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Global Stability Analysis of an Influenza A (H1N1) Model with Two Discrete Delays

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Abstract: The dynamics of influenza A (H1N1) model with delays has been studied. We begin this model with proving the positivity and boundedness of the solution. We establish sufficient conditions for the global stability of equilibria (infection-free equilibrium and infected equilibrium) are obtained by means of Lyapunov LaSalle invariance principle. We prove that if the basic reproduction number $R_0 < 1$ the infectious population disappear so the disease dies out, while if $R_0 > 1$ the infectious population persist. Numerical simulations with application to H1N1 model is given to verify the analytical results.

Keywords: H1N1 Model, Delays, Global stability analysis

1 Introduction

Mathematical models describing the dynamics of infectious diseases are of great public health importance because they provide insights on implementing practical and efficient disease-control strategies [1,2,3]. Epidemic models have long been an important tool for understanding and controlling the spread of infectious diseases. Most of them are described by delayed differential equations. The introduction of time delay is often used to model the latent period, that is, the time from the acquisition of infection to the time when the host becomes infectious [4]. Most of the authors assume that the latent period of diseases is negligible, i.e. once infected, each susceptible individual (S) instantaneously becomes infectious (I), and later recovers (R) with a permanent or temporary acquired immunity. These epidemic models are customarily called SIR (susceptible, infectious, recovered) models [5,6,7,8]. It is known that for some diseases, such as influenza and tuberculosis, on adequate contact with an infectious individual, a susceptible becomes exposed for a while; that is, infected but not yet infectious. Thus it is realistic to introduce a latent compartment.

Time delays of one type or another have been incorporated into biological models by many authors (for example, [9,10,11,12,13,14,15] and the references cited therein). In 2012, Xueyong Zhou and Zhen Guo [16] developed a simple ode model for influenza A (H1N1) dynamics. They defined the model as five compartments: but they were considering the four compartments: cells that are suspected, cells that are vaccination, cells that are exposed, and cells that are infectious. They described the dynamics of these populations by a system of four ordinary differential equations.

In this paper, we incorporate a two discrete delays to the model to describe the time between infectious and susceptible cells and the emission of exposed cells. The resulting model is a system of two delay-differential equations. To determine the dynamics of the delay model, we study the transcendental characteristic equation of the linearized system at the positive infected steady state and obtain analytic conditions on the parameters under which the infected steady state is globally asymptotically stable. Numerical simulations are carried out to illustrate the obtained results.

The paper is organized as follows. We investigate the model description for H1N1 model dynamics in section 2. The local and global stability of the infected-free equilibrium and infected equilibrium are studied in section 3. In section 4, we examine the stability results through numerical illustration. Finally, we end with conclusion in section 5.

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2 Model Description

In this paper, we propose the following SEIR epidemic model for (H1N1) influenza with two delays. Xueyong Zhou and Zhen Guo [16], proposed on ODE model with vaccination. In their study shows that higher values of vaccination rate Φ significantly reduce the number of infected individuals, and lead to disease eradication. Our model consisted of four types of cells: susceptible (those who are capable of contracting the disease), exposed (those who are infected but not yet infectious), infectious (those who are infected and capable of transmitting the disease) and recovered (those who are permanently immune), denoted by $S(t), E(t), I(t)$ and $R(t)$ respectively. $N(t)$ is now given by $N(t) = S(t) + E(t) + I(t) + R(t)$.

From [16], we have the following set of equation as our basic model

$$\begin{aligned}
\frac{dS}{dt} &= A - \beta(I(t) + \eta E(t))S(t) - (\Phi + \mu)S(t),\\
\frac{dV}{dt} &= \Phi S(t) - (1-\sigma)\beta(I(t) + \eta E(t))V(t) - \mu V(t),\\
\frac{dE}{dt} &= \beta(I(t) + \eta E(t))S(t) + (1-\sigma)\beta(I(t) + \eta E(t))V(t)\\
&\quad -k_1 E(t) - \mu E(t),\\
\frac{dI}{dt} &= k_1 E(t) - dI(t) - \delta I(t) - \mu I(t),\\
\frac{dR}{dt} &= \delta I(t) - \mu R(t). \qquad (1)
\end{aligned}$$

We begin by considering sub-models of (1) and to introduce the two delays into the above system, we obtain the model as follows:

$$\begin{aligned}
\frac{dS}{dt} &= A - \beta I(t)S(t) - \mu S(t),\\
\frac{dE}{dt} &= \beta I(t-\tau_1)S(t-\tau_1) - k_1 E(t) - \mu E(t),\\
\frac{dI}{dt} &= k_1 E(t-\tau_2) - dI(t) - \delta I(t) - \mu I(t),\\
\frac{dR}{dt} &= \delta I(t) - \mu R(t). \qquad (2)
\end{aligned}$$

Where τ_1 represents the infectious and susceptible individuals and τ_2 is the time necessary for exposed to become a infectious. The first equation from system (2), positive constant A represents the birth or immigration rate, and the positive constant μ represents the death rate of susceptible. β is the infection rate. The second equation of system (2), k_1 represents the transfer rate between the exposed and infectious and μ represents the death rate of exposed. The third equation of system (2), d represents the disease death rate, μ represents the death rate of infectious and also δ represent the rate of recovery from the disease. The fourth equation of system (2), μ represents the death rate of recovery. Parameter values are described in Table I.

Now, we simplified our model (2), it has two steady states: The infection free steady state

$$E_0(S,E,I,R) = \left(\frac{A}{\mu}, 0, 0, 0\right).$$

The infected steady state

$$E^*(S^*,E^*,I^*,R^*) = \left(\frac{(k_1+\mu)(d+\delta+\mu)}{\beta k_1}, \frac{(d+\delta+\mu)}{k_1\beta}(R_0-1), \frac{1}{\beta}(R_0-1), \frac{\delta}{\mu\beta}(R_0-1)\right),$$

where

$$R_0 = \frac{\beta k_1 A}{\mu(k_1+\mu)(d+\delta+\mu)}.$$

Table 1: Parameters description

Parameters	Values	Reference
A	variable	Assumed
μ	5.48×10^{-5}/day	[17]
d	0.001/day	[18]
k_1	0.2/day	[19]
β	variable	Assumed
δ	0.14/day	[20]

3 Analysis of H1N1 model

It is important to show that the positivity and the boundedness for the system (2) as they represent cell populations. Positivity implies that the cell population survives and boundedness may be interpreted as a natural restriction to growth as a consequence of limited resources. In this Section, we present some basic results, such as the positivity and the boundedness of solution of model (2).

Now, we find out the positive solution of the newly discussed model (2). We denote by $X = C([-\tau,0],\mathbb{R}^4_+)$, the Banach space of continuous function mapping the interval $[-\tau,0]$ into $\mathbb{R}^4_+$, equipped with the sup-norm, where $\tau = \max\{\tau_1,\tau_2\}$. By the standard theory of functional differential equation [21,22,13], we know that for any $\phi \in C([-\tau,0],\mathbb{R}^4_+)$, there exists a unique solution

$$Z(t,\phi) = (S(t,\phi),E(t,\phi),I(t,\phi),R(t,\phi)),$$

of the delayed system (2), which satisfy $Z_0 = \phi$, where $\phi = (\phi_1,\phi_2,\phi_3,\phi_4) \in \mathbb{R}^4_+$ with $\phi_i(\xi) \geq 0 : (\xi \in [-\tau,0], i = 1,\ldots,4)$, and $\phi_1(0),\phi_2(0),\phi_3(0),\phi_4(0) > 0$. And the initial conditions are given by,

$$S(\xi) = \phi_1(\xi), \quad E(\xi) = \phi_2(\xi), \quad I(\xi) = \phi_3(\xi), \quad R(\xi) = \phi_4(\xi). \qquad (3)$$

Proposition 3.1. Let $Z(t,\phi)$ be the solution of the delayed system (2) with the initial conditions (3). Then $S(t),E(t),I(t)$ and $R(t)$ are all non-negative and bounded $(\tau \geq 0)$ at which the solution exists.

Proof. Note that from (2), we obtain

$$\begin{aligned}
S(t) &= S(0)e^{-\int_0^t(\beta I(\eta)+\mu)d\eta} + \int_0^t Ae^{-\int_\gamma^t(\beta I(\eta)+\mu)d\eta}d\gamma,\\
E(t) &= E(0)e^{-(k_1+\mu)t} + \int_0^t \beta I(\gamma-\tau_1)S(\gamma-\tau_1)\\
&\quad e^{-(k_1+\mu)(t-\gamma)}d\gamma,\\
I(t) &= I(0)e^{-(d+\delta+\mu)t} + \int_0^t k_1E(\gamma-\tau_2)\\
&\quad e^{-(d+\delta+\mu)(t-\gamma)}d\gamma,\\
R(t) &= R(0)e^{-\mu t} + \int_0^t \delta I(\gamma)e^{-\mu(t-\gamma)}d\gamma. \qquad (4)
\end{aligned}$$

Using (3), we have $Z(t,\phi) \geq 0, \forall t \geq 0$. Hence for all $t \geq 0$, our solution $(S,E,I,R) \in \mathbb{R}^4_+$ with all parameters in $\mathbb{R}^4_+$.

Positivity immediately follows from the above integral forms and equation (3). For boundedness of the solution, we define

$$V(t) = S(t-\tau_1)+E(t)+I(t+\tau_2)+R(t+\tau_2)$$

and $p = \min\{\mu,\mu,d+\mu,\mu\}$. By non-negativity of the solution, it follows that

$$\begin{aligned}
\frac{dV}{dt}(t) &= A - p\{S(t-\tau_1)+E(t)+I(t+\tau_2)+R(t+\tau_2)\}\\
&\leq A - pV(t).
\end{aligned}$$

This implies that $V(t)$ is bounded, and so are $S(t),E(t),I(t)$ and $R(t)$. This completes the proof.

The system (2) will be analyzed in biologically feasible region as follows. Consider the feasible region

$$\Omega = \left\{(S,E,I,R) \in \mathbb{R}^4_+ : S \leq \frac{A}{\mu},\ E,I,R \geq 0\right\}$$

From the above, we can establish the following theorem.

Theorem 3.2. The region Ω is positively invariant for the system (2) with initial conditions in $\mathbb{R}^4_+$.

Thus, the epidemic model of the H1N1 will be considered in $C([-\tau,0],\mathbb{R}^4_+)$. Further we will find the sufficient conditions on the parameters for the stability of the infection free and the infected steady states.

3.1 Local stability analysis

To study the local stability of the steady state of the system (2), we linearized the system and obtained the characteristic equation, given by the following Jacobian matrix,

$$\begin{bmatrix}
-(\beta I^*+\mu) & 0 & -\beta S^* & 0\\
\beta I^* e^{-\lambda\tau_1} & -(k_1+\mu) & \beta S^* e^{-\lambda\tau_1} & 0\\
0 & k_1e^{-\lambda\tau_2} & -(d+\delta+\mu) & 0\\
0 & 0 & \delta & -\mu.
\end{bmatrix} \qquad (5)$$

From the above matrix (5), the characteristic equation for the infection free steady state of the model (2) is

$$(\lambda+\mu)^2[(\lambda+(k_1+\mu))(\lambda+(d+\delta+\mu))] + \frac{\beta A}{\mu}k_1e^{-\lambda\bar{\tau}} = 0, \qquad (6)$$

where $\bar{\tau} = \tau_1+\tau_2$ is the time delay. Thus the eigen values of the infection free steady state is $-\mu,-\mu$. Simplifying the above equation (6), we lead the following transcendental characteristic equation such as

$$\begin{aligned}
&\lambda^2+\lambda(k_1+\mu+d+\delta+\mu)\\
&+(k_1+\mu)(d+\delta+\mu)(1-R_0e^{-\lambda\bar{\tau}}) = 0. \qquad (7)
\end{aligned}$$

Theorem 3.3. The infection free steady state of model (2) is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$.

Proof. The characteristic Equation (7) at the infection free steady state can be rewritten as,

$$(\lambda+(k_1+\mu)(\lambda+(d+\delta+\mu)) = (k_1+\mu)(d+\delta+\mu) R_0e^{-\lambda\bar{\tau}}. \qquad (8)$$

If the eigenvalue of λ in (8) has a non-negative real part, then the modulus of the LHS of (8) satisfies,

$$|(\lambda+(k_1+\mu)(\lambda+(d+\delta+\mu))| \geq (k_1+\mu)(d+\delta+\mu). \qquad (9)$$

while the modulus of the RHS of (9) satisfies

$$\begin{aligned}
|(k_1+\mu)(d+\delta+\mu)R_0e^{-\lambda\bar{\tau}}| &< |(k_1+\mu)(d+\delta+\mu)R_0|\\
&< (k_1+\mu)(d+\delta+\mu).
\end{aligned}$$

This leads a contradiction to (8). Thus, all the eigenvalues of (8) have negative real part and hence the infected free steady state of the model (2) is locally asymptotically stable when $R_0 < 1$.

When $R_0 > 1$, we define a function,

$$\begin{aligned}
p(\lambda) &= (\lambda+(k_1+\mu)(\lambda+(d+\delta+\mu))\\
&\quad -(k_1+\mu)(d+\delta+\mu)R_0e^{-\lambda\bar{\tau}}. \qquad (10)
\end{aligned}$$

It is clear that $p(0) < 0$ and $p(\lambda) \to \infty$ as $\lambda \to \infty$. By the continuity, we know that, there exist atleast one positive root when $R_0 > 1$. Thus,the infection free steady state of the model (2) is unstable when $R_0 > 1$. From the above matrix (5), the characteristic equation of the infected steady state of the model (2) is

$$\begin{aligned}
&(\lambda+\mu+\beta I^*)\{(\lambda+\mu)(\lambda+(k_1+\mu))\\
&\quad (\lambda+(d+\delta+\mu))+\beta S^*k_1e^{-\lambda\bar{\tau}}\}\\
&\quad +\beta^2S^*I^*k_1e^{-\lambda\bar{\tau}}(\lambda+\mu) = 0. \qquad (11)
\end{aligned}$$

Proposition 3.4. All the roots of the equation (11) with $\bar{\tau} = 0$ have negative real parts if and only if $R_0 > 1$.

Now return to the study of equation (11) with $\bar{\tau} \geq 0$.

Theorem 3.5. The infected steady state of model (2) is locally asymptotically stable when $R_0 > 1$ in the case of $\bar{\tau} \geq 0$.

Proof. Suppose that $R_0 > 1$. Then from Proposition 3.4, the characteristic equation (11) has negative real parts for $\bar{\tau} = 0$. Obviously the characteristic equation (11) does not have any real solution. By Rouche's theorem [4, p.no.248], it follows that if instability occurs for a particular value of the delay $\bar{\tau}$, a characteristic root of the equation (11) must intersect the imaginary axis.

If the equation (11) has a purely imaginary root $\lambda = i\omega$, with $\omega > 0$, we get

$$(i\omega+\mu+\beta I^*)\left((i\omega+\mu)(i\omega+(k_1+\mu))\right.$$
$$\left.(i\omega+(d+\delta+\mu))+\beta S^* k_1 e^{-i\omega\bar{\tau}}\right)$$
$$+\beta^2 S^* I^* k_1 e^{-i\omega\bar{\tau}}(i\omega+\mu) = 0. \quad (12)$$

Separating real and imaginary parts, we've

$$\omega^2 a_1 - a_3 = b_1 \cos(\omega\bar{\tau}),$$
$$\omega^3 - \omega_2 = -b_1 \sin(\omega\bar{\tau}). \quad (13)$$

where

$$a_1 = 3\mu + d + \delta + k_1 + R_0 - 1,$$
$$a_2 = 3\mu^2 + (R_0-1)(k_1+2\mu+d+\delta) + k_1 d + k_1\delta$$
$$+\mu(2k_1+d+3\delta),$$
$$a_3 = \mu^3 + (R_0-1)(d\mu + dk_1 + \mu^2 + \mu\delta + \mu k_1 + \delta k_1)$$
$$+\mu k_1 d + \mu^2 d + \mu\delta k_1 + \delta\mu^2 + \mu^2 k_1,$$
$$b_1 = (k_1+\mu)(d+\delta+\mu)R_0.$$

Squaring and adding (13), we obtain

$$\omega^6 + A_1\omega^4 + A_2\omega^2 + A_3 = 0. \quad (14)$$

where

$$A_1 = a_1^2 - 2a_2,$$
$$A_2 = a_2^2 - 2a_1 a_3,$$
$$A_3 = a_3^2 - b_1^2.$$

Put $\omega^2 = \rho$ in (14), we get

$$h(\rho) = \rho^3 + A_1\rho^2 + A_2\rho + A_3 = 0. \quad (15)$$

From the hypothesis of $R_0 > 1$, we deduce that $A_3 = a_3^2 - b_1^2 > 0$, since for $R_0 > 1$, A_1 and A_2 are also positive. Thus the equation (15) has no positive solution for $R_0 > 1$. This completes the proof.

Suppose that if $A_3 < 0$ or $A_3 \geq 0$ and $A_2 < 0$, by using the Descartes' rule of sign equation (15) has positive root ρ^* and thus equation (14) has a purely imaginary roots $\pm i\omega_0$. From transcendental equation (12), we obtain

$$\bar{\tau_j} = \frac{1}{\omega_0}\arccos\left(\frac{a_1\omega_0^2 - a_3}{b_1}\right) + \frac{2j\Pi}{\omega_0}, \quad j = 0,1,2,... \quad (16)$$

Also, we can verify that the following transversality condition:

$$\frac{d}{d\bar{\tau}} Re\lambda(\bar{\tau})|_{\bar{\tau}=\bar{\tau_0}} = \frac{d}{d\bar{\tau}}\eta(\bar{\tau})|_{\bar{\tau}=\bar{\tau_0}} > 0$$

holds. By continuity, the real part of $\lambda(\bar{\tau})$ becomes positive when $\bar{\tau} > \bar{\tau_0}$ and the steady state becomes unstable. Moreover, a Hopf bifurcation occurs when $\bar{\tau}$ passes through the critical value $\bar{\tau_0}$ (see [9]).

3.2 Global stability analysis

We shall consider the global stability of the infection free and the infected steady state of model (2) by the Lyapunov direct method. We define a function $G : \mathbb{R}_{>0} \to \mathbb{R}_{\geq 0}$ as

$$G(u) = u - 1 - \ln u.$$

We note that $G(u) \geq 0$ for any $u > 0$ and has the global minimum 0 at $u = 1$.

Theorem 3.6. The infected free steady state of model (2) is globally asymptotically stable when $R_0 < 1$.

Proof. By Theorem 3.3, it suffices to prove that the infection free steady state E_0 of model (2) is globally attracting. We consider a Lyapunov functional $U_1(t)$ as follows:

$$U_1(t) = \left(S - S_0 - S_0\ln\frac{S}{S_0}\right) + E + I + \beta$$
$$\int_{t-\tau_1}^{t} I(\xi)S(\xi)d(\xi) + k_1\int_{t-\tau_2}^{t} E(\xi)d(\xi). \quad (17)$$

Calculating the time derivative of U_1 along the positive solutions of the model (17), we obtain

$$\frac{dU_1}{dt} = \left(1 - \frac{S_0}{S}\right)\frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt}$$
$$+\beta\left(I(t)S(t) - I(t-\tau_1)S(t-\tau_1)\right) +$$
$$k_1(E(t) - E(t-\tau_2))$$
$$= \left(1 - \frac{S_0}{S}\right)(A - \beta IS - \mu S) +$$
$$(\beta I(t-\tau_1)S(t-\tau_1) - k_1E(t) - \mu E(t)) +$$
$$(k_1E(t-\tau_2) - dI - \delta I - \mu I)$$
$$+\beta\left(I(t)S(t) - I(t-\tau_1)S(t-\tau_1)\right) +$$
$$k_1(E(t) - E(t-\tau_2)). \quad (18)$$

Using the infection free steady state condition of model (2) $A = \mu S_0$ in (18), then the equation (18) becomes

$$\frac{dU_1}{dt} = -\frac{\mu}{S}(S - S_0)^2 + (\beta S_0 - (d+\delta+\mu))I - \mu E$$
$$\leq 0. \quad (19)$$

It follows that $U_1(t)$ is bounded and non-increasing and thus $\lim_{t\to\infty} U_1(t)$ exists. Note that, $\frac{dU_1}{dt} = 0$ if and only if $S = S_0, I = R = 0$. Using $R = 0$ in (2), we get $E = I = 0$. Therefore, the maximal compact invariant set in $\left\{\frac{dU_1}{dt} = 0\right\}$ is the singleton E_0. By the LaSalle invariance principle for delay systems [23], the infection free steady state of model (2) is globally attracting.

Further, it was showed in Theorem 3.3, the infection free steady state is locally asymptotically stable when $R_0 < 1$. Therefore, the infection free steady state of model (2) is globally asymptotically stable when $R_0 < 1$.

Theorem 3.7. The infected steady state of model (2) is globally asymptotically stable when $R_0 > 1$.

Proof. We consider a Lyapunov functional as follows:

$$\begin{aligned} U_2(t) &= S^* g\left(\frac{S}{S^*}\right) + E^* g\left(\frac{E}{E^*}\right) + I^* g\left(\frac{I}{I^*}\right) \\ &\quad + \left(\frac{d+\delta+\mu}{\delta}\right) R^* g\left(\frac{S}{S^*}\right) \\ &\quad + \beta S^* I^* \int_{t-\tau_1}^{t} \left(\frac{S(\xi)I(\xi)}{S^*I^*}\right) d\xi \\ &\quad + k_1 E^* \int_{t-\tau_2}^{t} \left(\frac{E(\xi)}{E^*}\right) d\xi. \end{aligned} \tag{20}$$

Where

$$g(u_i) = u_i - 1 - \ln(u_i)$$

and $u_1 = \frac{S}{S^*}, u_2 = \frac{E}{E^*}, u_3 = \frac{I}{I^*}, u_4 = \frac{R}{R^*}$. Moreover $g(u_i) \geq 0$ for $i = 1,2,3,4$. Positiveness and boundedness of the solution of the model (2) implies that $U_2(t)$ is well defined and $U_2(t) \geq 0$ for all $t \geq 0$. We calculate the derivative of $U_2(t)$ along the solution of the system (2), we obtain

$$\begin{aligned} \frac{dU_2}{dt} &= \left(1-\frac{S^*}{S}\right)\frac{dS}{dt} + \left(1-\frac{E^*}{E}\right)\frac{dE}{dt} + \left(1-\frac{I^*}{I}\right)\frac{dI}{dt} \\ &\quad + \left(\frac{d+\delta+\mu}{\delta}\right)\left(1-\frac{R^*}{R}\right)\frac{dR}{dt} + \\ &\quad \beta S^* I^* \left(\frac{SI}{S^*I^*} - \frac{S(t-\tau_1)I(t-\tau_1)}{S^*I^*}\right. \\ &\quad \left. + \ln\frac{S(t-\tau_1)I(t-\tau_1)}{SI}\right) + \\ &\quad k_1 E^* \left(\frac{E}{E^*} - \frac{E(t-\tau_2)}{E^*} + \ln\frac{E(t-\tau_2)}{E}\right) \end{aligned}$$

$$\begin{aligned} &= \left(1-\frac{S^*}{S}\right)(A - \beta IS - \mu S) \\ &+ \left(1-\frac{E^*}{E}\right)(\beta I(t-\tau_1)S(t-\tau_1) - k_1 E(t) - \mu E(t)) \\ &+ \left(1-\frac{I^*}{I}\right)(k_1 E(t-\tau_2) - dI(t) - \delta I(t) - \mu I(t)) \\ &+ \left(\frac{d+\delta+\mu}{\delta}\right)\left(1-\frac{R^*}{R}\right)(\delta I - \mu R) \\ &+ \beta S^* I^* \left(\frac{SI}{S^*I^*} - \frac{S(t-\tau_1)I(t-\tau_1)}{S^*I^*}\right. \\ &\quad \left. + \ln\frac{S(t-\tau_1)I(t-\tau_1)}{SI}\right) \\ &+ k_1 E^* \left(\frac{E}{E^*} - \frac{E(t-\tau_2)}{E^*} + \ln\frac{E(t-\tau_2)}{E}\right) \end{aligned} \tag{21}$$

Using the infected steady state condition $A = \beta I^* S^* + \mu S^*$ and $\delta I^* = \mu R^*$ in (21), then equation (21) becomes

$$\begin{aligned} &= -\frac{\mu}{S}(S-S^*)^2 - \beta I^* S^* \left(1 + g\left(\frac{S^*}{S}\right)\right. \\ &+ \left. g\left(\frac{I(t-\tau_1)S(t-\tau_1)E^*}{I^*S^*E}\right) + g\left(\frac{EI^*}{E^*I}\right) - \ln\left(\frac{E^*I}{EI^*}\right)\right) \\ &\quad -k_1 E^* \left(g\left(\frac{E(t-\tau_2 I^*)}{IE^*}\right) - \ln\left(\frac{IE^*}{I^*E}\right)\right) \\ &- \frac{(d+\delta+\mu)}{\delta}\frac{IR^*}{R} \\ &\quad - \frac{(d+\delta+\mu)I^*\mu}{\delta}(R-R^*) - \mu(E-E^*) \\ &\leq 0 \end{aligned}$$

since

$$\begin{aligned} \ln\frac{S(t-\tau_1)I(t-\tau_1)}{SI} &= \ln\frac{S^*}{S} + \ln\frac{S(t-\tau_1)I(t-\tau_1)E^*}{S^*I^*E} \\ &\quad + \ln\frac{EI^*}{E^*I} \end{aligned}$$

$$\ln\frac{E(t-\tau_2)}{E} = \ln\frac{E(t-\tau_2)I^*}{E^*I} + \ln\frac{E^*I}{EI^*}.$$

It follows that $U_2(t)$ is bounded and non-increasing and thus $\lim_{t\to\infty} U_2(t)$ exists. Note that $\frac{dU_2(t)}{dt} = 0$ if and only if $I = I^*$, $E = E^*$, $E(t-\tau_2) = E^*$, $S = S^*$, $S(t-\tau_1)I(t-\tau_1) = S^*I^*$. Therefore, the maximal compact invariant set in $\frac{dU_2(t)}{dt} = 0$ is the singleton E^*. By the LaSalle invariance principle for delay systems in [23], the infected steady state of model (2) is globally attracting. Further,it was showed in Theorem 3.5, the infected steady state is locally asymptotically stable when $R_0 > 1$ and $\overline{\tau} \geq 0$. Hence the infected steady state of model (2) is globally asymptotically stable when $R_0 > 1$, in the case of $\overline{\tau} \geq 0$.

4 Numerical simulation

In this section, we carry out some numerical simulations to display the qualitative behaviours of H1N1 model (2)(see Figs. 10 (a) - 11 (b)) fit the model to given data. The numerical simulations confirmed the theoretical results obtained in Section 3. We have seen in previous sections that the basic reproduction number R_0 plays a decisive rule in determining the H1N1 dynamics. It is known that infected free and infected steady state is locally asymptotically stable if all the roots of the corresponding characteristic equations (7) and (11) have negative real parts (roots are located on the open left side of the complex plane *i.e.*, $Re\lambda_i < 0, i = 1,2,...$). The precise values of the time delays τ_1 and τ_2 are unknown. Here, we defined physiologically feasible intervals for some parameter based on information, we assumed that τ_1 is ≤ 3 days and τ_2 is ≤ 6 days, and estimated both of them by using Table I values.

4.1 Application

For $A = 0.4,\ \beta = 0.000018,\ \tau_1 = 3,\ \tau_2 = 6$ and the parameter values are taken from Table I. The system (2), as follows

$$\begin{aligned}
\frac{dS}{dt} &= 0.4 - 0.000018I(t)S(t) - 0.0000548S(t),\\
\frac{dE}{dt} &= 0.000018I(t-\tau_1)S(t-\tau_1) - 0.2E(t)\\
&\quad -0.0000548E(t)\\
,\frac{dI}{dt} &= 0.2E(t-\tau_2) - 0.001I(t) - 0.14I(t)\\
&\quad -0.0000548I(t),\\
\frac{dR}{dt} &= 0.14I(t) - 0.0000548R(t). \qquad (22)
\end{aligned}$$

For the infected free steady state, we can get $R_0 = 0.9312045472 \leq 1$. Moreover, the eigenvalues associated with the characteristic equation of (22),

$$\begin{aligned}
L(\lambda, \tau_1+\tau_2) &= \lambda^2 + 0.3411096\lambda + 0.02821868980\\
&\quad -0.026773722e^{(-9\lambda)} = 0. \qquad (23)
\end{aligned}$$

Finally, we can see that the Theorem 3.3 is satisfied, when $R_0 < 1$. Hence the infection free-steady state of model (22) is locally asymptotically stable. This, together with Theorems 3.6 implies that the global stability of equilibria for system (2) is completely determined by the reproduction number R_0.

For the infected steady state, $R_0 = 1.164005684 > 1$ and using $A = 0.5$, with the above same values of β, τ_1 and τ_2, we obtain,

$$\begin{aligned}
\frac{dS}{dt} &= 0.5 - 0.000018I(t)S(t) - 0.0000548S(t),\\
\frac{dE}{dt} &= 0.000018I(t-\tau_1)S(t-\tau_1) - 0.2E(t)\\
&\quad -0.0000548E(t),\\
\frac{dI}{dt} &= 0.2E(t-\tau_2) - 0.001I(t) - 0.14I(t)\\
&\quad -0.0000548I(t),\\
\frac{dR}{dt} &= 0.14I(t) - 0.0000548R(t). \qquad (24)
\end{aligned}$$

Then the characteristic equation of (24),

$$\begin{aligned}
L(\lambda, \tau_1+\tau_2) &= \lambda^3 + 0.505170084\lambda^2 + 0.0841889131\lambda\\
&\quad +0.00462957190\\
&\quad +0.03284671532e^{(-9\lambda)} = 0. \qquad (25)
\end{aligned}$$

Finally, we can see that the Theorem 3.5 is satisfied, when $R_0 > 1$. Hence the infected steady state of model (24) is locally asymptotically stable. This, together with Theorems 3.7 implies that the global stability of equilibria for system (24) is completely determined by the reproduction number R_0.

Using the Table I values, all the characteristic roots of the characteristic equation for the model (23) has negative real parts, when $R_0 < 1$. Similarly for infected steady state if $R_0 > 1$, then all the characteristic roots of the characteristic equation for the model (25) has negative real parts. Therefore our model (2) is always stable. The plots of the characteristic equations as shown in Fig. 1(a) - 2(b).

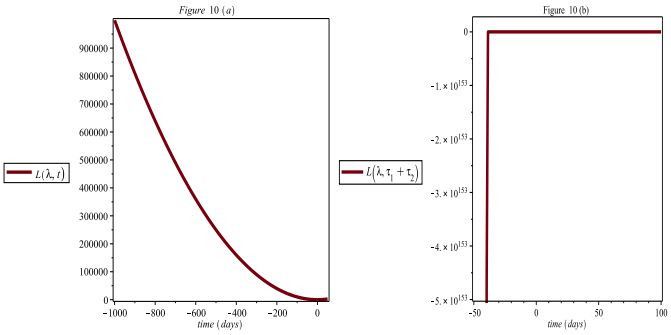

Fig. 1 (a) shows that the plot of the characteristic equation of the system (22) for non-delay case ($R_0 < 1$). Fig. 1 (b) shows that the plot of characteristic equation of the system (22) for delay case ($R_0 < 1$).

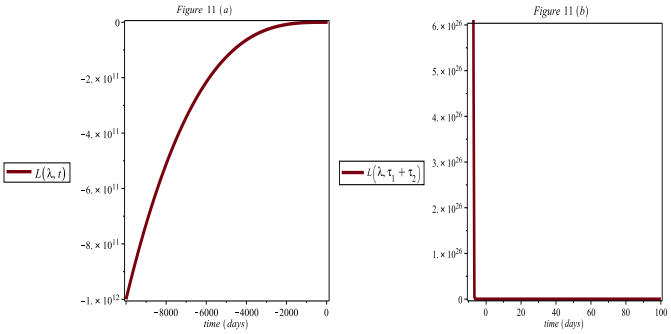

Fig. 2 (a) shows that the plot of the characteristic equation of the system (24) data for non-delay case ($R_0 > 1$). Fig. 2 (b) shows that the plot of characteristic equation of the system (24) for delay case ($R_0 > 1$).

From the above analysis, we can easily see that the delay model seems to fit and it could be better than using without delay. Thus, our numerical results are reasonable representatives of our model. Moreover, small perturbations of parameters will give small perturbation of the matrix entries used in finding eigenvalues for determining the stability of two steady state points. The stability results in our numerical calculation are biologically reasonable and represent a qualitative outcome that is possible for the parameter values.

5 Discussion and Conclusion

In this paper, we have incorporated time delay into our H1N1 models. We showed that the threshold value R_0 plays an important role in determining the stability of the steady states of the delay model of H1N1 model dynamics. The global stability of the infected free and the infected steady states have been established by using suitable Lyapunov functionals and LaSalle invariant principle. More specifically, we have proven that, if the threshold value R_0 is less than unity, then the infected free steady state is locally asymptotically stable and globally attracting, and if R_0 is greater than unity the infected steady state is locally asymptotically stable and globally attracting.

Xueyong Zhou and Zhen Guo [16], discussed ODE models for influenza A (H1N1). They were considered in their paper SIE model with vaccination only. They took under consideration that only a susceptible person can be vaccinated and that the vaccine is not 100% efficient. Their findings shows that higher values of vaccination rate Φ significantly reduce the number of infected individuals, and lead to disease eradication.

We point out the essential differences between our results and the results in [16]. On the other hand, the results in [16] are analyzed the local and global stability only for infected free steady states with vaccination reproduction ratio number, but we have obtained a global stability result for infected free and infected steady states by applying Lyapunov functional under certain conditions with two time delays. Our described model (2), is much better than the ODE model in [16]. We compare the ODE model without using vaccination, we found the smaller value of infection rate β and the birth of the immigration rate A provided the permanence of H1N1 system disappears and the epidemic disease dies out. The ultimate scenario makes intuitive biological sense: if the exposed takes too long to transfer to the infectious, then the infectious population will suffer low survival, as a result we will drop the transmission rate k_1, leading to the extinction of infectious level.

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