

STABILITY ANALYSIS OF A SEIV EPIDEMIC MODEL WITH SATURATED INCIDENCE RATE

O. Adebimpe

Department of Mathematics and Physical Science,

Osun State University, Oshogbo, Nigeria

E-mail:olukayode.adebimpe@uniosun.edu.ng

ABSTRACT

In this paper, a SEIV epidemic model with saturated incidence rate that incorporates polynomial information on current and past states of the disease is investigated. The model exhibits two equilibria, disease-free equilibrium (DFE) and the endemic equilibrium (EE). It is shown that if the basic reproduction number, $R_0 < 1$, the DFE is locally asymptotically stable and by the use of Lyapunov function, DFE is globally asymptotically stable and in such a case, the EE is unstable. Moreover, if $R_0 > 1$, the endemic equilibrium is locally asymptotically stable. The effects of the rate at which vaccine wanes (ω) are investigated through numerical stimulations.

Mathematics Subject Classification: 34C05, 92D25

Keywords: SEIV epidemic model, saturated incidence rate, basic reproduction number, locally and globally stable.

Tel.: +2348060438613

E-mail address: olukayode.adebimpe@uniosun.edu.ng

1. INTRODUCTION

Vaccinating susceptible against disease infections is an effective measure to control and prevent the spread of the infection. Kribs-Zaleta and Velasco-Hemandez (2000) investigated SIS model with vaccination, standard incidence and no disease-induced deaths. Arino et al., (2003) formulated an SIRS model with vaccinations standard incidence and no disease-induced deaths. Li et al., (2006) studied an SIS model with vaccination, standard incidence and the disease induced death. Li and Ma (2002, 2004b) all analyzed global behaviour of simple SIS vaccination epidemic models under the condition that the vaccine is perfectly efficient. Li and Ma (2004a) introduced a vaccination compartment into an SIS model. They assumed that in vaccine takes effect in duration of length τ .

Long and Xiang (2011) studied an SEIV epidemic model with vaccination and vertical transmission. Their results were written in form of basic reproduction number, R_0 and they carried out a bifurcation analysis and obtain the conditions ensuring that the system exhibits backward bifurcation. Chika and Ezeofor (2011) extended Cai and Li (2009) model by incorporating important practical factors as the proportion of recruited individuals that are exposed or infectious, the recovery rate of exposed individuals and the mortality rate due to the infection. Abdulrazak et al. (2012) discussed a vaccination model with non-linear incidence rate and vaccination waning period like (Cai and Li, 2009) but they numerically simulated the model to see how variations in rate of the variables. Capasso and Serio (1978) introduced a saturated incidence rate $g(I)$ into epidemic models, where $g(I)$ tends to a saturation level when I gets large, i.e.

$$g(I) = \frac{kI}{1 + \alpha I} \text{ where } kI \text{ measures the infection force of the disease and } \frac{1}{1 + \alpha I} \text{ measures the}$$

inhibition effect from the behavioural change of the susceptible individuals when their number increases or from the crowding effect of the infective individual. In this paper, we extend the work of Cai and Li

(2009) to incorporate a saturated incidence rate as used by Capasso and Serio (1978).

$$\begin{aligned}
\frac{dS}{dt} &= (1-\rho)\pi - \frac{\beta SI}{1+\alpha I} - \mu S + \omega V \\
\frac{dE}{dt} &= \frac{\beta SI}{1+\alpha I} - (\mu + \sigma)E \\
\frac{dI}{dt} &= \sigma E - (\mu + \gamma)I \\
\frac{dV}{dt} &= \rho\pi - \mu V + \gamma I - \omega V
\end{aligned} \tag{1.1}$$

where

π = recruitment of individuals that includes new born and immigrants into the susceptible population S ,

ρ = fraction of recruited individuals who are vaccinated, β = **rate at which susceptible individual become infected by those who are infectious**, μ = natural death rate, σ = rate at which exposed

individuals become infectious so that $\frac{1}{\sigma}$ is the mean latent period. γ = rate at which infected

individuals are treated or recovered, $\frac{1}{1+\alpha(I)}$ = measurement of psychological or inhibition effect of the

behavioural change of the susceptible individuals when there is an increase in the number of infective

individuals, ω = rate at which vaccine wanes. The total population size $N(t)$ can be determined by

$N(t) = S(t) + E(t) + I(t) + V(t)$, and is a solution of the differential equation

$$\frac{dN(t)}{dt} = \pi - \mu N(t)$$

Therefore, in the rest of the paper, we will study (1.1) in the closed set

$$D = \left\{ (S(t), E(t), I(t), V(t)) \in R_+^4 \left| S(t) + E(t) + I(t) + V(t) \leq \frac{\pi}{\mu} \right. \right\}$$

2. THE BASIC REPRODUCTION NUMBER

It is easy to see that the region $\{(S, E, I, V), S > 0, I \geq 0, E \geq 0, V > 0\}$ is positively invariant for the model (1.1). Summing up the four equations in model (1.1), we have

$$\frac{d}{dt}(S + E + I + V) = \mu \left[\frac{\pi}{\mu} - (S + E + I + V) \right].$$

Then, $\limsup_{t \rightarrow \infty} (S + E + I + V) \leq \frac{\pi}{\mu}$. So, we study the dynamic behaviour of model (1.1) on the region

$$\Sigma = \{(S, E, I, V) \mid S > 0, I \geq 0, E \geq 0, V > 0, S + E + I + V \leq \frac{\pi}{\mu}\},$$

which is a positive invariant set for (1.1)

Corresponding to $E = I = 0$, model (1.1) always has a disease-free equilibrium,

$$P_0 = \left(\frac{(\mu + \omega - \rho\mu)\pi}{\mu(\mu + \omega)}, 0, 0, \frac{\rho\pi}{\mu + \omega} \right).$$

Let $x = (S, E, I, V)^T$. Then the model (1.1) can be written as $\frac{dx}{dt} = F(x) - V(x)$

$$\text{where } F(x) = \begin{pmatrix} \frac{\beta SI}{1 + \alpha I} \\ 0 \\ 0 \\ 0 \end{pmatrix}, \quad V(x) = \begin{pmatrix} \mu E + \sigma E \\ \gamma + \mu I - \sigma E \\ -(1 - \rho)\pi + \frac{\beta SI}{1 + \alpha I} - \omega V + \mu S \\ \mu V + \omega V - \rho\pi - \gamma \end{pmatrix}$$

We have

$$F = \begin{pmatrix} 0 & \beta S_0 \\ 0 & 0 \end{pmatrix} \quad V = \begin{pmatrix} \mu + \sigma & 0 \\ -\sigma & \mu + \gamma \end{pmatrix}$$

So,

$$V^{-1} = \begin{pmatrix} \frac{1}{\mu + \sigma} & 0 \\ \frac{\sigma}{(\mu + \sigma)(\mu + \gamma)} & \frac{1}{\mu + \gamma} \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} \frac{\sigma \beta S_0}{(\mu + \sigma)(\mu + \gamma)} & \frac{\beta S_0}{(\mu + \gamma)} \\ 0 & 0 \end{pmatrix}$$

In van den Driessche and Watmough (2002), the basic reproduction number is defined as the spectral radius of the next generation matrix

$$FV^{-1} \left(\rho(FV^{-1}) \right).$$

So, according to Theorem (2) in van den Driessche and Watmough (2002), the basic reproduction number of model (1.1), is

$$R_0 = \ell(FV^{-1}) = \frac{\sigma \beta S_0}{(\mu + \sigma)(\mu + \gamma)}$$

where
$$S_0 = \frac{(\mu + \sigma)(1 - \rho)\pi + \omega \rho \pi}{\mu(\mu + \omega)}$$

Therefore,

$$R_0 = \frac{\sigma\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)(\mu + \sigma)(\mu + \gamma)}$$

Note: The spectral radius $(\rho[FV^{-1}])$ is the dominant eigenvalue of the matrix FV^{-1} .

3. LOCAL AND GLOBAL STABILITY OF DISEASE FREE EQUILIBRIUM

$$\text{Let } x = S - S_0, \quad I = I, \quad E = E, \quad y = V - V_0 \quad (3.1)$$

Then, equation (1.1) becomes

$$\begin{aligned} \frac{dS}{dt} &= (1 - \rho)\pi - \beta I \left(x + \frac{(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi}{\mu(\mu + \omega)} \right) (1 + \alpha I)^{-1} - \\ &\quad \mu \left(x + \frac{(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi}{\mu(\mu + \omega)} \right) + \omega \left(y + \frac{\rho\pi}{\mu + \omega} \right) \\ \frac{dE}{dt} &= \beta I \left(x + \frac{(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi}{\mu(\mu + \omega)} \right) (1 + \alpha I)^{-1} - (\mu + \sigma)E \\ \frac{dI}{dt} &= \sigma E - (\mu + \gamma)I \\ \frac{dV}{dt} &= \rho\pi - (\mu + \omega) \left(y + \frac{\rho\pi}{\mu + \omega} \right) + \gamma I \end{aligned} \quad (3.2)$$

The Jacobian matrix of equation (3.2) after linearization is

$$A = \begin{pmatrix} -\mu & 0 & -\frac{\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} & \omega \\ 0 & -(\mu + \sigma) & \frac{\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} & 0 \\ 0 & \sigma & -(\mu + \gamma) & 0 \\ 0 & 0 & \gamma & -(\mu + \omega) \end{pmatrix}$$

$$\text{Let } \frac{\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} = \Gamma$$

$$|A - \lambda I| = \begin{vmatrix} -(\mu + \lambda) & 0 & -\Gamma & \omega \\ 0 & -(\mu + \sigma + \lambda) & \Gamma & 0 \\ 0 & \sigma & -(\mu + \gamma + \lambda) & 0 \\ 0 & 0 & \gamma & -(\mu + \omega + \lambda) \end{vmatrix} = 0$$

Therefore, $\lambda_1 = -\mu$, $\lambda_2 = -(\mu + \omega)$, and the roots of the quadratic

$$\lambda^2 + (2\mu + \sigma + \gamma)\lambda + \mu^2 + \mu\gamma + \sigma\mu + \sigma\gamma - \sigma\Gamma = 0$$

For negative roots, we must have by Descartes' rule of signs

$$\mu^2 + \mu\gamma + \sigma\mu + \sigma\gamma - \sigma\Gamma > 0$$

That is,

$$(\mu + \sigma)(\mu + \gamma) > \sigma\beta \frac{[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)}$$

$$\sigma\beta \frac{[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)(\mu + \sigma)(\mu + \gamma)} < 1$$

Therefore,

$$R_0 = \frac{\sigma\beta [(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)(\mu + \sigma)(\mu + \gamma)} < 1$$

Theorem 3.1: If $R_0 < 1$, the disease free equilibrium P_0 is locally asymptotically stable; if $R_0 = 1$, P_0 is stable; if $R_0 > 1$, P_0 is unstable

Proof: We shall check the stability of the disease-free equilibrium P_0 , from the model, thus the linearization of model of the disease-free equilibrium P_0 gives the following characteristics equation.

$$-(\mu + \lambda)(\mu + \omega + \lambda) \left[(\mu + \gamma + \lambda)(\mu + \sigma + \lambda) - \frac{\sigma\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} \right] = 0 \quad (3.3)$$

Thus, we have

$$-(\mu + \lambda)(\mu + \omega + \lambda) \left[\lambda^2 + (2\mu + \gamma + \sigma)\lambda + \mu^2 + \mu\gamma + \sigma\mu + \sigma\gamma - \frac{\sigma\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} \right] = 0 \quad (3.4)$$

From equation (3.4), it can be seen that $\lambda_1 = -\mu$, $\lambda_2 = -(\mu + \omega)$ are two of the eigenvalues and they are always negative. To obtain the other eigenvalues of equation (3.4) we consider the equation

$$\lambda^2 + (2\mu + \gamma + \sigma)\lambda + \mu^2 + \mu\gamma + \sigma\mu + \sigma\gamma - \frac{\sigma\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} = 0 \quad (3.5)$$

From equation (3.5) we see that all roots have negative real parts if

$$\mu^2 + \mu\gamma + \sigma\mu + \sigma\gamma - \frac{\sigma\beta[(\mu + \omega)(1 - \rho)\pi + \omega\rho\pi]}{\mu(\mu + \omega)} > 0$$

That is, if $R_0 < 1$.

$\therefore$ The disease-free equilibrium P_0 , is locally asymptotically stable.

If $R_0 = 1$, one eigenvalue of equation (3.5) is zero and it is simple. Then P_0 is stable.

If $R_0 > 1$, one of the roots of equation (3.5) has a positive real part, then P_0 is unstable.

Theorem 3.2: If $R_0 < 1$, the disease-free equilibrium P_0 is globally asymptotically stable in D .

Proof: Consider the Lyapunov function $L(t) = \sigma E + (\mu + \sigma) I$. Its derivative along the system

(1.1) is

$$L^1(t) = \frac{\sigma\beta S_0 I}{1 + \alpha I} - (\mu + \sigma)(\mu + \gamma)I$$

$$L^1(t) = \left[\frac{\sigma\beta S_0}{(1 + \alpha I)(\mu + \sigma)(\mu + \gamma)} - 1 \right] I$$

$$L^1(t) = \left[\frac{R_0}{(1 + \alpha I)} - 1 \right]$$

If $R_0 < 1$, $I \neq 0$, $L^1(t) < 0$

Therefore, disease-free equilibrium is globally asymptotically stable

4. LOCAL STABILITY OF THE ENDEMIC EQUILIBRIUM

It is a known fact that the disease is endemic if the infectious part of the population persists above a certain positive level for sufficiently large time. The disease is endemic if (1.1) is uniformly persistent (Butler and Waltman, 1986).

Theorem 1: $R_0 > 1$, then unique endemic equilibrium P_* of (1.1) is locally asymptotically stable in D .

Proof: The method of Routh-Hurwitz will be used to show the local asymptotic stability of the equilibrium, P_* . The Jacobian matrix of (1.1) at a point $D = (S(t), E(t), I(t), V(t))$ is

$$J(P) = \begin{bmatrix} -(\beta I_* + \mu) & 0 & -\beta S_* & \omega \\ \beta I_* & -(\mu + \sigma) & \beta S_* & 0 \\ 0 & \sigma & -(\mu + \gamma) & 0 \\ 0 & 0 & \gamma & -(\mu + \omega) \end{bmatrix} \begin{pmatrix} x \\ y \\ z \\ q \end{pmatrix} + \text{nonlinear terms}$$

It is proved that the matrix P is stable with all its eigenvalues have negative real parts. From the Jacobian matrix, the characteristics equation is

$$\lambda^3 + a_1 \lambda^2 + a_2 \lambda + a_3 = 0$$

where

$$a_1 = \sigma + \gamma + 3\mu + \beta I_* > 0$$

$$a_2 = 2\beta\mu I_* + \beta\sigma I_* + \beta\gamma I_* + 3\mu^2 + 2\mu\sigma + 2\mu\gamma + \sigma\gamma - \sigma\beta S_*$$

$$a_3 = \beta\mu^2 I_* + \beta\mu\gamma I_* + \beta\sigma\mu I_* + \beta\sigma\gamma I_* + \mu^3 + \mu^2\gamma + \mu^2\sigma + \mu\sigma\gamma - \sigma\beta\mu S_* - \omega\sigma\beta\gamma I_*$$

If $a_1 a_2 > a_3$ the endemic equilibrium P^* is locally asymptotically stable in D .

5. NUMERICAL SIMULATION

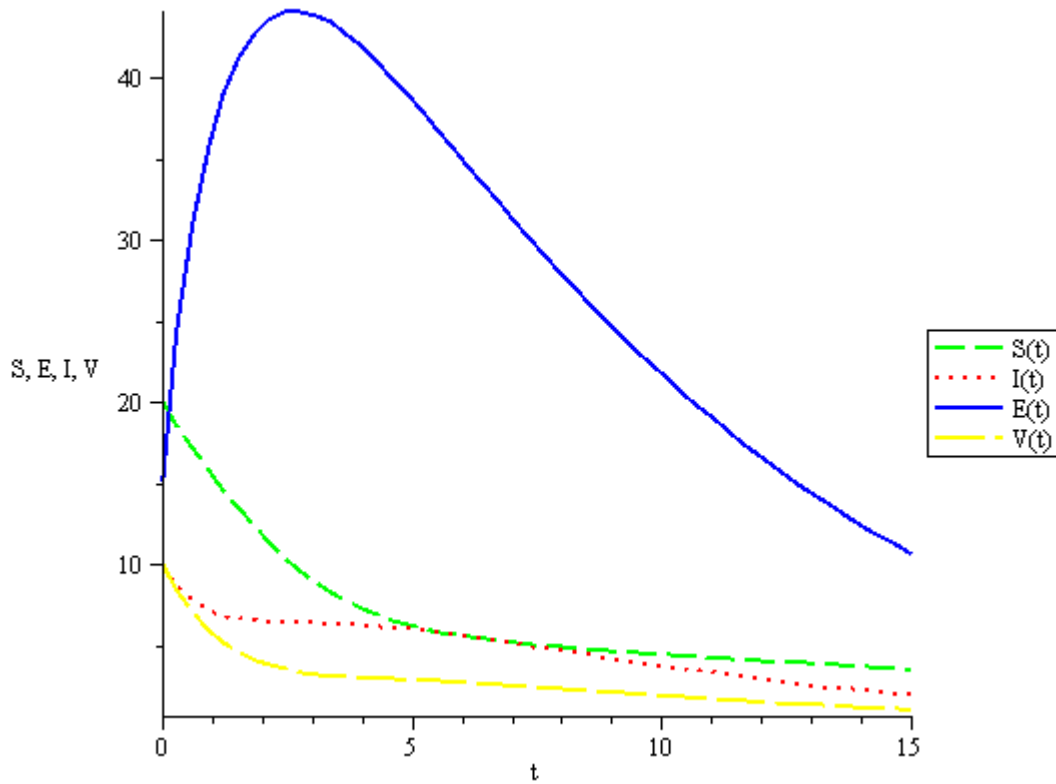


Figure 5.1: Graph of $S(t)$, $E(t)$, $I(t)$, $V(t)$ against time (t) when $\rho = 0.1$, $\pi = 0.2$, $\beta = 0.1$, $\alpha = 0.1$,

$\mu = 0.2$, $\omega = 0.9$, $\sigma = 0.1$, $\gamma = 0.5$

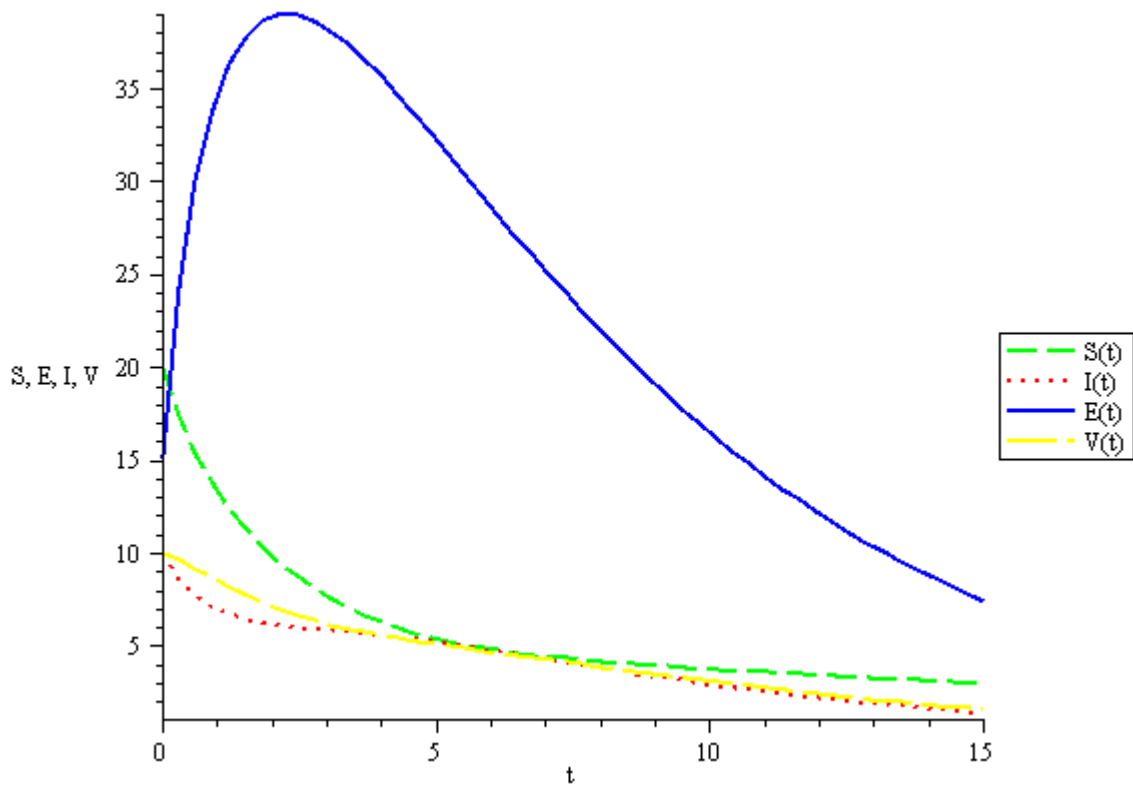


Figure 5.2: Graph of $S(t)$, $E(t)$, $I(t)$, $V(t)$ against time (t) when $\rho = 0.1$, $\pi = 0.2$, $\beta = 0.1$, $\alpha = 0.1$, $\mu = 0.2$, $\omega = 0.4$, $\sigma = 0.1$, $\gamma = 0.5$

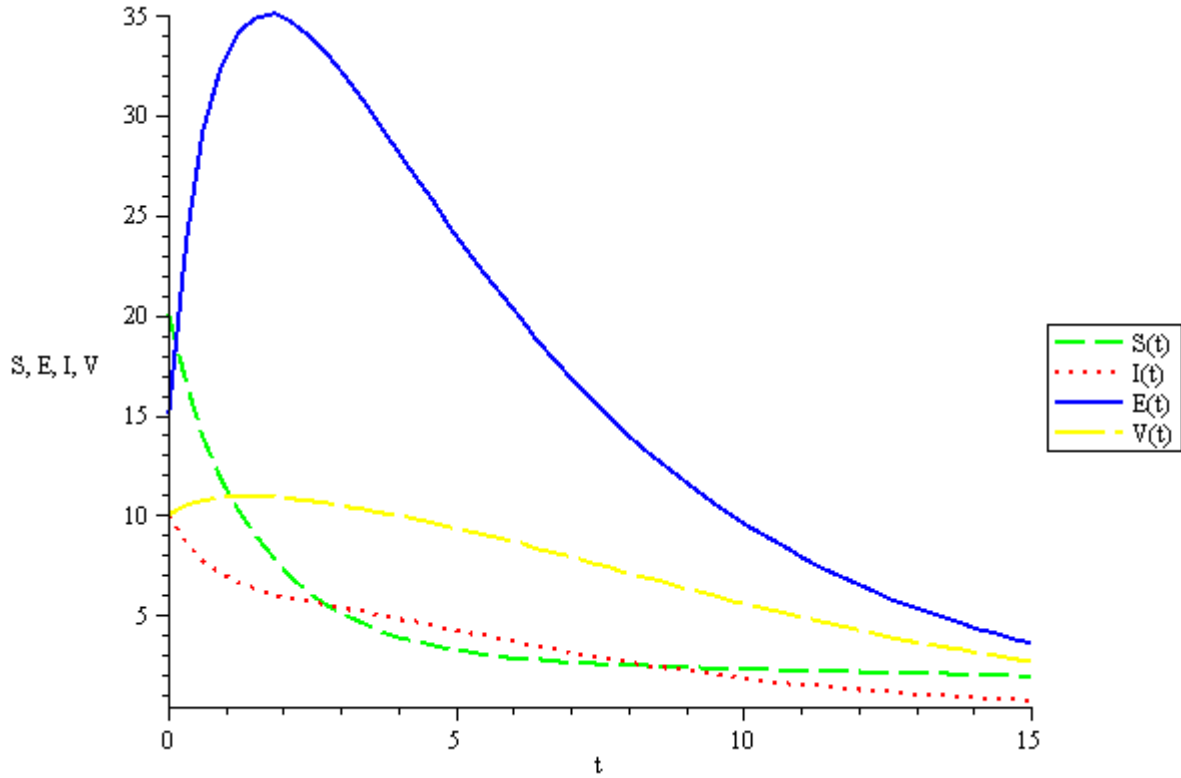


Figure 5.3: Graph of $S(t)$, $E(t)$, $I(t)$, $V(t)$ against time (t) when $\rho = 0.1$, $\pi = 0.2$, $\beta = 0.1$, $\alpha = 0.1$, $\mu = 0.2$, $\omega = 0.1$, $\sigma = 0.1$, $\gamma = 0.5$

6. CONCLUSION AND DISCUSSION

This paper has considered a SEIV model that incorporates an incidence rate of the form $\frac{\beta SI}{1 + \alpha I}$. We discussed the local and global stabilities of the disease-free equilibrium and as well as the local stability of the endemic equilibrium. We presented the results in the form of basic reproduction number, R_0 . The effects at which vaccine wanes were investigated and it is discovered that the smaller the value the greater the effect on the model. This implies that vaccination has a role to play in any disease eradication and that the rate at which vaccine wanes should be reduced to the bearest minimum for the vaccine to be effective in the population.

ACKNOWLEDGEMENT

The author acknowledged the support received from Institute of Mathematical Sciences (IMS), National University of Singapore (NUS), Singapore during his 2-month stay at the institute and also thank the anonymous referees for their useful feedback and helpful comments and suggestions which have improved the manuscript. The author wishes to dedicate the research work to the memory of his late supervisor and mentor, Professor Reuben Olafenwa Ayeni.

REFERENCES

1. Butler, G. J. and Waltman, P. (1986): Persistence in Dynamical Systems, J. Differential Equations, 63, pp., 225-263.
2. Kribs-Zaleta, C.M. and Velasco-Hernandez, J.K.: A simple vaccination model with multiple endemic states. Math Biosci (2000), 164:183-201.
3. Li, J. and Ma, Z. and Zhou, Y. : Global Analysis of SIS epidemic model with a simple vaccination and multiple endemic equilibria. Acta Math Sci (2006), 26B:83-93.
4. Arino, J., Mccluskey, C. C. and van den Driessche, P.: Global Results for an epidemic model with vaccination that exhibits backward bifurcation. SIAM J Appl Math (2003), 64: 260-276.
5. Li, J. and Ma, Z.: Qualitative analyzes of SIS epidemic model with vaccination and varying total population size. Math Comp Model (2002), 35: 1235-1243.
6. Li, J. and Ma, Z.: Stability analysis for SIS epidemic model with vaccination and constant population size. Disc Cont Dyn Sys (2004a), B 4: 637-644.
7. Li, J. and Ma, Z. : Global analysis of SIS epidemic models with variable total population size. Math Comput Model (2004b), 39: 1231-1242.
8. Cai, L. and Li, X.: Analysis of a SEIV epidemic model with a non-linear incidence rate. Applied Mathematical Modelling (2009), 33: 2919-2926.
9. Chika, M. and Ezeofor, O. V. : Extension and modification of an SEIV vaccination model. Journal of the Nigerian Mathematical Society, (2011), vol.30, pp. 163-177.
10. Abdulrazak, A. J., Ibrahim, M. O. and Usman, I. O. : A Seiv Vaccination Model with General Non-Linear Incidence Rate and Wanning Preventive Vaccine. IOSR Journal of Mathematics, (2012), volume 4, Issue 2, pp. 44-51
11. Capasso, V. and Serio, G.: A generalization of the Kermack-Mckendrick deterministic epidemic model, Math. Biosci. (1978) 42, pp. 43-61.
12. Long, D. and Xiang, Z.: On the study of an SEIV epidemic model concerning vaccination and vertical transmission, (2011), vol.1, no.1, pp. 21-30.
13. van den Driessche, P. and Watmough, J.: Reproduction numbers and sub- threshold endemic equilibria for compartmental models of disease transmission, Math, Biosci, (2002), 180, pp. 29-48.