

# Dynamical analysis of an epidemic model with saturated incidence rate and vaccination

A. W. Ogunsola <sup>1</sup>\*, O. Adebimpe <sup>2</sup>, B. A. Popoola <sup>3</sup>

<sup>1</sup> Department of Pure and Applied Mathematics, Ladoke Akintola University of Technology, Ogbomoso, Nigeria

<sup>2</sup> Department of Physical Sciences, Landmark University, Omuaran, Nigeria

<sup>3</sup> Department of Mathematics, Federal College of Education, Osiele, Nigeria

\*Corresponding author E-mail: amossolawale@yahoo.com

Copyright © 2014 A. W. Ogunsola et al. This is an open access article distributed under the <u>Creative Commons Attribution License</u>, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

### Abstract

An epidemic model with saturated incidence rate and vaccination is investigated. The model exhibits two equilibria namely disease-free and endemic equilibria. It is shown that if the basic reproduction number  $(R_0)$  is less than unity, the disease-free equilibrium is locally asymptotically stable and in such case, the endemic equilibrium does not exist. Also, it is shown that if  $R_0 > 1$ , the disease is persistent and the unique endemic equilibrium of the system with saturation incidence is locally asymptotically stable. Lyapunov function and Dulac's criterion plus Poincare-Bendixson theorem are applied to prove the global stability of the disease-free and endemic equilibria respectively. The effect of vaccine in the model is critically looked into.

Keywords: Basic Reproduction Number, Dulac's Criterion, Epidemic Model, Lyapunov Function, Poincare-Bendixson Theorem, Vaccination.

## 1. Introduction

Vaccinating susceptible against disease infections is an effective measure to control and prevent the spread of the infection. Kribs-Zaleta and Velasco Hernadez [1] investigated an SIS model with vaccination, standard incidence and no disease-induced diseases. Arino et al. [2] formulated an SIRS epidemic model with vaccination, standard incidence and no disease-induced deaths. Li et al. [3] studied an SIS model with vaccination, standard incidence and disease-induced deaths while Brauer [4] investigated an SIS model with vaccination, general incidence and no disease-induced death. Li and Ma [5], [6] also analyzed global behaviour of simple SIS vaccination epidemic models under the condition that the vaccine is perfectly efficient.

Adebimpe [7] investigated a SEIV epidemic model with saturated incidence rate that incorporates polynomial information on current and past states of the disease. He showed that if the basic reproduction number  $R_0 < 1$ , the

Disease-Free Equilibrium (DFE) is locally asymptotically stable and by the use of Lyapunov function, DFE is globally asymptotically stable and in such a case, the Endemic Equilibrium (EE) is unstable.

Adebimpe et al. [8] investigated the global stability of a SEIR epidemic model with saturating incidence rate. They identified a threshold  $R_0$  which determines the outcome of the disease. They used Dulac's criterion plus Poincare-Bendixson theorem and Lyapunov functions are used to prove the global stability of the disease-free and endemic equilibrium respectively.

Ullah et al. [9] investigated an epidemic model with a vaccination program. They determined the vaccine-induced reproduction number  $R_0(k)$  and discussed the impact of vaccination in reducing  $R_0(k)$ . Islam et al. [10] constructed a new deterministic model and used to analyze the effect of a preventive vaccine on the transmission dynamics of an infectious disease.

In this paper, we extend the work done by Islam et al. [10] to incorporate saturated incidence rate of the form

$$\frac{\rho SI}{1+mS+mI} \text{ as below:}$$

$$\frac{dS}{dt} = \delta - \frac{\beta SI}{1+\alpha S+\alpha I} - \gamma S - \mu S$$

$$\frac{dV}{dI} = \gamma S - \mu V - c \beta V I$$

$$\frac{dI}{dt} = c \beta V I - \frac{\beta SI}{1+\alpha S+\alpha I} - \mu I$$

$$I = \frac{1}{2}$$
(1)

Where S (t), V (t) and I (t) denote the number of the susceptible individuals, vaccinated individuals and recovered individuals respectively. All of the parameters are positive and have the following meaning:  $\pi$  is the recruitment of individuals (assumed susceptible) into the population,  $\mu$  is the natural death rate,  $\gamma$  is the rate of vaccination of the susceptible,  $\beta$  is the effective contact rate. Since the vaccine only provides partial protection to the infection, vaccinated individual may still become infected but at the lower rate  $c\beta$  than fully susceptible individuals. Here  $0 \ll 1$  and 1-C describes vaccine efficacy, when c=0, the vaccine is perfectly effective and has no effect on the immunity of vaccinated individuals at all when c=1.  $\alpha_1$  and  $\alpha_2$  Are the parameters that measure the effects of sociological, psychological or other mechanisms?

## 2. Local stability of the disease-free equilibrium

The model (1) has a disease-free equilibrium given by  $P_0 = \left(\frac{\delta}{\mu + \gamma}, 0, \frac{\gamma \delta}{\mu(\mu + \gamma)}\right)$ . It is obvious that  $P_0$  attracts the region

(stable manifold of  $P_0$ )

 $P_0 = \{(S, I, V) \in \varphi : I = 0\}$ 

The stability of this equilibrium  $P_0$  will be investigated using the linearization method governed by the basic reproduction number,  $R_0$ .

Now, by linearizing the system (1) about the point  $P_0$ , we have the following:

Let 
$$S = x + S_0 \cdot V = y + V_0 \cdot I = I$$
  

$$\frac{dx}{dt} = -\frac{\beta S_0 I}{1 + \alpha_1 S_0} - (\gamma + \mu) x + higher order terms$$

$$\frac{dy}{dt} = \gamma x - \mu y - c \beta V_0 I + higher order terms$$

$$\frac{dI}{dt} = c \beta V_0 I + \frac{\beta S_0 I}{1 + \alpha_1 S_0} - \mu I + higher order terms$$
(2)
The Jacobian matrix is
$$\begin{pmatrix} \frac{dx}{dt} \\ \frac{dI}{dt} \\ \frac{dy}{dt} \end{pmatrix} = \begin{pmatrix} -(\gamma + \mu) & -\frac{\beta S_0}{1 + \alpha_1 S_0} & 0 \\ 0 & c \beta V_0 + \frac{\beta S_0}{1 + \alpha_1 S_0} - \mu & 0 \\ \gamma & -c \beta V_0 & -\mu \end{pmatrix} \begin{pmatrix} x \\ I \\ y \end{pmatrix} + higher order terms$$
(3)
$$(\gamma + \mu + \lambda) [(c \beta V_0 + \frac{\beta S_0}{1 + \alpha_1 S_0} - \mu - \lambda)(\mu + \lambda)] = 0$$
(4)

$$\lambda_1 = -(\gamma + \mu), \ \lambda_2 = c \beta V_0 + \frac{\beta S_0}{1 + \alpha_1 S_0} - \mu, \ \lambda_3 = -\mu$$

Since all parameters are assumed positive, so it follows that  $\lambda_1 < 0$  and  $\lambda_3 < 0$ . So, the disease-free equilibrium  $P_0$  is locally asymptotically stable if and only if  $\lambda_2 = c \beta V_0 + \frac{\beta S_0}{1 + \alpha_1 S_0} - \mu < 0$ .

Let 
$$R = \frac{\beta\delta}{\mu(\mu+\gamma+\alpha\ \delta)} + \frac{c\ \beta\gamma\delta}{\mu^2(\mu+\gamma)}$$

**Lemma:** The disease-free equilibrium  $P_0$ , of the model (1) is locally asymptotically stable (CAS) if  $R_0 < 1$ , and unstable if  $R_0 > 1$ .

The quality  $R_0$  refers to the average number of secondary cases generated by a single infectious individual in a completely susceptible population. Since  $\lambda_1$ ,  $\lambda_3$  are negative, if  $R_0 < 1$ ,  $\lambda_2 < 0$ . Therefore, the disease-free equilibrium is locally asymptotically stable

## 3. Local stability of the endemic equilibrium

**Theorem 1:** If the endemic equilibrium  $P_*(S^*, I^*, V^*)$  of system () exists, then it is locally asymptotically stable **Proof:** According to Theorem (1), the endemic equilibrium  $P_*(S^*, I^*, V^*)$  exists if and only if  $R_0 > 1$ . The Jacobian matrix of the system (1) is

$$\begin{pmatrix} \frac{dx}{dt} \\ \frac{dy}{dt} \\ \frac{dy}{dt} \\ \frac{dz}{dt} \\ \frac{dz}{dt} \end{pmatrix} = \begin{pmatrix} -(\frac{\beta l*}{1+\alpha_l S*+\alpha_2 l*} + \gamma + \mu) & 0 & -\frac{\beta S*}{1+\alpha_l S*+\alpha_2 l*} \\ \gamma & -(c\beta l*+\mu) & 0 \\ \frac{\beta l*}{1+\alpha_l S*+\alpha_2 l*} & c\beta l* & c\beta V* \end{pmatrix} \begin{pmatrix} x \\ y \\ z \end{pmatrix} + higher order terms \\ \lambda^3 + (2\mu + 2\gamma + c\beta l* + \frac{\beta l*}{1+\alpha_s S*+\alpha_2 l*} - \frac{\beta S*}{1+\alpha_s S*+\alpha_1} - c\beta V*)\lambda^2 + (c^2\beta^2 V*l* + \frac{c\beta^2 l*}{1+\alpha_s S*+\alpha_1} + 2c\beta l*\mu \\ 1*2^* \\ \frac{\beta l}{1+\alpha_s S} + \frac{\beta l*}{1+\alpha_s S*+\alpha_1} + 2\gamma \mu + \gamma^2 + \frac{\mu\beta l*}{1+\alpha_s S*+\alpha_1} - c\beta V*)\lambda^2 + (c^2\beta^2 V*l* + \frac{c\beta^2 l*}{1+\alpha_s S*+\alpha_1} - \frac{\beta S*}{1+\alpha_s S*+\alpha_1} + 2\mu^2 \\ \frac{c\beta l}{1+\alpha_s S} + \frac{\beta l}{1+\alpha_s S*+\alpha_1} + 2\gamma \mu + \gamma^2 + \frac{\mu\beta l*}{1+\alpha_s S*+\alpha_1} + 2\mu^2 - \frac{c\beta^2 s}{1+\alpha_s S*+\alpha_1} - \frac{2\beta S*\mu}{1+\alpha_s S*+\alpha_1} - \frac{\beta S*}{1+\alpha_s S*+\alpha_1} + c\beta l*\mu + c\beta l*\mu \gamma + \beta l*\mu \gamma + \beta l*\mu^2 + \mu^3 \\ \frac{\mu^2 \gamma}{1+\alpha_s S*+\alpha_1} - \frac{c\beta^2 V*l}{1+\alpha_s S*+\alpha_1} - c\beta V*\mu - c\beta V*\gamma)\lambda + \frac{c\beta^2 l*^2 \mu}{1+\alpha_s S*+\alpha_1} + c\beta l*\mu \gamma + c\beta l*\mu \gamma + \beta l*\mu^2 + \mu^3 \\ \mu^2 \gamma - \frac{\beta S*\mu^2}{1+\alpha_s S*+\alpha_1} - \frac{c\beta^2 S*^2 \mu}{1+\alpha_s S*+\alpha_1} - \frac{c\beta^2 V*l*\mu}{1+\alpha_s S*+\alpha_1} - \frac{\beta S*\mu}{1+\alpha_s S*+\alpha_1} - c\beta V*\mu^2 - c\beta V*\mu^2 - c\beta V*\mu^2 - c\beta V*\mu^2 + \mu^3 \\ \mu^2 \gamma - \frac{\beta S*\mu^2}{1+\alpha_s S*+\alpha_1} - \frac{c\beta^2 l*^2}{1+\alpha_s S*+\alpha_2 l*} - \frac{\beta S*}{1+\alpha_s S*+\alpha_2 l*} - c\beta V*\mu^2 - c\beta V*\mu^2 - c\beta V*\mu^2 - c\beta V*\mu^2 + \mu^3 \\ \mu^2 \gamma - \frac{\beta S*\mu^2}{1+\alpha_s S*+\alpha_1} - \frac{c\beta^2 l*^2}{1+\alpha_s S*+\alpha_2 l*} - \frac{\beta S*\mu^2}{1+\alpha_s S*+\alpha_2 l*} - c\beta V*\mu^2 - c\beta V*\mu^2 - c\beta V*\mu^2 + \mu^3 \\ \mu^2 \gamma - \frac{\beta S*\mu^2}{1+\alpha_s S*+\alpha_2 l*} - \frac{c\beta^2 l*\mu^2}{1+\alpha_s S*+\alpha_2 l*} - \frac{\beta S*\mu^2}{1+\alpha_s S*+\alpha_2 l*} - c\beta V*\mu^2 + \frac{\mu\beta l*\mu^2}{1+\alpha_s S*+\alpha_2 l*} + 2\mu^2 - \frac{c\beta^2 S*l*\mu^2}{1+\alpha_s S*+\alpha_2 l*} + 2\mu$$

$$a_{3} = \frac{c \beta^{2} I_{*}^{2} \mu}{1 + \alpha_{1} S_{*} + \alpha_{2} I_{*}} + c \beta I_{*} \mu^{2} + c \beta I_{*} \mu^{2} + \mu^{3} \mu^{2} \gamma - \frac{\beta S_{*} \mu^{2}}{1 + \alpha_{1} S_{*} + \alpha_{2} I_{*}} - \frac{c \beta^{2} S_{*} I_{*}^{2} \mu}{1 + \alpha_{1} S_{*} + \alpha_{2} I_{*}} - \frac{c \beta^{2} V_{*} I_{*} \mu}{1 + \alpha_{1} S_{*} + \alpha_{2} I_{*}}$$

$$- \frac{\beta S_{*} \mu \gamma}{1 + \alpha_{1} S_{*} + \alpha_{2} I_{*}} - c \beta V_{*} \mu^{2} - c \beta V_{*} \mu \gamma$$
If  $a_{1} a_{2} > a_{0} a_{3}$ , by

Routh Hurwitz criterion, the endemic equilibrium is locally asymptotically stable.

#### Global stability of disease-free equilibrium 4.

In order to prove the global stability of the endemic equilibrium  $P_*$  of the equation (1) we apply Dulac's criterion plus Poincare-Bendixson Theorem.

**Theorem 2:** (Dulac's Criterion)

Consider the following general nonlinear autonomous system of de (\*)

 $x(t) = f(x), x \in E$ 

Let  $f = C^{1}(E)$  where E is a simple connected region in R<sup>2</sup>. If the exists a function it  $H \in C^{1}(E)$  such that  $\nabla (Hf)$  is not identically zero and does not change sign in E, the system (\*) has no close orbit lying entirely in E. if A is an annular region contained in E on which  $\nabla$ .(*Hf*) does not change sign, then there is at most one limit cycle of the system (\*) in A.

**Theorem 3:** (The Poincare-Bendixson Theorem): Suppose that  $f \in C^{1}(E)$  where E is an open subset of  $\mathbb{R}^{n}$  and that the system (\*) has a rejecting  $\Gamma$  contained in a compact subset f of E. assume that the system (\*) has only one unique equilibrium point  $x_0$  in f, then one of the following possibilities holds.

- a)  $w(\Gamma)$  is the equilibrium point  $x_0$
- b)  $w(\Gamma)$  is a periodic orbit
- c)  $w(\Gamma)$  is a graphic

**Theorem 4:** Let  $P_*$  be the unique positive equilibrium point of the system (1). If  $R_0>1$ , then  $P_*$  of the system (\*) is globally asymptotically stable.

**Proof:** We use Dulac's criterion plus Poincare'-Bendixson Theorem to analyze the system (1). Consider.

$$H(S,V,I) = \frac{1}{SVI}$$

Where S>0, V>0, I>0. Then,

$$\begin{split} \nabla .(Hf) &= \frac{\partial}{\partial S} (H.f_1) + \frac{\partial}{\partial V} (H.f_2) + \frac{\partial}{\partial I} (H.f_3) \\ &= \frac{\partial}{\partial S} [(\frac{1}{SVI} (\delta - \frac{\beta SI}{1 + \alpha_1 S + \alpha_2 I} - \gamma S - \mu S) + \frac{\partial}{\partial V} [(\frac{1}{SVI} (\gamma S - \mu V - c \beta VI) + \frac{\partial}{\partial I} [(\frac{1}{SVI} (c \beta VI + \frac{\beta SI}{1 + \alpha_1 S + \alpha_2 I} - \gamma I)] \\ &= -\frac{\delta}{S^2 VI} + \frac{\beta \alpha_1}{(1 + \alpha_1 S + \alpha_2 I)^2} - \frac{\gamma}{V^2 I} - \frac{\beta \alpha_2}{(1 + \alpha_1 S + \alpha_2 I)^2} \end{split}$$

If  $\alpha_1 = \alpha_2$ ,  $\nabla \cdot (Hf) < 0$ . Hence, by the Dulac's criterion, there is no closed orbit in the first quadrant. Therefore, the endemic equilibrium is globally asymptotically stable.

#### Numerical simulations 5.

In this section, we perform numerical calculations to support our theoretical analysis of this paper. Below are the graphs emanated from the numerical computations?

#### 6. **Discussion of results**

Simulation was carried out with different values of the parameters and stability analysis and values of the threshold were obtained.

From figures 1-4 above,  $R_0 < 1$  and different values of c were used. It was discovered that as c increases, the more stability the models become. This means that the vaccine has a lot to do with the eradication of the disease.

From figure 5, we have  $R_0 > 1$  and different values were used and it was discovered that there is endemic and that means that disease may break out and become endemic.

We established that when  $R_0 < 1$ , the disease may die out at the long run and when  $R_0 > 1$ , there may be endemic.



Fig. 1: Graph Of S (T), I (T) And V (T) Against Time (T) When  $\delta = 15$ ,  $\beta = 0.5$ ,  $\alpha_1 = 0.5$ ,  $\alpha_2 = 0.3$ ,  $\gamma = 0.5$ ,  $\mu = 2.5$ , c = 0.1 and  $R_0 < 1$ 



**Fig. 2:** Graph of S (T), I (T) and V (T) Against Time (T) When  $\delta = 15$ ,  $\beta = 0.5$ ,  $\alpha_1 = 0.5$ ,  $\alpha_2 = 0.3$ ,  $\gamma = 0.5$ ,  $\mu = 2.5$ , c = 0.4 and  $R_0 < 1$ 



Fig. 3: Graph of S (T), I (T) And V (T) Against Time (T) When  $\delta = 15$ ,  $\beta = 0.5$ ,  $\alpha_1 = 0.5$ ,  $\alpha_2 = 0.3$ ,  $\gamma = 0.5$ ,  $\mu = 2.5$ , c = 0.7 and  $R_0 < 1.5$ 



Fig. 4: Graph of S (T), I (T) and V (T) Against Time (T) when  $\delta = 15$ ,  $\beta = 0.5$ ,  $\alpha_1 = 0.5$ ,  $\alpha_2 = 0.3$ ,  $\gamma = 0.5$ ,  $\mu = 2.5$ , c = 0.95 and  $R_0 < 1$ 



**Fig. 5:** Graph of S (T), I (T) and V (T) Against Time (T) when  $\delta = 15$ ,  $\beta = 0.3$ ,  $\alpha_1 = 0.5$ ,  $\alpha_2 = 0.3$ ,  $\gamma = 0.1$ ,  $\mu = 0.1$ , c = 0.1 and  $R_0 > 1$ 

## 7. Conclusion

In this paper, an SVI deterministic model with saturating incidence rate is investigated. Some of the main findings of this study are:

- i) The model has a globally-asymptotically stable disease-free equilibrium whenever the associated reproduction number is less than unity;
- ii) The model has a unique endemic equilibrium under certain conditions. Under these conditions, the endemic equilibrium is locally-asymptotically stable whenever the associated reproduction number exceeds unity. The endemic equilibrium is shown to be globally-asymptotically stable using Dulac's criterion plus Poincare's Bendixson theorem.
- iii) Using Dulac's criterion plus Poincare's –Bendixson theorem and  $\alpha_1 = \alpha_2$ , the model is globally asymptotically stable.
- iv) Numerical Simulations illustrate that the parameter 1-c which describes the vaccine efficacy has a lot to do in disease eradication. As c increases when  $R_0 < 1$ , there is stability.

This study shows that the disease being considered can be eliminate from the population whenever the basic reproduction number  $R_0$  is less than unity. The disease persists in the community whenever the basic reproduction

number  $R_0$  exceeds unity.

## References

- C. M.Kribs-Zaleta, J. X.Velasco-Hernadez, A simple vaccination model with multiple endemic states. Math Biosci 164 (2000) 183-201. http://dx.doi.org/10.1016/S0025-5564 (00)00003-1.
- [2] J.Arino, C. C.McCluskey, P.van den Driessche, Global results for an epidemic model with vaccination that exhibits backward bifurcation. SIAM J. Appl. Math. Vol.64 No.1 (2003) pp. 260-276. http://dx.doi.org/10.1137/S0036139902413829.
- [3] J. Li, Z. Ma, Z., Y. Zhou, Global Analysis of SIS epidemic model with a simple vaccination and multiple endemic equilibrium. Acta Mathematica Scientia B (1): (2006) 83-93.
- F. Brauer, Backward bifurcations in simple vaccination models, J. Math. Anl. Appl. 298, (2004) pp. 418-431. http://dx.doi.org/10.1016/j.jmaa.2004.05.045.
- J. Li, Z. Ma, Qualitative analyses of SIS epidemic model with vaccination and varying total population size. Math. Comp. Model 35, (2002) 1235-1243. http://dx.doi.org/10.1016/S0895-7177 (02)00082-1.
- J. Li, Z. Ma, Global Analysis of SIS epidemic models with variable total population size. Math Comput Model 39 (2004) 1231-1242. http://dx.doi.org/10.1016/j.mcm.2004.06.004.
- [7] O. Adebimpe, Stability Analysis of a SEIV Epidemic Model with Saturated incidence Rate, British Journal of Mathematics and Computer Science 4(23): (2014), pp. 3358-3368 http://dx.doi.org/10.9734/BJMCS/2014/2758.
- [8] O. Adebimpe, B. O. Moses, O. J. Okoro, Global Stability Analysis of a SEIR Epidemic Model with Saturated Incidence Rate, International Journal of Mathematical Sciences, vol.34, Issue 1, (2014) 1504-1512.
- [9] R. Ullah, G. Zahman, S. Islam, I. Ahmad, Dynamical features and vaccination Strategies in an SEIR epidemic model, Research Journal of Recent Sciences, vol.2(10), (2013), pp. 48-56
- [10] Md. Saiful Islam, Md. Asaduzzaman, Md. Nazrul Islam Mondal, Stability Analysis of DFE of an Epidemic Model in the presence of a Preventive Vaccine, IOSR Journal of Mathematics, volume 3, issue 2, (2012) pp. 25-31.