Stability and Sensitivity Analysis of a Deterministic Epidemiological Model with Pseudo-recovery

Samson Olaniyi, Maruf A. Lawal, Olawale S. Obabiyi

***Abstract*—A deterministic epidemiological model describing the spread of infectious disease characterized by pseudo-recovery due to incomplete treatment is studied. The resulting SEIRI model in a closed system is robustly analysed. Trans-critical bifurcation at the threshold, $\mathcal{R}_0 = 1$, is investigated and the global asymptotic dynamics of the model around the disease-free and endemic equilibria are explored by the aid of suitable Lyapunov functionals. Further, sensitivity analysis complemented by simulations are performed to determine how changes in parameters affect the dynamical behaviour of the system.**

***Index Terms*—epidemiological model, pseudo-recovery, trans-critical bifurcation, global stability, sensitivity analysis.**

I. Introduction

In mathematical epidemiology, deterministic models are widely used to describe the transmission and spread of infectious diseases in a population. These models are often referred to as compartmental models since the individuals in the population are divided into classes or compartments depending on their disease status.

For instance, the popular epidemic model in Kermack and McKendrick [1] divides the population into three compartments: susceptible (S), in which individuals are not currently harbouring the disease but are liable to contract the disease; infectious class (I), in which individuals in the population are infected and are capable of transmitting the disease to other individuals; recovered class (R), in which individuals are recovered from the disease and subsequently acquire permanent immunity.

Arising from the classical SIR model in [1], several extensions have been made with a view to developing a more realistic epidemiological models. The choice of which classes or compartments to incorporate into a model depends on the features of the infectious disease under consideration (see [2], [3], [4], [5], [6], [7] for some collections of these models among others).

In recent times, a number of mathematical models have been developed in the literature to study the transmission and spread of diseases with relapse (see, e.g., [8], [9], [10] and the references cited therein). A relapse phenomenon is a condition whereby signs and symptoms of a disease are reverted after a period of improvement. This phenomenon is what we call *pseudo-recovery* and is due to incomplete treatment of the disease.

Manuscript received September 1, 2015; revised January 30, 2016.

S. Olaniyi and M. A. Lawal are with the Department of Pure and Applied Mathematics, Ladoke Akintola University of Technology, Ogbomoso, Nigeria, e-mail: solaniyi@lautech.edu.ng.

O. S. Obabiyi is with the Department of Mathematics, University of Ibadan, Ibadan, Nigeria.

Some diseases such malaria, herpes and bovine and human tuberculosis exhibit pseudo-recovery or relapse in which the recovered individuals do not acquire permanent immunity but return to the infectious class. For malaria, pseudo-recovery is commonly seen with *Plasmodium* vivax and *Plasmodium* ovale infections when the malaria symptoms reapper after the parasites had been cleared from the blood but persist as dormant hypnozoites in the liver cells [9]. For herpes (see, e.g., [11]), an individual once infected remains infected all his life, passing regularly through episodes of relapse of infectiousness while for tuberculosis, pseudo-recovery can be caused by incomplete treatment or by reactivation of latent infection, being observed that HIV-positive patients are significantly more likely to relapse than HIV-negative patients (see, [12]).

In [13], Vargas-De-León studied SIRI models with bilinear incidence rate (similar to that in [8]) and standard incidence rate. By constructing suitable Lyapunov functionals, the global asymptotic stability of the disease-free and endemic equilibria were established. Georgescue and Zhang [11] analyzed a SIRI model with nonlinear incidence of infection. They obtained sufficient conditions for the local stability of equilibria by means of Lyapunov's second method and it was shown that the global stability can be attained under suitable monotonicity conditions. Guo et al [14] studied an SIRI epidemic model with a certain nonlinear incidence rate and latent period where the stability and hopf bifurcation for the model were analyzed. In [15], the global stability results were extended to a delayed SIRI epidemic model with a general nonlinear incidence function. It was established that the basic reproduction number R_0 is a threshold for the stability of a delayed SIRI model.

In another development, an integro-differential equation was proposed in [16] to model a general relapse phenomenon in infectious diseases. The basic reproduction number R_0 for the model was identified and the global stability results were established by employing Lyapunov-Razumikhin technique and monotone dynamical systems theory. In a related work [17], a SEIRI model, among other disease models, was used to demonstrate the applications of matrix-theoretic and graph-theoretic methods to establish the global stability of the disease-free equilibrium and endemic equilibrium respectively. However, there is limited information on whether or not a pseudo-recovery can cause a forward or backward bifurcation as $\mathcal{R}_0$ crosses the threshold, $\mathcal{R}_0 = 1$. Further, how changes in parameters affect the basic reproduction number R_0 of the model with pseudo-recovery is scarce in the literature.

In this study, we consider an epidemiological model de-

scribing the spread of infectious disease characterized by pseudo-recovery due to incomplete treatment. The SEIRI model governed by a closed system of ordinary differential equations (ODEs) is robustly analyzed. The transcritical bifurcation at $R_0 = 1$ is investigated and the global asymptotic stabilities of the disease-free and endemic equilibria are explored by the aid of suitable Lyapunov functions. In addition, sensitivity analysis complemented by simulations are carried out to determine the impact of the key parameters on the behaviour of the system.

The rest of this study is organized as follows: The model formulation and its basic properties are shown in Section II. In Section III, local stability and transcritical bifurcation of the model are examined. In section IV, the global dynamics of the model around the disease-free and endemic equilibria are explored. In Section V, sensitivity analysis and numerical simulations are performed while concluding remarks are provided in Section VI.

II. Model Formulation

Consider a deterministic compartmental model which divides the total human population size at time t, denoted by $N(t)$, into susceptible individuals $S(t)$ (those who are not currently harbouring the disease but are liable to be infected), exposed individuals $E(t)$ (those who are infected but are incapable of transmitting the disease), infectious individuals $I(t)$ (those already infected and are able to transmit the disease), and pseudo-recovered individuals $R(t)$ (those who are recovered from the disease without permanent immunity but relapse). Assuming that the disease transmits in a closed system which translates into the simplifying assumption of a constant population size (see, e.g., [16], [18]) so that $N(t) = N$. Hence, we have the following system of ODEs with standard incidence:

$$\begin{aligned} \frac{dS}{dt} &= \mu N - \frac{\beta S(t) I(t)}{N} - \mu S(t) \\ \frac{dE}{dt} &= \frac{\beta S(t) I(t)}{N} - (\alpha + \mu) E(t) \\ \frac{dI}{dt} &= \alpha E(t) - (\gamma + \mu) I(t) + \theta R(t) \\ \frac{dR}{dt} &= \gamma I(t) - (\mu + \theta) R(t) \end{aligned} \tag{1}$$

together with the initial conditions:

$$S(0) = S_0,\ E(0) = E_0,\ I(0) = I_0,\ R(0) = R_0\ , \tag{2}$$

where μ represents the per capita birth (recruitment) rate and natural death (removal) rate, β is the effective contact rate, α denotes the progression rate of the exposed individuals to the infectious class, γ describes the rate at which infectious individuals become pseudo-recovered individuals and θ represents the pseudo-recovery (relapse) rate due to incomplete treatment.

We rescale the state variables of the formulated model (1) by normalizing as follows:

$$\bar{S} = \frac{S}{N},\ \ \bar{E} = \frac{E}{N},\ \ \bar{I} = \frac{I}{N},\ \ \bar{R} = \frac{R}{N},$$

so that $\bar{S} + \bar{E} + \bar{I} + \bar{R} = 1$. Thus, after dropping of bars, $(\bar{})$, model (1) leads to the following:

$$\begin{aligned} \frac{dS}{dt} &= \mu - \beta S(t) I(t) - \mu S(t) \\ \frac{dE}{dt} &= \beta S(t) I(t) - (\alpha + \mu) E(t) \\ \frac{dI}{dt} &= \alpha E(t) - (\gamma + \mu) I(t) + \theta R(t) \\ \frac{dR}{dt} &= \gamma I(t) - (\mu + \theta) R(t) \end{aligned} \tag{3}$$

A. Positivity of Solutions

Since model (3) represents interaction between individuals in the population, it makes sense to state that all the parameters involved are non-negative. It is also pertinent to show that all the state variables of the model are non-negative for all time. Hence, we have the following result:

Theorem 1. *The solution set $\{S, E, I, R\}$ of the epidemiological model* (3) *with non-negative initial data* (2) *remains non-negative for all time $t > 0$.*

Proof. Given that the initial data $S(0), E(0), I(0), R(0)$ are non-negative. It is clear from the first sub-equation of the model (3) that

$$\frac{dS}{dt} + [\beta I(t) + \mu] S(t) \geq 0,$$

so that,

$$\frac{d}{dt}\left[S(t) \exp\left(\mu t + \beta \int_0^t I(\zeta) d\zeta\right)\right] \geq 0. \tag{4}$$

Integrating (4) gives

$$S(t) \geq S(0) \exp\left[-\left(\mu t + \beta \int_0^t I(\zeta) d\zeta\right)\right] > 0, \forall t > 0. \tag{5}$$

Further, one sees from the second sub-equation of the model (3) that

$$\frac{dE}{dt} + (\alpha + \mu) E(t) \geq 0,$$

so that,

$$\frac{d}{dt}\left[E(t) \exp\left(\alpha + \mu\right) t\right] \geq 0, \tag{6}$$

which on integration yields

$$E(t) \geq E(0) \exp\left[-\left(\alpha + \mu\right) t\right] > 0, \forall t > 0. \tag{7}$$

In a similar fashion, it can be shown that $I(t) > 0$ and $R(t) > 0$ for all time $t > 0$. This completes the proof. □

It is crucial to note that model (3) will be analysed in a feasible region $\mathfrak{D}$ given by

$$\mathfrak{D} = \left\{(S, E, I, R) \in \mathbb{R}_+^4 : S + E + I + R = 1\right\}, \tag{8}$$

which can be easily verified to be positively invariant with respect to the model (3). In what follows, model (3) is epidemiologically and mathematically well-posed in $\mathfrak{D}$ (see, [2]).

III. Local Stability and Transcritical Bifurcation

This section deals with the local asymptotic stability of the disease-free and endemic equilibria with respect to the basic reproduction number, $\mathcal{R}_0$, and investigates whether model (3) exhibits supercritical or subcritical bifurcation as $\mathcal{R}_0$ crosses the threshold, $\mathcal{R}_0 = 1$.

A. Disease-Free Equilibrium

The disease-free equilibrium point of the model (3) is obtained as

$$\mathcal{E}_0 = (1,\ 0,\ 0,\ 0)\,. \tag{9}$$

It is noteworthy to state that, unlike the other epidemiological models without relapse, E, I and R are the diseased classes of the model (3) since there are traces of infection in the recovered individuals that make them to relapse.

To examine the local stability of $\mathcal{E}_0$ given by (9), it is important to first obtain the *basic reproduction number*, $\mathcal{R}_0$, defined as the average number of secondary infections caused by a typical infectious individual during its period of infectiousness in a completely susceptible population. Thus, using the next generation matrix approach [19], noting that

$$\frac{d}{dt}\begin{pmatrix} E \\ I \\ R \\ S \end{pmatrix} = \begin{pmatrix} \beta SI \\ 0 \\ 0 \\ 0 \end{pmatrix} - \begin{pmatrix} (\alpha+\mu)E \\ (\gamma+\mu)I - \alpha E - \theta R \\ (\theta+\mu)R - \gamma I \\ (\beta I+\mu)S - \mu \end{pmatrix},$$

from which the infection matrix $\mathbf{F}$ and transition matrix $\mathbf{V}$ are given, respectively, by

$$\mathbf{F} = \begin{pmatrix} 0 & \beta & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

and

$$\mathbf{V} = \begin{pmatrix} \alpha+\mu & 0 & 0 \\ -\alpha & \gamma+\mu & 0 \\ 0 & -\gamma & \theta+\mu \end{pmatrix}.$$

Consequently, we obtain the spectral radius of the matrix $\mathbf{FV^{-1}}$, known as the the basic reproduction number of the model (3) as

$$\mathcal{R}_0 = \frac{\alpha\beta(\theta+\mu)}{\mu(\alpha+\mu)(\theta+\gamma+\mu)}. \tag{10}$$

By Theorem 2 in [19], the result hereunder is established.

Lemma 1. *The disease-free equilibrium, $\mathcal{E}_0$, of the system* (3) *is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.*

The epidemiological implication of the above result is that the infectious disease governed by model (3) can be eliminated from the population whenever an influx by infectious individual into the population is small such that $\mathcal{R}_0 < 1$.

B. Transcritical Bifurcation

It is observed from the previous result that whenever $\mathcal{R}_0 > 1$, the asymptotic local stability of the disease-free equilibrium is lost. Here, we explore how the asymptotic local stability of the disease-free equilibrium is exchanged for asymptotic local stability of the endemic equilibrium of model (3) as the threshold quantity, $\mathcal{R}_0$, crosses the unity. In other words, we investigate the transcritical bifurcation at $\mathcal{R}_0 = 1$ using a center manifold theory of bifurcation analysis described in [20] and used in some disease models (see, e.g., [4], [5], [21], [22]). For convenience, the theorem in [20] is reproduced hereunder.

Theorem 2. *Consider the following general system of ordinary differential equations with a parameter ϕ:*

$$\frac{dx}{dt} = f(x,\phi),\quad f : \mathbb{R}^n \times \mathbb{R} \longrightarrow \mathbb{R} \text{ and } f \in \mathbb{C}^2(\mathbb{R}^n \times \mathbb{R}), \tag{11}$$

where 0 is an equilibrium point of the system (that is, $f(0,\phi) \equiv 0$ for all ϕ) and assume

A1: $A = D_x f(0,0) = \left(\dfrac{\partial f_i}{\partial x_j}(0,0)\right)$ *is the linearization matrix of the system given by (11) around the equilibrium 0 with ϕ evaluated at 0. Zero is a simple eigenvalue of A and other eigenvalues of A have negative real parts;*

A2: *Matrix A has a nonnegative right eigenvector w and a left eigenvector v corresponding to the zero eigenvalue.*

Let f_k be the kth component of f and

$$a = \sum_{k,i,j=1}^{n} v_k w_i w_j \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0),$$
$$b = \sum_{k,i=1}^{n} v_k w_i \frac{\partial^2 f_k}{\partial x_i \partial \phi}(0,0).$$

The local dynamics of (11) around 0 are totally determined by a and b.

(i) $a > 0, b > 0$. *When $\phi < 0$ with $|\phi| \ll 1$, 0 is locally asymptotically stable and there exists a positive unstable equilibrium; when $0 < \phi \ll 1$, 0 is unstable and there exists a negative, locally asymptotically stable equilibrium;*

(ii) $a < 0, b < 0$. *When $\phi < 0$ with $|\phi| \ll 1$, 0 is unstable; when $0 < \phi \ll 1$, 0 is locally asymptotically stable, and there exists a positive unstable equilibrium;*

(iii) $a > 0, b < 0$. *When $\phi < 0$ with $|\phi| \ll 1$, 0 is unstable, and there exists a locally asymptotically stable negative equilibrium; when $0 < \phi \ll 1$, 0 is stable, and a positive unstable equilibrium appears;*

(iv) $a < 0, b > 0$. *When ϕ changes from negative to positive, 0 changes its stability from stable to unstable. Correspondingly a negative unstable equilibrium becomes positive and locally asymptotically stable.*

In what follows, let the model (3) be written in the vector form

$$\frac{dX}{dt} = H(X),$$

where $X = (x_1, x_2, x_3, x_4)^T$ and $H = (h_1, h_2, h_3, h_4)^T$, so that $S = x_1, E = x_2, I = x_3, R = x_4$. Then model (3) becomes

$$\begin{aligned} \frac{dx_1}{dt} &= \mu - \beta x_1 x_3 - \mu x_1 := h_1 \\ \frac{dx_2}{dt} &= \beta x_1 x_3 - (\alpha+\mu)x_2 := h_2 \\ \frac{dx_3}{dt} &= \alpha x_2 - (\gamma+\mu)x_3 + \theta x_4 := h_3 \\ \frac{dx_4}{dt} &= \gamma x_3 - (\mu+\theta)x_4 := h_4 \end{aligned}. \tag{12}$$

Choosing β as the bifurcation parameter, then at $\mathcal{R}_0 = 1$ in (10), we obtain

$$\beta = \beta^* := \frac{\mu(\alpha+\mu)(\theta+\gamma+\mu)}{\alpha(\theta+\mu)}, \tag{13}$$

so that the disease-free equilibrium, $\mathcal{E}_0$, is locally stable when $\beta < \beta^*$, and is unstable when $\beta > \beta^*$. Thus, β^* is a bifurcation value.

The linearized matrix of the system (12) around the disease-free equilibrium $\mathcal{E}_0$ and evaluated at β^* is given by

$$J(\mathcal{E}_0,\beta^*)=\begin{pmatrix} -\mu_h & 0 & -\beta^* & 0\\ 0 & -(\alpha+\mu) & \beta^* & 0\\ 0 & \alpha & -(\gamma+\mu) & \theta\\ 0 & 0 & \gamma & -(\theta+\mu)\end{pmatrix}, \tag{14}$$

The eigenvalues (λ), of $J(\mathcal{E}_0,\beta^*)$ given by (14) are the roots of the characteristic equation of the form:

$$(\lambda+\mu)P(\lambda)=0, \tag{15}$$

where $P(\lambda)$ is a polynomial of degree three whose roots are real and negative except one zero eigenvalue. The right eigenvector, $\mathbf{w}=(w_1,w_2,w_3,w_4)^T$, associated with this simple zero eigenvalue can be obtained from $J(\mathcal{E}_0,\beta^*)\mathbf{w}=0$. As a result, we have

$$w_1=-\frac{(\alpha+\mu)(\theta+\gamma+\mu)w_3}{\alpha(\theta+\mu)},\ w_2=\frac{\mu(\theta+\gamma+\mu)w_3}{\alpha(\theta+\mu)},$$

$$w_3=w_3,\ w_4=\frac{\gamma w_3}{\theta+\mu}.$$

Further, the left eigenvector, $\mathbf{v}=(v_1,v_2,...,v_7)$, corresponding to the simple zero eigenvalue of (15) is obtained from $\mathbf{v}J(\mathcal{E}_0,\beta^*)=0$ as

$$v_1=0,\ v_2=\frac{\alpha v_3}{(\alpha+\mu)},\ v_3=v_3,\ v_4=\frac{\theta v_3}{\theta+\mu}$$

In order that **v.w=**1 as required in [20], w_3 and v_3 are given, respectively, by

$$w_3=\frac{1}{\mu(\theta+\mu)(\theta+\gamma+\mu)+(\alpha+\mu)[\gamma\theta+(\theta+\mu)^2]}$$

and

$$v_3=(\alpha+\mu)(\theta+\mu)^2.$$

All the second-order partial derivatives of $h_i, i=1,2,3,4$, from the system (12) are zero at point $(\mathcal{E}_0,\beta^*)$ except the following:

$$\frac{\partial^2 h_1}{\partial x_1\partial x_3}=\frac{\partial^2 h_1}{\partial x_3\partial x_1}=-\beta^*,$$

$$\frac{\partial^2 h_2}{\partial x_1\partial x_3}=\frac{\partial^2 h_2}{\partial x_3\partial x_1}=\beta^*$$

with

$$\frac{\partial^2 h_1}{\partial x_3\partial\beta}=-1,\ \frac{\partial^2 h_2}{\partial x_3\partial\beta}=1.$$

The direction of the bifurcation at $\mathcal{R}_0=1$ is determined by the signs of the bifurcation coefficients a and b, obtained from the above partial derivatives, given, respectively, by

$$\begin{aligned} a &= \sum_{k,i,j=1}^{4} v_k w_i w_j \frac{\partial^2 h_k}{\partial x_i\partial x_j}(\mathcal{E}_0,\beta^*)\\ &= -\frac{2v_3w_3^2\mu(\alpha+\mu)}{\alpha}\left[\frac{\theta+\gamma+\mu}{\theta+\mu}\right]^2 \end{aligned} \tag{16}$$

and

$$\begin{aligned} b &= \sum_{k,i=1}^{4} v_k w_i \frac{\partial^2 h_k}{\partial x_i\partial\beta}(\mathcal{E}_0,\beta^*)\\ &= \frac{\alpha v_3 w_3}{\alpha+\mu} \end{aligned} \tag{17}$$

From the fact that all the parameters of model (3) are positive and since w_3 and v_3 are positive, one sees that $a<0$ and $b>0$. Thus, by Theorem 2 item (iv), the model (3) exhibits a supercritical (forward) bifurcation as $\mathcal{R}_0$ crosses the threshold, $\mathcal{R}_0=1$ (or, equivalently, a locally asymptotically stable endemic equilibrium $\mathcal{E}_e$:= (S^*,E^*,I^*,R^*) representing the non-trivial positive steady-states of model (3) exists). This result is theorized hereunder:

Theorem 3. *The transcritical bifurcation at $\mathcal{R}_0=1$ of the model* (3) *is supercritical* (*or, equivalently, there exists a locally asymptotically stable endemic equilibrium, $\mathcal{E}_e$, for $\mathcal{R}_0>1$ near $\mathcal{R}_0=1$*).

The implication of the above result is that a small inflow of infectious individuals into a completely susceptible population will lead to the persistence of the disease in the community whenever $\mathcal{R}_0>1$. In other words, the exchange of the local asymptotic stability of the equilibria depends on the initial number of the infectious individuals in the population. However, it is important to show that the exchange or transfer of the local asymptotic stability of the equilibria is independent of the initial sizes of the subpopulations of the model (3). This is done in the next section.

IV. Global stability analysis

One of the effective methods used in addressing the problem associated with the global stability analysis of epidemiological models is the use of Lyapunov functions. For insights on the useful construction of suitable Lyapunov functions for disease models with different forms of incidence rates, see [13], [23], and the references therein. First, the following result investigates the global dynamics of the model (3) around the disease-free equilibrium.

Theorem 4. *The disease-free equilibrium, $\mathcal{E}_0$, given by* (9)*, of the model* (3)*, is globally asymptotically stable in $\mathfrak{D}$ if $\mathcal{R}_0\le 1$.*

Proof. The proof is based on the use of the linear Lyapunov function (see [17], for a different construction via the matrix-theoretic approach) defined by

$$\mathfrak{L}=\frac{\alpha}{\alpha+\mu}E+I+\frac{\theta}{\theta+\mu}R \tag{18}$$

The time derivative of $\mathfrak{L}$ given by (18) along the solutions of the model (3) yields

$$\begin{aligned} \dot{\mathfrak{L}} &= \frac{\alpha}{\alpha+\mu}\left[\beta SI-(\alpha+\mu)E\right]\\ &\quad+\left[\alpha E-(\gamma+\mu)I+\theta R\right]\\ &\quad+\frac{\theta}{\theta+\mu}\left[\gamma I-(\theta+\mu)R\right]\\ &= \frac{\alpha\beta SI}{\alpha+\mu}-(\gamma+\mu)I+\frac{\gamma\theta I}{\theta+\mu}\\ &\le \left[\frac{\alpha\beta}{\alpha+\mu}-\frac{\mu(\gamma+\theta+\mu)}{\theta+\mu}\right]I\\ &= \frac{\mu(\gamma+\theta+\mu)}{\theta+\mu}\left[\mathcal{R}_0-1\right]I. \end{aligned}$$

Therefore $\dot{\mathfrak{L}}\le 0$ for $\mathcal{R}_0\le 1$ with $\dot{\mathfrak{L}}=0$ if and only if $I=0$. Further, one sees that $(S,E,R)\to(1,0,0)$ as $t\to\infty$

since $I \to 0$ as $t \to \infty$. It follows that the largest compact invariant set in $\{(S, E, I, R) \in \mathfrak{D} : \dot{\mathfrak{L}} = 0\}$ is the singleton $\{\mathcal{E}_0\}$ and by Lyapunov-LaSalle's invariance principle [24], $\mathcal{E}_0$ is globally asymptotically stable in $\mathfrak{D}$ if $\mathcal{R}_0 \leq 1$. Hence, the proof. □

The above result implies that the disease elimination is possible irrespective of the initial sizes of the sub-populations of the model whenever the threshold parameter, $\mathcal{R}_0$, is less than unity.

Remark 1. It is worth mentioning that the global asymptotic stability of the disease-free equilibrium, $\mathcal{E}_0$, shown in the previous result, can also be established using the method in [25] (see, also, [5]). This can be achieved by re-writing model system (3) as

$$\begin{aligned} \frac{dY}{dt} &= F(Y, Z) \\ \frac{dZ}{dt} &= G(Y, Z), \qquad G(Y, 0) = 0, \end{aligned} \tag{19}$$

where $Y = S \in \mathbb{R}_+$ denotes uninfected individuals in the population and $Z = (E, I, R) \in \mathbb{R}^3_+$ denotes the infected individuals in the population (noting that the compartment R contains pseudo-recovered individuals with traces of infection). Further, $\mathcal{E}_0 = (Y^\star, 0)$ represents the disease-free equilibrium of (19), where $Y^\star = 1$. Thus, the conditions (H1) and (H2) below guarantee global asymptotic stability of $\mathcal{E}_0$:

H1: For $\dfrac{dY}{dt} = F(Y, 0)$, $Y^\star$ is globally asymptotically stable.

H2: $G(Y, Z) = AZ - \widehat{G}(Y, Z)$, $\widehat{G}(Y, Z) \geq 0$, for $(Y, Z) \in \mathbb{R}^4_+$,

where $A = D_Z G(Y^\star, 0)$ is the jacobian of $G(Y, Z)$ taken in (E, I, R) and evaluated at $(Y^\star, 0) = (1, 0, 0, 0)$.

Next, we explore the global dynamics of the model (3) around the endemic equilibrium, $\mathcal{E}_e = (S^*, E^*, I^*, R^*)$, which has been shown to exist when $\mathcal{R}_0 > 1$ (see, Theorem 3).

Theorem 5. *The endemic equilibrium, $\mathcal{E}_e$, of the model* (3) *is globally asymptotically stable whenever $\mathcal{R}_0 > 1$.*

Proof. Using the following nonlinear Volterra-type Lyapunov function (see, e.g., [17], [22], [26], for similar approach).

$$\begin{aligned} \mathfrak{L} &= S - S^* - S^* \ln\left(\frac{S}{S^*}\right) \\ &\quad + E - E^* - E^* \ln\left(\frac{E}{E^*}\right) \\ &\quad + \frac{\alpha + \mu}{\alpha}\left[I - I^* - I^* \ln\left(\frac{I}{I^*}\right)\right] \\ &\quad + \frac{\theta(\alpha + \mu)}{\alpha(\theta + \mu)}\left[R - R^* - R^* \ln\left(\frac{R}{R^*}\right)\right], \end{aligned} \tag{20}$$

with the Lyapunov derivative given by

$$\begin{aligned} \dot{\mathfrak{L}} &= \dot{S} - \frac{S^*}{S}\dot{S} + \dot{E} - \frac{E^*}{E}\dot{E} \\ &\quad + \frac{\alpha + \mu}{\alpha}\left(\dot{I} - \frac{I^*}{I}\dot{I}\right) \\ &\quad + \frac{\theta(\alpha + \mu)}{\alpha(\theta + \mu)}\left(\dot{R} - \frac{R^*}{R}\dot{R}\right), \end{aligned} \tag{21}$$

where dot represents the differentiation with respect to time t. If we substitute the equations in model (3) appropriately into (21), we have

$$\begin{aligned} \dot{\mathfrak{L}} &= \mu - \beta SI - \mu S - \tfrac{S^*}{S}\left(\mu - \beta SI - \mu S - \tfrac{S^*}{S}\right) \\ &\quad + \beta SI - [\alpha + \mu]E - \tfrac{E^*}{E}\left(\beta SI - [\alpha + \mu]E\right) + \tfrac{\alpha+\mu}{\alpha} \\ &\quad \times \left(\alpha E - [\gamma + \mu]I + \theta R - \tfrac{I^*}{I}\left[\alpha E - [\gamma + \mu]I + \theta R\right]\right) \\ &\quad + \tfrac{\theta(\alpha+\mu)}{\alpha(\theta+\mu)}\left(\gamma I - [\theta + \mu]R - \frac{R^*}{R}\left[\gamma I - [\theta + \mu]R\right]\right), \end{aligned}$$

and further simplification yields

$$\begin{aligned} \dot{\mathfrak{L}} &= \mu\left(1 - \frac{S^*}{S}\right) - \mu S\left(1 - \frac{S^*}{S}\right) \\ &\quad + \beta S^* I - \frac{E^* \beta SI}{E} \\ &\quad + (\alpha + \mu)E^* - \frac{(\alpha + \mu)(\gamma + \mu)I}{\alpha} \\ &\quad - \frac{(\alpha + \mu)I^* E}{I} + \frac{(\alpha + \mu)(\gamma + \mu)I^*}{\alpha} \\ &\quad - \frac{(\alpha + \mu)\theta I^* R}{\alpha I} + \frac{(\alpha + \mu)\theta\gamma I}{\alpha(\theta + \mu)} \\ &\quad - \frac{(\alpha + \mu)\theta\gamma R^* I}{\alpha(\theta + \mu)R} + \frac{(\alpha + \mu)\theta R^*}{\alpha}. \end{aligned} \tag{22}$$

At the endemic steady state, the following relations obtained from model (3) hold:

$$\begin{aligned} \mu &= \beta S^* I^* + \mu S^* \\ \alpha + \mu &= \frac{\beta S^* I^*}{E^*} \\ \gamma + \mu &= \frac{\alpha E^* + \theta R^*}{I^*} \\ \theta + \mu &= \frac{\gamma I^*}{R^*} \end{aligned} \tag{23}$$

By using (23) in (22) and simplifying, we get

$$\begin{aligned} \dot{\mathfrak{L}} &= \mu S^*\left[2 - \frac{S^*}{S} - \frac{S}{S^*}\right] \\ &\quad + \beta S^* I^*\left[3 - \frac{S^*}{S} - \frac{E^* SI}{ES^* I^*} - \frac{I^* E}{IE^*}\right] \\ &\quad + \frac{\beta\theta S^* I^* R^*}{\alpha E^*}\left[2 - \frac{I^* R}{IR^*} - \frac{IR^*}{I^* R}\right]. \end{aligned} \tag{24}$$

Since the arithmetic mean is greater or equal to the geometric mean (AM-GM inequality), one sees that

$$\left[2-\frac{S^*}{S}-\frac{S}{S^*}\right]\leq 0,$$

$$\left[3-\frac{S^*}{S}-\frac{E^*SI}{ES^*I^*}-\frac{I^*E}{IE^*}\right]\leq 0,$$

$$\left[2-\frac{I^*R}{IR^*}-\frac{IR^*}{I^*R}\right]\leq 0.$$

It follows from (24) that $\dot{\mathfrak{L}}\leq 0$ with $\dot{\mathfrak{L}}=0$ if and only if $S=S^*$, $E=E^*$, $I=I^*$, $R=R^*$. Thus, by Lyapunov-LaSalle's invariance principle [24], the largest compact invariant subset of the set where $\dot{\mathfrak{L}}=0$ is the singleton $\{\mathcal{E}_e=(S^*,E^*,I^*,R^*)\}$ and we conclude that the endemic equilibrium, $\mathcal{E}_e$, is globally asymptotically stable. This completes the proof. □

The epidemiological implication of the above result is that the disease will establish itself in the community whenever $\mathcal{R}_0>1$ irrespective of the initial sizes of the infectious individuals in the population (see Figure 3 for a graphical illustration).

V. SENSITIVITY ANALYSIS AND SIMULATIONS

This section examines the changing effects of the model parameters with respect to the basic reproduction number, $\mathcal{R}_0$, of the model (3). Numerical simulations are also carried out to complement the theoretical results obtained.

A. Sensitivity Analysis

To determine how changes in parameters affect the transmission and spread of the disease with pseudo-recovery, a sensitivity analysis of the model (3) is carried out in the sense of [22], [27].

Definition 1. *The normalized forward-sensitivity index of a variable, v, that depends differentiably on a parameter, p, is defined as:*

$$\Upsilon_p^v=\frac{\partial v}{\partial p}\times\frac{p}{v}. \tag{25}$$

In particular, sensitivity indices of the basic reproduction number, $\mathcal{R}_0$, with respect to the model parameters are examined. For examples, using (25), we obtain:

$$\begin{aligned}\Upsilon_\theta^{\mathcal{R}_0}&=\frac{\partial\mathcal{R}_0}{\partial\theta}\times\frac{\theta}{\mathcal{R}_0}=\frac{\theta\gamma}{(\theta+\mu)(\theta+\gamma+\mu)},\\ \Upsilon_\gamma^{\mathcal{R}_0}&=\frac{\partial\mathcal{R}_0}{\partial\gamma}\times\frac{\gamma}{\mathcal{R}_0}=-\left(\frac{\gamma}{\gamma+\theta+\mu}\right),\\ \Upsilon_\alpha^{\mathcal{R}_0}&=\frac{\partial\mathcal{R}_0}{\partial\alpha}\times\frac{\alpha}{\mathcal{R}_0}=\frac{\mu}{\alpha+\mu}.\end{aligned} \tag{26}$$

The sensitivity index (S.I.) of $\mathcal{R}_0$ to μ can be obtained in a similar manner and the signs of S.I. are summarized in the Table I. The positive sign of S.I. of $\mathcal{R}_0$ to the model parameters shows that an increase (or decrease) in the value of each of the parameter in this case will lead to an increase (or decrease) in $\mathcal{R}_0$ of the model (3) and asymptotically results into persistence (or elimination) of the disease in the community (see, Theorem 4 and Theorem 5). For instance,

TABLE I
SIGNS OF S.I. OF $\mathcal{R}_0$

Parameter	S.I.
β	positive
μ	negative
α	positive
θ	positive
γ	negative

TABLE II
THE VALUES OF MODEL PARAMETERS

Parameter	Value	Source
β	0.1	[15]
μ	0.01	[15]
α	varied	Assumed
θ	varied	Assumed
γ	0.6	[11]

$\Upsilon_\beta^{\mathcal{R}_0}=1$ means that increasing (or decreasing) β by 10% increases (or decreases) $\mathcal{R}_0$ by 10%. On the contrary, the negative sign of S.I. of $\mathcal{R}_0$ to the model parameters indicates that an increase (or decrease) in the value of each of the parameter in this case leads to a corresponding decrease (or increase) in $\mathcal{R}_0$ of the model (3). Hence, with sensitivity analysis, one can get insight on the appropriate intervention strategies to prevent and control the spread of the disease described by model (3).

B. Simulations

We illustrate the results of the sensitivity analysis by numerically simulating the behaviour of the model (3) using the parameter values given in Table II. In particular, we illustrate the changing effects of the pseudo-recovery rate, θ, and that of α on the size of infectious individuals. This is done because an increase or decrease in the basic reproduction number, $\mathcal{R}_0$, is determined by the influx of the infectious individuals in the community.

Considering the initial conditions $S_0=0.99$, $E_0=0.01$, $I_0=0$, $R_0=0$, the results of the simulations are provided in the Figures 1-3.

VI. CONCLUSION

This study presented both theoretical and quantitative analyses of a deterministic epidemiological model that is characterized by pseudo-recovery phenomenon. The results obtained are highlighted as follows:

(i) The disease-free equilibrium is locally asymptotically stable when the threshold quantity, $\mathcal{R}_0$, is less than unity.

(ii) The transcritical bifurcation at the threshold, $\mathcal{R}_0=1$, is forward and a locally asymptotically stable endemic equilibrium exists when $\mathcal{R}_0>1$ as the threshold, $\mathcal{R}_0$, crosses unity.

(iii) The model has a globally asymptotically stable disease-free equilibrium when the threshold parameter $\mathcal{R}_0<1$.

(iv) The endemic equilibrium of the formulated model is globally asymptotically stable whenever the threshold quantity, $\mathcal{R}_0$, is greater than unity.

(v) Increasing the value of any of the parameters, β, α, or θ, increases the basic reproduction number, $\mathcal{R}_0$, and the magnitude of the infectious individuals in the community

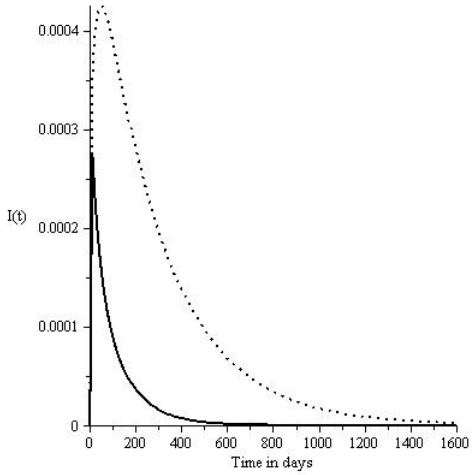

Fig. 1. The changing effects of the pseudo-recovery rate θ on the number of infectious individuals. For a fixed value $\alpha = 0.02$ with $\theta = 0.01(\mathcal{R}_0 = 0.2151)$: (solid curve) and $\theta = 0.05(\mathcal{R}_0 = 0.6061)$: (dotted curve), the solutions approach the disease-free equilibrium asymptotically (in line with Theorem 4)

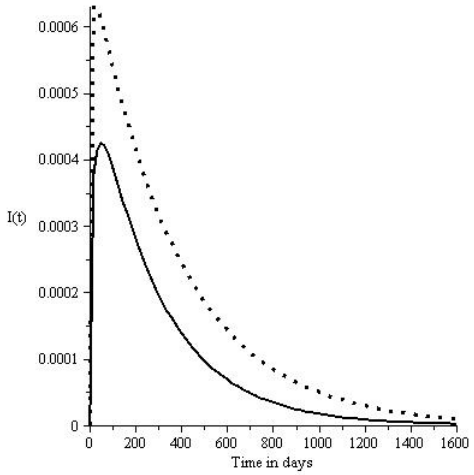

Fig. 2. The changing effects of the progression rate α on the number of infectious individuals. For a fixed value $\theta = 0.05$ with $\alpha = 0.02(\mathcal{R}_0 = 0.6061)$: (solid curve) and $\alpha = 0.04(\mathcal{R}_0 = 0.7272)$: (dotted curve) which are in line with the sensitivity analysis results, increasing value of α increases the magnitude of the infectious individuals that eventually approach the disease-free equilibrium (in line with Theorem 4)

increases accordingly. Conversely, increasing the value of either μ or γ, decreases the basic reproduction number, $\mathcal{R}_0$, and the magnitude of the infectious individuals in the community decreases accordingly.

Therefore, it is pertinent to conclude that efforts at reducing the basic reproduction number of a disease should be encouraged in order to achieve a disease-free population. Above all, prevention, early detection and arresting any disease with or without pseudo-recovery at its onset is a panacea for the disease endemicity.

ACKNOWLEDGMENT

The improvement of the original manuscript is due to the constructive comments and valuable suggestions of the reviewers and handling editor.

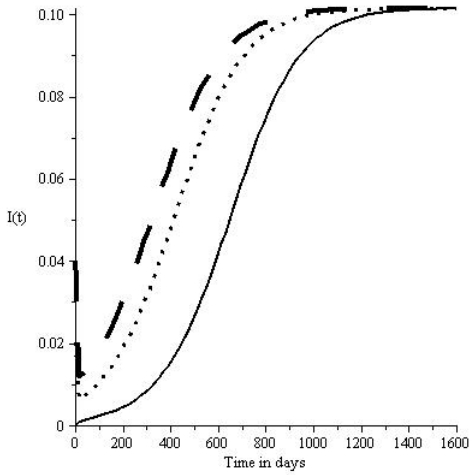

Fig. 3. The changing effects of initial conditions as $\mathcal{R}_0 > 1$. For fixed values of $\alpha = 0.02$ with $\theta = 0.25; (\mathcal{R}_0 = 2.0155)$, and $S_0 = 0.99$, $E_0 = 0.01$, $I_0 = 0$, $R_0 = 0$: (solid curve), $S_0 = 0.97$, $E_0 = 0.01$, $I_0 = 0.02$, $R_0 = 0$: (dotted curve), $S_0 = 0.95$, $E_0 = 0.01$, $I_0 = 0.04$, $R_0 = 0$: (dashed curve). The solutions asymptotically approach the endemic equilibrium (in line with Theorem 5)

REFERENCES

[1] W. O. Kermack and A. G. McKendrick, "Contributions to the mathematical theory of epidemics, part I," *Proceedings of the Royal Society of London Series A*, vol. 115, 700–721, 1927.

[2] H. W. Hethcote, "The mathematics of infectious diseases," *SIAM Review*, vol. 42, no. 4, pp. 599–653, 2000.

[3] M. Zhien, Z. Yicang and W. Jianhong, *Modeling and Dynamics of Infectious Disease*, World Scientific Publishing Co Pte Ltd., Singapore, 2009.

[4] S. M. Garba, A. B. Gumel and N. Hussaini, "Mathematical analysis of an age-structured vaccination model for measles," *Journal of the Nigerian Mathematical Society*, vol. 33, pp. 41–76, 2014.

[5] C. P. Bhunu and S. Mushayabasa, "Modelling the transmission dynamics of pox-like infections," *IAENG International Journal of Applied Mathematics*, vol. 41, no. 2, pp. 141–149, 2011.

[6] S. Olaniyi and O. S. Obabiyi, "Mathematical model for malaria transmission dynamics in human and mosquito populations with nonlinear forces of infection," *International Journal Pure and Applied Mathematics*, vol. 88, no. 1, pp. 125–156, 2013.

[7] C. Xu and M. Liao, "Stability and bifurcation analysis in a SEIR epidemic model with nonlinear incidence rates," *IAENG International Journal of Applied Mathematics*, vol. 41, no. 3, pp. 191–198, 2011.

[8] D. Tudor, "A deterministic model for herpes infections in human and animal populations," *SIAM Review*, vol. 32, no. 1, pp. 136–139, 1990.

[9] H. F. Huo and G. M. Qiu, "Stability of a mathematical model of malaria transmission with relapse," *Abstract and Applied Analysis*, vol. 2014, Article ID 289349, 9 pages, 2014.

[10] R. Xu, "Global dynamics of an SEIRI epidemiological model with time delay," *Applied Mathematics and Computation*, vol. 232, pp. 436–444, 2014.

[11] P. Georgescu and H. Zhang, "A Lyapunov functional for a SIRI model with nonlinear incidence of infection and relapse," *Applied Mathematics and Computation*, vol. 219, pp. 8496–8507, 2013.

[12] H. Cox, Y. Kebeda, S. Allamuratova, G. Ismailov, Z. Davletmuratova, G. Byrnes, C. Stone, S. Niemann, S. Rsch-Gerdes, L. Blok and D. Doshetov, "Tuberculosis recurrence and mortality after successful treatment: impact of drug resistance," *PLoS Med.*, vol. 3, no. 10, pp. 1836–1843, 2006.

[13] C. Vargas-De-León, "On the global stability of infectious diseases models with relapse", *Abstraction & Application*, vol. 9, pp. 50-61, 2013.

[14] P. Guo, X. Yang and Z. Yang, "Dynamical behaviors of an SIRI epidemic model with nonlinear incidence and latent period," *Advances in Difference Equations*, vol. 2014, pp. 164, 2014.

[15] A. Bernoussi, A. Kaddar and S. Asserda, "Global stability of a delayed SIRI epidemic model with nonlinear incidence," *International Journal of Engineering Mathematics*, vol. 2014, Article ID 487589, 6 pages, 2014.

[16] P. van den Driessche and X. Zou, "Modeling relapse in infectious diseases," *Mathematical Biosciences*, vol. 207, pp. 89–103, 2007.

[17] Z. Shuai and P. van den Driessche, "Global stability of infectious disease models using Lyapunov functions," *SIAM Journal on Applied Mathematics*, vol. 73, no. 4, pp. 1513–1532, 2013.
[18] P. van den Driessche, L. Wang and X. Zou, "Modeling diseases with latency and relapse," *Mathematical Biosciences and Engineering*, vol. 4, no. 2, pp. 205–219, 2007.
[19] P. van den Driessche and J. Watmough, "Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission," *Mathematical Biosciences*, vol. 180, no. 1-2, pp. 29–48, 2002.
[20] C. Castillo-Chavez and B. Song, "Dynamical models of tuberculosis and their applications," *Mathematical Biosciences and Engineering*, vol. 1, no. 2, pp. 361–404, 2004.
[21] E. Ávila-Vales, B. Buonomo and N. Chan-Chi, "Analysis of a mosquito-borne epidemic model with vector stages and saturating forces of infection," arXiv:1402.1719v1, 2014.
[22] S. Olaniyi and O. S. Obabiyi, "Qualitative analysis of malaria dynamics with nonlinear incidence function," *Applied Mathematical Sciences*, vol. 8, no. 78, pp. 3889–3904, 2014.
[23] A. Korobeinikov, "Global properties of infectious disease models with nonlinear incidence," *Bulletin of Mathematical Biology*, vol. 69, pp. 1871–1886, 2007.
[24] J. P. LaSalle, *The Stability of Dynamical Systems*, Regional Conference Series in Applied Mathematics, SIAM, Philadelphia, Pa, USA, 1976.
[25] C. Castillo-Chavez, S. Blower, P. van den Driessche, D. Kirschner and A. Yakubu, *Mathematical Approaches for Emerging and Reemerging Infectious Diseases: Models, Methods and Theory*, Springer, New York, 2002.
[26] M. A. Safi and S. M. Garba, "Global stability analysis of SEIR model with holling type II incidence function," *Computational and Mathematical Methods in Medicine*, vol. 2012, Article ID 826052, 8 pages, 2012.
[27] S. Mushayabasa and C. P. Bhunu, "Modeling HIV transmission dynamics among male prisoners in sub-saharan africa," *IAENG International Journal of Applied Mathematics*, vol. 41, no. 1, pp. 62–67, 2011.