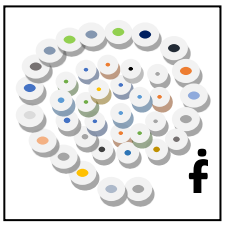

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SVEIR model of an infectious disease among infected immigrants with nonlinear incidence rate

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Abstract

In this paper, the effect of a saturated incidence rate and infectious immigrants on the transmission dynamics of an infectious disease is studied using an SVEIR model. The model exhibits three equilibrium states: the disease-free and endemic equilibrium states when there is no influx of infective immigrants and the endemic equilibrium state when there is an influx of infective immigrants in the population. Besides, the model shows a forward bifurcation when there is no entry of infective immigrants and this aid in establishing the local and global asymptotically stability when the basic reproduction number, $R_0 < 1$ and $R_0 > 1$ respectively. Numerical results are performed to examine the effect of the saturated incidence rate and the infective immigrants on disease transmission. The results indicate that the disease could be controlled or eradicated if there is a strict check to ensure that the infected immigrants are treated before they join the population.

Keywords: SVEIR model; Infectious disease; Non-linear incidence rate; basic reproduction number; global stability; infective immigrants

1 Introduction

Infectious diseases are inconveniences, disorders and a leading cause of death across the globe that man has been fighting to control [1]. They are deadly diseases characterized by rapid progressive deterioration and premature death and this includes severe acute respiratory syndrome (SARS), middle-east respiratory syndrome (MERS), Ebola virus disease, Lassa virus disease, and Yellow fever [2]. They constitute a public health burden to mankind and have profound negative effects on human life and socio-economic activities. These have compelled people of various fields to search for means of halting the spread of infectious diseases in the population. Controlling the spread of infectious diseases could be the administration of herbal and/or traditional remedies, surgery, vaccination, quarantine of infected individuals, and a thorough check on immigrants [3]. The impact of screening

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and vaccination of immigrants on the spread of infectious diseases in any population is considered in this work.

Vaccination is the administration of antigenic material called vaccine which produces immunity to a disease. Immunity can be temporary or permanent. It has proven to be one of the most effective preventive measures of combating infectious diseases, such as smallpox, measles, hepatitis B, and polio [4]. Vaccines are substances used to build the body's immune system. It produces responses that fight pathogens like viruses, fungi, bacteria, and protects humans from the diseases these pathogens cause. A vaccine can be given by oral, injection, puncture, transdermal, or intranasal. The effect of vaccines is either for life or temporary in the body of the vaccinated person and where it is temporary, the person will become susceptible to the disease again [3, 5].

Immigration is the movement of people from their legal place of origin to another place where they are not native settlers which results in a permanent residence or future citizens. Immigrants are inspired to leave their legal place of origin for some reason, which includes socio-economic, political issues, education (quality of institutions), family reunion, environmental factors like conflict or natural disaster, and the desire of changing one's surroundings. Thus, immigrants from areas where there are infectious diseases can pose a challenge to another area and this makes human migration a major means of spreading infectious diseases to other countries. Infectious immigrants are immigrants with no overt disease who harbors infectious organisms. Infectious immigrants are increasingly important risk factors and sometimes becomes the index case for infections to the host population.

The mathematical modeling of infectious diseases is used to study the mechanisms of the transmission dynamics, the prediction of the future course of an outbreak, and the evaluation of strategies to control the disease. The saturated incidence rate is about the behavioural attitude of susceptible individuals and the crowding effects of infective individuals when there is an outbreak of disease [4, 6]. Significant work on compartmental models such as SEIRS, SEIQV, SIR, SEIR, SEIV with a saturated incidence rate has been done to examine the transmission dynamics of infectious diseases. The global analysis was carried out for these compartmental models except the work of Capasso and Serio [7] who initiated a saturated type incidence rate for generalized Kermack-Mckendrick deterministic model. Authors like Cai and Li [8] studied a SEIV model while Khan et al. [9] considered an SEIRS. Both models [8, 9] incorporate the general incidence rate and a waning preventive vaccine. Liu and Yang [10] used a saturated incidence rate, $\frac{\beta SI}{(1+aI)}$ for a SEIQV with vaccination and quarantine measures. Enatsu et al. [11] discussed a SIR with distributed time delay and found that the global dynamics are not affected by the distributed time delay. Li and Cui [12] incorporate different incidence rates for exposed and infected classes for an SEIR model and assumed permanent immunity for recovered class while Safi and Garba [13] incorporated a Holling type II incidence function with public health education and counseling as control measures for an SEIR. The effect of infected immigrants is considered by Zhang *et al.* [14] with bilinear incidence rate and temporary immunity. They developed an SEIRS model. From the aforementioned authors, none has considered the effect of infected immigrants on the spread of infectious disease with generalized incidence rate. This study investigates the impact of screening and vaccination of infected immigrants on disease dynamics by extending the work of Cai and Li [8]. Our model incorporates the influx of infected immigrants, the recovered class and mortality rate in the work of Cai and Li [8] since the infected immigrants become the index case to the host population as it was seen in the occurrence of the Ebola virus disease and the COVID-19 in Nigeria. It is also important to include the mortality rate because some sufferers can die from the disease itself and most times interventions in place are

non-pharmaceutical interventions. Our work is different from the work of Zhang *et al.* [14] because of the generalized nonlinear incidence rate and the permanent immunity of the recovered class considered in this paper. Thus, an SVEIR compartmental model with a generalized incidence rate and the proportion of infected immigrants is considered in this study. The impact of the different incidence rates is examined.

Based on the above motivation, an SVEIR compartmental model with a saturated incidence rate and the proportion of infected immigrants is considered in this paper. The rest of the paper is organized as follows: Section 2, is the formulation of the SVEIR model. The model analysis is presented in Section 3. In Section 4, numerical simulation is carried out to verify some analytical results while a brief discussion and conclusion are described in Section 5.

2 Model Formulation

We considered a non-linear saturated incidence rate of the form, $\frac{\beta SI}{\varphi(I)}$, which is a more general form of $\frac{\beta I^p S}{(1+\propto I^q)}$ that is used by some researchers (Liu *et al.* [15], Liu *et al.* [16]). The incidence rate is bilinear when $\varphi(I) = 1$. The function, $\varphi(I)$, satisfies $\varphi(0) = 1$ and $\dot{\varphi}(I) \geq 0$. This implies that $\varphi(I) \geq 0$ for $I(t) \geq 0$. The function, $\frac{1}{\varphi(I)}$, is used to measure the psychological or inhibition effect of the behavioral change of susceptible individuals when there is an increase in the number of infectious individuals. We develop a five compartmental model which consists of Susceptible individuals, $S(t)$, Vaccinated individuals, $V(t)$, Exposed individuals, $E(t)$, Infectious individuals $I(t)$, and Recovered individuals $R(t)$ with a general non-linear incidence rate, $\frac{\beta SI}{\varphi(I)}$ and a waning preventive vaccine at the rate, ω. Our model assumed that some proportion, k, of immigrants are infected [14] while some proportions, p, are given vaccination at the point of entrance [9]. Infected immigrants are sometimes the index case to the host population as it happened in Nigeria for the Ebola virus disease and COVID-19 [17, 18]. Also, we assumed that the recovered class has permanent immunity as in the work of [13]. COVID-19 can be a good example of an SVEIR since it has not been confirmed with temporary immunity. This makes up the SVEIR model that is given as follows with the parameter description in Table 1.

$$\frac{dS}{dt} = (1-p-k)\pi - \frac{BSI}{\varphi(I)} - \mu S + \omega V \,, \tag{1}$$

$$\frac{dV}{dt} = p\pi - (\mu+\omega)V \,, \tag{2}$$

$$\frac{dE}{dt} = \frac{BSI}{\varphi(I)} - (\mu+\varkappa)E \,. \tag{3}$$

$$\frac{dI}{dt} = k\pi + \varkappa E - (\mu+\delta+d)I, \tag{4}$$

$$\frac{dR}{dt} = \delta I - \mu R, \tag{5}$$

subject to the initial conditions, $S(0) = S_0, V(0) = V_0,\ E(0) = E_0\,,\ I(0) = I_0,\ \ R(0) = R_0$.

Table 1. Parameter description

Parameters	Description
$\boldsymbol{\pi}$	The recruitment rate of individuals including newborns and immigrants into the population.
$\boldsymbol{p}$	A proportion of recruited individuals that are vaccinated
$\boldsymbol{k}$	A proportion of infected immigrants in the population
$\boldsymbol{\beta}$	The transmission rate
$\boldsymbol{\mu}$	Natural death rate
$\boldsymbol{d}$	The mortality rate due to infection
$\boldsymbol{r}$	The rate at which exposed individuals become infectious
$\boldsymbol{\delta}$	The rate at which infected individuals are treated and recovered
$\boldsymbol{\omega}$	The rate at which the vaccine wanes

3 Model Analysis

3.1 Boundedness of the Solutions

The SVEIR model (1) – (5) is shown to be well-posed and makes biological sense. This is done by proving that the existence of a non-negative solution and its boundedness for an initial solution.

Theorem 1. Let the initial solutions satisfy $S(0) > 0, V(0) \geq 0,\ E(0) \geq 0,\ I(0) \geq 0, R(0) \geq 0$. The SVEIR model of equation (1) - (5) has non-negative solutions which are contained in the feasible region, $\Omega = \left\{\left(S(t), V(t), E(t), I(t), R(t)\right) \in \mathbb{R}_+^5 : N \leq \frac{\pi}{\mu}\right\}$.

Proof. First, we prove the non-negative solution set for the SVEIR model (1) – (5). It follows from (1) that

$$\frac{dS}{dt} = (1-p-k)\pi - \frac{\beta SI}{\varphi(I)} - \mu S + \omega V \geq (1-p-k)\pi - \beta(t)S\,, \qquad (6)$$

where $\beta(t) = \frac{\beta I}{\varphi(I)} + \mu$.

Solving (6), a first-order linear equation in S , using the method of integrating factor on $[0, t]$ with the initial condition, $S(0) > 0$, we have

$$S(t) \geq S(0)exp\left(\int_0^t -\beta(s)ds\right) + exp\left(\int_0^t -\beta(s)ds\right) \times \int_0^t (1 - p - k)\pi exp\left(\int_0^u \beta(\omega)d\omega\right) \geq 0 .$$

Hence, $S(t) \geq 0$ since $S(0) > 0$.

The remaining equations are obtained in a similar way that

$$V(t) \geq V(0)exp\big(-(\mu + \omega)\big)t \geq 0 ,$$

$$E(t) \geq E(0)\exp\big(-(\mu + \curlyvee)\big)\, t \geq 0 ,$$

$$I(t) \geq I(0)\exp\big(-(\mu + \delta + d)\big)\, t \geq 0 ,$$

and

$$R(t) \geq R(0)\exp(-\mu t) \geq 0.$$

Hence, the solution set $\big(S(t), V(t), E(t), I(t), R(t)\big)$ of the SVEIR model of equations (1)-(6) is non-negative for all $t > 0$ since exponential functions and initial solutions are non-negative.

Next, we prove that the non-negative solution set is contained in the feasible region, Ω, which is the boundedness of the solution. This is done by adding the equations of SVEIR model to get the rate of the total population, $N(t)$,

$$\frac{dN}{dt} = \pi - \mu N - dI . \tag{7}$$

If we ignore d, equation (7) yields

$$\frac{dN_h}{dt} \leq \pi - \mu N . \tag{8}$$

Applying the Gronwall's inequality to equation (8) with the initial condition, $N(0) = N_0$, we get

$$N(t) \leq \frac{\pi}{\mu} + \left[N_0 - \frac{\pi}{\mu}\right] e^{-\mu t}. \tag{9}$$

If $N_0 < \frac{\pi}{\mu}$ as $t \to \infty$, the trajectories approach $\frac{\pi}{\mu}$; If $N_0 > \frac{\pi}{\mu}$, the solutions $N(t)$ decreases to $\frac{\pi}{\mu}$ as $t \to \infty$. Therefore, in either case, the total population, $N(t) \to \frac{\pi}{\mu}$ as $t \to \infty$ in (9). This

means that $0 \leq N(t) \leq \frac{\pi}{\mu}$. Hence, the non-negative solution set of the SVEIR model equations (1)-(5) enters the feasible region, Ω, which is a positively invariant set.

3.2 Existence and Stability of Disease-free Equilibrium State and Basic Reproduction Number

3.2.1 Disease-free Equilibrium State

The equilibrium state for the SVEIR model is obtained when $\frac{dS}{dt} = 0$, $\frac{dV}{dt} = 0$, $\frac{dE}{dt} = 0$, $\frac{dI}{dt} = 0$, and $\frac{dR}{dt} = 0$. This yields

$$(1 - p - k)\pi - \frac{BSI}{\varphi(I)} - \mu S + \omega V = 0 , \tag{10}$$

$$p\pi - hV = 0 , \tag{11}$$

$$\frac{BSI}{\varphi(I)} - fE = 0 , \tag{12}$$

$$k\pi + \curlyvee E - gI = 0 , \tag{13}$$

$$\delta I - \mu R = 0, \tag{14}$$

where

$$h = (\mu + \omega), f = (\mu + \curlyvee), \text{and } g = (\mu + \delta + d). \tag{15}$$

Solving equations (10) – (14) when there are no infective immigrants in the population $(i.e. k = 0)$, we have the disease-free equilibrium (DFE) state, E_0, as $E_0 = (S_0, V_0, 0, 0, 0) = \left(\frac{\pi\{(1-p)\mu+\omega\}}{\mu(\mu+\omega)}, \frac{p\pi}{\mu+\omega}, 0, 0, 0\right)$.

This implies that when there is no exposed infective and recovery individuals in the population, the level of susceptible will be approaching $\frac{\pi\{(1-p)\mu+\omega\}}{\mu(\mu+\omega)}$ and the vaccination population will remain at is equilibrium state, $V_0 = \frac{p\pi}{\mu+\omega}$.

3.2.2 Basic Reproduction Number, $\mathbf{R_0}$

The basic reproduction number of an infection denoted by R_0, is a threshold quantity that provides useful information regarding the spreading and control of infectious disease in a population. If $R_0 < 1$, the infection will fizzle out, but, if $R_0, > 1$, the infection will be able to spread and persist in the population. To compute the basic reproduction number for the SVEIR model using the next generation operator, we follow the approach of Van den Driessche and Watmough, [19]. Let $X = (E, I)$, be the vector that represents the infected compartments. Then from the model (1) – (5), we have the rate of new infection in the infected compartments as

$$F = \begin{bmatrix} \frac{\beta SI}{\varphi(I)} \\ 0 \end{bmatrix},$$

and the rate of transfer from in and out the infected compartments as

$$V = \begin{bmatrix} fE \\ -k\pi - \gamma E + gI \end{bmatrix}.$$

Taking the partial derivatives of F and V at the DFE, E_0, yield

$$G = \frac{\partial F(E_0)}{\partial X} = \begin{bmatrix} 0 & \beta S_0 \\ 0 & 0 \end{bmatrix} \text{ and } \qquad U = \frac{\partial V(E_0)}{\partial X} = \begin{bmatrix} f & 0 \\ -\gamma & g \end{bmatrix}.$$

We have the matrix, GU^{-1}, as

$$GU^{-1} = \begin{bmatrix} \frac{\beta S_0 \gamma}{fg} & \frac{\beta S_0}{g} \\ 0 & 0 \end{bmatrix},$$

and the basic reproduction number, R_0, which is the spectral radius of the matrix, GU^{-1}, given as

$$R_0 = \frac{\beta S_0 \gamma}{fg}. \tag{16}$$

Substituting, S_0, and the definition (15) in (21) gives

$$R_0 = \frac{\beta \gamma \pi \{(1-p)\mu + \omega\}}{\mu(\mu+\omega)(\mu+\gamma)(\mu+\delta+d)}. \tag{17}$$

Equation (17) is the basic reproduction number, R_0, for the SVEIR model (1) – (5). The effect of these parameters, $\tau, \beta, \omega, \delta$ on R_0 is illustrate numerically in Figure 1 using the parameter values in [7]. Figure 1 shows that increasing τ, β, ω, and decreasing δ, increases the basic reproduction number, R_0 while other parameters are keep constant.

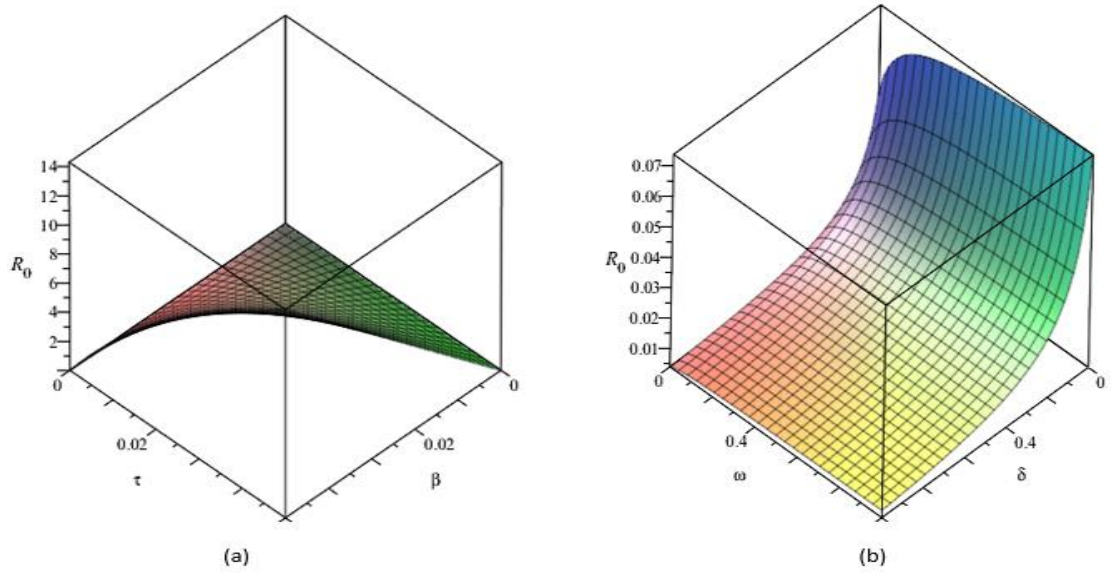

Figure 1. The effect of $\tau, \beta, \omega, \delta$ on the basic reproduction number, R_0. For (a),$p = 0.4,\ \delta = 0.009, \mu = 0.09, d = 0.004, \pi = 10, \omega = 0.05$ and for (b), $p = 0.4,\ \beta = 0.002, \mu = 0.09, d = 0.004, \pi = 10, \tau = 0.003$.

3.2.3 Local Stability of Disease-free Equilibrium (DFE)

Here, we investigate the local stability of the disease-free equilibrium state,$E_0 = (S_0, V_0, 0,\ 0,\ 0)$ without the recovery class, since it does not involve other classes using linearization method by computing its Jacobian matrix at the DFE, $J(E_0)$, as follows

$$J(E_0) = \begin{bmatrix} -\mu & 0 & -\beta S_0 & \omega \\ 0 & -f & \beta S_0 & 0 \\ 0 & r & -g & 0 \\ 0 & 0 & 0 & -h \end{bmatrix}. \tag{18}$$

The characteristics equation of the $J(E_0)$ in (18) is given by

$$(\lambda + \mu)(\lambda + h)[\lambda^2 + (f + g)\lambda + fg - \beta S_0 r] = 0. \tag{19}$$

The SVEIR model (1) – (5) has two negative real roots $-\mu, -h,$ and the roots of the characteristics equation given as

$$\lambda^2 + (f + g)\lambda + fg - \beta S_0 r = 0. \tag{20}$$

Using Routh-Hurwitz criteria, equation (20) has negative root if $A > 0,\ AB > 0$ which implies that $B > 0$.

In equation (20), $A = f + g$; $B = fg - \beta S_0 r$. It is clear that $A > 0$ and $B > 0$ if $fg > \beta S_0 r$ which means that $\frac{\beta S_0 r}{fg} < 1$. Therefore, using the definition in equation (16), we have that DFE, E_0 is locally asymptotically stable if $R_0 < 1$.

3.3 Existence and Stability of Endemic Equilibrium State

3.3.1 Existence of Endemic Equilibrium State

The endemic equilibrium state is established when there is infection in the population ($i.e. I \neq 0$). The endemic equilibrium state for SVEIR model (1) – (5) is obtained by solving equations (10) – (14) simultaneously which gives

$$S^\star = \frac{fA(gI - k\pi)}{r\beta I}, E^\star = \frac{gI - k\pi}{r}, V^\star = \frac{P\pi}{h}. \quad (21)$$

Substituting (21) in (12) and simplifying gives

$$PI^{\star 2} - QI^\star - R = 0, \quad (22)$$

where $A = \varphi(I^\star), P = \beta fgh$, $Q = fgh\mu\left(R_0 + \frac{\beta\pi k}{fg} - A\right)$, $R = A\pi fhk\mu$.

If $k = 0,$ we have $R = 0$ and $A = 1,$ so equation (22) will becomes

$$PI^{\star 2} - Q^* I^\star = 0 \quad (23)$$

with $Q^* = fgh\mu R_0$.

From equation (23), it implies that $I^\star = 0$ or $I^\star = \frac{\mu R_0}{\beta}$. $I = 0$ corresponds to DFE, E_0. So, we have endemic equilibrium state, $E_1,$ when $k = 0$ as

$$E_1 = \left(\frac{fg}{r\beta}, \frac{gR_0}{r\beta fgh}, \frac{R_0}{\beta fgh}, \frac{\mu R_0}{\beta}, \frac{p\pi}{h}\right).$$

When $k > 0,$ we have from equation (22) that

$$I^\star = \frac{Q + \sqrt{Q^2 + 4PR}}{2P}. \quad (24)$$

Substituting equation (24) into equation (21), we have the endemic equilibrium state for $k > 0$ given as

$$E_{1k} = \left(\frac{fAg(Q + \sqrt{Q^2 + 4PR}) - 2pk\pi fA}{r\beta(Q + \sqrt{Q^2 + 4PR})}, \frac{p\pi}{h}, \frac{g(Q + \sqrt{Q^2 + 4PR}) - 2pk\pi}{2pr}, \frac{Q + \sqrt{Q^2 + 4PR}}{2P}, \frac{\delta\left(Q + \sqrt{Q^2 + 4PR}\right)}{2P\mu}\right). \quad (25)$$

Equations (24) and (25) give the endemic equilibrium state,E_{1k}, provided it satisfy the inequality $g\left(Q+\sqrt{Q^2+4PR}\right)>2pk\pi$.

3.3.2 Local Stability of Endemic Equilibrium State

We establish the local stability of endemic equilibrium using the centre manifold theorem by Castillo - Chavez and Song [20] which depends on the existence of bifurcation near $R_0=1$. A forward bifurcation implies that disease-free equilibrium is locally asymptotically stable for $R_0<1$ and also endemic equilibrium is locally asymptotically stable for $R_0>1$ near one. It is possible to have the global asymptotical stability of the two equilibrium states and disease cannot invade the population when $R_0<1$.

Using the concept of Castillo - Chavez and Song [21], we choose $\beta=\beta^*$ as bifurcation parameter so at $R_0=1$ from equation (17) gives

$\beta=\beta^*=\frac{fg\mu(\mu+\varphi)}{\pi\sigma\left((1-p)\mu+\varphi\right)}$.

Also, let represent $S=x_1,\ \ V=x_2,\ E=x_3,\ I=x_4,\ \ \ R=x_5,$ in equations (1) – (5).

If we replacing $\beta=\beta^*$ in the Jacobian matrix $J(E_0)$ of equation (18) at $R_0=1$, we have a simple zero eigenvalue and negative eigenvalues by solving (19) and this yields

$\lambda=-\mu,\lambda=-h,\lambda=-(f+g)$, and $\lambda=0$, since $fg-\beta S_0\gamma=0$ at $R_0=1$.

We derived the right and left eigenvectors associated with zero eigenvalue using the centre manifold theory as $\boldsymbol{w}=(w_1,w_2,w_3,w_4)=\left(-\frac{f}{\mu}w_2,w_2,\frac{\sigma}{g}w_2,0\right)$ and $\boldsymbol{v}=(v_1,v_2,v_3,v_4)=\left(0,v_2,\frac{f}{\sigma}v_2,0\right)$.

Using Theorem 4.1 of [16], the coefficients a and b are given as

$a=-v_2w_2^2\frac{\beta^*f\sigma}{g\mu}$ and $b=v_2w_2\frac{\sigma}{g}S_0$.

It is clear that $a<0$ and $b>0$. This shows the SVEIR model of equations (1) – (5) exhibits a forward bifurcation. This means that the endemic equilibrium state is locally asymptotical stability for $R_0>1$ near one and the disease-free equilibrium state is locally asymptotical stability for $R_0<1$ when $k=0$ and there is the possibility of global stability of the equilibrium states when $k=0$. This is shown graphically in Figure 2.

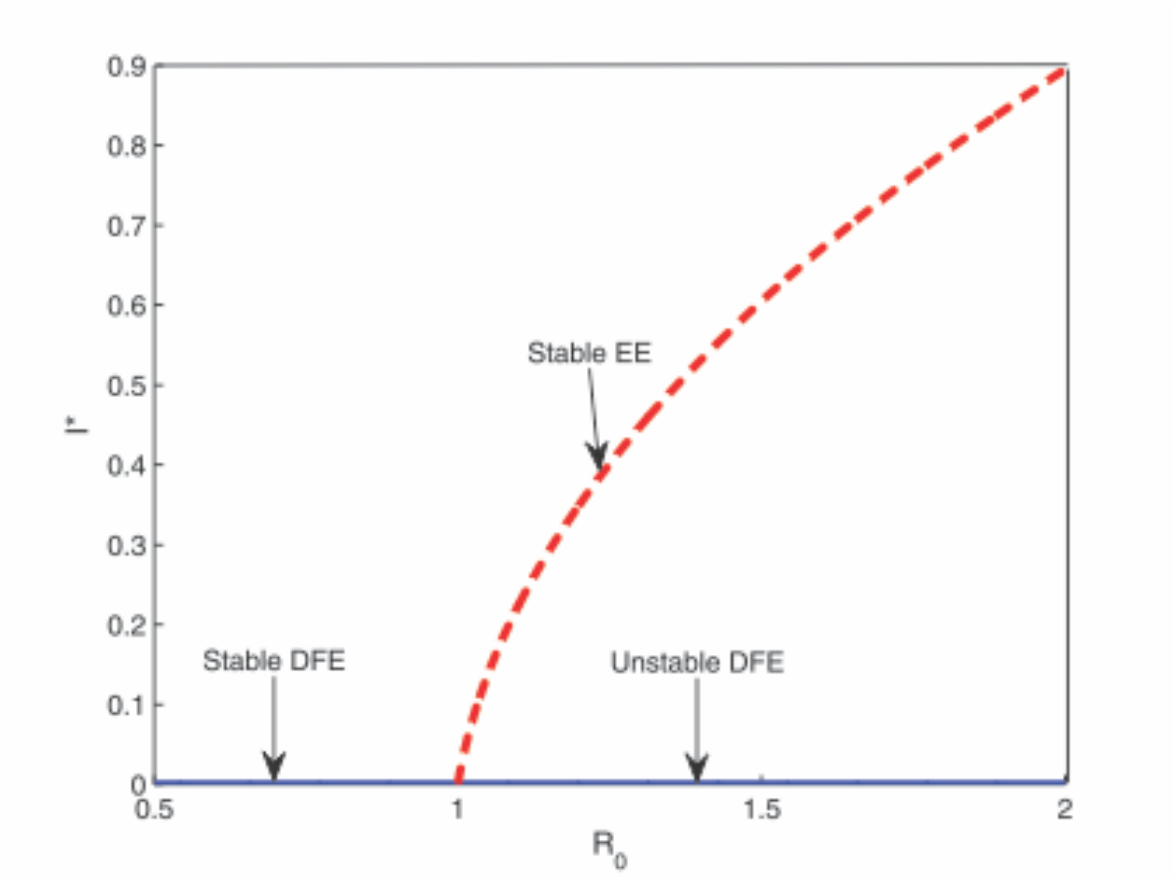

Figure 2. Forward bifurcation plot for the SVEIR model displaying I^* as a function of R_0. Here, $\varphi(I^*) = 1 + I^{*2}$ and the parameter values are $p = 0.4,\ \delta = 0.09, \mu = 0.09, d = 0.004, \pi = 10, \omega = 0.05, \beta = 0.02, \tau = 0.03, k = 0.0, R_0 = 2.243$.

3.4 Global Stability of Equilibrium States

In this subsection, the global stability of the equilibrium states when $k = 0$ is considered. This is done by constructing Lyapunov functions.

3.4.1 Global Stability of Disease-free Equilibrium State

The global stability of the disease-free equilibrium of the SVEIR model equations (1) - (5) is considered by constructing a Lyapunov function and applying LaSalle's invariance principle.

Theorem 2: The DFE, E_0, of the SVEIR model equations (1)-(5) is globally asymptotically stable if $R_0 \leq 1$ in Ω.

Proof: we construct a Lyapunov function using a matrix-theoretic method by Shuai and van Den Driessche [19]. The function is given by

$$L = \frac{r}{fg}E + \frac{1}{g}I \ . \tag{26}$$

Taking the time derivative of equation (26) along the solution of the SVEIR model, we get

$$L' = \frac{r}{fg}E' + \frac{1}{g}I' \ ,$$

$$= \frac{r}{fg}\left(\frac{\beta SI}{\varphi(I)} - fE\right) + \frac{1}{g}(rE - gI) \ . \tag{27}$$

Expanding and simplifying equation (27) yields

$$L' = \left(\frac{\beta rS}{fg\varphi(I)} - 1\right) I \ ,$$

which can be written as

$$L' = \left[\frac{\beta r}{fg}\left(\frac{S}{\varphi(I)} - \frac{S_0}{\varphi(I_0)} + \frac{S_0}{\varphi(I_0)}\right) - 1\right] I \ .$$

But $\varphi(I_0) = 1$ at DFE, E_0. Therefore, we have

$$L' = \left(\frac{\beta rS_0}{fg\varphi(I_0)} - 1\right) I + \frac{\beta r}{fg}\left(\frac{S}{\varphi(I)} - \frac{S_0}{\varphi(I_0)}\right) I \ ,$$

$$= (R_0 - 1)I + \frac{\beta r}{fg}\left(\frac{S}{\varphi(I)} - S_0\right) I \ .$$

Since $\varphi(I) \geq 1,$ then $\frac{S}{\varphi(I)} - S_0 \leq 0.$

Hence,

$$L' \leq (R_0 - 1)I \ .$$

Therefore, it follows that $L' \leq 0$ for $R_0 \leq 1$ with $L' = 0,$ if and only if $E = I = 0.$ This shows that the singleton $\{E_0\}$ is the largest compact invariant set in $\{(S(t), V(t), E(t), I(t), R(t)) \in \Omega : L' = 0\}$. Hence, applying LaSalle's invariance principle, the disease-free equilibrium, $\{E_0\}$ is globally asymptotically stable in Ω If $R_0 \leq 1$.

3.4.2 Global Stability of Endemic Equilibrium State

Theorem 3. The endemic equilibrium, E_1, of the SVEIR model equations (1)-(5) is globally asymptotically stable if $R_0 > 1$ in Ω.

Proof. The global stability of the endemic equilibrium is proved by constructing the Volterra-Lyapunov function.

$$L = \left(S - S^* - S^* ln\frac{S}{S^*}\right) + \left(E - E^* - E^* ln\frac{E}{E^*}\right) + \frac{f}{r}\left(I - I^* - I^* ln\frac{I}{I^*}\right) + \left(V - V^* - V^* ln\frac{V}{V^*}\right).$$

Taking the time derivatives of L along the solutions of the equations (1) – (5), we get

$$L' = \left(1 - \frac{S^*}{S}\right)S' + \left(1 - \frac{E^*}{E}\right)E' + \frac{f}{r}\left(1 - \frac{I^*}{I}\right)I' + \left(1 - \frac{V^*}{V}\right)V',$$

$$L' = \left(1 - \frac{S^*}{S}\right)\left((1-\rho)\pi - \frac{\beta SI}{\varphi(I)} - \mu S + \omega V\right) + \left(1 - \frac{E^*}{E}\right)\left(\frac{\beta SI}{\varphi(I)} - fE\right) + \frac{f}{r}\left(1 - \frac{I^*}{I}\right)(rE - gI) + \left(1 - \frac{V^*}{V}\right)(\rho\pi - hV) \quad . \tag{28}$$

At the endemic equilibrium state, we have

$$(1-\rho)\pi = \frac{\beta S^*I^*}{\varphi(I)} + \mu S^* - \omega V^*, f = \frac{\beta S^*I^*}{\varphi(I^*)E^*}\ ,\ \rho\pi = hV^*,\ g = \frac{rE^*}{I^*}. \tag{29}$$

Substituting equation (29) into equation (28) yields

$$L' = \left(1 - \frac{S^*}{S}\right)\left(\frac{\beta S^*I^*}{\varphi(I^*)} + \mu S - \omega V^* - \frac{\beta SI}{\varphi(I)} - \mu S + \omega V\right) + \left(1 - \frac{E^*}{E}\right)\left(\frac{\beta SI}{\varphi(I)} - \frac{\beta S^*I^*E}{\varphi(I^*)E^*}\right) + \frac{f}{r}(1 - \frac{I^*}{I})\left(rE - \frac{rE^*}{I^*}I\right) + \left(1 - \frac{V^*}{V}\right)(hV^* - hV) \quad . \tag{30}$$

Expanding equation (30) gives

$$L' = \frac{\beta S^*I^*}{\varphi(I^*)} + \mu S^* - \omega V^* - \mu S + \omega V - \frac{\beta S^{*2}I^*}{\varphi(I^*)S} - \frac{\mu S^{*2}}{S} + \omega V^*\frac{S^*}{S} + \frac{\beta S^*I}{\varphi(I)} + \mu S^* - \omega V\frac{S^*}{S} - \frac{\beta S^*I^*E}{\varphi(I^*)E^*} - \frac{\beta SIE^*}{\varphi(I)E} + \frac{\beta S^*I^*}{\varphi(I^*)} + \frac{\beta S^*I^*E}{\varphi(I^*)E^*} - \frac{\beta S^*I}{\varphi(I^*)} - \frac{\beta S^*I^{*2}E}{\varphi(I^*)IE^*} + \frac{\beta S^*I^*}{\varphi(I^*)} + hV^* - hV - \frac{hV^{*2}}{V} + hV^*,$$

which is simplify to get

$$L' = \mu S^*\left(2 - \frac{S^*}{S} - \frac{S}{S^*}\right) + \frac{\beta S^*I}{\varphi(I^*)}\left(3 - \frac{S^*}{S} - \frac{S}{S^*}\frac{I}{I^*}\frac{E^*}{E} - \frac{I^*}{I}\frac{E}{E^*}\right) + \frac{\beta S^*I^*}{\varphi(I^*)}\left(\frac{I}{I^*}\frac{\varphi(I^*)}{\varphi(I)} - \frac{I}{I^*}\right) + hV^*\left(2 - \frac{V}{V^*} - \frac{V^*}{V}\right) + \omega V^*\left(\frac{V}{V^*} + \frac{S^*}{S} - \frac{V}{V^*}\frac{S^*}{S} - 1\right).$$

But $h = \mu + \omega$ in equation (15), then

$$L' = F(S,I,E) + \mu V^*\left(2 - \frac{V}{V^*} - \frac{V^*}{V}\right) + \omega V^*\left(\frac{S^*}{S} - \frac{V}{V^*}\frac{S^*}{S} + 1 - \frac{V^*}{V}\right) + \frac{\beta S^*I^*}{\varphi(I^*)}\left(\frac{I}{I^*}\frac{\varphi(I^*)}{\varphi(I)} - \frac{I}{I^*}\right),$$

where $F(S,I,E) = \mu S^*\left(2 - \frac{S^*}{S} - \frac{S}{S^*}\right) + \frac{\beta S^*I^*}{\varphi(I^*)}\left(3 - \frac{S^*}{S} - \frac{S}{S^*}\frac{I}{I^*}\frac{E^*}{E} - \frac{I^*}{I}\frac{E}{E^*}\right)$.

So,

$$L' = F(S,I,E) + \mu V^*\left(2 - \frac{V}{V^*} - \frac{V^*}{V}\right) + \omega V^*\left(1 - \frac{V^*}{V} + \frac{S^*}{S} - \frac{V}{V^*}\frac{S^*}{S}\right) + \frac{\beta S^* I^*}{\varphi(I^*)}\left(\frac{I}{I^*}\frac{\varphi(I^*)}{\varphi(I)} - \frac{I}{I^*}\right).$$

But, $1 - \frac{V^*}{V} + \frac{S^*}{S} - \frac{V}{V^*}\frac{S^*}{S} \leq 2 - \frac{V^*}{V} - \frac{V}{V^*}$, and $\frac{\varphi(I^*)}{\varphi(I)} - 1 \leq 0$ for $I^* \leq I$ since $S^* < S$ and $\varphi(I)$ is an increasing function.

Therefore,

$$L' \leq \mu S^*\left(2 - \frac{S^*}{S} - \frac{S}{S^*}\right) + \frac{\beta S^* I^*}{\varphi(I^*)}\left(3 - \frac{S^*}{S} - \frac{S}{S^*}\frac{I}{I^*}\frac{E^*}{E} - \frac{I^*}{I}\frac{E}{E^*}\right) + (\mu + \omega)V^*\left(2 - \frac{V}{V^*} - \frac{V^*}{V}\right). \quad (31)$$

Applying the arithmetic-geometric mean inequality theorem to equation (31), we have

$$2 \leq \frac{S^*}{S} + \frac{S}{S^*}, \quad 3 \leq \frac{S^*}{S} + \frac{S}{S^*}\frac{I}{I^*}\frac{E^*}{E} + \frac{I^*}{I}\frac{E}{E^*}, \text{ and } 2 \leq \frac{V}{V^*} + \frac{V^*}{V}.$$

Hence, $L' \leq 0$ for all $\big(S(t), V(t), E(t), I(t), R(t)\big)$ in the region, Ω and $L' = 0$, if and only if $S^* = S,\ E^* = E,\ V^* = V, I^* = I, R^* = R$. This shows that the singleton $\{E_1\}$ is the largest compact invariant set in $\big\{\big(S(t), V(t), E(t), I(t), R(t)\big) \in \Omega : L' = 0\big\}$. Therefore, applying LaSalle's invariance principle, the endemic equilibrium state, $\{E_1\}$ is globally asymptotically stable in Ω If $R_0 > 1$ when $k = 0$.

Global stability implies that with different initial conditions, the model will always converge to the disease-free and endemic equilibrium states when $R_0 < 1$ and $R_0 > 1$ respectively. This is shown in Figure 3 for the infected population. The Infected population is choosing to illustrate the global stability of the equilibrium states.

4 Numerical Simulations

In this section, the numerical simulations for the SVEIR model are implemented to quantify the impact of different incidence rates and proportions of infective immigrants on disease dynamics. The parameter values used in this simulation are mainly from Khan et al. [7] except stated otherwise. The saturated incidence rate, $\varphi(I) = 1 + I^2$ is also used.

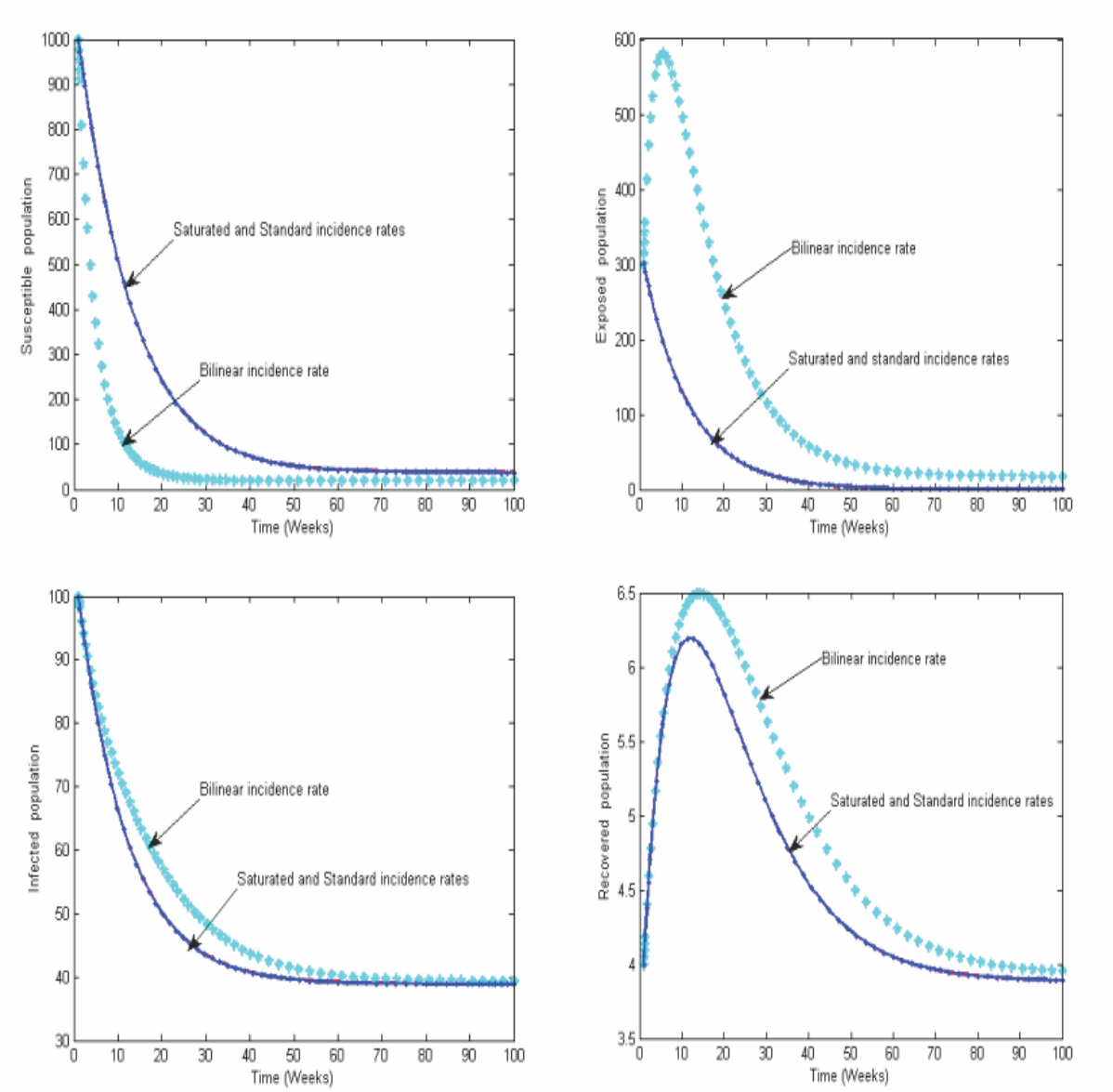

Figure 3. The dynamical behavior of the SVEIR model with different incidence rates. The parameter values are $\beta = 0.002, p = 0.4, k = 0.4, \tau = 0.003, \delta = 0.009, \mu = 0.09, d = 0.004, \pi = 10, \omega = 0.05$.

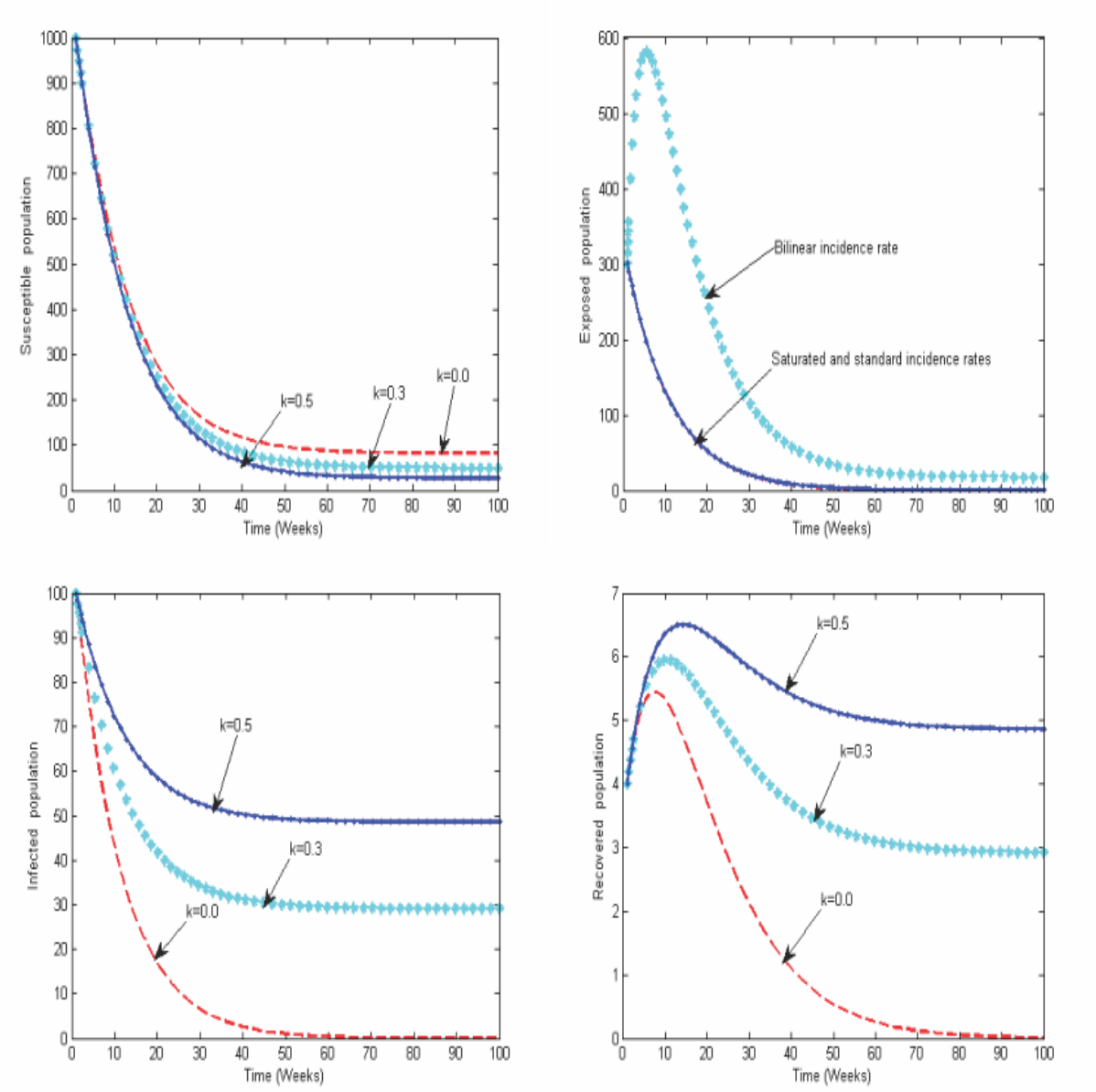

Figure 4. The dynamical behavior of the SVEIR model with different proportions of infective immigrants. The parameter values are $\beta = 0.002, p = 0.4,\ \tau = 0.003, \delta = 0.009, \mu = 0.09, d = 0.004, \pi = 10, \omega = 0.05$.

5 Discussion and Conclusion

This study investigates the transmission dynamics of infectious diseases with a saturated incidence rate and the influx of infected immigrants in the population. The model is a deterministic SVEIR model. The basic reproduction number, R_0, is computed using the next-generation approach. The disease-free and endemic equilibrium states without the influx of infected immigrants are shown to be local

and global asymptomatically stable when $R_0 < 1$ and $R_0 > 1$ respectively. Also, the endemic equilibrium state when there is an influx of infected immigrants in the population is established under certain conditions. A forward bifurcation existed when there is no infective immigrant in the population. Numerical results show that the saturated incidence and the standard incidence rates produce the same results that reduce the number of infected individuals in the population compared to the bilinear incidence rate (Figure 3). The important of infected immigrants is considered and the outcome reveals that infected immigrants do not affect exposed individuals in the population. However, infected individuals increase as the proportion of infected immigrants increase (see Figure 4) and this is comparable with the work of [12] that considered the entrance of infected immigrants in the population for an SEIRS model. This indicates that measures should be taken to reduce the influx of infected immigrants in the population. One of these measures could be screening at the entry point in the population especially for infectious diseases like COVID-19, SARS, MERS, Ebola virus disease and Lassa virus.

References

[1] The Red Cross and the World Health Organization Regional Office for Europe (2001). Infection and Infectious diseases: A manual for nurses and midwives in the WHO Europe Region. https:// www.euro.who.int > assets > pdf_files

[2] Baldassi, F., Carestia, M., Moramarco, S., Malizia, A., and Gaudio, P. (2021). Infectious Diseases Seeker (IDS): An Innovative Tool for Prompt Identification of Infectious Diseases during Outbreaks. Int. J. Environ. Res. Public Health, 18: 3216. https://doi.org/10.3390/ijerph18063216.

[3] Li-Ming Cai and Xue-Zhi Li (2008). Analysis of a SEIV Epidemic Model with a Nonlinear Incidence Rate. J. of Appl. Math Modelling doi: 10.1016/j.apm.2008.01.005.

[4] Liu, W.M., Hethcote, H.W. and Levin, S.A. (1987). Dynamical behavior of epidemiological models with nonlinear incidence rates. J. Math. Biol., 25: 359-380.[5] Zhang, T. and Teng, Z. (2007). Pulse vaccination delayed SEIRS epidemic model with saturated incidence. Appl. Math. Model. doi: 10.1016/J. amp. 2007.06.005.

[6] Liu, W.M., Levin, S.A. and Iwasa, Y. (1986). Influence of nonlinear incidence rates upon the behavior of SIRS epidemiological models. J.Math.Biol., 23:187-204.

[7] Capasso, V. and Serio, G. (1978). A generalization of the Kermack-Mckendrick deterministic epidemic model. Math. Biosci., 42:43-61.

[8] Li-Ming Cai and Xue-Zhi Li (2009). Analysis of a SEIV Epidemic Model with a Nonlinear Incidence Rate. Applied Mathematical Modelling, 33: 2919 – 2926.

[9] Khan, M. A., Badshah, Q., Islam, S, Khan, I., Shafie, S. and Khan, S. A. (2015). Global dynamics of SEIRS epidemic model with non-linear generalized incidences and preventive vaccination. Advances in Difference Equations, 2015:88.

[10] Liu, X. and Yang, L. (2012). Stability Analysis of an SEIQV epidemic model with saturated incidence rate. Nonlinear Analysis. Real World Applications,13(2012):2671-2679.

[11] Enatsu, Y., Nakata, Y. and Muroya, Y. (2012). Global stability of SIRS epidemic models with a class of nonlinear incidence rates and distributed delays. Acta Mathematica Scientia. 32(3): 851-865.

[12] Li, J. and Cui, N. (2013). Dynamics Analysis of an SEIR Model with Distinct Incidence for Exposed and infectives. The Scientific World Journal, 2013: Article ID 871393.
[13] Safi, M. A. and Garba, S. M. (2012). Global Stability Analysis of SEIR Model with Holling Type II incidence Function. Computational and Mathematical Method in Medicine, 2012:Article ID 826052.
[14] Zhang, L., Li, Y., Ren, Q. and Huo, Z. (2013). Global dynamics of an SEIRS epidemic model with constant immigration and immunity. WSEAS Trans. Math. 12(5): 630-640.
[15] Liu, W.M., Hethcote, H.W. and Levin, S.A. (1987). Dynamical behavior of epidemiological models with nonlinear incidence rates. J. math. Boil., 25: 359-380.
[16] Liu, W.M., Levin, S.A. and Iwasa, Y. (1986). Influence of nonlinear incidence rates upon the behavior of SIRS epidemiological models. J.math.Biol., 23:187-204.
[17] CDC (2014). Ebola Disease Outbreak – Nigeria, July – September 2014. Morbidity and Mortality Weekly Report (MMWR), October 3, 2014/ 63(39):867-872.
[18] NCDC (2020). First Case of Corona Virus Disease confirmed in Nigeria. https://ncdc.gov.ng/nes/227/first-case-of-corona-virus-disease-confirmed-in-nigeria. Accessed on 14th July, 2021.
[19] Van den Driessche, P and Watmough, J. (2002). Reproduction number and sub-threshold endemic equilibrium for compartmental models of disease of transmission. Math Biosci. 180: 29-48.
[20] Castillo – Chavez, C. and Song, B. (2004). Dynamical models of tuberculosis and their applications. Mathematical Biosciences and Engineering, 1(2): 361-404.
[21] Shaui, Z. and van den Driessche, P. (2013). Global Stability of Infectious Disease Models Using Lyapunov Functions. SIAM J. Appl. Math., 73(4): 1513 – 1532.