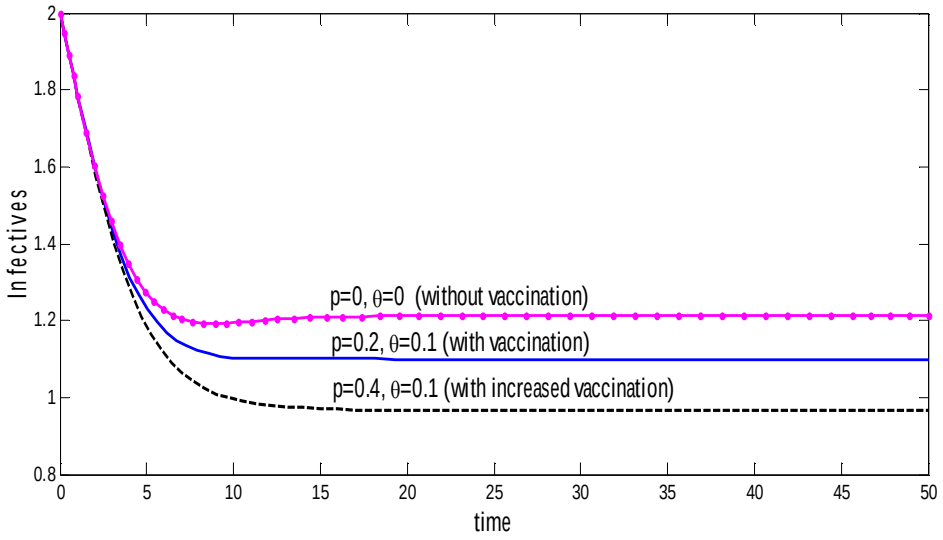

Figure 4: Effect of vaccination coverage on size of infected population.

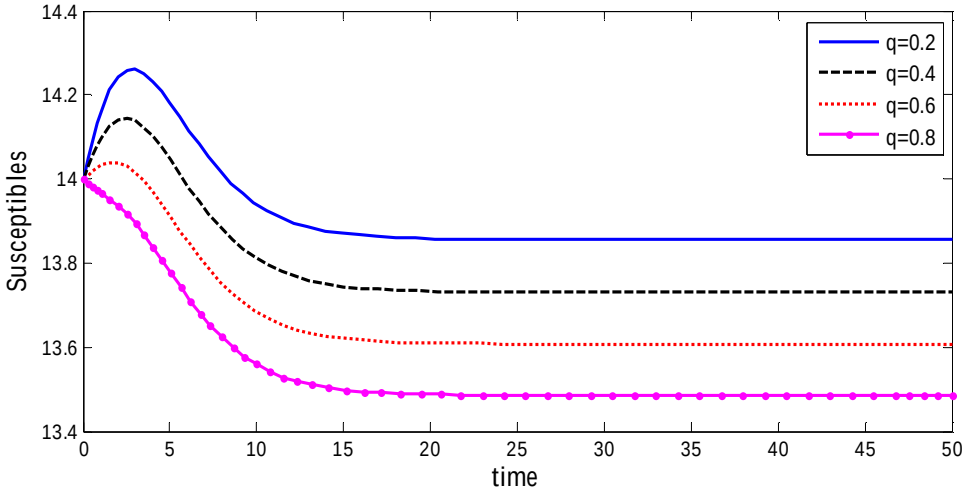

Figure 5: Effect of q on the size of the susceptible population.

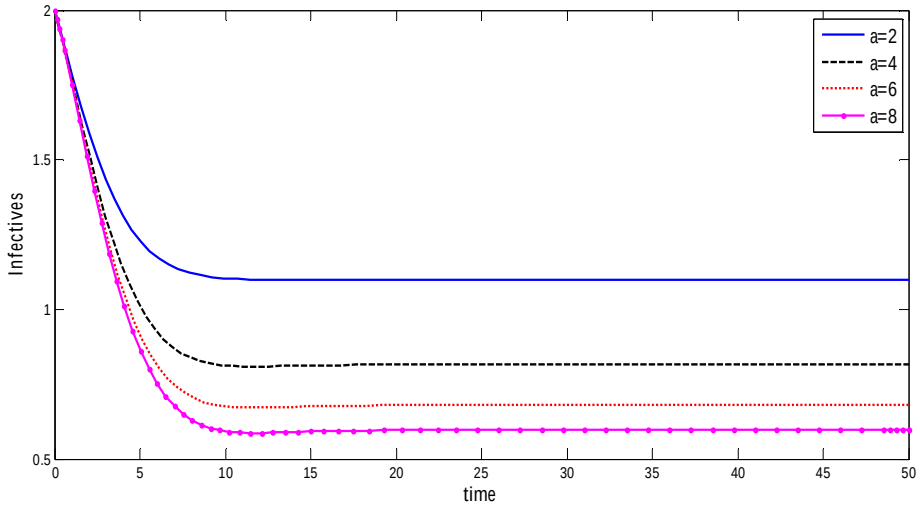

Figure 6: The steady-state values of I_* decreases as a increases.

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