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# Mathematical Modeling and Analysis of Seqiahr Model: Impact of Quarantine and Isolation on COVID-19

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## Abstract

At this moment in time, an outbreak of COVID-19 is transmitting from human to human. Different parts have different quality of life (e.g., India compared to Russia), which implies the impact varies in each part of the world. Although clinical vaccines are available to cure, the question is how to minimize the spread without considering the vaccine. In this paper, via a mathematical model, the transmission dynamics of novel coronavirus with quarantine and isolation facilities have been proposed. The examination of the proposed model is set in motion with the boundedness and positivity of the solution, sole disease-free equilibrium, and local stability. Then, the condition for the existence of sole endemic equilibrium and its local stability has established. In addition, the global stability of the endemic equilibrium for a special case has been investigated. Further, it has shown that the system undergoes a transcritical bifurcation. A threshold analysis has also performed to examine the effect of quarantine on transmission dynamics. Lastly, numerical simulations are giving support to theoretical results.

**Keywords:** Novel coronavirus; Quarantine; Isolation; Stability; Asymptomatic; Lienard Chipart criterion; Transcritical bifurcation

**MSC 2020 No.:** 92B05, 34C60, 92D30, 93B45

# 1. Introduction

Humanity faces hardships from time to time; outbreaks of infectious diseases are one of them. Whenever the environment gets disturbed due to human activities, factors opposing nature become reasons for such a breakout to come into existence. These breakouts affect our society physically, mentally, economically as well as sociologically. From an era, whether its Plague from 1346 to 1353 that was an outbreak ended up killing 75 to 200 million individuals in Europe, Africa and Asia or its Influenza of 1956, an outbreak in China, Singapore, Hong Kong, and the United States, everything was devastated. The Influenza outbreak in 1968 brought silence to approximately one million residents of Singapore, Vietnam, Australia, Philippines, United States, India, Australia and Europe. HIV/AIDS killed more than 36 million people in the world since 1981, while 31-35 million people still live with HIV.

Recently, the SARS-CoV-2 virus has infected a chunk of people, approximately 162,177,376 individuals and caused more than 3,364,178 deaths worldwide as of May 16, 2021 (WHO (2021)). The novelty infected case of the COVID-19 was clocked in the Huanan seafood market in Wuhan, China, on the thirty-first of December, 2019. On the twenty-fourth of January, 2020, World Health Organization (WHO) stated the SARS-CoV-2 virus could be passed on from one mortal to another (WHO (2020)). In India, the foremost case of COVID-19 was reported in Kerala on the thirtieth of January 2020. On the eleventh of March 2020, WHO stated COVID-19 as a pandemic and announced its Public Health Emergency of International Concern (PHEIC). WHO formally asked nations to take an instantaneous action to reduce transmission. Quarantine and isolation are the best first steps to reduce transmission from one individual to another.

To evaluate the dynamics of infectious diseases, mathematical models are the finest. The pattern deduction of the spread in the host population is essential and which mathematical models help us to understand concerning both time and space. In 1760, England's change in mortality rate due to smallpox made Daniel Bernoulli (Bernoulli (1760)) develop the first mathematical model. After a big gap, at the beginning of the nineteenth century, some authors came up with new epidemiological models (Ross (1911)). In recent times authors ideas evolved realistic mathematical epidemiological models to investigate the transmission dynamics of infection as well as asymptotic behaviors of these models (Misra et al. (2018); Sahu and Dhar (2012); Dhar and Sharma (2009); Lee et al. (2019); Wang et al. (2017); Zhou and Cui (2011); Xing and Cardona (2009)).

Infectious disease outbreaks are dangerous for society due to their unknown effects and unavailability of vaccines and specific drugs. In favour of this situation, one could minimize the infection by reducing people's movement through isolation and quarantine of infected individuals (Brauer and Chavez (2011)). In various transmissible diseases such as smallpox, tuberculosis commonly called TB, AIDS and SARS, etc., isolation and quarantine have resulted in great success as a control measure (Hethcote et al. (2002); Gani et al. (1997); Hyman and Li (1998)). In 2013, Safi and Gumel (2013) proposed a mathematical model taking control strategy into account to study the transmission of a communicable disease in which quarantine was applied. They found that the proposed model undergoes a backward bifurcation when the associated reproduction threshold is less than unity. They quantitatively analyzed the quarantine efficiency and showed that when the efficacy of quarantine is perfect and the reproduction threshold is less than unity, the disease-free equilibrium is globally-asymptotically stable. Sahu and Dhar (2015) proposed a SEQIHRS epidemic model and analyzed the behaviour of disease-free and unique endemic equilibrium by keeping quarantine and isolation as control measures. In 2017, Erdem et al. (2017) proposed a SIQR endemic model with quarantine as control measures. They analyzed the stability of the equilibria of their model. Using numerical analysis, they also showed that the proposed model exhibits Hopf bifurcation when the quarantine effectiveness values vary. The article is targeting to inspect the ability of quarantine and isolation on the communication of SARS-CoV-2 virus in context of India.

## 2. Model formulation and basic properties

### 2.1. Mathematical model

Khan and Atangana (2020) assumed that the transmission of novel coronavirus first occurred within the bats' population and then it occurred to the wild animals (host). Afterwards, the transmission of novel coronavirus happened in the human population. They proposed the following two models:

(i) bat and hosts mathematical model:

$$\begin{cases} \frac{dS_b}{dt} = \Pi_b - \mu_b S_b - \frac{\eta_b S_b I_b}{N_b}, \\ \frac{dE_b}{dt} = \frac{\eta_b S_b I_b}{N_b} - (\mu_b + \theta_b) E_b, \\ \frac{dI_b}{dt} = \theta_b E_b - (\tau_b + \mu_b) I_b, \\ \frac{dR_b}{dt} = \tau_b I_b - \mu_b R_b, \\ \frac{dS_h}{dt} = \Pi_h - \mu_h S_h - \frac{\eta_{bh} S_h I_b}{N_h} - \frac{\eta_h S_h I_h}{N_h}, \\ \frac{dE_h}{dt} = \frac{\eta_{bh} S_h I_h}{N_h} + \frac{\eta_h S_h I_h}{N_h} - (\mu_h + \theta_h) E_h, \\ \frac{dI_h}{dt} = \theta_h E_h - (\tau_h + \mu_h) I_h, \\ \frac{dR_h}{dt} = \tau_h I_h - \mu_h R_h. \end{cases} \tag{1}$$

(ii) Coronavirus (sea food market) versus people (ignored the interaction among bats and hosts)

$$\begin{cases} \frac{dS_p}{dt} = \Pi_p - \mu_p S_p - \frac{\eta_p S_p (I_p + \psi A_P)}{N_p} - \eta_w S_p M, \\ \frac{dE_p}{dt} = \frac{\eta_p S_p (I_p + \psi A_P)}{N_p} + \eta_w S_p M - (1-\theta_p)\omega_p E_p - \theta_p \rho_p E_p - \mu_p E_p, \\ \frac{dI_p}{dt} = (1-\theta_p)\omega_p E_p - (\tau_p + \mu_p) I_p, \\ \frac{dA_p}{dt} = \theta_p \rho_p E_p - (\tau_{ap} + \mu_p) A_p, \\ \frac{dR_p}{dt} = \tau_p I_p + \tau_{ap} A_p - \mu_p R_p, \\ \frac{dM}{dt} = \overline{\rho}_p I_p + \overline{\omega}_p A_p - \pi M. \end{cases} \tag{2}$$

In the present paper, we have taken into account human interaction is the main route of transmission of COVID-19. Also, assume that quarantine and isolation are the best strategies to break the chain of human social interactions. We improve the model (2) in India's context by incorporating imperfect quarantine and isolation facilities and ignoring the seafood market. Thusly, we propose the following mathematical model with total population $(N_p(t))$ of India at time $t$ is splitted into seven mutually exclusive classes of susceptible $(S_p(t))$ citizens, exposed $(E_p(t))$ citizens, quarantine $(Q_p(t))$ citizens, infectious $(I_p(t))$ citizens, asymptomatic $(A_p(t))$ citizens, Isolated (Hospitalized) $(H_p(t))$ citizens and recovered $(R_p(t))$ citizens. Accordingly, $S_p(t) + E_p(t) + Q_p(t) + I_p(t) + A_p(t) + H_p(t) + R_p(t)$ will come to $N_p(t)$.

$$\begin{cases} \frac{dS_p}{dt} = \Pi_p - \mu_p S_p - \frac{\eta_p S_p (I_p + \psi A_p + \eta H_p)}{N_p}, \\ \frac{dE_p}{dt} = \frac{\eta_p S_p (I_p + \psi A_p + \eta H_p)}{N_p} - (\gamma_Q + \omega_p + \rho_p + \mu_p) E_p, \\ \frac{dQ_p}{dt} = \gamma_Q E_p - (\mu_H + \mu_p) Q_p, \\ \frac{dI_p}{dt} = \omega_p E_p - (\tau_p + \mu_p + \alpha_{IH}) I_p, \\ \frac{dA_p}{dt} = \rho_p E_p - (\tau_{ap} + \mu_p + \alpha_{aH}) A_p, \\ \frac{dH_p}{dt} = \mu_H Q_p + \alpha_{IH} I_p + \alpha_{aH} A_p - (\mu_p + \tau_H) H_p, \\ \frac{dR_p}{dt} = \tau_p I_p + \tau_{ap} A_p + \tau_H H_p - \mu_p R_p. \end{cases} \tag{3}$$

The parameter $0 \leq \eta < 1$ represents the reduction in virus transmission by isolated being compared to the non-hospitalized one. In the $I$ class, $\gamma_Q$ stands for quarantine rate to exposed people, $\mu_H$ represents the hospitalization rate for quarantined people, $\alpha_{IH}$ represents the hospitalized rate of infected people, $\alpha_{aH}$ represents the hospitalized rate of asymptomatically infected people and $\tau_H$ represents recovery rate of hospitalized people. The schematic flow diagram of the proposed model is in Figure 1.

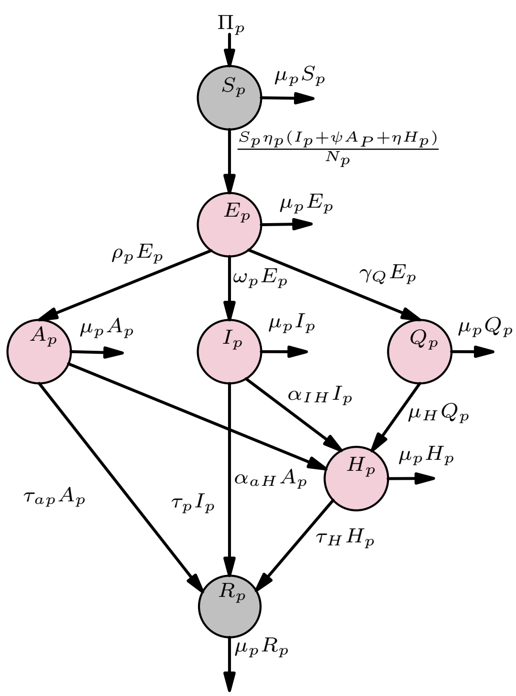

**Figure 1.** Flow chart of the desired compartmental endemic model (3)

**Table 1.** Description of the models state variables

| State variables | Description |
|---|---|
| $N_b$ | Total population of bats |
| $N_h$ | Total population of hosts |
| $S_b$ | Population of susceptible bats |
| $E_b$ | Population of exposed bats |
| $I_b$ | Population of infected bats |
| $R_b$ | Population of recovered bats |
| $S_h$ | Population of susceptible hosts |
| $E_h$ | Population of exposed hosts |
| $I_h$ | Population of infected hosts |
| $R_h$ | Population of recovered hosts |
| $N_p$ | Total population of people |
| $S_p$ | Population of susceptible people |
| $E_p$ | Population of exposed people |
| $I_p$ | Population of infected people |
| $A_p$ | Population of asymptomatically infected people |
| $Q_p$ | Population of quarantined peoples |
| $H_p$ | Population of hospitalized peoples |
| $R_p$ | Population of recovered people |
| $M$ | Reservoir or sea food market |

## 2.2. Basic Properties

For the sake of epidemiologically meaningful interpretation of the transmission model (3), it is assumed that all its associated parameters and initial data $S_p(0) = S_0,\ E_p(0) = E_0,\ Q_p(0) = Q_0,\ I_p(0) = I_0,\ A_p(0) = A_0,\ H_p(0) = H_0,\ R_p(0) = R_0$ are non-negative. Turning over a new leaf, it is managed to show that the solution of the model (3) with non-negative initial data will be non-negative and bounded for all time.

**Theorem 2.1.**

Let $S_p(0) = S_0 \geq 0,\ E_p(0) = E_0 \geq 0,\ Q_p(0) = Q_0 \geq 0,\ I_p(0) = I_0 \geq 0,\ A_p(0) = A_0 \geq 0,\ H_p(0) = H_0 \geq 0,\ R_p(0) = R_0 \geq 0$. The solutions $S_p(t),\ E_p(t),\ Q_p(t),\ I_p(t),\ A_p(t),\ H_p(t)$ and $R_p(t)$ of the system (3) are non-negative for all $t > 0$.

***Proof:***

Consider

$$\tilde{t} = \sup\{t > 0 : S_0 > 0,\ E_0 > 0,\ Q_0 > 0,\ I_0 > 0,\ A_0 > 0,\ H_0 > 0,\ R_0 > 0\} \in [0, t].$$

From the first equation of system (3), we get

$$\frac{dS_p}{dt} \geq -\Big(\mu_p + \frac{\eta_p(I_p + \psi A_P + \eta H_p)}{N_p}\Big)S_p. \tag{4}$$

On integrating the inequality (4), we have

$$S_p(\tilde{t}) \geq S_0.\exp\Big[-\Big(\mu_p\tilde{t} + \int_o^{\tilde{t}} \frac{\eta_p(I_p(s) + \psi A_P(s) + \eta H_p(s))}{N_p(s)}ds\Big)\Big] > 0.$$

Similarly,

$$\begin{aligned}
&E_p(\tilde{t}) \geq E_0.\exp[-(\omega_p + \rho_p + \mu_p + \gamma_Q)\tilde{t}] > 0,\\
&Q_p(\tilde{t}) \geq Q_0.\exp[-\Big(\mu_H + \mu_p\Big)\tilde{t}] > 0,\\
&I_p(\tilde{t}) \geq I_0.\exp[-\Big(\tau_p + \mu_p + \alpha_{IH}\Big)\tilde{t}] > 0,\\
&A_p(\tilde{t}) \geq A_0.\exp[-\Big(\tau_{ap} + \mu_p + \alpha_{aH}\Big)\tilde{t}] > 0,\\
&H_p(\tilde{t}) \geq H_0.\exp[-\Big(\mu_p + \tau_H\Big)\tilde{t}\Big] > 0,\\
&R_p(\tilde{t}) \geq R_0.\exp[-\mu_p\tilde{t}] > 0.
\end{aligned}$$

Ergo, the solution of the proposed model (3) with non-negative initial figures will be non-negative for all time $t > 0$. ■

**Theorem 2.2.**

Let $S_p(0) = S_0 \geq 0$, $E_p(0) = E_0 \geq 0$, $Q_p(0) = Q_0 \geq 0$, $I_p(0) = I_0 \geq 0$, $A_p(0) = A_0 \geq 0$, $H_p(0) = H_0 \geq 0$, $R_p(0) = R_0 \geq 0$. Then, the feasible region $\Omega = \big\{(S_p, E_p, Q_p, I_p, A_p, H_p, R_p) \in \mathbb{R}^7_+ : 0 \leq N \leq \max\big\{N_0, \frac{\Pi_p}{\mu_p}\big\}\big\}$ is positively invariant for the system (3) for all $t \geq 0$.

***Proof:***

Summing up all the equations of (3), the following differential equation is formed,

$$\frac{dN_p}{dt} = \Pi_p - \mu_p N_P. \tag{5}$$

The solution of differential equation (5) is given by

$$N_p(t) = \frac{\Pi_p}{\mu_p} + \Big(N_0 - \frac{\Pi_p}{\mu_p}\Big)\exp(-\mu_p t). \tag{6}$$

Equation (6) implies $N_p(t) \to \frac{\Pi_p}{\mu_p}$, when $t \to \infty$. The following two scenarios arise:

(i) $N_0 < \frac{\Pi_p}{\mu_p}$. In this case $N_p(t)$ increases to $\frac{\Pi_p}{\mu_p}$ as $t \to \infty$, i.e., $\lim_{t\to\infty} N_p(t) = \frac{\Pi_p}{\mu_p}$.
(ii) $N_0 > \frac{\Pi_p}{\mu_p}$. In this case $N_p(t)$ decreases to $\frac{\Pi_p}{\mu_p}$ as $t \to \infty$, i.e., $\lim_{t\to\infty} N_p(t) = \frac{\Pi_p}{\mu_p}$.

Thus, we have $0 \leq N_p(t) \leq \max\left\{N_0, \frac{\Pi_p}{\mu_p}\right\}$, i.e., $N_p(t)$ is bounded above. Subsequently, $S_p(t), E_p(t), Q_p(t), I_p(t), A_p(t), H_p(t), R_p(t)$ are bounded above. ■

## 3. Dynamical behavior of the proposed model

In this part, we focus on the dynamics of the proposed system (3). In Section 2, it is proved that the region $\Omega = \left\{(S_p, E_p, Q_p, I_p, A_p, H_p, R_p) \in \mathbb{R}^7_+ : 0 \leq N_p \leq \max\left\{N_0, \frac{\Pi_p}{\mu_p}\right\}\right\}$ is positively-invariant for the system (3) for all $t \geq 0$. It is sufficient to study the dynamics of the system (3) with initial data inside $\Omega$.

### 3.1. Local stability of disease-free equilibrium

The disease-free equilibrium (DFE) of the system of equations (3) is given by $\mathbb{E}^0 = (S^0, E^0, Q^0, I^0, A^0, H^0, R^0) = \left(\frac{\Pi_p}{\mu_p}, 0, 0, 0, 0, 0, 0\right)$. The local stability of the system (3) at DFE ($\mathbb{E}^0$) is explored using the next generation matrix operator method. We have adopted the method applied by P. Van den Driesschea and J. Wamough (2002); the matrices $F$ and $V$, for the new infection terms and the remaining transfer terms associated with the system (3) at DFE ($\mathbb{E}^0$), are computed, respectively, as follows,

$$F = \begin{bmatrix} 0 & 0 & \eta_p & \psi\eta_p & \eta_p\eta \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix},$$

$$V = \begin{bmatrix} \alpha_2 & 0 & 0 & 0 & 0 \\ -\gamma_Q & \alpha_3 & 0 & 0 & 0 \\ -\omega_p & 0 & \alpha_4 & 0 & 0 \\ -\rho_p & 0 & 0 & \alpha_5 & 0 \\ 0 & -\mu_H & -\alpha_{IH} & -\alpha_{aH} & \alpha_6, \end{bmatrix},$$

where $\alpha_2 = \omega_p + \rho_p + \mu_p + \gamma_Q, \quad \alpha_3 = \mu_H + \mu_p, \quad \alpha_4 = \tau_p + \mu_p + \alpha_{IH}, \quad \alpha_5 = \tau_{ap} + \mu_p + \alpha_{aH}, \quad \alpha_6 = \mu_p + \tau_H.$

**Table 2.** Description of the model parameters

| Parameter | Description | Value (per day) | Source |
|---|---|---|---|
| $\Pi_b$ | Birth rate of bats | - | - |
| $\mu_b$ | Death rate of bats | - | - |
| $\eta_b$ | Disease transmission rate among bats | - | - |
| $\theta_b$ | Infection rate after completing incubation period bats | - | - |
| $\tau_b$ | Recover rate infected bats | - | - |
| $\Pi_h$ | Birth rate of host | - | - |
| $\mu_h$ | Death rate of hosts | - | - |
| $\eta_h$ | Disease transmission rate among hosts | - | - |
| $\theta_h$ | Infection rate of exposed hosts | - | - |
| $\tau_h$ | Recover rate infected hosts | - | - |
| $\pi$ | Removing rate of virus from $M$ | - | - |
| $\overline{\rho}_p$ | Disease transmission coefficient from $I_p$ to $M$ | - | - |
| $\overline{\omega}_p$ | Disease transmission coefficient from $A_p$ to $M$ | - | - |
| $\eta_w$ | Disease transmission coefficient from $M$ to $S_p$ | - | - |
| $\Pi_p$ | Birth rate of people | 67446.82054 | (Biswas et al. (2020)) |
| $\mu_p$ | Natural death rate of people | 0.0000391 | (Biswas et al. (2020)) |
| $\psi$ | Transmissibility multiple of $A_p$, $0 \leq \psi \leq 1$ | 0.02 | (Khan and Atangana (2020)) |
| $\eta_p$ | Disease transmission coefficient among people | 0.67047 | (Biswas et al. (2020)) |
| $\omega_p$ | Progression rate from exposed to infectious class | 0.24757 | (Biswas et al. (2020)) |
| $\rho_p$ | Progression rate from exposed to asymptomatic class | 0.24176 | (Biswas et al. (2020)) |
| $\tau_p$ | Recovery rate of infected people | 0.05090 | (Biswas et al. (2020)) |
| $\tau_{ap}$ | Recovery rate of asymptomatically infected people | 0.05311 | (Biswas et al. (2020)) |
| $\eta$ | Modification parameter for reduction in infectiousness of hospitalized individuals | 0.09 | Assumed |
| $\gamma_Q$ | Quarantine rate of exposed people | 0.26556 | (Biswas et al. (2020)) |
| $\mu_H$ | Hospitalization rate for quarantined people | 0.397875 | (Biswas et al. (2020)) |
| $\alpha_{IH}$ | Hospitalized rate of infected people | 0.26267 | (Biswas et al. (2020)) |
| $\alpha_{aH}$ | Hospitalized rate of asymptomatically infected people | 0.0001 | Assumed |
| $\tau_H$ | Recovery rate of hospitalized people | 0.07048 | (Biswas et al. (2020)) |

The eigenvalues of $FV^{-1}$ matrix are

$$\frac{\eta_p(\alpha_4\alpha_5\eta\gamma_Q\mu_H + \alpha_3\alpha_4\alpha_6\psi\rho_p + \alpha_3\alpha_4\eta\alpha_{aH}\rho_p + \alpha_3\alpha_5\alpha_6\omega_p + \alpha_3\alpha_5\eta\omega_p\alpha_{IH})}{\alpha_2\alpha_3\alpha_4\alpha_5\alpha_6},\ 0,\ 0,\ 0, 0.$$

Thus, the basic reproduction number of system (3), at DFE is

$$\Re_0 = \frac{\eta_p(\alpha_4\alpha_5\eta\gamma_Q\mu_H + \alpha_3\alpha_4\alpha_6\psi\rho_p + \alpha_3\alpha_4\eta\alpha_{aH}\rho_p + \alpha_3\alpha_5\alpha_6\omega_p + \alpha_3\alpha_5\eta\omega_p\alpha_{IH})}{\alpha_2\alpha_3\alpha_4\alpha_5\alpha_6}.$$

Epidemiologically, the basic reproduction number $\Re_0$ measures the average number of secondary infections that a single infected individual can create in a susceptible population over the duration of the period of infection (Van den Driesschea and Wamough (2002)).

**Theorem 3.1.**

The DFE $(\mathbb{E}^0)$ of the system of equations (3) is locally asymptotically stable if $\Re_0 < 1$ and unstable otherwise.

***Proof:***

The Jacobian matrix of the system of equations (3) at DFE $(\mathbb{E}^0)$ can be written as

$$J_{\mathbb{E}^0} = \begin{bmatrix} -\mu_p & 0 & 0 & -\eta_p & -\eta_p\psi & -\eta_p\eta & 0 \\ 0 & -\alpha_2 & 0 & \eta_p & \eta_p\psi & \eta_p\eta & 0 \\ 0 & \gamma_Q & -\alpha_3 & 0 & 0 & 0 & 0 \\ 0 & \omega_p & 0 & -\alpha_4 & 0 & 0 & 0 \\ 0 & \rho_p & 0 & 0 & -\alpha_5 & 0 & 0 \\ 0 & 0 & \mu_H & \alpha_{IH} & \alpha_{aH} & -\alpha_6 & 0 \\ 0 & 0 & 0 & \tau_p & \tau_{ap} & \tau_H & -\mu_p \end{bmatrix}.$$

The characteristic equation of the Jacobian matrix $J_{\mathbb{E}^0}$ is

$$(-\lambda - \mu_p)^2(\lambda^5 + A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5) = 0, \tag{7}$$

where $A_1 = \alpha_2 + \alpha_3 + \alpha_4 + \alpha_5 + \alpha_6, A_2 = \alpha_2\alpha_3 + \alpha_2\alpha_4 + \alpha_2\alpha_5 + \alpha_2\alpha_6 + \alpha_3\alpha_4 + \alpha_3\alpha_5 + \alpha_3\alpha_6 + \alpha_4\alpha_5 + \alpha_4\alpha_6 + \alpha_5\alpha_6 - \psi\eta_p\rho_p - \eta_p\omega_p, A_3 = \alpha_2\alpha_3\alpha_4 + \alpha_2\alpha_3\alpha_5 + \alpha_2\alpha_3\alpha_6 + \alpha_2\alpha_4\alpha_5 + \alpha_2\alpha_4\alpha_6 + \alpha_2\alpha_5\alpha_6 + \alpha_3\alpha_4\alpha_5 + \alpha_3\alpha_4\alpha_6 + \alpha_3\alpha_5\alpha_6 - \gamma_Q\eta\eta_p\mu_H - \psi\alpha_3\eta_p\rho_p - \psi\alpha_4\eta_p\rho_p - \psi\alpha_6\eta_p\rho_p - \alpha_3\eta_p\omega_p - \alpha_5\eta_p\omega_p - \alpha_6\eta_p\omega_p - \eta\alpha_{aH}\eta_p\rho_p - \eta\alpha_{IH}\eta_p\omega_p, A_4 = \alpha_2\alpha_3\alpha_4\alpha_5 + \alpha_2\alpha_3\alpha_4\alpha_6 + \alpha_2\alpha_3\alpha_5\alpha_6 + \alpha_2\alpha_4\alpha_5\alpha_6 + \alpha_3\alpha_4\alpha_5\alpha_6 - \alpha_4\eta\eta_p\gamma_Q\mu_H - \alpha_4\eta\eta_p\gamma_Q\mu_H - \alpha_3\alpha_4\psi\eta_p\rho_p - \alpha_3\alpha_6\psi\eta_p\rho_p - \alpha_4\alpha_6\psi\eta_p\rho_p - \alpha_3\eta\alpha_{aH}\eta_p\rho_p - \alpha_4\eta\alpha_{aH}\eta_p\rho_p - \alpha_3\alpha_5\eta_p\omega_p - \alpha_3\alpha_6\eta_p\omega_p - \alpha_5\alpha_6\eta_p\omega_p - \alpha_3\eta\eta_p\alpha_{IH}\omega_p - \alpha_5\eta\eta_p\alpha_{IH}\omega_p,$ and $A_5 = \alpha_2\alpha_3\alpha_4\alpha_5\alpha_6 - \alpha_4\alpha_5\eta\gamma_Q\eta_p\mu_H - \alpha_3\alpha_4\alpha_6\psi\eta_p\rho_p - \alpha_3\alpha_5\alpha_6\eta_p\omega_p - \alpha_3\alpha_4\eta\eta_p\rho_p\alpha_{aH} - \alpha_3\alpha_5\eta\eta_p\omega_p\alpha_{IH}.$

From Equation (7), it is clear the two eigenvalues of the Jacobian matrix $J_{\mathbb{E}^0}$ are real and negative. The remaining five eigenvalues of the Jacobian matrix $J_{\mathbb{E}^0}$ are the roots of the equation

$$\lambda^5 + A_1\lambda^4 + A_2\lambda^3 + A_3\lambda^2 + A_4\lambda + A_5 = 0. \tag{8}$$

Our aim here is to know the sign of the real parts of the roots of the equation (8). The Liénard Chipart (Daud (2021)) criterion provides necessary and sufficient condition for a polynomial equation to have all the roots with negative real part. The real parts of the roots of the equation (8) will be negative if $A_1, A_2, A_3, A_4, A_5 > 0, A_1A_2 - A_3 > 0$ and $A_1A_2A_3A_4 - A_1A_2^2A_5 - A_1^2A_4^2 + 2A_1A_4A_5 - A_3^2A_4 + A_2A_3A_5 - A_5^2 > 0$. We have the basic reproduction number

$$\mathfrak{R}_0 = \frac{\eta_p(\alpha_4\alpha_5\eta\gamma_Q\mu_H + \alpha_3\alpha_4\alpha_6\psi\rho_p + \alpha_3\alpha_4\eta\alpha_{aH}\rho_p + \alpha_3\alpha_5\alpha_6\omega_p + \alpha_3\alpha_5\eta\omega_p\alpha_{IH})}{\alpha_2\alpha_3\alpha_4\alpha_5\alpha_6}.$$

Consider $\mathfrak{R}_0 = \mathfrak{R}_1 + \mathfrak{R}_2 + \mathfrak{R}_3 + \mathfrak{R}_4 + \mathfrak{R}_5$, where

$$\mathfrak{R}_1 = \frac{\eta_p\eta\gamma_Q\mu_H}{\alpha_2\alpha_3\alpha_6}, \mathfrak{R}_2 = \frac{\eta_p\psi\rho_p}{\alpha_2\alpha_5}, \mathfrak{R}_3 = \frac{\eta_p\eta\alpha_{aH}\rho_p}{\alpha_2\alpha_5\alpha_6},\ \mathfrak{R}_4 = \frac{\eta_p\omega_p}{\alpha_2\alpha_4},\ \mathfrak{R}_5 = \frac{\eta_p\eta\omega_p\alpha_{IH}}{\alpha_2\alpha_4\alpha_6}.$$

We have

$$\begin{aligned}
A_2 &= \alpha_2\alpha_3 + \alpha_2\alpha_4(1-\mathfrak{R}_4) + \alpha_2\alpha_5(1-\mathfrak{R}_2) + \alpha_2\alpha_6 + \alpha_3\alpha_4 + \alpha_3\alpha_5 + \alpha_3\alpha_6 \\
&\quad + \alpha_4\alpha_5 + \alpha_4\alpha_6 + \alpha_5\alpha_6, \\
A_3 &= \alpha_2\alpha_3\alpha_4(1-\mathfrak{R}_4) + \alpha_2\alpha_3\alpha_5(1-\mathfrak{R}_2) + \alpha_2\alpha_3\alpha_6(1-\mathfrak{R}_1) \\
&\quad + \alpha_2\alpha_4\alpha_5(1-\mathfrak{R}_2-\mathfrak{R}_4) + \alpha_2\alpha_4\alpha_6(1-\mathfrak{R}_4-\mathfrak{R}_5) + \alpha_2\alpha_5\alpha_6(1-\mathfrak{R}_2-\mathfrak{R}_3) \\
&\quad + \alpha_4\alpha_5\alpha_6 + \alpha_3\alpha_4\alpha_5 + \alpha_3\alpha_4\alpha_6 + \alpha_3\alpha_5\alpha_6, \\
A_4 &= \alpha_2\alpha_3\alpha_4\alpha_5(1-\mathfrak{R}_2-\mathfrak{R}_4) + \alpha_2\alpha_3\alpha_4\alpha_6(1-\mathfrak{R}_1-\mathfrak{R}_4-\mathfrak{R}_5) \\
&\quad + \alpha_2\alpha_3\alpha_5\alpha_6(1-\mathfrak{R}_1-\mathfrak{R}_2-\mathfrak{R}_3) \\
&\quad + \alpha_2\alpha_4\alpha_5\alpha_6(1-\mathfrak{R}_2-\mathfrak{R}_3-\mathfrak{R}_4-\mathfrak{R}_5) + \alpha_3\alpha_4\alpha_5\alpha_6, \\
A_5 &= \alpha_2\alpha_3\alpha_4\alpha_5\alpha_6(1-\mathfrak{R}_0), \\
A_1A_2 - A_3 &= \alpha_2^2\alpha_3 + \alpha_2\alpha_3^2 + \alpha_2^2\alpha_4(1-\mathfrak{R}_4) + 2\alpha_2\alpha_3\alpha_4 + \alpha_3^2\alpha_4 + \alpha_2\alpha_4^2(1-\mathfrak{R}_4) \\
&\quad + \alpha_3\alpha_4^2 + \alpha_2^2\alpha_5(1-\mathfrak{R}_2) + 2\alpha_2\alpha_3\alpha_5 + \alpha_3^2\alpha_5 + 2\alpha_2\alpha_4\alpha_5 + 2\alpha_3\alpha_4\alpha_5 + \alpha_4^2\alpha_5 \\
&\quad + \alpha_2\alpha_5^2(1-\mathfrak{R}_2) + \alpha_3\alpha_5^2 + \alpha_4\alpha_5^2 + \alpha_2^2\alpha_6 + 2\alpha_2\alpha_3\alpha_6 + \mathfrak{R}_1\alpha_2\alpha_3\alpha_6 + \alpha_3^2\alpha_6 \\
&\quad + 2\alpha_2\alpha_4\alpha_6 + \mathfrak{R}_5\alpha_2\alpha_4\alpha_6 + 2\alpha_3\alpha_4\alpha_6 + \alpha_4^2\alpha_6 + 2\alpha_2\alpha_5\alpha_6 + \mathfrak{R}_3\alpha_2\alpha_5\alpha_6 \\
&\quad + 2\alpha_3\alpha_5\alpha_6 + 2\alpha_4\alpha_5\alpha_6 + \alpha_5^2\alpha_6 + \alpha_2\alpha_6^2 + \alpha_3\alpha_6^2 + \alpha_4\alpha_6^2 + \alpha_5\alpha_6^2.
\end{aligned}$$

Also,

$$\begin{aligned}
&A_1A_2A_3A_4 - A_1A_2^2A_5 - A_1^2A_4^2 + 2A_1A_4A_5 - A_3^2A_4 + A_2A_3A_5 - A_5^2 \\
&= (A_1A_2 - A_3)A_3A_4 + (A_2A_3 + 2A_1A_4 - A_5)A_5 + A_1(-A_1A_4^2 + A_2^2A_5) \\
&= \alpha_2^4\alpha_3^3\alpha_4^2\alpha_5 - \mathfrak{R}_2\alpha_2^4\alpha_3^3\alpha_4^2\alpha_5 - 2\mathfrak{R}_4\alpha_2^4\alpha_3^3\alpha_4^2\alpha_5 + (\cdots\ 4541\ \text{ terms }\ \cdots) + \alpha_3\alpha_4^2\alpha_5^3\alpha_6^4.
\end{aligned}$$

Evidently, $A_1, A_2, A_3, A_4, A_5 > 0, A_1A_2 - A_3 > 0$ and $(A_1A_2 - A_3)A_3A_4 + (A_2A_3 + 2A_1A_4 - A_5)A_5 + A_1(-A_1A_4^2 + A_2^2A_5) > 0$, when $\mathfrak{R}_0 < 1$. Thus, all the eigenvalues of the Jacobian matrix

$J_{\mathbb{E}^0}$ have negative real part, if $\mathfrak{R}_0 < 1$. This implies that the DFE $(\mathbb{E}^0)$ is locally asymptotically stable, if $\mathfrak{R}_0 < 1$. ■

From an epidemiological point, the above statement, that, if $\mathfrak{R}_0 < 1$, then the disease show the decrement in its spread because of the less able to infect the individuals, whereas, if $\mathfrak{R}_0 > 1$, the disease spreads as the infection ability is more than 1, means one infected individual infects a group of individual, generating the more number of infected individuals.

### 3.2. Existence and local stability of the endemic equilibrium

The subsection discusses about the feasibility and stability of the endemic equilibrium point.

**Theorem 3.2.**

The system (3) has a unique feasible endemic equilibrium $\mathbb{E}^* = (S_p^*,\ E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R^*)$ if and only if $\mathfrak{R}_0 > 1$. Moreover, no endemic equilibrium exists if $\mathfrak{R}_0 \leq 1$.

***Proof:***

Let the endemic equilibrium point $\mathbb{E}^* = (S_p^*,\ E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R_p^*)$ of the system of equations (3), obtained by solving equations as follows

$$\frac{dS_P^*}{dt} = \frac{dE_p^*}{dt} = \frac{dQ_P^*}{dt} = \frac{dI_P^*}{dt} = \frac{dA_P^*}{dt} = \frac{dH_P^*}{dt} = \frac{dR_P^*}{dt} = 0. \tag{9}$$

On solving the system (9), we get

$$S_p^* = \frac{\Pi_p}{\lambda^* + \mu_p}, \tag{10}$$

$$E_p^* = \frac{\lambda^* S_p^*}{(\gamma_Q + \omega_p + \rho_p + \mu_p)}, \tag{11}$$

$$Q_p^* = \frac{\gamma_Q E_p^*}{(\mu_H + \mu_p)}, \tag{12}$$

$$I_p^* = \frac{\omega_p E_p^*}{(\tau_p + \mu_p + \alpha_{IH})}, \tag{13}$$

$$A_p^* = \frac{\rho_p E_p^*}{(\tau_{ap} + \mu_p + \alpha_{aH})}, \tag{14}$$

$$H_p^* = \frac{\mu_H Q_p^* + \alpha_{IH} I_p^* + \alpha_{aH} A_p^*}{(\mu_p + \tau_H)}, \tag{15}$$

$$R_p^* = \frac{\tau_p I_p^* + \tau_{ap} A_p^* + \tau_H H_p^*}{\mu_p}, \tag{16}$$

where

$$\lambda^* = \frac{\eta_p(I_p^* + \psi A_P^* + \eta H_p^*)}{S_p^* + E_p^* + Q_p^* + I_p^* + A_p^* + H_p^* + R_p^*}. \tag{17}$$

Substitution of $S_p^*,\ E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R_p^*$ in the equation (17) shows that the endemic equilibrium of the system (3) satisfies the equation

$$a_1(\lambda^*)^2 + a_2\lambda^* = 0, \tag{18}$$

where

$$\begin{aligned}
a_1 &= (\tau_H + \mu_p)\alpha_{aH}\rho_p\alpha_3\alpha_4 + (\tau_H + \mu_p)\omega_p\alpha_{IH}\alpha_3\alpha_5 + (\tau_H + \mu_p)\mu_H\gamma_Q\alpha_4\alpha_5 \\
&\quad + (\mu_p + \tau_{ap})\rho_p\alpha_3\alpha_4\alpha_6 + (\mu_p + \tau_p)\omega_p\alpha_3\alpha_5\alpha_6 + (\gamma_Q + \alpha_3)\mu_p\alpha_4\alpha_5\alpha_6, \\
a_2 &= \mu_p\alpha_2\alpha_3\alpha_4\alpha_5\alpha_6(1 - \mathfrak{R}_0).
\end{aligned}$$

The solutions of the quadratic equation (18) are $\lambda^* = 0$ and $\lambda^* = -\frac{a_2}{a_1}$. The value $\lambda^* = 0$ is corresponding to DFE ($\mathbb{E}^0$). If $\mathfrak{R}_0 < 1$, then $\lambda^* = -\frac{a_2}{a_1}$ will be negative. Thus, if $\mathfrak{R}_0 < 1$ no endemic equilibrium point will exist. If $\mathfrak{R}_0 > 1$, then $\lambda^* = -\frac{a_2}{a_1}$ will be positive. Thus, an endemic equilibrium point $\mathbb{E}^* = (S_p^*,\ E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R^*)$ will exist. ■

Now we will derive the condition for local stability of the endemic equilibrium point $\mathbb{E}^*$ of the system (3) by using Krasnoselskii sub-linearity trick (Hethcote and Thieme (1985); Esteva et al. (2009); Esteva and Vargas (2000)).

**Theorem 3.3.**

The endemic equilibrium $\mathbb{E}^* = (S_p^*,\ E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R^*)$ of the system (3) with $N_p = N_p^*$ is locally asymptotically stable if $\mathfrak{R}_0 > 1$.

***Proof:***

Since $N_p = S_p + E_p + Q_p + I_p + A_p + H_p + R_p$ and $N_p = N_p^*$, the system (3) becomes equation (19) and the corresponding endemic equilibrium point is $\tilde{E} = (E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R_p^*)$.

$$\begin{cases}
\frac{dE_p}{dt} = \frac{\eta_p(N_P^* - E_p - Q_p - I_p - A_p - H_p - R_p)(I_p + \psi A_P + \eta H_p)}{N_p} - (\gamma_Q + \omega_p + \rho_p + \mu_p)E_p, \\
\frac{dQ_p}{dt} = \gamma_Q E_p - (\mu_H + \mu_p)Q_p, \\
\frac{dI_p}{dt} = \omega_p E_p - (\tau_p + \mu_p + \alpha_{IH})I_p, \\
\frac{dA_p}{dt} = \rho_p E_p - (\tau_{ap} + \mu_p + \alpha_{aH})A_p, \\
\frac{dH_p}{dt} = \mu_H Q_p + \alpha_{IH} I_p + \alpha_{aH} A_p - (\mu_p + \tau_H)H_p, \\
\frac{dR_p}{dt} = \tau_p I_p + \tau_{ap} A_p + \tau_H H_p - \mu_p R_p.
\end{cases} \tag{19}$$

On linearizing the system (19) around the endemic equilibrium point $\tilde{E}$, we get

$$\begin{cases} \frac{dE_p}{dt} = -(\lambda^* + \alpha_2)E_p - \lambda^* Q_p + (\lambda_1^* - \lambda^*)I_p + (\psi\lambda_1^* - \lambda^*)A_p \\ \qquad + (\eta\lambda_1^* - \lambda^*)H_p - \lambda^* R_p, \\ \frac{dQ_p}{dt} = \gamma_Q E_p - (\mu_H + \mu_p)Q_p, \\ \frac{dI_p}{dt} = \omega_p E_p - (\tau_p + \mu_p + \alpha_{IH})I_p, \\ \frac{dA_p}{dt} = \rho_p E_p - (\tau_{ap} + \mu_p + \alpha_{aH})A_p, \\ \frac{dH_p}{dt} = \mu_H Q_p + \alpha_{IH} I_p + \alpha_{aH} A_p - (\mu_p + \tau_H)H_p, \\ \frac{dR_p}{dt} = \tau_p I_p + \tau_{ap} A_p + \tau_H H_p - \mu_p R_p, \end{cases} \tag{20}$$

where, $\lambda_1^* = \frac{\eta_p S_p^*}{N_p^*}$.

The Jacobian matrix of the system (20) at the equilibrium point $\tilde{E}$ is

$$J_{\tilde{E}} = \begin{bmatrix} -(\lambda^* + \alpha_2) & -\lambda^* & (\lambda_1^* - \lambda^*) & (\psi\lambda_1^* - \lambda^*) & (\eta\lambda_1^* - \lambda^*) & -\lambda^* \\ \gamma_Q & -\alpha_3 & 0 & 0 & 0 & 0 \\ \omega_p & 0 & -\alpha_4 & 0 & 0 & 0 \\ \rho_p & 0 & 0 & -\alpha_5 & 0 & 0 \\ 0 & \mu_H & \alpha_{IH} & \alpha_{aH} & -\alpha_6 & 0 \\ 0 & 0 & \tau_p & \tau_{ap} & \tau_H & -\mu_p \end{bmatrix},$$

where $\alpha_2 = \gamma_Q + \omega_p + \rho_p + \mu_p, \quad \alpha_3 = (\mu_H + \mu_p), \quad \alpha_4 = (\tau_p + \mu_p + \alpha_{IH}), \quad \alpha_5 = (\tau_{ap} + \mu_p + \alpha_{aH}), \quad \alpha_6 = (\mu_p + \tau_H)$. The solution of the system (20) can be considered in form

$$\mathbf{Z}(t) = \mathbf{Z}_0 e^{\omega t}, \tag{21}$$

where $\mathbf{Z}_0 = (Z_1, Z_2, Z_3, Z_4, Z_5, Z_6)$ and $\omega, Z_1, Z_2, Z_3, Z_4, Z_5, Z_6 \in \mathbb{C}$. Using Equation (21), system (20) becomes

$$\begin{cases} \omega Z_1 = -(\lambda^* + \alpha_2)Z_1 - \lambda^* Z_2 + (\lambda_1^* - \lambda^*)Z_3 + (\psi\lambda_1^* - \lambda^*)Z_4 + (\eta\lambda_1^* \\ \qquad - \lambda^*)Z_5 - \lambda^* Z_6, \\ \omega Z_2 = \gamma_Q Z_1 - \alpha_3 Z_2, \\ \omega Z_3 = \omega_p Z_1 - \alpha_4 Z_3, \\ \omega Z_4 = \rho_p Z_1 - \alpha_5 Z_4, \\ \omega Z_5 = \mu_H Z_2 + \alpha_{IH} Z_3 + \alpha_{aH} Z_4 - \alpha_6 Z_5, \\ \omega Z_6 = \tau_p Z_3 + \tau_{ap} Z_4 + \tau_H Z_5 - \mu_p Z_6. \end{cases} \tag{22}$$

Evidently, the system (22) is a homogeneous linear system in $Z_1, Z_2, Z_3, Z_4, Z_5, Z_6$. Now, the system (22) can be rewritten as

$$\begin{cases} (1+f_1(\omega))Z_1 = \frac{\lambda_1^*}{\alpha_2}Z_3 + \frac{\psi\lambda_1^*}{\alpha_2}Z_4 + \frac{\eta\lambda_1^*}{\alpha_2}Z_5, \\ (1+f_2(\omega))Z_2 = \frac{\gamma_Q}{\alpha_3}Z_1, \\ (1+f_3(\omega))Z_3 = \frac{\omega_p}{\alpha_4}Z_1, \\ (1+f_4(\omega))Z_4 = \frac{\rho_p}{\alpha_5}Z_1, \\ (1+f_5(\omega))Z_5 = \frac{\mu_H}{\alpha_6}Z_2 + \frac{\alpha_{IH}}{\alpha_6}Z_3 + \frac{\alpha_{aH}}{\alpha_6}Z_4, \\ (1+f_6(\omega))Z_6 = \frac{\tau_p}{\mu_p}Z_3 + \frac{\tau_{ap}}{\mu_p}Z_4 + \frac{\tau_H}{\mu_p}Z_5, \end{cases} \tag{23}$$

where

$$\begin{aligned} f_1(\omega) = \frac{\omega}{\alpha_2} + \frac{\lambda}{\alpha_2}\Big[1 + \frac{\gamma_Q}{\omega+\alpha_3} + \frac{\omega_p}{\omega+\alpha_4} + \frac{\rho_p}{\omega+\alpha_5} + \Big(\frac{\mu_H\gamma_Q}{\omega+\alpha_3} + \frac{\alpha_{IH}\omega_p}{\omega+\alpha_4} \\ + \frac{\alpha_{aH}\rho_p}{\omega+\alpha_5}\Big)\Big(\frac{\tau_H}{\omega+\mu_p}+1\Big)\frac{1}{\omega+\alpha_6} + \frac{1}{\omega+\mu_p}\Big(\frac{\tau_p\omega_p}{\alpha_4+\omega} + \frac{\tau_{ap}\rho_p}{\omega+\alpha_5}\Big)\Big], \\ f_2(\omega) = \frac{\omega}{\alpha_3}, \quad f_3(\omega) = \frac{\omega}{\alpha_4}, \quad f_4(\omega) = \frac{\omega}{\alpha_5}, \quad f_5(\omega) = \frac{\omega}{\alpha_6}, \quad f_6(\omega) = \frac{\omega}{\mu_p}. \end{aligned}$$

Let

$$M = \begin{bmatrix} 0 & 0 & \frac{\lambda_1^*}{\alpha_2} & \frac{\psi\lambda_1^*}{\alpha_2} & \frac{\eta\lambda_1^*}{\alpha_2} & 0 \\ \frac{\gamma_Q}{\alpha_3} & 0 & 0 & 0 & 0 & 0 \\ \frac{\omega_p}{\alpha_4} & 0 & 0 & 0 & 0 & 0 \\ \frac{\rho_p}{\alpha_5} & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\mu_H}{\alpha_6} & \frac{\alpha_{IH}}{\alpha_6} & \frac{\alpha_{aH}}{\alpha_6} & 0 & 0 \\ 0 & 0 & \frac{\tau_p}{\mu_p} & \frac{\tau_{ap}}{\mu_p} & \frac{\tau_H}{\mu_p} & 0 \end{bmatrix}.$$

It is easy to verify that $\tilde{E} = (E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R^*)$ is the solution of the system

$$\tilde{E} = M\tilde{E}. \tag{24}$$

If $\mathbf{Z}$ is the solution of the system (22), there exist a real positive number $r$ (Esteva et al. (2009); Esteva and Vargas (2000)) such that

$$\|\mathbf{Z}\| \leq r\tilde{E}, \tag{25}$$

where $\|\mathbf{Z}\| = (\|Z_1\|, \|Z_2\|, \|Z_3\|, \|Z_4\|, \|Z_5\|, \|Z_6\|)$ with lexicographic order, and $\|.\|$ is a norm in $\mathbb{C}$. In order to prove that endemic equilibrium $\tilde{E}$ is locally asymptotically stable, it is sufficient to prove that Re $\omega < 0$.

If possible suppose Re $\omega \geq 0$. The following two cases arise:

$(i)$ $\omega = \mathbf{0}$ :
In this case the determinant of the coefficient matrix of the system (22) is

$$\begin{aligned}\Delta = &\alpha_2\alpha_3\alpha_4\alpha_5\alpha_6\mu_p(1-\lambda_1^*\mathfrak{R}_0) + \alpha_3\alpha_5\alpha_6\lambda^*\mu_p\omega_p + \alpha_3\alpha_5\lambda^*\mu_p\alpha_H\omega_p \\ &+ \alpha_3\alpha_5\lambda^*\alpha_h\tau_H\omega_p + \alpha_3\alpha_5\alpha_6\lambda^*\tau_p\omega_p + \alpha_3\alpha_4\alpha_5\alpha_6\lambda^*\mu_p + \alpha_4\alpha_5\alpha_6\gamma_Q\lambda^*\mu_p \\ &+ \alpha_4\alpha_5\gamma_Q\lambda^*\mu_p\mu_H + \alpha_3\alpha_4\alpha_6\lambda^*\mu_p\rho_p + \alpha_3\alpha_4\lambda\mu_p\alpha_{aH}\rho_p + \\ &+ \alpha_3\alpha_4\alpha_6\lambda^*\rho_p\tau_{ap} + \alpha_4\alpha_5\gamma_q\lambda^*\mu_H\tau_H + \alpha_3\alpha_4\lambda^*\alpha_{aH}\rho_p\tau_H\ .\end{aligned}$$

Using the values $E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R_p^*$ , we get $(1-\lambda_1^*\mathfrak{R}_0) = 0$, Thus, $\Delta > 0$. This implies that the system (22) has a trivial solution $Z_1 = 0,\ Z_2 = 0,\ Z_3 = 0,\ Z_4 = 0,\ Z_5 = 0,\ Z_6 = 0$, i.e., $S_p^* = 0,\ E_p^* = 0,\ Q_p^* = 0,\ I_p^* = 0,\ A_p^* = 0,\ H_p^* = 0,\ R_p^* = 0$.

$(ii)$ Re $\omega > 0$:
Evidently, we have $|1 + f_i(\omega)| > 1, i = 1, 2, ...6$. Define $F(\omega) = \min_i |1 + f_i|$. Thus, we have $F(\omega) > 1$. This implies

$$\frac{r}{F(\omega)} < r. \tag{26}$$

Using inequalities (25) and (26), we get

$$\|\mathbf{Z}\| \geq \frac{r}{F(\omega)}\tilde{E}. \tag{27}$$

Now from definition of $F(\omega)$, we have

$$F(\omega)\|Z_2\| \leq |1 + f_2(\omega)|\|Z_2\|. \tag{28}$$

Using second equation of system (23), Equation (28) becomes

$$F(\omega)\|Z_2\| \leq \frac{\gamma_Q}{\alpha_3}\|Z_1\|. \tag{29}$$

Using inequality (25), inequality (29), becomes

$$F(\omega)\|Z_2\| \leq \frac{\gamma_Q}{\alpha_3} r E_p^*. \tag{30}$$

That is

$$F(\omega)\|Z_2\| \leq r Q_p^*. \tag{31}$$

Inequality (31) implies

$$\|Z_2\| \leq \frac{r}{F(\omega)} Q_p^*. \tag{32}$$

We can see that inequality (32) contradicts the inequality (27). Thus, our assumption Re$\omega >$ $0$ is wrong. Hence, the unique endemic equilibrium point $\mathbb{E}^*$ is locally asymptotically stable if $\Re_0 > 1$. ∎

### 3.3. Global stability of endemic equilibrium for special case

In this paragraph, the global asymptotic stability property of the endemic equilibrium of the model (3) for the special case has been discussed. Consider $\psi = 0$ (transmissibility multiple of asymptotically infected people) and $\eta = 0$ (modification parameter for reduction in infectiousness of hospitalized individuals). Let $\lambda = \beta I_P$, where $\beta = \frac{\eta_p}{N_p}$. In this case $\Re_0 = \frac{\eta_p \omega_p}{\alpha_2 \alpha_4}$.

**Theorem 3.4.**

The unique endemic equilibrium $\mathbb{E}^* = (S_p^*,\ E_p^*,\ Q_p^*,\ I_p^*,\ A_p^*,\ H_p^*,\ R_p^*)$ of the system (3) with $\psi = 0,\ \eta = 0$ is globally asymptotically stable if $\Re_0 > 1$.

***Proof:***

Consider a Lyapunov function

$$V = S - S^* - S^* \log\Big(\frac{S}{S^*}\Big) + E - E^* - E^* \log\Big(\frac{E}{E^*}\Big) + \frac{\alpha_2}{\omega_p}\Big[I - I^* - I^* \log\Big(\frac{I}{I^*}\Big)\Big].$$

Thus, we have

$$\dot{V} = \dot{S} - \frac{S^*}{S}\dot{S} + \dot{E} - \frac{E^*}{E}\dot{E} + \frac{\alpha_2}{\omega_p}\Big(\dot{I} - \frac{I^*}{I}\dot{I}\Big).$$

Using the first, second and fourth equations of (3), we get

$$\begin{aligned}\dot{V} \ &= \ \Pi_p - \mu_p S_p - \beta S_p I_p - \frac{S_p^*}{S_p}(\Pi_p - \mu_p S_p - \beta S_p I_p) + \beta S_p I_p - \alpha_2 E_p \\ &\quad - \frac{E_p^*}{E_p}(\beta S_p I_p - \alpha_2 E_p) \ + \frac{\alpha_2}{\omega_p}\Big[\omega_p E_p - \alpha_4 I_p - \frac{I_p^*}{I_p}\Big(\omega_p E_p - \alpha_4 I_p\Big)\Big]. \qquad (33)\end{aligned}$$

At the endemic steady-state $\tilde{E}$, we have $\Pi_p = \mu_p S_p^* + \beta S_p^* I_p^*, \alpha_2 = \frac{\beta S_p^* I_p^*}{E_p^*}$ and $\alpha_4 = \frac{\omega_p E_p^*}{I_p^*}$. Thus, (33) becomes

$$\dot{V} = \mu_p S_p^*\Big(2 - \frac{S_p}{S_p^*} - \frac{S_p^*}{S_p}\Big) + \beta S_P^* I_p^*\Big(3 - \frac{S_P^*}{S_P} - \frac{S_P I_p E_p^*}{S_P^* I_p^* E_p} - \frac{E_p I_p^*}{E_p^* I_p}\Big). \qquad (34)$$

It is easy to verify that

$$2 - \frac{S_p}{S_p^*} - \frac{S_p^*}{S_p} < 0 \qquad (35)$$

and

$$3 - \frac{S_P^*}{S_P} - \frac{S_P I_p E_p^*}{S_P^* I_p^* E_p} - \frac{E_p I_p^*}{E_p^* I_p} < 0. \tag{36}$$

Using inequalities (35) and (36) in Equation (34), we get

$$\dot{V} < 0 \quad \text{for} \quad \Re_0 > 1.$$

Thus, LaSalle's Invariance Principle (Hale (1969)) implies

$$\lim_{t\to\infty} S_p = S_P^*, \qquad \lim_{t\to\infty} E_p = E_P^*, \qquad \lim_{t\to\infty} I_p = I_P^*. \tag{37}$$

From definition, we have

$$\liminf_{t\to\infty} E_p = \liminf_{t\to\infty} E_p = E_p^*.$$

Thus, for sufficiently small positive numbers $\epsilon_1$ and $\epsilon_2$ there exists a positive number $T$ such that

$$\limsup_{t\to\infty} E_p \leq E_p^* + \epsilon_1, \qquad \forall t > T, \tag{38}$$

$$\liminf_{t\to\infty} E_p \geq E_p^* + \epsilon_2, \qquad \forall t > T. \tag{39}$$

Using inequality (38), the third equation of system (3) gives

$$\frac{dQ_p}{dt} \leq \gamma_Q(E_p^* + \epsilon_1) - \alpha_3 Q_p(t).$$

Using comparison theorem (Lakshmikantham et al. (1989)), we get

$$\limsup_{t\to\infty} Q_p(t) \leq \frac{\gamma_Q(E_p^* + \epsilon_1)}{\alpha_3}.$$

Let $\epsilon_1 \to 0$, we have

$$\limsup_{t\to\infty} Q_p(t) \leq \frac{\gamma_Q E_p^*}{\alpha_3}. \tag{40}$$

Similarly, we have

$$\liminf_{t\to\infty} Q_p(t) \geq \frac{\gamma_Q E_p^*}{\alpha_3}. \tag{41}$$

Inequalities (40) and (41) imply $\lim_{t\to\infty} Q_p(t) = Q_p^*$. Proceeding in this way, we get $\lim_{t\to\infty} A_p(t) = A_p^*$, $\lim_{t\to\infty} H_p(t) = H_p^*$, $\lim_{t\to\infty} R_p(t) = R_p^*$. Thus, each solution of the model (3) approaching to the endemic equilibrium, whenever $\psi = 0,\ \eta = 0$ and initial data lies inside $\Omega$. ■

From an epidemiological point of view, the above theorem states that if $\psi = 0, \eta = 0$, the disease spreads in the population whenever $\Re_0 > 1$.

### 3.4. Transcritical Bifurcation

It has been shown that the system (3) has two equilibrium points: i) disease-free equilibrium point $(\mathbb{E}^0)$, and ii) endemic equilibrium point $(\mathbb{E}^*)$. Further, it has been shown that if $\mathfrak{R}_0 < 1$, the DFE is asymptotically stable and EEP is infeasible. Moreover, if $\mathfrak{R}_0 > 1$, DFE losses its stability and becomes a saddle point, while the EEP becomes locally asymptotically stable. Thus, there is an exchange of stability between the two equilibrium points DFE and EEP which may be due to the existence of transcritical bifurcation.

**Theorem 3.5.**

The system (3) undergoes a transcritical bifurcation between DFE $(\mathbb{E}^0)$ and EEP $(\mathbb{E}^*)$ with respect to the parameter $\mu_H$ at $\mathfrak{R}_0 = 1$.

***Proof:***

We will use Sotomayor's theorem (Perko (1996)) to verify the transversality conditions of transcritical bifurcation. If $\mathfrak{R}_0 = 1$, then we have $A_5 = 0$. This implies that one eigenvalue of the Jacobian matrix $J_{\mathbb{E}^0}$ will be zero and remaining has negative real part. Let

$$V = \begin{bmatrix} v_1 & v_2 & v_3 & v_4 & v_5 & v_6 & v_7 \end{bmatrix}^T$$

and

$$W = \begin{bmatrix} w_1 & w_2 & w_3 & w_4 & w_5 & w_6 & w_7 \end{bmatrix}^T$$

be the two eigenvectors corresponding to the zero eigenvalue of the matrices $J_{\mathbb{E}^0}$ and $J^T_{\mathbb{E}^0}$, respectively, where $v_1 = -\frac{\eta_p v_4 + \psi \eta_p v_5 + \eta_p \eta v_6}{\mu_p}$, $v_2 = 1$, $v_3 = \frac{\gamma_Q}{\alpha_3}$, $v_4 = \frac{\omega_p}{\alpha_4}$, $v_5 = \frac{\rho_p}{\alpha_5}$, $v_6 = \frac{\alpha_{aH} v_5 + \alpha_{IH} v_4 + \mu_H v_3}{\alpha_6}$, $v_7 = \frac{\tau_{ap} v_5 + \tau_H v_6 + \tau_p v_4}{\mu_p}$, $w_1 = 0$, $w_2 = \frac{\alpha_6}{\eta_p \eta}$, $w_3 = \frac{\mu_H w_6}{\alpha_3}$, $w_4 = \frac{\alpha_{IH} w_6 + \eta_p w_2}{\alpha_4}$, $w_5 = \frac{\psi \eta_p w_2 + \alpha_{aH} w_6}{\alpha_5}$, $w_6 = 1$, $w_7 = 0$.

Furthermore, we have

$$F_{\mu_H}(\mathbb{E}^0, \mu_H^{TC}) = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}^T,$$

$$DF_{\mu_H}(\mathbb{E}^0, \mu_H^{TC})V = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \\ v_5 \\ v_6 \\ v_7 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ -v_3 \\ 0 \\ 0 \\ v_3 \\ 0 \end{bmatrix},$$

$$D^2F_{\mu_H}(\mathbb{E}^0, \mu_H^{TC})(V,V) = \begin{bmatrix} \zeta & -\zeta & 0 & 0 & 0 & 0 & 0 \end{bmatrix}^T,$$

where

$$\zeta = \frac{2\eta_p \mu_p}{\Pi_p}(v_4 + \psi v_5 + \eta v_6)(v_2 + v_3 + v_4 + v_5 + v_6 + v_7).$$

Now

$$W^T.F_{\mu_H}(\mathbb{E}^0, \mu_H^{TC}) = 0,$$

$$W^T.[DF_{\mu_H}(\mathbb{E}^0, \mu_H^{TC})V] = -v_3 w_3 + v_3 w_6 = v_3(1 - \frac{\mu_H}{\mu_H + \mu_p}) \neq 0,$$

$$W^T.[D^2 F_{\mu_H}(\mathbb{E}^0, \mu_H^{TC})(V, V)] = -\zeta w_2 \neq 0.$$

Thus, the transversality conditions for transcritical bifurcation are satisfied. This ensures the existence of transcritical bifurcation. ■

### 3.5. Threshold Analysis

Now, we scrutiny the effect of quarantine to see the transmission variability of the proposed model (3). By means of computation of partial derivative of $\mathfrak{R}_0$ with respect to the parameter $\gamma_Q$, a threshold analysis is performed.

**Theorem 3.6.**

The work of quarantine on the exposed individuals have positive (negative) population-level aftermath if $\eta < (>) \eta^*$, where $\eta^* = \frac{\alpha_3(\psi\alpha_4\alpha_6\rho_p + \alpha_4\eta\alpha_{aH}\rho_p + \alpha_5\alpha_6\omega_p)}{\alpha_4\alpha_5\mu_H(\omega_p + \rho_p + \mu_p) - \alpha_3\alpha_5\omega_p\alpha_{IH}}$.

***Proof:***

Differentiating partially the $\mathfrak{R}_0$ with respect to $\gamma_Q$, we get

$$\frac{\partial \mathfrak{R}_0}{\partial \gamma_Q} = \frac{\alpha_4\alpha_5\eta_p\mu_H\eta(\omega_p + \rho_p + \mu_p) - \alpha_3\eta_p(\psi\alpha_4\alpha_6\rho_p + \alpha_4\eta\alpha_{aH}\rho_p + \alpha_5\alpha_6\omega_p + \alpha_5\eta\omega_p\alpha_{IH})}{\alpha_2^2\alpha_3\alpha_4\alpha_5\alpha_6}.$$

Let

$$\eta^* = \frac{\alpha_3(\psi\alpha_4\alpha_6\rho_p + \alpha_4\eta\alpha_{aH}\rho_p + \alpha_5\alpha_6\omega_p)}{\alpha_4\alpha_5\mu_H(\omega_p + \rho_p + \mu_p) - \alpha_3\alpha_5\omega_p\alpha_{IH}}.$$

We can see that $\frac{\partial \mathfrak{R}_0}{\partial \gamma_Q} < 0$, if $\eta < \eta^*$ and $\frac{\partial \mathfrak{R}_0}{\partial \gamma_Q} > 0$ if $\eta > \eta^*$. ■

Thus, the basic reproduction number will depend on $\gamma_Q$ and will be decreasing function when quarantined people do not exceed the threshold value $\eta^*$ and therefore, disease burden will reduce.

Further, the basic reproduction number will be an increasing function of the parameter $\gamma_Q$ when quarantined individuals exceed the threshold value $\eta^*$, and therefore, the disease will increase in the society.

## 4. Numerical Simulations

In this part, analytical findings of model (3) are verified through numerical simulations. We consider the following data from Table 2 (Biswas et al. (2020)).

$N_p(0) = 1352642280$ (Biswas et al. (2020)), $S_p(0) = 1352642280$ (Biswas et al. (2020)), $E_p(0) = 131$ (Biswas et al. (2020)), $Q_p(0) = 647$ (Biswas et al. (2020)), $I_P(0) = 482$ (Biswas et al. (2020)), $A_p(0) = 506$ (Biswas et al. (2020)), $H_p(0) = 657$ (Biswas et al. (2020)), $R_p(0) = 20$ (Assumed).

For the parametric values given in Table 2, the basic reproduction number $\mathfrak{R}_0 = 1.3183 \ > 1$. Thus, the proposed model (3) have a disease-free equilibrium point that will be locally asymptotically unstable (Figure 2). Figure 3 depicts the total number of infected individuals for different values of $\eta$ when $\mathfrak{R}_0 \ > 1$. One can easily see that number of infected individuals are directly proportional to "modification parameter for reduction in infectiousness of hospitalized individuals" ($\eta$). The basic reproduction number $\mathfrak{R}_0 = 1$ when $\eta = 0.03661$, and there is an exchange of stability between the two equilibrium points DFE and EEP which shows that the system (3) undergoes a Transcritical bifurcation (Figure 4). Thus, there exist a threshold value $\eta^{TC} \ = \ 0.03661$ for the parameter $\eta$ such that if $\eta > 0.03661$, the disease-free equilibrium will be locally asymptotically stable and if $\eta < 0.03661$, the endemic equilibrium will be locally asymptotically stable. Further, if $\eta = 0.005$, the proposed model (3) has an endemic equilibrium point that will be locally asymptotically stable for $\mathfrak{R}_0 \ < 1$ which can be seen in Figure 5. In Figure 6 it is readily visible that the decrement rate of the infected individual is directly proportional to the "modification parameter for reduction in infectiousness of hospitalized individuals" ($\eta$) whenever $\mathfrak{R}_0 \ < 1$. Figure 7, depicts that parameter $\eta$ has a threshold value $\eta^* = 0.2$, such that, parameter $\gamma_Q$ has positive population-level impact for $\eta < 0.2$ and negative population-level impact for $\eta > 0.2$.

## 5. Results and discussion

The future is so un-predictive that one can not tell when another epidemic will fall out. A mathematical epidemiological model (3) has been proposed and analyzed to evaluate the strategies for preventing future outbreaks with the help of epidemiological information and guide society in managing the disease. The dynamical transmission behaviour of the proposed model has studied theoretically and numerically. We have obtained the following mathematical and epidemiological results of the proposed model:

$(i)$ The solution of the model is non-negative and bounded for all time $t \ > \ 0$, when initial data are non-negative (Theorem 2.1 and 2.2). Thus, the proposed mathematical model (3) is mathematically well-posed and epidemiologically reasonable.

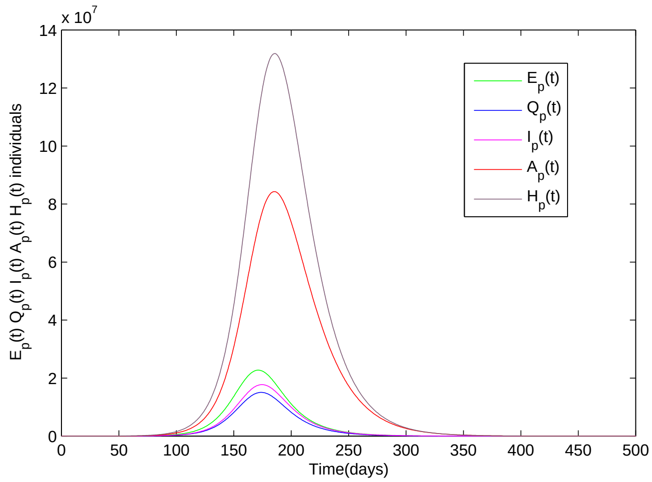


**Figure 2.** The variation of the scaled population in scaled-time for $\Re_0 > 1$. The parameter values used are as in Table 2 except $\eta = 0.01$

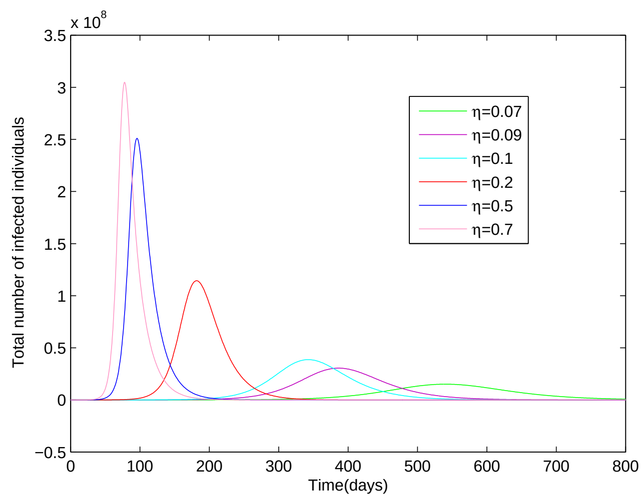


**Figure 3.** The total number of infected people as a function of time for $\Re_0 > 1$. The parameter values used are as in Table 2 except $\eta$

$(ii)$ The model has a disease-free equilibrium that is locally-asymptotically stable whenever the associated basic reproduction number is less than unity (Theorem 3.1). Epidemiologically speaking, if the associated basic reproduction number is less than unity, every infected person will infect less than one person in the entire period of infection, which means that the disease will be exhausted. Thus, we can conclude that it is possible to control the disease by keeping the associated basic reproduction number less than one in the absence of a vaccine.

$(iii)$ The mathematical model has one and only one endemic equilibrium if the basic reproduction number exceeds unity. This endemic equilibrium is locally asymptotically stable (Theorem 3.3) and globally-asymptotically stable for special case (Theorem 3.4). Epidemiologically speaking, if the associated basic reproduction number exceeds unity, then each infected person will infect more than one person in the entire infection period, which implies that the

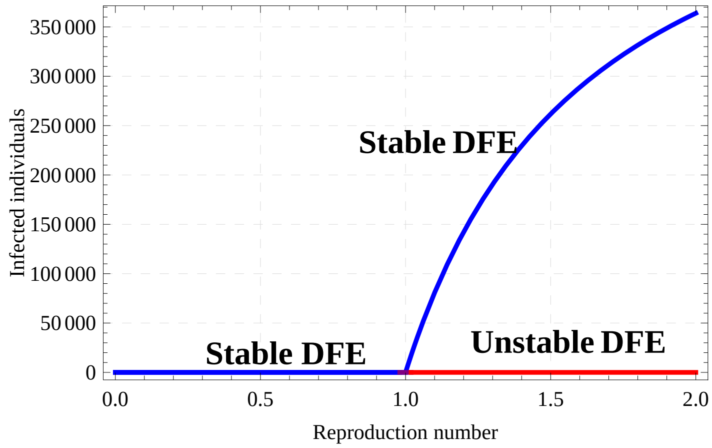


**Figure 4.** Transcritical bifurcation diagram for the model (3)

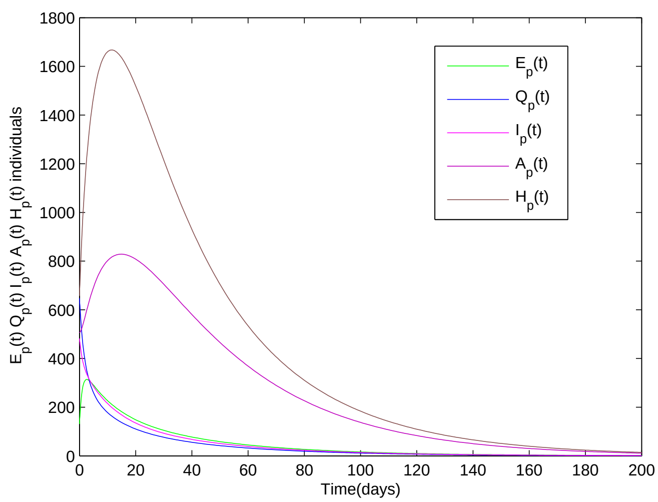


**Figure 5.** The variation of the scaled population in scaled-time for $\mathfrak{R}_0 < 1$. The parameter values used are as in Table 2 except value of $\eta = 0.005$

disease invading the susceptible population.

$(iv)$ The model exhibits a transcritical bifurcation concerning the parameter $\mu_H$ (hospitalization rate for quarantined individuals). Epidemiologically speaking, a threshold value $\mu_H = \mu_H^{TC}$ of $\mu_H$ exists, such that, if $\mu_H > \mu_H^{TC}$ then disease eradication may be obtained.

$(v)$ The quarantine of exposed people can control the reproduction number (Theorem 3.6). Epidemiologically speaking, by keeping $\eta < \eta^*$ we can reduce new infections. Thus, in the control of disease, one can conclude that the facility of quarantine is utile.

## 6. Conclusion

Epidemics and pandemics are so sudden that they need strict instantaneous restrictions and boundaries to be implemented in society. Quarantine and isolation are two of them. The sudden reaction

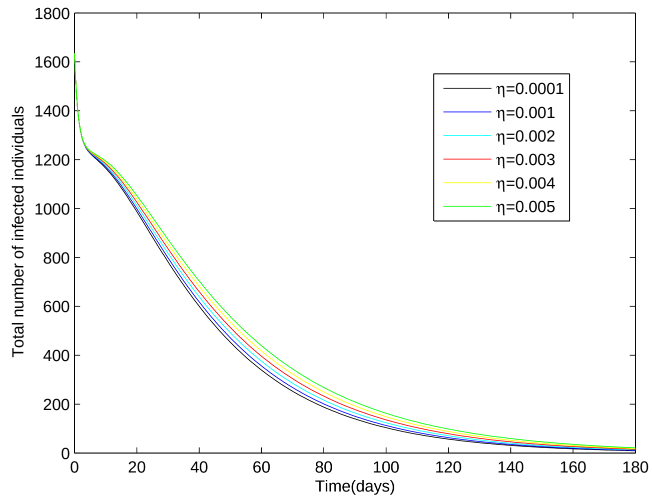


**Figure 6.** The total number of infected people as a function of time for $\Re_0 < 1$. The parameter values used are as in Table 2, but with different values of $\eta$

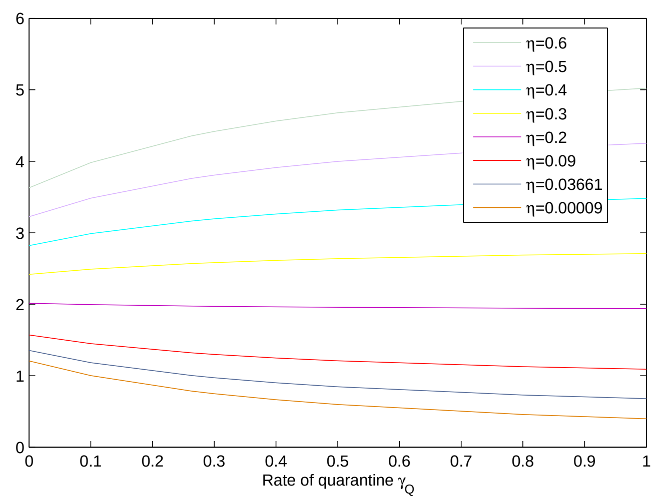


**Figure 7.** Effect of quarantine parameter $\gamma_Q$ on basic reproduction number $\Re_0$

of government authorities and citizens can affect the rise or fall in the cases of a disease at that time. Depending on the geographical area, spread rate, reproduction number and prevention strategies, it may last for days, one year, or more. Isolation and quarantine can be highly effective as it helps separate infected and exposed citizens from the healthy people. Breaking the spread chain can effectively result in to decrease in the spread. It is challenging to impose a perfect quarantine; however, if imposed, it will reduce the virus blowout, as discussed in the paper. The reproduction number can also be controlled with the quarantine, and a threshold number can provide the predictions related to an outbreak to impose restrictions efficiently. Also, if no such imposition is there, the reproduction number increases and result in the disease staying in the environment, which could result in a dangerous situation, and hence, one can easily conclude that isolation and quarantine can play a crucial role in controlling an outbreak from expanding all around in the environment.


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