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GLOBAL DYNAMICS OF A COUPLED EPIDEMIC MODEL WITH GENERAL INCIDENCE FUNCTION

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Abstract. In this paper, we propose a novel epidemic model coupling direct and indirect transmission of disease with general incidence function and study the global dynamic of the model system. Despite the nonlinearity and complexity of the system, the basic reproduction number exhibits a nice linear property: it is simply the sum of two basic reproduction numbers for direct and indirect disease transmissions respectively. We further demonstrate that the local and global dynamic of the system are related to the basic reproduction number. The new model has the advantage that it generalizes or connects to various disease models on HIV, Zika virus and so on.

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1. Introduction

Historically the mathematical modeling of epidemics has started since the time of Graunt [6]. In fact, Kermack and Mckendric [9] describe some classical deterministic mathematical models of epidemiology by considering the total population into three classes namely susceptible (S) individuals, infected (I) individuals and recovered (R) individuals which is known to us as SIR epidemic model. This SIR epidemic model is very important in analysis of diseases.

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In recent years, epidemiological models have been studied by a number of authors [4,5,7]. The basic and important research subjects for these systems are the existence of the threshold value which distinguishes whether the infectious disease will die out, the local and global stability of the disease-free equilibrium and the endemic equilibrium, the existence of periodic solutions, the persistence and extinction of the disease, etc

Motivated by the works above, in the present paper, we are concerned the dynamics of a coupled epidemic model with general incidence function.

The paper is organized as follow: The model is described and the previous results are given in section 2. In section 3, the basic properties are presented. Section 4 contains the local and global stability of the free-equilibrium point. Therefore, we study the global stability of the endemic equilibrium. Section 5 is devoted to numerical simulation. Finally, in section 6, we end by a conclusion.

2. Mathematical model

The model we propose in this section is a generalization of the following problem [8]:

$$\begin{cases} x'(t) = b - \dfrac{\beta_1 x(t)y(t)}{x(t)+y(t)} - \beta_2 x(t)z(t) - \mu x(t), \\ y'(t) = \dfrac{\beta_1 x(t)y(t)}{x(t)+y(t)} + \beta_2 x(t)z(t) - \gamma y(t), \\ z'(t) = py(t) - \delta z(t) \end{cases} \tag{2.1}$$

where x and y denote respectively the susceptible and infected population sizes.

The constants μ and γ are death rates of these two groups, and b is a constant birth rate. The disease could transmit directly via a standard incidence function $\dfrac{\beta_1 x(t)y(t)}{x(t)+y(t)}$ and indirectly via a mass-action infection term $\beta_2 x(t)z(t)$, where z accounts for the vector of the indirect transmission. We assume in the third equation that the growth of disease vector is proportional to the number of infected individuals, and its decay rate is a constant δ.

Our aim is to generalyse model (2.1) by considering general incidence function $f(x,y)$ and $g(x,z)$ in the equation x' and y'. $f(x,y)$(direct transmission) and $g(x,z)$ (indirect transmission) are designed by taking into account a wide range of incidences.

As general as possible, the incidence function f and g must satisfy technical conditions. Thus, we assume that:

(H1) f and g are non-negative C^1 functions on the non-negative quadrant,

(H2) for all $(x, y) \in \mathbb{R}^2_+$, $f(x, 0) = f(0, y) = 0$ and $g(x, 0) = g(0, z) = 0$.

Let us denote by f_1 and f_2 the partial derivatives of f with respect to the first and to the second variable.

Let us denote by g_1 and g_2 the partial derivatives of g with respect to the first and to the second variable. Considering general incidence function as previously define, the model (2.1) is then written as:

$$\begin{cases} x'(t) = b - f(x, y) - g(x, z) - \mu x(t), \\ y'(t) = f(x, y) + g(x, z) - \gamma y(t), \\ z'(t) = py(t) - \delta z(t) \end{cases} \tag{2.2}$$

If $f(x, y) = 0$ (namely, there is no direct transmission), the above system (2.2) reduces to the classical HIV model [17], where x, y, z represent the densities of target cells, infected cells and virus, respectively. It is well-know that the global dynamics of this reduced system is fully determined by the reproduction number [21]

$$R_0^i = \frac{pg_2(x^0, 0)}{\gamma\delta} \tag{2.3}$$

To be more specific, if $R_0^i < 1$, then the infection-free equilibrium is globally asymptotically stable; if $R_0^i > 1$, then there exists a unique positive equilibrium which is globally asymptotically stable. Here, the superscript i means indirect disease transmission and $x^0 = \frac{b}{\mu}$.

On the other hand, if the indirect transmission is ignored (i.e g(x,z)=0), then the equation (2.2) can be decoupled from the original system, and the remaining system is the same as the Kermack-McKendrick epidemic model [9] with standard incidence function. The basic reproduction number for the reduced direct-transmission-only model is given by

$$R_0^d = \frac{f_2(x^0, 0)}{\gamma} \tag{2.4}$$

where the superscript d corresponds to the direct disease transmission [21]. A similar dichotomy results holds: if $R_0^d < 1$, then the disease-free equilibrium is globally asymptotically stable; if $R_0^d > 1$, then there exists a unique positive equilibrium which is globally asymptotically stable. For global stability analysis on epidemic models with more general direct transmission rates, we refer to [10, 11, 16] and the references therein.

The proposed system (2.2) is motivated by the observations of cell-to-cell transmission of HIV [20] and human-to-human transmission of Zika virus [3]. It is of both biological and mathematical interests to study a disease model that couples direct transmission with indirect transmission. The coupled virus models with both transmissions being assumed to be mass-actions have been studied in [12,13], where the basic reproduction number for the coupled system is simply the sum of two basic reproduction numbers for the subsystems with only direct or indirect disease transmissions respectively. Similar results were also obtained for cholera models [19], pathogen models [1] and treatment models [23]. The coupled model proposed in [23] incorporated two virions with sensitive and resistant strains, respectively, and the basic reproduction number for the full system is the maximum of two basic reproduction numbers of viral strains. However, the basic reproduction number corresponds to each viral strain is still the sum of two basic reproduction numbers for the direct and the indirect transmissions when both transmission functions are chosen as mass-actions. One nature question is whether this linear property of basic reproduction number of nonlinear coupled systems is universal, regardless of the choices of nonlinear incidence functions. Biologically, we may still define the basic reproduction number of this coupled system as the sum of R_0^i and R_0^d:

$$R_0 = \frac{pg_2(x^0,0)}{\gamma\delta} + \frac{f_2(x^0,0)}{\gamma} \tag{2.5}$$

Hence, $E_0 = (x^0, 0, 0)$ is an equilibrium point of system (2.2). Biologically, E_0 represents the disease-free equilibrium.

The jacobian matrix of (2.2) at E_0 is

$$J_0 = \begin{pmatrix} -f_1(x^0,0) - g_1(x^0,0) - \mu & -f_2(x^0,0) & -g_2(x^0,0) \\ f_1(x^0,0) + g_1(x^0,0) & f_2(x^0,0) - \gamma & g_2(x^0,0) \\ 0 & p & -\delta \end{pmatrix}$$

The submatrix of J_0 to the infectious compartments can be split as follows:

$$J_{01} = \begin{pmatrix} f_2(x^0,0) - \gamma & g_2(x^0,0) \\ p & -\delta \end{pmatrix} = \begin{pmatrix} f_2(x^0,0) & g_2(x^0,0) \\ p & 0 \end{pmatrix} - \begin{pmatrix} \gamma & 0 \\ 0 & \delta \end{pmatrix} := F - V$$

Algebric computation shows that the next generation matrix is given by

$$FV^{-1} = \begin{pmatrix} \frac{f_2(x^0,0)}{\gamma} + \frac{pg_2(x^0,0)}{\gamma\delta} & \frac{g_2(x^0,0)}{\delta} \\ 0 & 0 \end{pmatrix}$$

The basic reproductive number, R_0, is defined as the spectral radius of FV^{-1} [21], hence

$$R_0 := \rho(FV^{-1}) = \frac{pg_2(x^0, 0)}{\gamma\delta} + \frac{f_2(x^0, 0)}{\gamma}$$

We intend to explore the relation of local and global dynamics for the model system with the basic reproduction number.

3. Basic properties

Theorem 3.1. *The positive orthant*

$$\{(x, y, z) \in \mathbb{R}^3 : x \geq 0, y \geq 0, z \geq 0\}$$

is positively invariant for system (2.2).

To prove Theorem 3.1, we need the following lemma.

Lemma 3.1. [2] *Let $L : \mathbb{R}^n \to \mathbb{R}$ be a differentiable function, and let $a \in \mathbb{R}$. Let $X(x)$ be the vector field, and let G be the closed set $G = \{x \in \mathbb{R}^n : L(x) \leq a\}$ such that $\nabla L(x) \neq 0$ for all $x \in L^{-1}(a) = \{x \in \mathbb{R}^n : L(x) = a\}$. If $< X(x), \nabla L(x) > \leq 0$ for all $x \in L^{-1}(a)$, then the set G is positively invariant.*

Proof of theorem 3.1 Let

$$t = (x, y, z) \tag{3.1}$$

We will prove that $\{S \geq 0\}$ is positively invariant. Then let

$$L(t) = -x.$$

L is differentiable, and $\nabla L(t) = (-1, 0, 0) \neq 0$ for all $t \in L(0)^{-1} = \{t \in \mathbb{R}^3 / L(t) = 0\}$.
The vector field on $\{x = 0\}$ is

$$X(t) = \begin{pmatrix} b \\ -\gamma y \\ py - \delta z \end{pmatrix}. \tag{3.2}$$

Then $< X(t), \nabla L(t) >= -b < 0$. This proves that $\{x \geq 0\}$ is positively invariant. Similarly, we prove that $\{y \geq 0\}$, $\{z \geq 0\}$ are positively invariant.
Then $\{(x, y, z) \in \mathbb{R}^3 : x \geq 0, y \geq 0, z \geq 0\}$ is positively invariant for system (2.2). Therefore, the model is mathematically well posed and epidemiologically reasonable since all the variables remain non-negatives for all $t > 0$. □

Theorem 3.2. *Any solution* (x, y, z) *of system* (2.2) *with the initial conditions satisfies* $\limsup_{t\to+\infty}(x(t)+y(t)) \leq \dfrac{B}{\overline{\mu}}$, *where* $\overline{\mu} = min\{\mu, \gamma\}$.

Proof. Adding the first and the second equations of (2.2) gives

$$x'(t) + y'(t) = b - \mu x(t) - \gamma y(t) \leq b - \min(\mu, \gamma)\Big(x(t) + y(t)\Big)$$

. Thus, we have $\limsup_{t\to\infty}(x(t)+y(t)) \leq \dfrac{b}{\overline{\mu}}$. Especially, $x(t)$ and $y(t)$ are ultimately bounded as $t \to \infty$. It is then easily seen from the third of (2.2) that $z(t)$ is also ultimately bounded as $t \to \infty$. □

The differential equation model described by (2.2) has two equilibrium points: a disease-free equilibrium E_0 given by

$$E_0 = \Big(x^0, 0, 0\Big) = \Big(\frac{b}{\mu}, 0, 0\Big)$$

and an endemic equilibrium $E^* = (x^*, y^*, z^*)$ where,

$$\begin{aligned} x^* &= \frac{b - \gamma y^*}{\mu} \\ y^* &= y^* \\ z^* &= \frac{p}{\delta} y^* \end{aligned}$$

Theorem 3.3. (i) *If* $R_0 < 1$, *the system* (2.2) *has only a unique disease-free equilibrium* $E_0 = (x^0, 0, 0)$.

(ii) *If* $R_0 > 1$, *the system*(2.2) *has a unique endemic equilibrium* $E^* = (x^*, y^*, z^*)$.

Proof. Let $E = (x, y, z)$ be an equilibrium point of system (2.2). Using the second and the last equations (2.2), we have

$$\begin{aligned} f(x, y) + g(x, z) &= \gamma y(t), \\ py(t) &= \delta z(t) \end{aligned}$$

so we have

$$\frac{f(x, y) + g(x, z)}{y}\frac{y}{z} = \gamma\frac{\delta}{p}$$

Let

$$\Phi(y, z) = \frac{f(x^0 - \frac{\gamma}{\mu}y, y) + g(x^0 - \frac{\gamma}{\mu}y, z)}{y}\frac{y}{z} - \gamma\frac{\delta}{p}$$

$$\lim_{(y,z)\to(0,0)} \Phi(y, z) = \Big(\frac{\delta}{p}f_2(x^0, 0) + g_2(x^0, 0)\Big) - \frac{\delta\gamma}{p} = \frac{\delta\gamma}{p}\Big(R_0 - 1\Big)$$

and we have also $\Phi(\bar{y},\bar{z}) = -\gamma\dfrac{\delta}{p}$ with $\bar{y} = \dfrac{\mu x^0}{\gamma}$ and $\bar{z} = z$.
When $R_0 < 1$, we have $\lim\limits_{(y,z)\to(0,0)} \Phi(y,z) < 0$, thus, there is not any $(y^*,z^*) > (0,0)$ such that $\Phi(y^*,z^*) = 0$. Therefore, system (2.2) has a unique disease-free equilibrium E_0.
When $R_0 > 1$, we have $\lim\limits_{(y,z)\to(0,0)} \Phi(y,z) > 0$, so there exists $y^* > 0$ and $z^* > 0$. This implies that the system (2.2) has a unique endemic equilibrium point E^*. □

4. Equilibria and analysis

Theorem 4.1. *When $\gamma < \mu$ and $R_0 < 1$, then the disease-free equilibrium is locally asymptotically stable.*

Proof. We calculate the jacobian matrix of the system (2.2) about the disease-free equilibrium $(x^0, 0, 0)$. In doing so, we note that $f(x,0) = 0$ for all x and so $f_1(E_0) = 0$. We also note that $g(x,0) = 0$ for all x and so $g_1(E_0) = 0$.
We have

$$J_0 = \begin{pmatrix} -\mu & -f_2(x^0,0) & -g_2(x^0,0) \\ 0 & f_2(x^0,0) - \gamma & g_2(x^0,0) \\ 0 & p & -\delta \end{pmatrix}$$

The corresponding characteristic equation is $\lambda^3 + a_2\lambda^2 + a_1\lambda + a_0 = 0$
where

$$\begin{aligned} a_2 &= \delta - f_2(x^0,0) + \gamma + \mu \\ a_1 &= \delta\Big(\gamma - f_2(x^0,0)\Big) + \mu\Big(\gamma - f_2(x^0,0)\Big) - pg_2(x^0,0) + \mu\delta \\ a_0 &= -\mu\Big(\delta f_2(x^0,0) + pg_2(x^0,0) - \delta\gamma\Big) \end{aligned}$$

Especially, $a_2 > 0$, $a_1 > 0$ $a_0 > 0$ and $a_2a_1 > a_0$. By Routh Hurwitz criterion, it follows that all eigenvalues of J_0 have negative real parts, which implies the local asymptotic stability of disease-free equilibrium. □

Now, we are ready to establish the global dynamics of the system (2.2). We first make the following additional assumption.
(H3) For all $(x,y,z) \in \mathbb{R}^3_+$, $f(x,y) \le f_2(x^0,0)y$ and $g(x,z) \le g_2(x^0,0)z$.

Theorem 4.2. *If $R_0 < 1$, then the disease-free equilibrium of system (2.2) with nonnegative initial conditions is globally asymptotically stable, namely, as $t \to \infty$, we have $(x(t),y(t),z(t)) \to (x^0,0,0)$*

Proof. Note that the equations of the infected components in system (2.2) can be used as

$$\begin{cases} y'(t) = f(x,y) + g(x,z) - \gamma y(t), \\ \\ z'(t) = py(t) - \delta z(t) \end{cases} \tag{4.1}$$

By using **H3**, we get

$$\begin{cases} y'(t) \leq f_2(x^0,0)y + g_2(x^0,0)z - \gamma y(t), \\ \\ z'(t) \leq py(t) - \delta z(t) \end{cases} \tag{4.2}$$

$$\begin{pmatrix} y'(t) \\ z'(t) \end{pmatrix} \leq \begin{pmatrix} f_2(x^0,0) - \gamma & g_2(x^0,0) \\ p & -\delta \end{pmatrix} \begin{pmatrix} y \\ z \end{pmatrix} \tag{4.3}$$

$$\begin{pmatrix} y'(t) \\ z'(t) \end{pmatrix} \leq (F+V) \begin{pmatrix} y \\ z \end{pmatrix} \tag{4.4}$$

We consider the following equation

$$\begin{pmatrix} \bar{y}'(t) \\ \bar{z}'(t) \end{pmatrix} = (F+V) \begin{pmatrix} \bar{y} \\ \bar{z} \end{pmatrix} \tag{4.5}$$

We have $F \geq 0$ and V is an asymptotic stable Metzler inversible matrix.

Since, $R_0 = \rho(-FV^{-1})$ then, by Varga lemma in [22], the matrix $M = F + V$ is asymptotically stable, that is to say the system (4.5) is asymptotically stable at origin $(0,0)$.

Thus,

$$(\bar{y}(t), \bar{z}(t)) \to (0,0) \text{ as } t \to +\infty$$

Consequently, by a standard comparison theorem in [14], $(y(t), z(t)) \to (0,0)$ as $t \to +\infty$ and substituting $y = z = 0$ into system (2.2) gives $x \to x^0$ as $t \to +\infty$.

Thus, $(x(t), y(t), z(t)) \to (x^0, 0, 0)$ as $t \to +\infty$ for $R_0 < 1$.

Therefore, E_0 is globally asymptotically stable if $R_0 < 1$. □

The next main result states the global asymptotic stability of endemic equilibrium.

Theorem 4.3. *If $R_0 > 1$, then the unique endemic equilibrium is globally asymptotically stable, namely, as $t \to \infty$, we have $(x(t), y(t), z(t)) \to (x^*, y^*, z^*)$*

Proof. Evaluating both sides of (2.2) at E^* gives

$$\begin{cases} b = f(x^*, y^*) + g(x^*, z^*) + \mu x^*, \\ \gamma y^* = f(x^*, y^*) + g(x^*, z^*), \\ \delta z^* = p y^*. \end{cases} \tag{4.6}$$

Let

$$h(x) = x - 1 - \ln x \tag{4.7}$$

$$\begin{aligned} V_x(t) &= \frac{1}{2}(x - x^*)^2, \\ V_y(t) &= \frac{1}{2}(y - y^*)^2, \\ V_z(t) &= \frac{1}{2}(z - z^*)^2, \end{aligned} \tag{4.8}$$

We can see that $h : \mathbb{R}_+^* \to \mathbb{R}_+^*$ has the strict global minimum $h(1) = 0$. Thus, $V_x(t) \geq 0$, $V_y(t) \geq 0$, $V_z(t) \geq 0$ with equality if and only if $x(t) = x^*$, $y(t) = y^*$ and $z(t) = z^*$. We will study the behaviour of the Lyapunov function

$$V(t) = V_x(t) + V_y(t) + V_z(t). \tag{4.9}$$

The derivatives of $V_x(t)$, $V_y(t)$ and $V_z(t)$ will be calculated separately and then combined to get the desired quantity $\frac{dV}{dt}$.

$$\begin{aligned} \frac{dV_x}{dt} &= \big(x - x^*\big)\frac{dx}{dt} \\ &= \big(x - x^*\big)\big(b - f(x, y) - g(x, z) - \mu x(t)\big) \\ &= x^*\big(\frac{x}{x^*} - 1\big)\big(b - f(x, y) - g(x, z) - \mu x(t)\big) \end{aligned}$$

Using the first equation of (4.6) to replace b gives

$$\begin{aligned} \frac{dV_x}{dt} &= x^*\left(\frac{x}{x^*} - 1\right)\Big(\mu(x^* - x) + (f(x^*, y^*) - f(x, y)) + (g(x^*, z^*) - g(x, z))\Big) \\ &= -\mu(x - x^*)^2 + x^* f(x^*, y^*)\left(\frac{x}{x^*} - 1\right)\left(1 - \frac{f(x, y)}{f(x^*, y^*)}\right) \\ &\quad + x^* g(x^*, z^*)\left(\frac{x}{x^*} - 1\right)\left(1 - \frac{g(x, z)}{g(x^*, z^*)}\right). \end{aligned} \tag{4.10}$$

Next, we calculate $\frac{dV_y}{dt}$

$$\begin{aligned}\frac{dV_y}{dt} &= \big(y-y^*\big)\frac{dy}{dt}\\ &= \big(y-y^*\big)\big(f(x,y)+g(x,z)-\gamma y(t)\big)\end{aligned}$$

Using the second equation of (4.6) to replace γy^* gives

$$\begin{aligned}\frac{dV_y}{dt} &= \big(y-y^*\big)\big(f(x,y)+g(x,z)+\gamma y^*-f(x^*,y^*)-g(x^*,z^*)-\gamma y(t)\big)\\ &= -\gamma\big(y-y^*\big)^2+y^*f(x^*,y^*)\left(\frac{y}{y^*}-1\right)\left(\frac{f(x,y)}{f(x^*,y^*)}-1\right)\\ &\quad +y^*g(x^*,z^*)\left(\frac{y}{y^*}-1\right)\left(\frac{g(x,z)}{g(x^*,z^*)}-1\right).\end{aligned}\tag{4.11}$$

Now, we calculate $\frac{dV_z}{dt}$

$$\begin{aligned}\frac{dV_z}{dt} &= \big(z-z^*\big)\frac{dz}{dt}\\ &= \big(z-z^*\big)\big(py(t)-\delta z(t)\big)\end{aligned}$$

Using the last equation of (4.6) to replace δz^* gives

$$\begin{aligned}\frac{dV_z}{dt} &= \big(z-z^*\big)\big(py(t)+\delta z^*-py^*-\delta z(t)\big)\\ &= -\delta\big(z-z^*\big)^2+py^*z^*\left(\frac{z}{z^*}-1\right)\left(\frac{y}{y^*}-1\right)\end{aligned}\tag{4.12}$$

Combining equations (4.10) – (4.12), we obtain

$$\frac{dV}{dt}\le -\mu(x-x^*)^2-\gamma\big(y-y^*\big)^2-\delta\big(z-z^*\big)^2+\xi Q(j),\tag{4.13}$$

where

$$\begin{aligned}Q(j) &= \left(\frac{x}{x^*}-1\right)\left(1-\frac{f(x,y)}{f(x^*,y^*)}\right)+\left(\frac{x}{x^*}-1\right)\left(1-\frac{g(x,z)}{g(x^*,z^*)}\right)\\ &\quad +\left(\frac{y}{y^*}-1\right)\left(\frac{f(x,y)}{f(x^*,y^*)}-1\right)+\left(\frac{y}{y^*}-1\right)\left(\frac{g(x,z)}{g(x^*,z^*)}-1\right)\\ &\quad +\left(\frac{z}{z^*}-1\right)\left(\frac{y}{y^*}-1\right)\end{aligned}\tag{4.14}$$

and

$$\xi=\max\{x^*f(x^*,y^*);x^*g(x^*,z^*);y^*f(x^*,y^*);y^*g(x^*,z^*);py^*z^*\}$$

By adding and substracting the quantity
$1+\ln\left(\frac{x}{x^*}\right)+\ln\left(\frac{y}{y^*}\right)+\ln\left(\frac{z}{z^*}\right)+\ln\left(\frac{zy}{z^*y^*}\right)+\ln\left(\frac{xf(x,y)}{x^*f(x^*,y^*)}\right)+\ln\left(\frac{xg(x,z)}{x^*g(x^*,z^*)}\right)+\ln\left(\frac{yf(x,y)}{y^*f(x^*,y^*)}\right)+\ln\left(\frac{yg(x,z)}{y^*g(x^*,z^*)}\right)$ to (4.14), we obtain

$$\begin{aligned}
Q(j) &= 2\left(\frac{x}{x^*}-1-\ln\left(\frac{x}{x^*}\right)\right)+\left(-\frac{xf(x,y)}{x^*f(x^*,y^*)}+1+\ln\left(\frac{xf(x,y)}{x^*f(x^*,y^*)}\right)\right)\\
&\quad+\left(-\frac{xg(x,z)}{x^*g(x^*,z^*)}+1+\ln\left(\frac{xg(x,z)}{x^*g(x^*,z^*)}\right)\right)+\left(\frac{yf(x,y)}{y^*f(x^*,y^*)}-1-\ln\left(\frac{yf(x,y)}{y^*f(x^*,y^*)}\right)\right)\\
&\quad+\left(\frac{yg(x,z)}{y^*g(x^*,z^*)}-1-\ln\left(\frac{yg(x,z)}{y^*g(x^*,z^*)}\right)\right)+3\left(-\frac{y}{y^*}+1+\ln\left(\frac{y}{y^*}\right)\right)\\
&\quad+\left(\frac{zy}{z^*y^*}-1-\ln\left(\frac{zy}{z^*y^*}\right)\right)+\left(-\frac{z}{z^*}+1+\ln\left(\frac{z}{z^*}\right)\right)\\
Q(j) &= 2h\left(\frac{x}{x^*}\right)-h\left(\frac{xf(x,y)}{x^*f(x^*,y^*)}\right)-h\left(\frac{xg(x,z)}{x^*g(x^*,z^*)}\right)+h\left(\frac{yf(x,y)}{y^*f(x^*,y^*)}\right)\\
&\quad+h\left(\frac{yg(x,z)}{y^*g(x^*,z^*)}\right)-3h\left(\frac{y}{y^*}\right)+h\left(\frac{zy}{z^*y^*}\right)-h\left(\frac{z}{z^*}\right)
\end{aligned}$$

Since the function h is monotone of each side of 1 and is minimized at 1, H4 implies

$$h\left(\frac{yf(x,y)}{y^*f(x^*,y^*)}\right)\le h\left(\frac{xf(x,y)}{x^*f(x^*,y^*)}\right) \text{ and } h\left(\frac{yg(x,z)}{y^*g(x^*,z^*)}\right)\le h\left(\frac{xg(x,z)}{x^*g(x^*,z^*)}\right)$$
$$h\left(\frac{x}{x^*}\right)\le h\left(\frac{y}{y^*}\right) \text{ and } h\left(\frac{zy}{z^*y^*}\right)\le h\left(\frac{z}{z^*}\right)$$

Since $h>0$, then $\frac{dV}{dt}\le 0$ for all x, y, z with egality only for $x(t)=x^*$, $y(t)=y^*$ and $z(t)=z^*$. Hence, the endemic equilibrium E^* is the only positively invariant set of the system (2.2) contained in $\{(x,y,z)\in\mathbb{R}^3_+; x(t)=x^*, y(t)=y^*; z(t)=z^*\}$
Then, it follows that E^* is globally asymptotically stable [15].

5. Numerical simulation and comments

In this section, we derive the computation work that supports our study. In this computation, the functions f and g are chosen as follows: $f(x;y)=\theta x(t)y(t)$ and $g(x(t),z(t))=\beta x(t)z(t)$ (mass action). Two different cases of computational simulations are studied: in the first case $R_0<1$ Figure 1, while in the second case $R_0>1$ Figure 2.

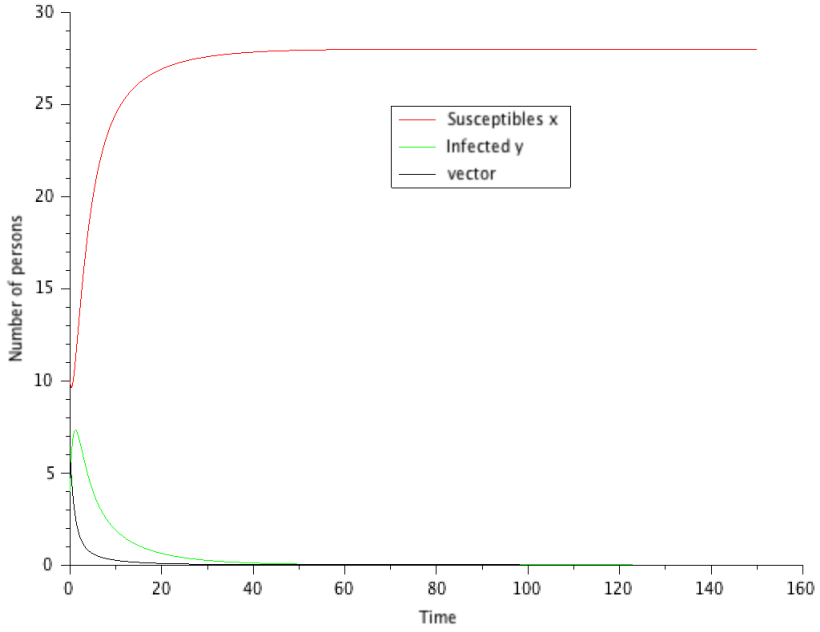

FIGURE 1. case where $R_0 < 1$

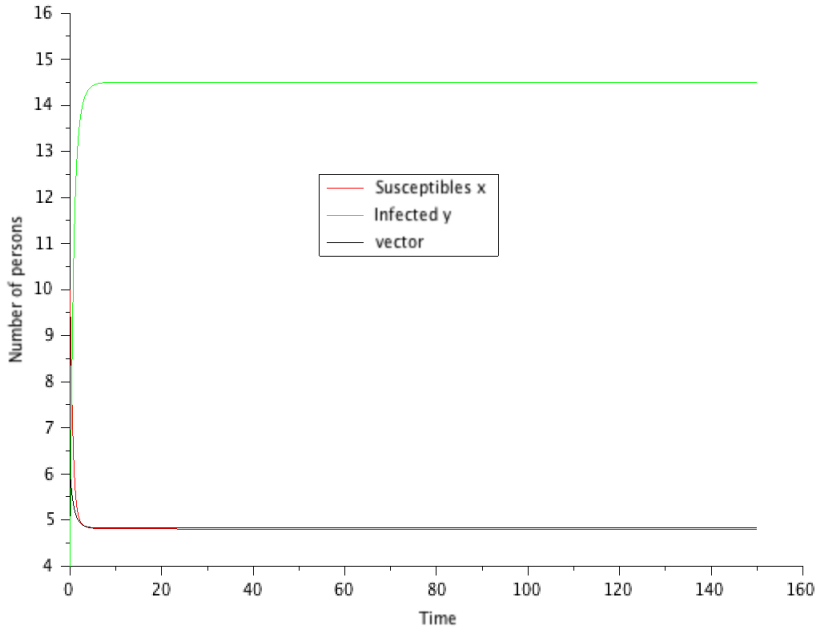

FIGURE 2. case where $R_0 > 1$

In other hand, to illustrate our results, we use the saturation incidence functions f and g in Figure 2 and Figure 4 denoted by

$$f(x(t), y(t)) = \frac{\theta x(t) y(t)}{1 + p y(t)}$$

$$g(x(t), z(t)) = \frac{\beta x(t) z(t)}{1 + q z(t)}$$

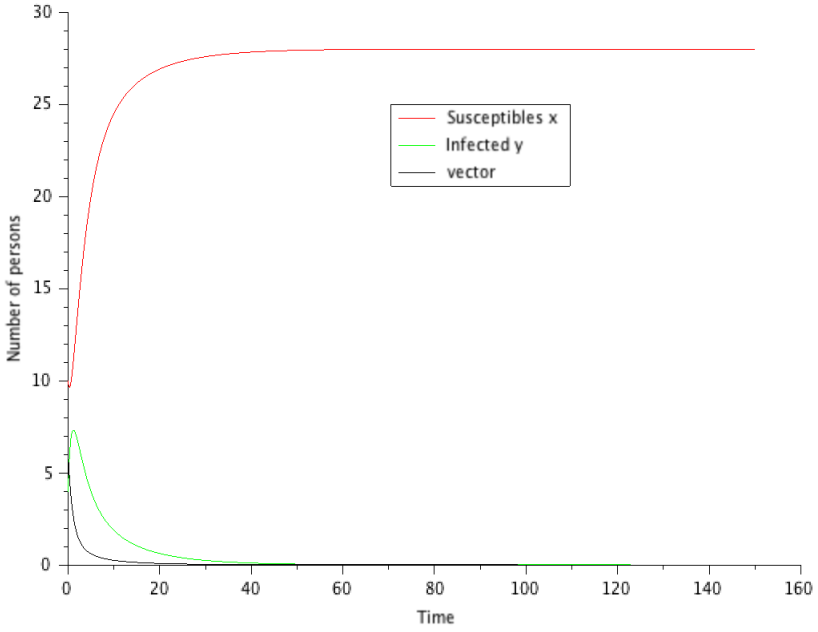

FIGURE 3. case where $R_0 < 1$

At the end, to illustrate our results, we use the standard incidence functions f and g in Figure 5 and Figure 6 denoted by

$$f(x(t), y(t)) = \frac{x(t) y(t)}{x(t) + y(t)}$$

$$g(x(t), z(t)) = \frac{x(t) z(t)}{x(t) + z(t)}$$

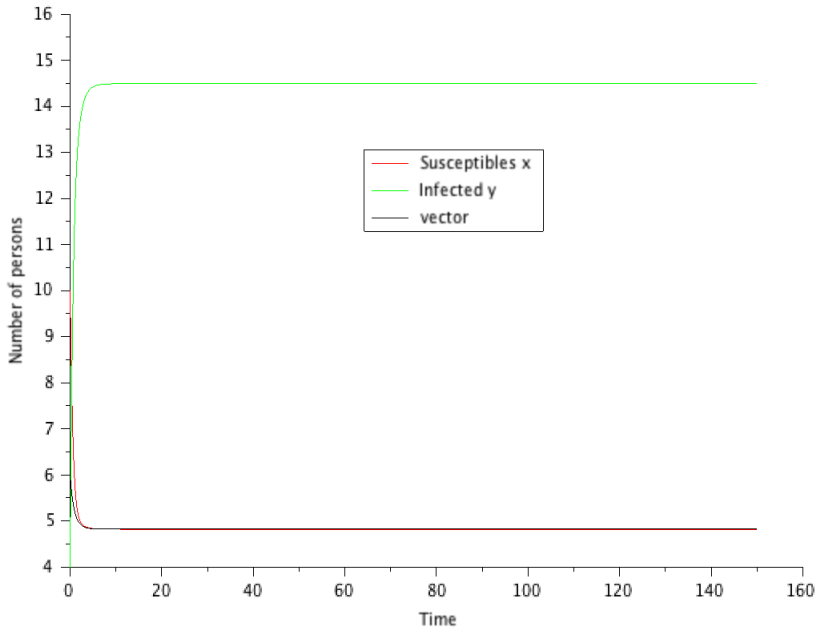

FIGURE 4. case where $R_0 > 1$

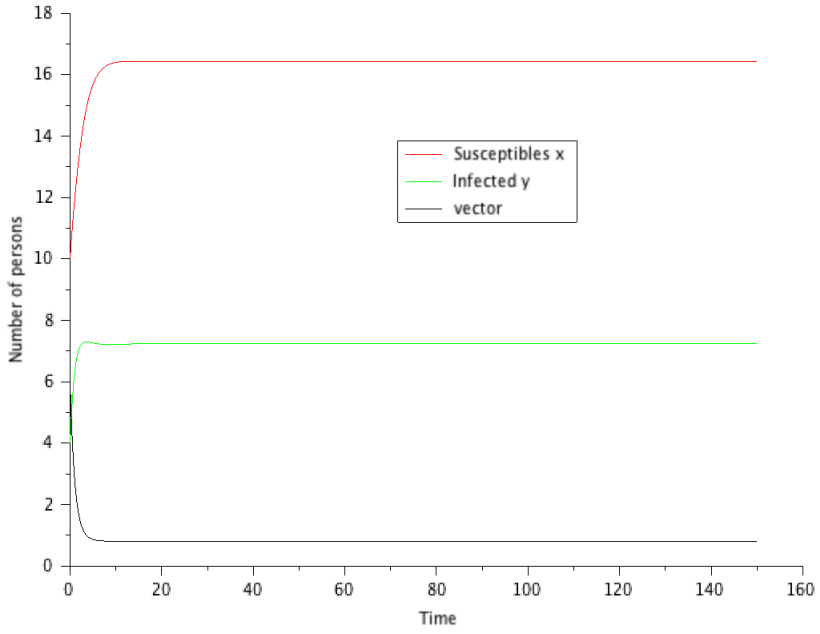

FIGURE 5. case where $R_0 < 1$

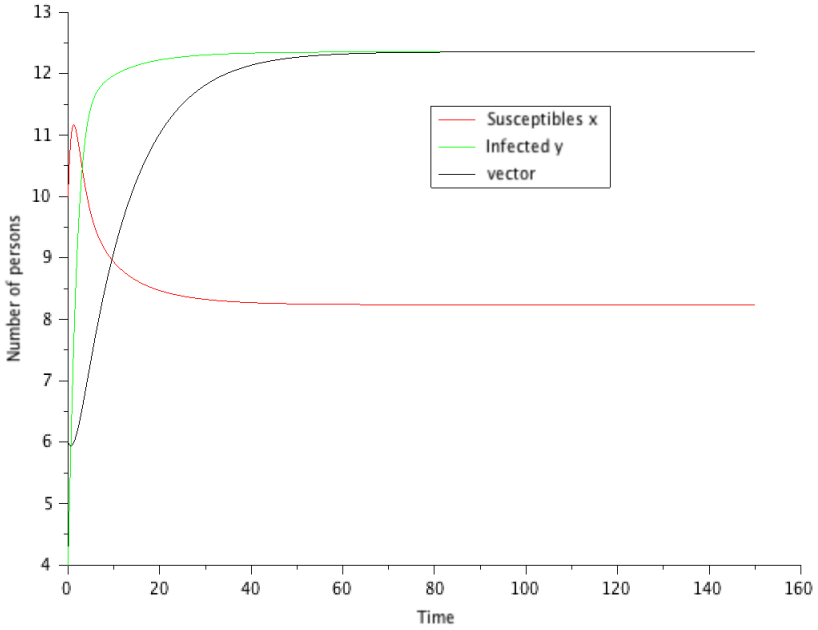

FIGURE 6. case where $R_0 > 1$

6. CONCLUSION

In this paper, a global dynamics of a coupled epidemic model with general incidence function is derived. The global behaviour of the model system was studied. We proved that, if $R_0 < 1$ holds, then the disease-free equilibrium is globally asymptotically stable, which implies that the disease fades out from the population. If $R_0 > 1$, then there exists a unique endemic equilibrium which is globally asymptotically stable, and this implies that the disease will persist in the population.

COMPETING INTERESTS

The author(s) declare(s) that there is no conflict of interest regarding the publication of this paper.

REFERENCES

[1] M. Bani-Yaghoub, R. Gautam, Z. Shuai, P. Van den Driesche and R. Ivanek, Reproduction numbers for infections with free-living pathogens growing in the environment, J. Biol. Dyn. **2** (2012), 923-940.

[2] Bony, JM: Principe du maximum, inégalité de Harnack et unicité du problème de Cauchy pour les operateurs elliptiques dégénérés . Ann. Inst. Fourier (Grenoble) **19**(1) (1969), 277-304.

[3] B. D. Foy, K. C. Kobylinski, J. L. C. Foy, B. J. Blitvich, A. Travassos da Rosa, A. D. Haddow, R. S. Lanciotti and R. B. Tech, Probable non-vector-borne transmission of Zika virus, Colorado, USA, Emerg. Infect. Dis. **17** (2011), 880-882.

[4] A. Guiro, D. Ngom, D. Ouedraogo, Global stability for a class of discrete Schistosomiasis models with general incidence. Adv. Differ. Equ. **2017** (2017), 116.

[5] A. Guiro, D. Ouedraogo and H. Ouedraogo, Global stability analysis for a discrete SIR epidemic model with delay and general nonlinear incidence function. Appl. Math. **9** (2018), 1039-1054.

[6] J. Graunt, Natural and political observations made upon the bills of mortality, Roycroft and Dicas, London, (1662).

[7] K. Hattaf, A.A. Lashari, Y. Louartassi, and N. Yousfi, A delayed SIR epidemic model with general incidence rate, Electron. J. Qual. Theory Differ. Equ. **2013** (2013), 3.

[8] H. Shu, X.S. Wang, Global dynamics of a coupled epidemic model, Discr. Continuous Dyn. Syst. Ser. B, **22** (2017), 1575-1585.

[9] W.O. Kermack, and A.G. Mckendric, Contribution to the mathematical theory of epidemics, Proc. R. Soc. Lond. Ser. A 115 (1927) 700-721.

[10] A. Korobeinikov, Lyapunov functions and global stability for SIR and SIRS epidemiological models with non-linear transmission, Bull. Math. Biol. **68** (2006), 615-626.

[11] A. Korobeinikov, Global properties of infectious disease models with nonlinear incidence, Bull. Math. Biol. **69** (2007), 1871-1886.

[12] X. Lai and X. Zou, Modeling HIV-1 virus dynamics with both virus-to-cell infection and cell-to-cell transmission, SIAM J. Appl. Math. **74** (2014), 898-917.

[13] X. Lai and X. Zou, Modeling cell-to-cell spread of HIV-1 with logistic target cell growth, Math. Anal. Appl. **426** (2015), 563-584 .

[14] V. Lakshmikantham, S. Leela, A. A. Martynyuk, Stability Analysis of Nonlinear Systems, Marcel Dekker, New York, 1989.

[15] J. P. Lasalle, The Stability of Dynamical Systems, SIAM, Philadelphia, 1976.

[16] C. C. McCluskey, Global stability of an SIR epidemic model with delay and general nonlinear incidence, Math. Biosci. Eng. **7** (2010), 837-850.

[17] A. Perelson, A. Neumann, M. Markowitz, J. Leonard and D. Ho, HIV-1 dynamics in vivo: Virion clearence rate, infected cell life-span, and viral generation time, Sciences, **271** (1996), 1582-1586.

[18] Z. Shuai and P. Van den Driesche, Global dynamics of cholera models with differential infectivity, Math. Biosci. **234** (2011), 118-126 .

[19] Z. Shuai and P. Van den Driesche, Global dynamics of cholera models with differential infectivity, Math. Biosci. **234** (2011), 118-126 .

[20] A. sigal, J. T. Kim, B. Balazs, E. Dekel, A. Mayo, R. Milo and D. Baltimore, Cell-to-cell spread of HIV permits ongoing replication despite antiretroviral therapy, Nature, **477** (2011), 95-98.

[21] P. Van den Driesche and J. Watmough, Reproduction Numbers and Substhreshold Endemic Equilibria for the Compartmental Models of Disease Transmission, Math. Biosci. **180** (2002), 29-48.

[22] R. Varga, Matrix iterative analysis, Prentice-Hall, 1962.

[23] Y. Xiao, F. Brauer and S. M. Moghadas, Can treatment increase the epidemic size? J. Math. Biol. **72** (2016), 343-361.