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Mathematical modeling and analysis for controlling the spread of infectious diseases

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In this work, we present and discuss the approaches, that are used for modeling and surveillance of dynamics of infectious diseases by considering the early stage asymptomatic and later stage symptomatic infections. We highlight the conceptual ideas and mathematical tools needed for such infectious disease modeling. We compute the basic reproduction number of the proposed model and investigate the qualitative behaviours of the infectious disease model such as, local and global stability of equilibria for the non-delayed as well as delayed system. At the end, we perform numerical simulations to validate the effectiveness of the derived results.

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1. Introduction

Over the past many years, various efforts have been made up worldwide in developing the establishment of a global surveillance network to combat the pandemics of emergent and re-emerging infectious diseases. Various researchers and scientists from different fields are working on rapid assessment of such potentially urgent situations. To achieve this, mathematical modeling plays a significant role focussing on prediction, assess and development of control strategies of potential outbreaks. For better understanding and modeling of the contagious dynamics such as Nipah virus infection (NIV), SARS, COVID..., etc., the impact of various variables, such as interaction terms along with prevailing social, ecological and demographic factors need to be analyzed. Due to these infectious diseases, many countries in this world encounter death and ailments. Besides this, it affects the economic and social structure of the respective country. Thus, one can conclude that these infectious diseases are a major threat to the society. In past years, mathematical modeling of infectious diseases has been the major topic of interest for researchers to capture their dynamics. The possible causes for the spread of an epidemic can be accurately predicted using mathematical modeling. In earlier mathematical models, only those factors were used to be considered that were closely related to disease, such as infectious period, mode of transmission, susceptibility, etc. But with time, the growth of epidemiology has made it mandatory to consider other factors too, such as economic, geographic and demographic conditions, which play a significant role in the transmission of these diseases. Thus, it becomes necessary to make the mathematical model more realistic by incorporating more parameters and variables. Various mathematical models have been proposed to analyze the dynamics of diseases considering above-mentioned factors. For more details on the various mathematical models proposed in literature, we refer to \cite{1}–\cite{16} and the references cited therein. These infectious diseases can be subdivided into various classes, such as vector-borne disease, water-
borne diseases, zoonotic disease,... etc. Among these, zoonotic diseases are very unique, as they are mainly caused by pathogens (such as fungi, bacteria, parasites, or viruses) and they have the capability to jump from animals to humans or vice versa. Moreover, these diseases can cause sickness or death in people. Thus these are more troublesome and deadly in particular. Recently, many zoonotic diseases have emerged out due to increase in human and wildlife interaction. With increase in farming or deforestation, humans and wildlife are compelled to reside in the same habitat. Due to this, the infected hosts transmit the disease to humans who come in contact with the infected animal through different modes. These modes include bites, scratches, animal secretions that include saliva, faeces or mucus. This family of zoonotic diseases includes West Nile, Rabies, Ebola, Dengue fever.

In late 2002 and early 2003, Severe acute respiratory syndrome (SARS) was such infectious disease, which was highly contagious and rapidly spreading, and had been transmitted to more than 28 countries through the medium of international travel. The evolution and spread of SARS resulted in an international effort coordinated by the World Health Organization (WHO). Due to the rapid increase in infection, complete data was collected and various kinds of research had been carried out. A new corona virus had been isolated from patients with SARS, and the sequence of the complete genome of SARS-CoV was determined [17,18]. To bring SARS under control, various measures and actions were taken [19]. Newspapers, radio, TV stations, and posters campaigned to educate and make the public aware of SARS prevention. In many public places, including streets, shopping centers, airports, railways, bus terminals, classrooms, offices, transportation vehicles, and residential areas, disinfectant was sprayed. Individuals who have had direct or indirect contact with probable SARS-infected cases were quarantined in their homes, hospitals, or campuses. Stern travel advisories were issued to students and workers. A body temperature check was done for all air passengers and passengers who failed a therm-imaging check at the entrance were checked by nurses and doctors at the station’s quarantine center. Many stock exchanges, cinemas, theaters, and internet cafes were closed temporarily. Quarantine outpatient departments were set up for fever patients in many large hospitals. Special hospitals for SARS treatment were specified in every large city.

In 2018, one of these zoonotic diseases, Nipah virus (NiV) emerged out as a prime suspect, a member of the Henipavirus genus in the Paramyxoviridae family with subfamily Paramyxovirinae. The natural host of the virus was fruit bats of the Pteropodidae Family, Pteropus genus. This virus had become a major concern in South-East Asia. Human NIV infection was first identified during an outbreak of disease, that took place in Kampung Sungai Nipah, Malaysia and Singapore from September 1998 to June 1999, in which 276 cases were reported. During this occasion, pigs were the intermediate hosts. However, in subsequent NiV outbreaks, there were no intermediate hosts. The human outbreak of Nipah infection terminated after widespread deployment of personal protective equipment to people contacting infected or sick pigs and hindering livestock movements and culling over 9,000,000 pigs [20]. In Bangladesh (2004), humans became infected with NiV due to consumption of date palm sap that had been contaminated by infected fruit bats. Human-to-human transmission has also been documented, including in a hospital setting in India. During the 1998 outbreak, about 40 percent of patients with encephalitis subsequently died. Very recently, the outbreak was reported in Kerala (India), in which 17 people died of those it infected. A total of 18 confirmed cases had been reported [21]. NiV infection in humans can be clinically represented in a wide range, from asymptomatic infection to acute respiratory syndrome and fatal encephalitis. NiV is also capable of causing disease in pigs and other domestic animals. There is no vaccine for either humans or animals. There is a vast literature discussing the NiV spread, causes, symptoms etc. For instance, we refer to [22–30] and references cited therein. Consequently, it becomes mandatory to respond urgently to this in order to combat against NiV infection effectively.

Very recently the Novel 2019 Corona virus, SARS-CoV-2 (COVID-19), emerged towards the end of 2019 in Wuhan city in the Peoples Republic of China, and it has spread to the entire world very fast and in a very short time. With the respiratory tract infection that it causes, the virus leads to pneumonia characterized by an appearance like frosted glass. This infection has progressed in a highly destructive manner in the whole world. Various preventive measures have been taken by countries to control this pandemic, such as complete lock down and efforts similar to taken during spread of SARS in 2003. Due to these reasons, the prevention of infectious diseases become one of the most important tasks in public health. To tackle these issues of infectious diseases successfully, it becomes mandatory to establish a supporting system of executing preventive measures sharing know-how of prevention from infectious diseases. Among such preventive measures, mathematical modelling of such disease models and their analysis plays a very important role to achieve these missions. In literature, various mathematical models have been proposed for the SARS-COV-2 model. In [31], Zhang et. al. investigated a delayed virus model with two different transmission methods and treatments. For more details on the mathematical models for 2019-nCoV, we refer to [32,33] and the references cited therein. Motivated by the above discussions, this work aims to provide a mathematical model for the infectious disease model and its qualitative analysis for the corresponding non-delayed and delayed model to explore the dynamics of the infections and reduce the spread and prevent the possible occurrence of such infections.

This work is organized as follows: In Section 2, we give the mathematical formulation of the proposed model. In Section 3, we determine the basic reproduction number using next generation matrix approach. In Section 4, we investigate the local and global stability of the proposed model. In Section 5, we analyze the delayed system for stability and Hopf Bifurcation. In Section 6, we give numerical simulation results to validate the analytical findings. Finally a concluding remark is presented in Section 7.

2. Model Formulation

Let \( N(t) \) denote the total human population at time \( t \). We subdivide \( N(t) \) into seven sub-populations; namely Susceptible individuals (\( S(t) \)), Exposed individuals (\( E(t) \)), Asymptomatic individuals at early stage (\( I_1(t) \)), Symptomatic individuals at later stage (\( I_2(t) \)), Hospitalized individuals (\( H(t) \)), Home Quarantined or Home treated individuals (\( T(t) \)) and Recovered individuals (\( R(t) \)), such that

\[
N(t) = S(t) + E(t) + I_1(t) + I_2(t) + H(t) + T(t) + R(t).
\]  

(2.1)

The model can be described by the following deterministic system of non linear differential equations:

\[
\frac{dS}{dt} = A - \mu S - \alpha S(I_1 + I_2)
\]

(2.2)

\[
\frac{dE}{dt} = \alpha S(I_1 + I_2) - (\lambda + \mu)E
\]

(2.3)

\[
\frac{dI_1}{dt} = \lambda E - (\tau_1 + \gamma + \mu)I_1
\]

(2.4)

\[
\frac{dI_2}{dt} = \gamma I_1 - (\tau_2 + \psi + \phi_1 + \mu + \delta)I_2
\]

(2.5)

\[
\frac{dT}{dt} = \psi I_2 - (\phi_2 + \mu + \theta_1 \delta)T
\]

(2.6)
Thus initial conditions are given by: 
\[ \text{Proof.} \]

Let \( S, E, I_1, I_2, H, T, R \) be any solution with positive initial conditions. Then from (2.1), the time derivative of total population \( N(t) \) is given by
\[
\frac{dN}{dt} = A - \mu N - \delta_2 - \theta \delta H.
\]
where \( S(t), E(t), I_1(t), I_2(t), H(t), T(t) \) and \( R(t) \) are non-negative.

Positivity and Boundedness of the solution

Theorem 2.1. The solutions of model system (2.2)-2.8) are bounded.

Proof. From equation (2.9), the time derivative of total population \( N \) is given by
\[
\frac{dN}{dt} = A - \mu N - \delta_2 - \theta \delta H,
\]
where \( S(t), E(t), I_1(t), I_2(t), H(t), T(t) \) and \( R(t) \geq 0 \). This implies that \( \frac{dN}{dt} \) is bounded by \( A - \mu N \). Using standard comparison theorem [34], we obtain
\[
0 < N(t) \leq \frac{A}{\mu} \left( 1 - e^{-\alpha t} \right) + N(0).
\]

Thus
\[
\lim_{t \to +\infty} N(t) = \frac{A}{\mu}.
\]

Further for \( I_2 = 0, H = 0 \), if \( N(t) > \frac{A}{\mu} \), then \( \frac{dN}{dt} < 0 \). Thus we have
\[
0 < N(t) \leq \frac{A}{\mu}.
\]

Also \( N(t) \leq \frac{A}{\mu} \) if \( N(0) \leq \frac{A}{\mu} \). Consequently, the region \( \Omega = \left\{(S, E, I_1, I_2, H, T, R) : S + E + I_1 + I_2 + H + T + R \leq \frac{A}{\mu}\right\} \) is invariant. Hence, all the solutions are bounded and independent of initial conditions. Furthermore, as \( A > 0, \mu > 0 \), we have \( A < \mu > 0 \).

Thus the invariant set is positive. Hence all solutions of model (2.2)-2.8) that initiate in \( \mathbb{R}^7 \setminus \{0\} \) are confined in the region \( \Omega \). □

Corollary 2.1. The closed set
\[
\Omega = \left\{(S, E, I_1, I_2, H, T, R) \in \mathbb{R}^7 : N(t) \leq \frac{A}{\mu}\right\}
\]
is positively invariant and attracting with respect to model (2.2)-2.8).

Proof. The proof follows directly from Theorem 2.1. □

From above, in the region \( \Omega \), the proposed model is well posed epidemiologically and mathematically. Thus it is sufficient to analyze qualitative dynamics of model (2.2)-2.8) in \( \Omega \).

3. Possible equilibria and basic reproduction number \( R_0 \)

The model involved system (2.2)-2.8) admits two equilibria, namely, disease free equilibrium (DFE) point \( E_0 = (S^0,0,0,0,0,0) = (\frac{\lambda}{\gamma},0,0,0,0,0) \) and endemic equilibrium point \( E_1 = (S^*,E^*,I_1^*,I_2^*,H^*,T^*,R^*) \). The existence of disease free equilibrium point is trivial.

The basic reproduction number \( R_0 \), is defined as number of secondary infections produced by a single infected individual when introduced to a completely susceptible population. It is a threshold quantity which enables us to analyze the disease dynamics. Due to this significance, various efforts have been made to calculate \( R_0 \).

Furthermore, the basic reproduction number is also defined as the largest eigenvalue of the next generation matrix.

In order to find out the basic reproduction number \( R_0 \), we use the next generation matrix approach [35]. We construct matrices \( F \) and \( V \) as
\[
F = \begin{pmatrix} \alpha S & 0 \\ 0 & \alpha S \end{pmatrix} = \begin{pmatrix} \alpha S(I_1 + I_2) \\ 0 \end{pmatrix}
\]
and
\[
V = \begin{pmatrix} -\lambda E + (\tau_1 + \gamma + \mu)I_1 \\ -\gamma I_1 + (\tau_2 + \psi + \phi_0 + \mu + \delta)I_2 \end{pmatrix}.
\]
We then find matrices \( F \) and \( V \) as
\[
F = \text{Jacobian of } F \text{ at } E_0 = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}
\]
and
\[
V = \text{Jacobian of } V \text{ at } E_0 = \begin{pmatrix} \lambda + \mu & 0 & 0 \\ -\gamma & \tau_2 + \psi + \phi_0 + \mu + \delta \end{pmatrix}.
\]
It then follows that
\[
FV^{-1} = \begin{pmatrix} m_1 & m_2 & m_3 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix},
\]
where
\[
m_1 = \frac{\lambda \alpha S^0 (\tau_2 + \psi + \phi_0 + \mu + \delta + \gamma)}{(\lambda + \mu)(\tau_1 + \gamma + \mu)(\tau_2 + \psi + \phi_0 + \mu + \delta)},
\]
\[
m_2 = \frac{-\alpha S^0 (\tau_2 + \psi + \phi_0 + \mu + \delta + \gamma)}{(\tau_1 + \gamma + \mu)(\tau_2 + \psi + \phi_0 + \mu + \delta)},
\]
\[
m_3 = \frac{\alpha S^0}{(\tau_1 + \gamma + \mu)(\tau_2 + \psi + \phi_0 + \mu + \delta)}.
\]
Then the basic reproduction number \( R_0 \), which is given by the largest eigenvalue of \( FV^{-1} \), is obtained as below:
\[
R_0 = \frac{\lambda \alpha S^0 (\tau_2 + \psi + \phi_0 + \mu + \delta + \gamma)}{(\tau_1 + \gamma + \mu)(\tau_2 + \psi + \phi_0 + \mu + \delta)},
\]

3
Let $s(A)$ denotes the spectral abscissa (i.e., the largest real part of any eigenvalue of $A$) for a matrix $A$ and $J_0$ denotes the Jacobian matrix evaluated at DFE. Then for a model defined in terms of prevalent numbers, the basic reproduction number $R_0$ is defined as the expected number of new infections produced by an infected individual in a population at DFE. The DFE is locally stable if $R_0 < 1$ (equivalently $s(J_0) < 0$) and unstable if $R_0 > 1$ (equivalently $s(J_0) > 0$) [36].

4. Existence and stability of equilibria

The DFE for model (2.2)-(2.8) is $E_0 = (S^0, 0, 0, 0, 0, 0, 0) = \left(\frac{A}{\mu}, 0, 0, 0, 0, 0, 0\right)$.

**Theorem 4.1.** The DFE for model (2.2)-(2.8) is locally asymptotically stable on $\Omega$.

**Proof.** The characteristic equation of the Jacobian matrix at DFE for the model (2.2)-(2.8) is given by

$$\det\begin{bmatrix}
A_{11} - x & 0 & A_{12} & A_{13} & A_{14} & 0 & 0 \\
0 & A_{22} - x & A_{23} & A_{24} & 0 & 0 & 0 \\
0 & A_{32} & A_{33} - x & A_{34} & 0 & 0 & 0 \\
0 & 0 & 0 & A_{43} & A_{44} - x & 0 & 0 \\
0 & 0 & 0 & A_{53} & A_{55} - x & 0 & 0 \\
0 & 0 & 0 & 0 & A_{64} & A_{66} - x & 0 \\
0 & 0 & 0 & 0 & 0 & A_{75} & A_{76} \\
\end{bmatrix} = 0,$$

where

$$A_{11} = -\mu, A_{13} = -\alpha S^0, A_{14} = -\alpha S^0, A_{22} = -(\lambda + \mu), A_{23} = \alpha S^0, A_{24} = \alpha S^0,$$

$$A_{32} = A, A_{33} = -(\tau_1 + \gamma + \mu), A_{34} = \gamma A, A_{44} = -(\tau_2 + \psi + \phi_t + \mu + \delta), A_{54} = \psi, A_{55} = -\phi_t, A_{66} = -\phi_t, A_{77} = -\mu.$$

Simplifying the above determinant, we obtain

$$H_0 + H_1 x + H_2 x^2 + H_3 x^3 + H_4 x^4 + H_5 x^5 + H_6 x^6 + H_7 x^7 = 0,$$

where

$$H_0 = -A_{35} A_{46} A_{77} \left[ A_{11}(A_{22} A_{33} A_{44} + A_{24} A_{32} A_{44} - 2 A_{23} A_{32} A_{44}) + A_{13} A_{32} A_{44} - A_{14} A_{33} A_{43} \right],$$

$$H_1 = (A_{55} A_{66} + A_{57} A_{67}) (A_{11} A_{22} A_{33} A_{44} + A_{11} A_{23} A_{32} A_{44} + A_{13} A_{24} A_{33} A_{43} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42}) + A_{55} A_{66} A_{77} \left[ A_{11} A_{22} A_{33} A_{44} + A_{12} A_{23} A_{32} A_{44} - A_{13} A_{24} A_{33} A_{43} + A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right]$$

$$+ (A_{55} A_{66} + A_{57} A_{67}) \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right],$$

$$H_2 = -A_{55} A_{66} + A_{57} A_{67} (A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42})$$

$$+ (A_{55} A_{66} + A_{57} A_{67}) \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right],$$

$$H_3 = (A_{55} A_{66} + A_{57} A_{67}) \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right]$$

$$+ (A_{55} A_{66} + A_{57} A_{67}) \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right],$$

$$H_4 = \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right]$$

$$+ (A_{55} A_{66} + A_{57} A_{67}) \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right],$$

$$H_5 = A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42}$$

$$+ (A_{55} A_{66} + A_{57} A_{67}) \left[ A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right],$$

$$H_6 = \left( A_{11} A_{22} A_{33} A_{44} + A_{11} A_{24} A_{32} A_{44} + A_{13} A_{23} A_{44} - A_{14} A_{33} A_{43} - 2 A_{11} A_{23} A_{32} A_{42} \right),$$

$$H_7 = 1.$$

Furthermore, if we have

$$H_0 > 0, \quad \det \begin{pmatrix} H_6 & 1 \\ H_4 & H_5 \\ \end{pmatrix} > 0, \quad \det \begin{pmatrix} H_6 & 1 & 0 \\ H_4 & H_5 & H_6 \\ H_2 & H_3 & H_4 \\ \end{pmatrix} > 0, \quad \det \begin{pmatrix} H_6 & 1 & 0 & 0 \\ H_4 & H_5 & H_6 & 1 \\ H_2 & H_3 & H_4 & H_5 \\ H_0 & H_1 & H_2 & H_3 \\ \end{pmatrix} > 0.$$
Then using Routh-Hurwitz criterion, all the eigenvalues of the Jacobian matrix have negative real parts. Thus the DFE is locally asymptotically stable. □

In addition to DFE, the system (2.2)-(2.8) admits a unique endemic equilibrium point

\[
E_\ast = \left( S^\ast, E^\ast, I_1^\ast, I_2^\ast, H^\ast, T^\ast, R^\ast \right),
\]

where

\[
S^\ast = \frac{1}{\mu} \left[ A - \frac{(\mu + \lambda)(\tau_1 + \gamma + \mu)\left(\tau_2 + \psi + \phi_2 + \mu + \delta\right)}{\gamma \lambda} \right] I_2^\ast,
\]

\[
E^\ast = \left( \frac{\tau_1 + \gamma + \mu}{\lambda \gamma} \left(\tau_2 + \psi + \phi_2 + \mu + \delta\right) I_2^\ast, \right.
\]

\[
l_1^\ast = \frac{1}{\gamma} \left(\tau_2 + \psi + \phi_2 + \mu + \delta\right) I_2^\ast,
\]

\[
H^\ast = \left( \phi_1 + \theta_1 \delta \right) I_2^\ast.
\]

\[
T^\ast = \left( \frac{1}{\phi_1 + \mu} \left( \frac{\tau_1}{\gamma} \left(\tau_2 + \psi + \phi_2 + \mu + \delta\right) + \tau_2 \right) I_2^\ast, \right.
\]

\[
R^\ast = \frac{1}{\mu} \left[ \phi_2 + \theta_2 \mu \left(\frac{\phi_1}{\phi_1 + \mu + \theta_2 \delta} + \frac{\phi_1}{\phi_1 + \theta_2 \mu} \left(\frac{\tau_1}{\gamma} \left(\tau_2 + \psi + \phi_2 + \mu + \delta\right) + \tau_2 \right) \right) I_2^\ast, \right.
\]

\[
l_2^\ast = \frac{\alpha \gamma}{(\lambda + \mu)(\tau_1 + \gamma + \mu)\left(\tau_2 + \psi + \phi_2 + \mu + \delta\right) - \alpha(\tau_2 + \psi + \phi_2 + \mu + \delta + \gamma)}.
\]

**Global stability analysis**

In order to prove the global asymptotic stability of DFE, we use theorem by Castillo-Chavez et al. [37].

**Theorem 4.2.** [38] The given mathematical model (2.2)-(2.8) can be represented in the form

\[
\frac{dX}{dt} = F(X, Y), \quad \frac{dY}{dt} = G(X, Y), \quad G(X, 0) = 0,
\]

where \( X = S, Y = (E, I_1, I_2)^T \) denote the classes of uninfected and infected individuals respectively.

The DFE is represented by \( E_0 = (X_0, 0) = (\frac{K}{S}, 0) \).

For global asymptotic stability of \( E_0 \), conditions (H1) and (H2) must be satisfied.

(H1) \( \frac{\partial F}{\partial X} = F(X_0, 0) \) is globally asymptotically stable.

(H2) \( G(X, Y) = MY - \hat{G}(X, Y) \), \( \hat{G}(X, Y) \geq 0 \). Here \( M = D_Y G(X_0, 0) \) is M-matrix, that is all off-diagonal elements are non-negative.

If given system (2.2)-(2.8) satisfies (4.2), then \( E_0 = (X_0, 0) \) is a globally asymptotically stable equilibrium of given mathematical model.

**Theorem 4.3.** The equilibrium \( E_0 = (X_0, 0) \) of system (2.2)-(2.8) is globally asymptotically stable provided the conditions in (4.2) are satisfied.

**Proof.** Using Theorem 4.2 to our model system (2.2)-(2.8), we obtain

\[
F(X_0, 0) = A - \mu S, \quad G(X, Y) = MY - \hat{G}(X, Y)
\]

where

\[
M = \begin{bmatrix}
-\lambda - \mu & \alpha S^0 \\
\alpha S^0 & \gamma - (\tau_1 + \gamma + \mu)
\end{bmatrix}, \quad \hat{G}(X, Y) = \begin{bmatrix}
\hat{G}_1(X, Y) \\
\hat{G}_2(X, Y) \\
\hat{G}_3(X, Y)
\end{bmatrix} = \begin{bmatrix}
\gamma (l_1 + l_2)(S^0 - S) \\
0 \\
0
\end{bmatrix}.
\]

We can observe that \( S^0 \geq S \). Hence \( \hat{G}(X, Y) \geq 0 \) \( V(X, Y) \). Furthermore, the matrix \( A \) is M-matrix. Thus the DFE \( E_0 \) is globally asymptotically stable.

**Theorem 4.4.** The endemic equilibrium point \( E_\ast = (S^\ast, E^\ast, I_1^\ast, I_2^\ast, H^\ast, T^\ast, R^\ast) \) of the model (2.2)-(2.8) is globally asymptotically stable.

**Proof.** We consider the following Lyapunov function

\[
V = K_1 \left[ S - S^\ast - S^\ast \ln \frac{S}{S^\ast} \right] + K_2 \left[ E - E^\ast - E^\ast \ln \frac{E}{E^\ast} \right] + K_3 \left[ l_1 - l_1^\ast - l_1^\ast \ln \frac{l_1}{l_1^\ast} \right] + K_4 \left[ l_2 - l_2^\ast - l_2^\ast \ln \frac{l_2}{l_2^\ast} \right].
\]

Calculating time derivative of \( V \) and substituting values from (2.2)-(2.8), we obtain

\[
\frac{dV}{dt} = K_1 \left[ 1 - \frac{S}{S^\ast} \right] (A - \mu S - \alpha S) + K_2 \left[ 1 - \frac{E}{E^\ast} \right] (\alpha S - \lambda E - \mu E)
\]

\[
+ K_3 \left[ 1 - \frac{l_1}{l_1^\ast} \right] (\lambda E - (\tau_1 + \gamma + \mu) l_1) + K_4 \left[ 1 - \frac{l_2}{l_2^\ast} \right] (\gamma l_1 - (\tau_2 + \psi + \phi_2 + \mu + \delta) l_2).
\]

(4.3)
At equilibrium point $E_*$, model (2.2)-(2.8) satisfies the following relations:

$$A = \mu S^* + \alpha S^*I^*, \quad \alpha S^*E^* = (\lambda + \mu).$$

$$\tau_1 + \gamma + \mu = \frac{\lambda E^*}{I^*_1}, \quad (\tau_2 + \psi + \phi_2 + \mu + \delta) = \frac{\gamma I^*_1}{I^*_2}.$$  \hspace{1cm} (4.4)

Substituting (4.4) into (4.3) and after simplifications, we obtain

$$\frac{dV}{dt} = K_3 \left[ \frac{S - S^*}{S} \right] (-\mu (S - S^*) + \alpha (S^*T - SI)) + K_1 \left(1 - \frac{E^*}{E} \right) \left(\alpha S^*E^* - \frac{\alpha S^*I^*E^*}{E^*} \right)$$

$$+ K_3 \left[1 - \frac{I^*_1}{I^*_2}\right] \left(\lambda E - \frac{\lambda E^*I^*_1}{I^*_1}\right) + K_4 \left[1 - \frac{I^*_1}{I^*_2}\right] \left(\gamma I^*_1 - \frac{\gamma I^*_1I^*_2}{I^*_2}\right).$$

We can rewrite the above equation as

$$\frac{dV}{dt} = -\frac{K_1 \mu (S - S^*)^2}{S} + g(y_1, y_2, y_3, y_4),$$  \hspace{1cm} (4.5)

where $\frac{S - S^*}{S} = y_1, \frac{E - E^*}{E^*} = y_2, \frac{I^*_1}{I^*_1} = y_3, \frac{I^*_2}{I^*_2} = y_4$. $S^*I^*_1 = a, S^*I^*_2 = b, \lambda E^* = c, \gamma I^*_1 = d$ and

$$g(y_1, y_2, y_3, y_4) = K_1a(b - a - by_1y_3 - by_1y_4) - K_1\frac{\alpha a}{y_1} + K_1\frac{\alpha ab}{y_1} + K_1\alpha ay_2 + K_1\alpha by_4$$

$$+ K_2a(ay_1y_3 + by_1y_4 - ay_2 - by_2) - K_2\frac{\alpha ay_1y_3}{y_2} + K_2\alpha ay_2 + K_2\alpha by_4$$

$$+ K_3y_2 - K_3\frac{c}{y_3}y_3 - K_3\frac{cy_2}{y_3} + K_3c + K_4dy_3 - K_4dy_4 + K_4\frac{dy_2}{y_4} + K_4d.$$
5. The delayed system

In this section, we analyze the global stability along with direction and stability of Hopf bifurcation for the infectious disease model with time delay. It is evident that time delay for system of differential equations is an important tool for many models of population interactions. We consider the following delayed model corresponding to the system (2.2)-(2.8):

\[
\begin{align*}
\frac{dS}{dt} &= A - \mu S - \alpha S(l_1(t - \tau) + l_2(t - \tau)) \\
\frac{dE}{dt} &= \alpha S(l_1(t - \tau) + l_2(t - \tau)) - (\lambda + \mu)E \\
\frac{dl_1}{dt} &= \lambda E - (\tau_1 + \gamma + \mu)l_1 \\
\frac{dl_2}{dt} &= \gamma l_1 - (\tau_2 + \psi + \phi_1 + \mu + \delta)l_2
\end{align*}
\]

(5.1)

The initial conditions are \( S_0(\theta) = \phi_1(\theta) > 0, \ E_0(\theta) = \phi_2(\theta) > 0, \ l_{10}(\theta) = \phi_3(\theta) > 0, \ l_{20}(\theta) = \phi_4(\theta) > 0 \) with \( \theta \in [-\tau, 0] \) where \( \phi_i \in C([-\tau, 0] \to \mathbb{R}_+) \). \( (r = 1, 2, 3, 4) \) are given functions and \( \tau \) is a positive constant.

5.1. Positive Invariance and Boundedness of the solution

We can rewrite system (5.1)-(5.4) in the vector form by setting \( X = (S, E, l_1, l_2)^T \in \mathbb{R}^4 \) and

\[
F(X) = \begin{pmatrix}
F_1(X) \\
F_2(X) \\
F_3(X) \\
F_4(X)
\end{pmatrix} = \begin{pmatrix}
A - \mu S - \alpha S(l_1(t - \tau) + l_2(t - \tau)) \\
\alpha S(l_1(t - \tau) + l_2(t - \tau)) - (\lambda + \mu)E \\
\lambda E - (\tau_1 + \gamma + \mu)l_1 \\
\gamma l_1 - (\tau_2 + \psi + \phi_1 + \mu + \delta)l_2
\end{pmatrix}
\]

(5.5)

where \( F : C_+ \to \mathbb{R}^4 \) and \( F \in C^\infty(\mathbb{R}^4) \). Then delayed model (5.1)-(5.4) becomes

\[
\dot{X}(t) = F(X_t).
\]

(5.6)

where \( \cdot = \frac{d}{dt} \) and \( X_i(\theta) = X(t + \theta), \theta \in [-\tau, 0] \). We can observe from (5.6) that whenever we choose \( X(\theta) \in C_+ \) such that \( X_i = 0 \), we obtain \( F_i(X)\big|_{X_i(t_0) = 0} \). \( X_i \in C_+ \). \( i = 1, 2, 3, 4 \). Following Lemma [39], any solution of (5.6) with \( X_i(\theta) \in C_+ \), say \( X(t) = X(t, X(0)) \) is such that \( X(t) \in \mathbb{R}_+^4 \). \( \forall \ t > 0 \).

Now, to prove the boundedness of the solution, we define

\[
V(t) = S(t) + E(t) + l_1(t) + l_2(t)
\]

and \( r = \min \{\mu, \lambda + \mu, \tau_1 + \gamma + \mu, \tau_2 + \psi + \phi_1 + \mu + \delta\} \). From non-negativity of the solutions, it follows that

\[
\frac{dV}{dt} = A - rV(t)
\]

This implies that \( V(t) \) is bounded and hence are \( S(t), E(t), l_1(t) \) and \( l_2(t) \). This completes the proof.

We analyze the delayed system (5.1)-(5.4) in biologically feasible region defined by

\[
\Omega = \left\{ (S, E, l_1, l_2) \in \mathbb{R}_+^4 : S \leq \frac{A}{\mu}, E, l_1, l_2 \geq 0 \right\}
\]

We can write the above analysis as the following theorem:

**Theorem 5.1.** The region \( \Omega \) is positively invariant for the delayed system (5.1)-(5.4) with initial conditions in \( \mathbb{R}_+^4 \).

Thus, we will consider the infectious disease epidemic model in \( C([-\tau, 0], \mathbb{R}_+) \). We will also find out the sufficient conditions on the parameters for the stability of the disease free and the infected steady state.

5.2. Linear stability analysis

**Theorem 5.2.** The disease free steady state of the delayed model (5.1)-(5.4) is linearly asymptotically stable for \( \tau \geq 0 \).

**Proof.** The delayed system (5.1)-(5.4) has an infected steady state \( E_\ast = (S_\ast, E_\ast, l_{1\ast}, l_{2\ast}) \). Then the linearized system at \( E_\ast \) results

\[
\begin{pmatrix}
-(\mu + \alpha l_1^\ast + \alpha l_2^\ast) - x \\
\alpha (l_1^\ast + l_2^\ast) e^{-xt} \\
0 \\
0
\end{pmatrix} + \begin{pmatrix}
0 \\
-(\lambda + \mu) - x \\
\lambda \\
0
\end{pmatrix} + \begin{pmatrix}
-\alpha S e^{-xt} \\
\alpha S e^{-xt} \\
0 \\
0
\end{pmatrix} + \begin{pmatrix}
-\alpha S e^{-xt} \\
\alpha S e^{-xt} \\
0 \\
0
\end{pmatrix} = 0.
\]

\( \square \)
This yields the following characteristic polynomial:
\[ x^4 + A_1x^3 + A_2x^2 + A_3x + A_4 + e^{-2\pi t}(B_1x + B_2) = 0. \]  
(5.7)

where
\[ A_1 = (\tau + \psi + \phi_1 + \mu + \delta) + \lambda + 2\mu + \alpha (l_1^* + l_2^*), \]
\[ A_2 = (\lambda + \mu) (t_1 + \gamma + 2\mu + t_2 + \psi + \phi_2 + \delta) + (t_1 + \gamma + \mu) (t_2 + \psi + \phi_3 + \mu + \delta) \]
\[ + \mu (\lambda + \alpha l_1^* + l_1^* (\lambda + 3\mu + t_1 + \gamma + t_2 + \psi + \phi_4 + \delta). \]
\[ A_3 = (\lambda + 2\mu + \alpha l^*) (t_1 + \gamma + \mu) (t_2 + \psi + \phi_1 + \mu + \delta) + (\mu + \alpha l^*) (\lambda + \mu) (t_1 + \gamma + 2\mu + t_2 + \psi + \phi_5 + \delta) - \alpha \lambda S', \]
\[ A_4 = (\mu + \alpha l^*) (\lambda + \mu) (t_1 + \gamma + \mu) (t_2 + \psi + \phi_3 + \mu + \delta) - \alpha \lambda S', \]
\[ B_1 = \alpha^2 S (l_1^* + l_2^*) \lambda, \]
\[ B_2 = \alpha^2 S (l_1^* + l_2^*) \lambda (t_2 + \psi + \phi_1 + \mu + \delta + \gamma). \]

If equation (5.7) admits purely imaginary root \( x = i\omega, \omega^* > 0 \), then separating real and imaginary parts, we obtain following system of transcendental equations
\[ \omega^4 - A_2 \omega^2 + A_4 = -B_2 \cos 2\omega^* \tau - B_1 \omega^* \sin 2\omega^* \tau \]
(5.8)
\[ A_1 \omega^4 - A_3 \omega^* = B_1 \omega^* \cos 2\omega^* \tau - B_2 \sin 2\omega^* \tau. \]
(5.9)

Further on squaring and adding above two equations and substituting \( \omega^2 = \rho \), we obtain
\[ \rho^4 + C_1 \rho^3 + C_2 \rho^2 + C_3 \rho + C_4 = 0. \]
(5.10)

We select the parameters in such a way that \( C_1, C_2, C_3, C_4 \) are all positive. Thus we conclude that equation (5.10) does not have any positive solution. This completes the proof.

**Theorem 5.3.** The infected equilibrium \( E_s \) is stable for \( \tau \in [0, \tau^*] \) and unstable for \( \tau > \tau^* \), where \( \tau^* \) denotes the critical time delay, at which Hopf Bifurcation takes place. As \( \tau \) passes through the critical value, the periodic solutions bifurcate from this infected equilibrium.

**Proof.** Now, we assume that \( A_2^* B_2^* \), that is \( C_4 < 0 \). Then equation (5.10) admits one positive root \( \xi \) and thus a pair of purely imaginary roots \( i\omega^* \). From (5.8) and (5.9), we obtain
\[ \tau^* = \frac{1}{2\omega^* \alpha} \arccos \left[ \frac{B_1^2 (A_1 \omega^3 - A_3 \omega^*) - B_1 \omega^* (\omega^4 - A_2 \omega^* + A_4)}{2\omega^* B_1^2 B_2^2} \right] + \frac{2n\pi}{\omega^*}, \quad n = 0, 1, 2, \ldots \]

Furthermore, after simple analysis, we obtain that \( \frac{d(\mathcal{R}(\xi))}{dt} \bigg|_{\omega = \omega^*, \tau = \tau^*} > 0 \). Thus the solution curve of characteristic equation (5.10) crosses the imaginary axis. This implies that Hopf Bifurcation takes place at \( 0 < \tau = \tau^* \). By continuity, we can interpret that the infected steady state is locally asymptotically stable at \( \tau < \tau^* \). \( \square \)

5.3. Direction and stability of Hopf Bifurcation

In this section, we study the direction of the Hopf bifurcations and stability of bifurcating periodic solutions by using the normal theory and the center manifold theorem introduced by Hassard et al. [40]. Let \( \bar{u_1} = S - S^*, \bar{u_2} = E - E^*, \bar{u_3} = I - I^* \) and \( \bar{u_4} = L_1 - L_1^* \) and \( \bar{t} = tt \). Further let \( a = \bar{t} - \bar{t} \), then \( a = 0 \) is the Hopf bifurcation value of the system (5.1)-(5.4). Dropping the bars for simplification of notation, the delayed system (5.1)-(5.4) is transformed into
\[ \frac{du_1}{dt} = j_{11} u_1(t) + j_{13} u_3(t - 1) + j_{14} u_4(t - 1) - \alpha u_1(t) (u_3(t - 1) + u_4(t - 1)) \]
(5.11)
\[ \frac{du_2}{dt} = j_{21} u_1(t) + j_{22} u_2(t) + j_{23} u_3(t - 1) + j_{24} u_4(t - 1) + \alpha u_1(t) (u_3(t - 1) + u_4(t - 1)) \]
(5.12)
\[ \frac{du_3}{dt} = j_{32} u_2(t) + j_{33} u_3(t) \]
(5.13)
\[ \frac{du_4}{dt} = j_{43} u_3(t) + j_{44} u_4(t) \]
(5.14)

where \( j_{11} = -\mu + \alpha l^*, j_{13} = -\alpha S^*, j_{14} = -\alpha S^*, j_{21} = -\alpha l^*, j_{22} = -(\lambda + \mu), j_{23} = \alpha l^*, j_{24} = \alpha S^*, j_{32} = \lambda, j_{33} = -(t_1 + \gamma + \mu), j_{43} = \gamma, j_{44} = (t_2 + \psi + \phi_4 + \mu + \delta) \). We can write the above system as following functional differential equation in \( C = C([-1, 0], \mathbb{R}^4) \) as
\[ \dot{x}(t) = Lx(t) + f(x, t) \]
(5.15)

where \( x(t) = (u_1(t), u_2(t), u_3(t), u_4(t))^T \in \mathbb{R}^4 \) and \( L_0 : C \to \mathbb{R}^4, F : \mathbb{R} \times C \to \mathbb{R}^4 \) are given by

\[
L_0(\phi) = (\tau^* + \alpha) \begin{pmatrix}
1 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 \\
0 & 0 & 1 & 0 \\
0 & 0 & 0 & 1
\end{pmatrix} \begin{pmatrix}
\phi_1(0) \\
\phi_2(0) \\
\phi_3(0) \\
\phi_4(0)
\end{pmatrix} + (\tau^* + \alpha) \begin{pmatrix}
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0
\end{pmatrix} \begin{pmatrix}
\phi_1(-1) \\
\phi_2(-1) \\
\phi_3(-1) \\
\phi_4(-1)
\end{pmatrix}
\]
Similarly, we have

\[ f(a, x_i) = (\tau^* + a) \begin{pmatrix} -\phi_1(0)\phi_3(-1) - \phi_1(0)\phi_4(-1) \\ \phi_1(0)\phi_3(-1) + \phi_1(0)\phi_4(-1) \\ 0 \\ 0 \end{pmatrix}. \]

By Riesz representation theorem [40], there exists a function \( \eta(\theta, a) \) of bounded variation for \( \theta \in [-1, 0] \) such that

\[ L_a(\phi) = \int_{-1}^{0} d\eta(\theta, 0)\phi(\theta), \quad \phi \in C. \quad (5.16) \]

In fact, we choose

\[ \eta(\theta, a) = (\tau^* + a) \begin{pmatrix} j_{11} & 0 & 0 & 0 \\ j_{21} & j_{22} & 0 & 0 \\ j_{31} & j_{32} & j_{33} & 0 \\ 0 & 0 & j_{43} & j_{44} \end{pmatrix} \delta(\theta) - (\tau^* + a) \begin{pmatrix} 0 & 0 & j_{13} & j_{14} \\ 0 & 0 & j_{23} & j_{24} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \delta(\theta + 1) \]

where \( \delta \) is dirac delta function and for \( \phi \in C([-1, 0], \mathbb{R}^4) \), define

\[ A(a)\phi = \begin{cases} \frac{d\phi(\theta)}{d\theta} & \text{for } \theta \in [-1, 0), \\ \int_{-1}^{0} d\eta(a, s)\phi(s) & \text{for } \theta = 0 \end{cases} \quad (5.17) \]

and

\[ R(a)\phi = \begin{cases} 0 & \text{for } \theta \in [-1, 0), \\ f(a, \phi) & \text{for } \theta = 0. \end{cases} \quad (5.18) \]

Then the system (5.15) is equivalent to

\[ \dot{x}_i = A(a)x_i + R(a)x_i \quad (5.19) \]

where \( x_i(\theta) = x(t + \theta) \) for \( \theta \in [0, -1] \).

For \( \psi \in C^1([0, 1], (\mathbb{R}^2)^*) \), define

\[ A^*\psi(s) = \begin{cases} -\frac{d\psi(s)}{ds} & \text{for } s \in [0, 1), \\ \int_{-1}^{0} d\eta^T(0, \phi)(-t) & \text{for } s = 0 \end{cases} \quad (5.20) \]

and a bilinear inner product

\[ <\psi(s), \phi(\theta)> = \tilde{\psi}(0)\phi(0) - \int_{-1}^{0} \int_{\sigma=0}^{\theta} \tilde{\psi}(\sigma - \theta)d\eta(\theta)\phi(\sigma)d\sigma, \quad (5.21) \]

where \( \eta(\theta) = \eta(\theta, 0) \). Then \( A(0) \) and \( A^* \) are adjoint operators and

\[ <\psi, A\phi> = <A^*\psi, \phi>. \]

Furthermore, if \( \pm i\omega^*\tau^* \) are eigenvalues of \( A(0) \) and they are also eigenvalues of \( A^* \). We first need to compute the eigenvectors of \( A(0) \) and \( A^* \) corresponding to \( \pm i\omega^*\tau^* \), respectively. Assume that \( q(\theta) = (1, q_1, q_2, q_3)^T e^{i\omega^*\tau^*} \) is the eigenvector of \( A(0) \) corresponding to \( i\omega^*\tau^* \). Then \( A(0)q(\theta) = i\omega^*\tau^*q(\theta) \). From definition of \( A(0) \), \( L_a(\phi) \), \( \eta \) (5.16) and for \( q(-1) = q(0)e^{-i\omega^*\tau^*} \), we have

\[ q_1 = \frac{(j_{11} + i\omega^*\tau^*)}{j_{21}}, \quad (5.22) \]

\[ q_2 = \frac{(j_{11} + i\omega^*\tau^*)}{j_{21}j_{32}}, \quad (5.23) \]

\[ q_3 = \frac{(j_{11} + i\omega^*\tau^*)(j_{24} + j_{11}j_{14} - j_{21}j_{14})}{j_{21}(j_{44} + i\omega^*\tau^*)}. \]
We normalize $q$ and $q^*$ by condition $<q^*(s), q(\theta) >= 1$. Clearly $<q^*(s), \tilde{q}(\theta) >= 0$. In order to assure $<q^*(s), q(\theta) >= 1$, we need to choose a suitable $D$ by evaluating

$$<\psi(s), \phi(\theta)>=\tilde{D}(1, \tilde{q}_1, \tilde{q}_2, \tilde{q}_3)(1, q_1, q_2, q_3)^T - \int_{-1}^{0} d\sigma \tilde{D}(1, \tilde{q}_1, \tilde{q}_2, \tilde{q}_3)e^{j\omega_0 r^* \sigma}dq(\theta)(1, q_1, q_2, q_3)^T e^{j\omega r^* \sigma} d\sigma.$$  

Following the algorithms given in [40] and using similar computation process in [41,42], we can obtain the following coefficients which will be used to determine the important quantities;

$$g_{20} = 2D\left[\frac{\alpha}{2} W_{20}^{(1)}(0)q_2(0)e^{-j\omega r^*}(\tilde{q}_1 - 1) + \alpha q_3(0)e^{-j\omega r^*}(\tilde{q}_1 - 1)\right]$$  

$$g_{11} = \tilde{D}\left[\alpha \tilde{q}_2(0)e^{j\omega r^*}(\tilde{q}_1 - 1) + \alpha \tilde{q}_3(0)e^{j\omega r^*}(\tilde{q}_1 - 1)\right]$$  

$$g_{02} = 2\tilde{D}\left[\alpha \tilde{q}_2(0)e^{j\omega r^*}(\tilde{q}_1 - 1) + \alpha \tilde{q}_3(0)e^{j\omega r^*}(\tilde{q}_1 - 1)\right]$$  

$$g_{21} = 2\tilde{D}\left[\alpha W_{11}^{(3)}(-1)(\tilde{q}_1 - 1) + \alpha W_{11}^{(4)}(-1)(\tilde{q}_1 - 1) + \alpha \left(\frac{W_{20}^{(3)}(-1)}{2} \frac{W_{20}^{(1)}(0)}{2} \tilde{q}_2 e^{j\omega r^*}\right) \right.$$  

$$+ \alpha \left(\frac{W_{20}^{(4)}(-1)}{2} \frac{W_{20}^{(1)}(0)}{2} \tilde{q}_1 e^{j\omega r^*}\right) \right]$$

where

$$W_{20}^{(\theta)} = \frac{ig_{20}}{\omega r^*} q(0)e^{j\omega r^* \theta} + \frac{ig_{02}}{3\omega r^*} \tilde{q}(0)e^{-j\omega r^* \theta} + E_1 e^{2j\omega r^*}$$

and

$$W_{11}^{(\theta)} = -\frac{ig_{11}}{\omega r^*} q(0)e^{j\omega r^* \theta} + \frac{ig_{11}}{\omega r^*} \tilde{q}(0)e^{-j\omega r^* \theta} + E_2.$$  

Moreover, $E_1$ and $E_2$ satisfy the following

$$(\begin{array}{cccc}
2\omega r^* - j_{11} & 0 & -j_{13} e^{2j\omega r^*} & -j_{14} e^{-2j\omega r^*} \\
-j_{21} & 2\omega r^* - j_{22} & -j_{23} e^{-2j\omega r^*} & -j_{24} e^{2j\omega r^*} \\
0 & -j_{32} & 2\omega r^* - j_{33} & 0 \\
0 & 0 & -j_{34} & 2\omega r^* - j_{44}
\end{array}) = E_1 = 2 \left(\begin{array}{cccc}
c_1 \\
c_2 \\
c_3 \\
c_4
\end{array}\right)$$

and

$$(\begin{array}{cccc}
j_{11} & 0 & j_{13} & j_{14} \\
j_{21} & j_{22} & j_{23} & j_{24} \\
0 & j_{32} & j_{33} & 0 \\
0 & j_{34} & j_{44}
\end{array}) = E_1 = 2 \left(\begin{array}{cccc}
d_1 \\
d_2 \\
d_3 \\
d_4
\end{array}\right)$$

with

$$\left(\begin{array}{cccc}
c_1 \\
c_2 \\
c_3 \\
c_4
\end{array}\right) = \left(\begin{array}{cccc}
-\alpha \tilde{q}_2 e^{-j\omega r^*} - \alpha \tilde{q}_3 e^{j\omega r^*} \\
\alpha \tilde{q}_2 e^{j\omega r^*} + \alpha \tilde{q}_3 e^{-j\omega r^*} \\
0 \\
0
\end{array}\right)$$

and

$$\left(\begin{array}{cccc}
d_1 \\
d_2 \\
d_3 \\
d_4
\end{array}\right) = \left(\begin{array}{cccc}
-\alpha Re[q_2] e^{j\omega r^*} - \alpha Re[q_3] e^{-j\omega r^*} \\
\alpha Re[q_2] e^{-j\omega r^*} + \alpha Re[q_3] e^{j\omega r^*} \\
0 \\
0
\end{array}\right).$$

From the above expressions for each $g_{ij}$, we can compute the following quantities:

$$c_1(0) = \frac{i}{2\omega r^*} \left(\frac{g_{20}g_{11}}{2} - \frac{|g_{02}|^2}{3}\right) + \frac{g_{21}}{2}.$$  

$$\mu_2 = \left(\frac{Re[c_1(0)]}{Re[\frac{\partial c_1}{\partial \tau}]}\right),$$

$$\beta_2 = 2Re\left\{c_1(0)\right\},$$

$$T_2 = \left(-\frac{Im[c_1(0)]\mu_2 Im[\frac{\partial c_1}{\partial \tau}]}{\omega r^*}\right).$$  

(5.27)
From the result of Hassard et al. [40], we have the following:

**Theorem 5.4.** [40] Under the condition of local asymptotic stability at \( E^* \) and let \( c_1(0) \) be given in (5.27), Then

1. \( \mu_2 \) determine the direction of Hopf bifurcation: if \( \mu_2 > 0 (\mu_2 < 0) \) then the Hopf bifurcation is supercritical (sub-critical) and bifurcating periodic solution exists for \( \tau > \hat{\tau} (\tau < \hat{\tau}) \).
2. \( \beta_2 \) determines the stability of the bifurcating periodic solution: The bifurcating periodic solution is stable (unstable) if \( \beta_2 < 0 (\beta_2 > 0) \).
3. \( T_2 \) determines the period of bifurcating periodic solution: If \( T_2 > 0 \), the period increases, otherwise decreases.

### 6. Numerical Examples

In this section, we perform numerical simulations to validate our analytical findings. We select the parameter values as \( A = 3000, \lambda = 0.0002, \alpha = 0.0004, \gamma = 0.0001, \delta = 0.002, \mu = 0.0421, \tau_1 = 0.25, \tau_2 = 0.75, \phi_2 = 0.45, \psi = 0.71, \phi_H = 0.75, \phi_T = 0.6, \theta = 0.25 \). For this set of parameter values, we have \( R_0 = 0.4612 < 1 \), which implies the existence of DFE point. The DFE
point for this case is given by $E_0 = (7.13 \times 10^4, 0, 0, 0, 0, 0, 0)^T$. The eigenvalues for the variational matrix corresponding to DFE point are $-0.0421, -0.0421, -0.7926, -0.6421, -0.3133, -0.0212, -1.9541$. Since all eigenvalues are negative, this implies that DFE point $E_0$ is locally asymptotically stable.

For these set of parameters, the corresponding delayed system is also asymptotically stable for $R_0 = 0.4612 < 1$. Also, corresponding to these parameters, Eq. (5.10) does not admit any non-negative solution. From the Figs. 1, we can observe that with time, the rate of transmission of infectious disease decreases in population and ultimately tends to zero, implying asymptotic stability. Since $R_0 < 1$, we expect that the rate of spread of the infectious disease should decrease with time. We can also observe the same behaviour from the figures that the individuals in early stage infection as well as later stage infection decrease with time, which signifies the reduction in the spread of the infectious disease. This results in the decrease of individuals to be hospitalized and under treatment. Now we investigate the variation of $I_2$ with variation in $\psi$ in Fig. 2. For higher values of $\psi$, $I_2$ decreases rapidly in comparison to lower values of $\psi$. This holds true in general belief also, as if more people are hospitalized for treatment, number of infectious individuals decreases and vice versa.

Further we investigate the variation of $I_2$ with variation in $\tau_2$ in Fig. 3. It can be observed from the figures that with increase in $\tau_2$, $I_2$ decreases rapidly and increases with decrease in values of $\tau_2$. This is also true in general belief also, as if more people opt for treatment on getting any symptoms, number of infectious individuals decreases and vice versa. As soon as one gets even any mild symptom, the individual should go for antiviral detection and hence its treatment. This will result in the decrease of spread of infectious disease to a large extent from the ground level.

Now we change the parameters as $A = 300$, $\lambda = 1.0002$, $\alpha = 1.0004$, $\gamma = 1.0001$, $\delta = 0.002$, $\mu = 1.0421$, $\tau_1 = 0.000025$, $\tau_2 = 0.000075$, $\phi_0 = 1.0045$, $\psi = 0.000071$, $\phi_1 = 0.000075$, $\phi_2 = 0.0006$. For this set of parameter values, we have $R_0 = 10.2777 > 1$. In this case, the endemic equilibrium point comes into existence and is given by $E_\ast = (1.3703, 146.1940, 71.5999, 34.9517, 0.0024, 0.0042, 33.6906)^T$. The real parts of eigenvalues for the variational matrix corresponding to endemic equilibrium point are $-1.04, -1.05, -1.04, -1.0765, -2.28, -1.92, -1.92$. Since all eigenvalues have negative real parts, this implies that the endemic equilibrium point $E_\ast$ is locally asymptotically stable. The solution trajectories for the second set of parameters are given in Fig. 4.

We investigate the variation of $I_2$ with variation in $\psi$ in Fig. 5. We observe that for higher values of $\psi$, $I_2$ decreases rapidly in comparison to lower values of $\psi$. This holds true in real life situation also, as if more people are hospitalized for treatment, number of infectious individuals decreases and vice versa.

Further we investigate the variation of $I_2$ with variation in $\tau_2$ in Fig. 6. It can be observed from the figures that with increase in $\tau_2$, $I_2$ decreases rapidly and increases with decrease in values of $\tau_2$, which holds true for real world situation also, as if more people are treated for symptoms, number of infectious individuals decreases and vice versa. Furthermore, for the corresponding delayed system, there exists a critical delay value $\tau^* = 2.118 > 0$, at which Hopf bifurcation takes place and the infected steady state is asymptotically stable for $\tau < \tau^* = 2.118$.

From the above analysis and graphical results, we can conclude that if the rate of treatment is small, then with increase in time, the infection passes into the population and number of infectious individuals increases. But if we increase the treatment rate, hospitalization and maintain proper hygiene, the spread of infection can be reduced and controlled to a large extent.
Future work directions

- Some new models can be proposed with different incidence rate.
- A more general model can also be proposed by considering the reaction-diffusion terms.
- Of course, a nice and worthwhile task can be taken for validation of mathematical results with empirical data.
- Fractional optimal control problem and iterative method can be proposed for the numerical solutions to the corresponding fractional-order model.

Credit Author Statement

All authors contributed in preparation and improving this paper.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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