

# Mathematical Modeling on Double Quarantine Process in the Spread and Stability of COVID-19



Jangyadatta Behera, Aswin Kumar Rauta, Yerra Shankar Rao,  
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**Abstract** The transmission of COVID-19 and its stability are formulated in this chapter. In the susceptible class, pre-quarantine technique is implemented for the individuals who have come from the disease prone areas. Similarly, in the infected compartment post-quarantine technique is implemented. As per the principle of mathematical epidemiology, the rate of change of each compartment is expressed in the form of ordinary differential equations (ODEs). The differential equations are nonlinear in nature which are associated with the disease parameters, namely rate of natural death, death due to COVID-19, immigrant's influx, spread, and recovery. The basic reproduction number is found mathematically which is useful to address the local and global stability. Fourth-order Runge–Kutta numerical technique is used to solve the ODEs. The trend of spread and stability of disease are visualized in the graphs with the help of MATLAB software. The stability analysis at disease-free state and endemic state is discussed. The global stability is explained on the basis of Lyapunov function. Routh–Hurwitz theorem is applied for the behavior of eigenvalues to discuss the disease-free equilibrium. Our investigation shows that the disease will be stable for a long run due to the quarantine process.

**Keywords** Eigenvalues · Endemic · Equilibrium · Quarantine · Stability · Virus

**Mathematics Subject Classification (2010)** 92D25 · 92D30 · 93D20 · 93D05

## Nomenclature

- A Rate of immigrants and newborn.  
S Susceptible population.

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$I$	Infected population.
$Q_H$	Home isolation population, i.e., pre-quarantine class.
$Q_1$	Quarantine populations in hospitals, i.e., post-quarantine class.
$R$	Recovered population.
$\beta$	Rate of infection from infective class to susceptible class.
$\theta$	Rate at which the susceptible population goes to home isolation.
$\omega$	Probability at which the home isolation population becomes susceptible.
$p$	Probability at which the infected population goes to hospital quarantine for treatment.
$\gamma$	Rate at which the population becomes recovered after hospitalities.
$d_1$	Natural death rate.
$d_2$	Rate of death due to COVID-19.
$d_3$	Rate of death due to preexisting diseases that are vulnerable to COVID-19.
$R_0$	Basic reproduction number of pre-quarantine class.
$R_{0H}$	Basic reproduction number after hospitalities.

## 1 Introduction

The infectious diseases due to different viruses are more harmful, quickly spread, and uncontrolled than the infectious diseases due to other microorganisms. Human being has been mostly affected by these diseases. The information from different sources witnessed that these diseases were originated from birds, animals, men, and changing climates, etc. Most of these diseases are seasonal in the remote areas, hilly areas, and unhygienic environment in the underdeveloped countries of the African continent but in December 2019, the present pandemic disease COVID-19 was detected in China (Wuhan city). The disease spread all over the world by the end of March 2020 and severely affected many developed countries like USA, Italy, France, Spain, England, Germany, and Belgium. As per WHO's (WORLD HEALTH ORGANIZATION) [1] report from December 31th, 2019, to May 7th, 2020, the disease has spread over 212 countries and 2 international conveyances with number of confirmed cases is more than 38 lakhs, at least 2.6 lakhs death and more than 13 lakhs recovered persons have been reported around the world. The disease shows the sign of enhancing body temperature, sneezing, itching of throat, and difficulty in breathing in most of the cases; also in some cases, headache and diarrhea are reported. COVID-19 spreads due to social contact, sneezing openly, and cough of infected individuals. On average of 5–6 days is the latency period; however, it can take up to 14 days. The time period of recovery from the COVID-19 is nearly about 2 weeks in case of mild cases, but it takes up to 3–6 weeks in case of critical patients. COVID-19 affects the people of different age groups; however, the older people and people with preexisting diseases like asthma, heart problem, kidney disease, and hypertension are appeared to be more vulnerable. Presently, the disease is not resistant to any vaccine or medicine. Based on the patient's clinical conditions, some prescribed antibiotics are given to the patients

and ICU or ventilator is used for treatment as per the guideline of WHO. Many persons are cured or recovered from the disease. The disease can be stabilized through home quarantine, washing hands with soap several times about 20 s, sanitization, not touching the face, eyes, ear, and wearing mask. So, it is a big challenge for researchers of different fields including the mathematicians to investigate, analyze, and interpret the available data including the model parameters to ascertain the cause, effect, and control of the disease. Mathematical models embedded with the rate of transmission, recovery rate, rate of quarantine, and death rate with stability analysis will be helpful for the researchers of other fields to investigate in a realistic way. Before beginning the study of a new problem, it is required to acquaint with the background of other infectious disease and research development of current pandemic disease COVID-19. Therefore, after reviewing, analyzing, and interpreting many past and present research articles on the epidemiology, we have cited the following limited numbers of research articles in this paper due to the paucity of article length.

Trawicki [2] has discussed the vaccination of newborn, temporary immunity, vital dynamics having unequal rate of birth, and death with help of SEIRS epidemic modeling. Also both local and global stability analyses are performed. The model has not included the quarantine class. Lu et al. [3] have explained predator–prey model using nonlinear perturbation method to investigate the SIS and SIQR epidemic models. Lyapunov function is established for stability analysis using an ergodic stationary point. Analysis of stability in biological system using differential equations is presented by Bastin [4]. Bin et al. [5] had modeled the disease that demonstrates the intervention of post-lockdown which mitigates COVID-19. Xu et al. [6] have explained the evolution of the disease in China and obtained the risk of human transmission by modeling its spike protein. Pederson et al. [7] have explained how the undetected patients quantify the number of infected cases and effort of containment to control the disease in Italy. Li et al. [8] have proposed COVID-19 mathematical model on the transmission of the disease and suggested the controlling measure that can die out the disease. Xia et al. [9] have proved the local stability using the delayed SEIQ epidemic model. Juhen et al. [10] examined the transmission of the disease from December 2019 to January 2020 in Wuhan and suggested the effective measures to stabilize the disease. Rothe et al. [11] have shown how the asymptomatic contact individuals of Germany have transmitted the disease and impact of severity on infection. Zhang et al. [12] have studied the SEIQR mathematical model and explained the stability analysis. Zhang et al. [13] have studied the different mathematical models of influenza viruses and discussed their stability analysis using vaccination. Lan et al. [14] studied the SIQR model with stochastic persistence of diseases using Markov semigroup theory. Erdem et al. [15] have observed the oscillatory behavior of SIQR model with imperfect quarantine that resembles the stability of the disease in South Korea and China. Ma et al. [16] have used the comparison principle to discuss the global stability of SIR model. Rao et al. [17] explored the individual mobility of the disease using the SEIVR model. They have explained that the disease is transmitted indirectly through the environment. Their numerical simulation exhibits global stability and equilibrium. Malik et al. [18] have proposed a fractional-order system of the disease for finding parameters using numerical method. They found that the

result agrees with real data. Zhang et al. [19] have searched hidden parameters that impact the resurgence of SARS-COV-2 pandemic due to the removal of lockdown and other social measures. Baba et al. [20] have presented a model for the stability of disease outbreaks using optimal control function. They established the Lyapunov function for global stability which shows the disease reduces drastically. Oliveria et al. [21] have conducted the study of disease in the city of TeraSanya, Brazil. They used descriptive bibliometric process to ascertain the scientific production through bibliometric analysis on new COVID-19. Savas et al. [22] have compared the estimated and real cases of COVID-19. They also calculated death cases for 45 days in Turkey. Their mathematical model suggested that the estimation accuracy was 90% and 66% for 30 days and 45 days of COVID-19 death, respectively. Gracia et al. [23] have studied the dynamics of coronavirus in the advanced and emerging country to forecast economic growth. They found the economic growth is expected to recover for the long term. Rauta et al. [24] have investigated the SIQRS model to study the transmission of disease and the impact of isolation. They found the disease can be controlled for a long run due to quarantine. Paul et al. [25] have investigated COVID-19 using simple population dynamics based on incidence–fitness relationships. They found the corona case peaked to the top using the concept of geometry. Murray [26] has forecasted the effect of death during the transmission of the disease in the first phase in USA and European economic areas in hospitals. He interpreted that the load on the health system in the USA was beyond the current capacity. He claimed that to mitigate the overload in hospital system and to prevent the death, it is required to enhance the medical facilities.

The literature survey reveals that mathematical modeling of the transmission of COVID-19 due to coronavirus is inadequate and has many limitations. Many researchers have investigated different epidemic models on COVID-19 but ignored some important parameters. So the research done till date is insufficient for this emerging pandemic disease. A few studies have been reported about the double quarantine effect using limited parameters but the stability analysis is hardly discussed. Therefore, the model developed in this research paper to investigate the pre- and post-quarantine effect on the transmission and stability of COVID-19 is new. The novelty of the proposed model in this chapter is original, and the discussion of both local and global stabilities will explore the new dimensions in the study of COVID-19.

## 2 Mathematical Model

Let  $S(t)$ ,  $I(t)$ ,  $Q_h(t)$ ,  $Q_1(t)$ , and  $R(t)$  are five disjoint classes whose union is total population  $N$  over the time  $t$ . The rate at which the average number of sufficient contacts by a single infected person per day from infected compartment ( $I$ ) to susceptible compartment ( $S$ ) is  $\beta$ . So the mean number of susceptible those who got infected by an infected individual is  $\beta S$ . Thus, the whole infected class is  $\beta SI$  which is called incidence (mass action law). The immigrants, newborn, and suspected individuals having travel history are kept in home quarantine class  $Q_h$  at rate ' $\theta$ ' for 14 days.

Therefore, the mean rate of home quarantine class is  $\frac{1}{\theta}$ . The probability of recovery due to  $Q_h$  is taken as ' $\omega$ ' that enters into susceptible class, and probability of showing symptoms of COVID-19 in  $Q_h$  is  $(1 - \omega)$  that enters into infected compartment. Again, the probability of infected showing mild symptoms to be kept in government quarantine  $Q_1$  for another 14 days during the treatment is taken as ' $p$ ' and the probability of recovered as  $(1 - p)$ . Let ' $\gamma$ ' is the recovery rate from post-quarantine class to recovery class. The natural mortality rate in each class is given by  $d_1$  with an average life time is  $\frac{1}{d_1}$ . The disease-induced death rate in infected class I and post-quarantine class  $Q_1$  are taken at the rate  $d_2$  and  $d_3$ , respectively. Thus, the rate of mortality due to disease induced and natural reason in infected compartment is  $(d_1 + d_2)$  with average mortality rate is  $\frac{1}{d_1+d_2}$ . Similarly, the average mortality rate of post-quarantine class  $Q_1$  is  $\frac{1}{d_1+d_3}$ . It is assumed that everyone has equal chance of infection. Every compartment is dynamic in nature with respect to time. Based on these assumptions, the flow diagram and modeling of COVID-19 are given in Fig. 1.

The net flow of quantity that enters into each compartment is taken as positive and exit from each compartment is taken as negative. Thus, as per Kermack–McKendrick model [27–29] the size of each class can be expressed in terms of the following differential equations

$$\begin{aligned} \frac{dS}{dt} &= A + \omega Q_H - (\beta SI + d_1 S + \theta S) \\ \frac{dQ_H}{dt} &= \theta S - (1 - \omega + \omega + d_1) Q_H = \theta S - (1 + d_1) Q_H \\ \frac{dI}{dt} &= \beta SI + (1 - \omega) Q_H - (p + d_1 + d_2 + (1 - p)) I \\ &= \beta SI + (1 - \omega) Q_H - (d_1 + d_2 + 1) I \\ \frac{dQ_1}{dt} &= p I - (d_1 + d_3 + \gamma) Q_1 \end{aligned}$$

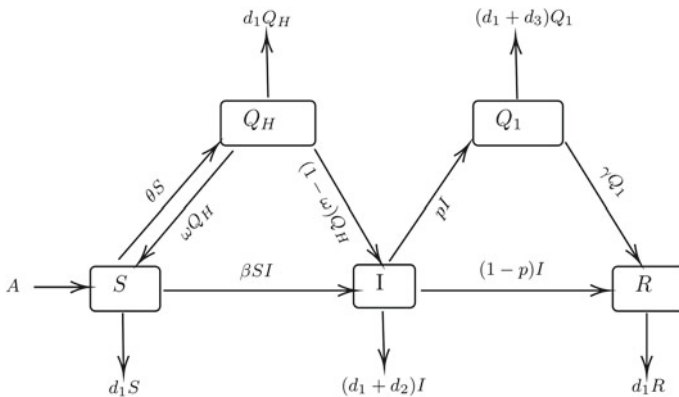


Fig. 1 Schematic diagram of the model

$$\frac{dR}{dt} = (1 - p)I + \gamma Q_1 - d_1 R \quad (1)$$

With initial conditions  $S(0) > 0$ ,  $Q_H(0) > 0$ ,  $I(0) > 0$ ,  $Q_1(0) > 0$ ,  $R(0) > 0$ . Since these systems of nonlinear differential equations are not in standard forms to solve analytically, so fourth-order Runge–Kutta numerical method is used for solving them with help of MATLAB software. Simulated results are interpreted graphically with detailed discussions.

## 2.1 Model Analysis

In epidemiology, the basic reproduction number ( $R_0$ ) is an important indicator that denotes the contagiousness of infectious agents. It is the average number of maximum contacts by an infected individual to the whole susceptible class during the infection period. Therefore,  $R_0 =$  number of new cases arising per day from one infective  $\times$  average days of infection. It is a threshold quantity. When a number of infectious is entered into a population, then the number of infected individuals in population will either decrease to zero or increase to a peak. These threshold conditions are characterized by the basic reproductive number in epidemiology. With initial infective is small and initial susceptible is large so that  $\beta S > 1$ , then  $I$  increase to a peak and  $S$  decrease eventually. In this case,  $R_0 > 1$ , i.e., the disease spread for longer time leads to epidemic and the system is said to be unstable. When  $R_0 < 1$ , i.e., infected replaces itself with less than one new infective, then the disease will extinct and the system is said to be stable. If  $R_0 = 1$ , then an infected person produces only one new case of the diseases, so disease will not grow significantly but the disease persists. It is the critical value of the threshold quantity. So, the analysis and interpretation of  $R_0$  are important for the study of COVID-19 and due to adoption of two quarantine process (pre- and post-quarantine) in this paper, we derived two basic reproduction numbers from the model.

The region in which solutions for the model are uniformly bounded is defined as  $\Omega \in R_+^5 = \{(S, Q_H, I, Q_1, R) \in R_+^5, S \geq 0, Q_H \geq 0, I \geq 0, Q_1 \geq 0, R \geq 0\}$ . The interactive functions of system (1) are continuously differentiable, so the solution of the system (1) exist and unique. The uniform boundedness of solutions for the system (1) having nonnegative initial conditions is discussed using different theorems.

**Theorem 1** *Solutions of the system (1) which are defined in  $R_+^5$  are uniformly bounded.*

**Proof** Let  $S(t)$ ,  $Q_H(t)$ ,  $I(t)$ ,  $Q_1(t)$ , and  $R(t)$  be any solution of system (1) having nonnegative initial condition  $S(0)$ ,  $Q_H(0)$ ,  $I(0)$ ,  $Q_1(0)$  and  $R(0)$ .

Therefore,  $N(t) = S(t) + Q_H(t) + I(t) + Q_1(t) + R(t)$ .

Then,  $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dQ_H}{dt} + \frac{dI}{dt} + \frac{dQ_1}{dt} + \frac{dR}{dt}$  so,  $\frac{dN}{dt} = A - d_1 N - d_2 I - d_3 Q_1$ .

In the dearth of any infection,  $N$  becomes  $\frac{A}{d_1}$ , i.e., as  $t \rightarrow \infty$ , then  $N \rightarrow \frac{A}{d_1}$ . Hence, the solution of the system (1) is well posed and confined in the region  $\Omega = \left\{ (S, Q_H, I, Q_1, R) \in R_+^5 : N \leq \frac{A}{d_1} \right\}$ .

### 2.2 Calculation of $R_0$ from $SIQ_1R$ Model

The  $SIQ_1R$  compartmental equations are

$$\begin{aligned} \frac{dS}{dt} &= A + \omega Q_H - (\beta SI + d_1 S + \theta S) \\ \frac{dI}{dt} &= \beta SI + (1 - \omega) Q_H - (d_1 + d_2 + 1) I \\ \frac{dQ_1}{dt} &= PI - (d_1 + d_3 + \gamma) Q_1 \\ \frac{dR}{dt} &= (1 - P)I + \gamma Q_1 - d_1 R \end{aligned} \tag{2}$$

This model is also positive and closed invariant.

$R_0$  = the largest positive eigenvalue of the matrix  $FV^{-1}$ , where  $F$  is called infection matrix and  $V$  is called transformation matrix between the compartments.

Linearization of Eq. (2) by taking two classes  $I$  and  $Q_1$ , we have

$$R_0 = \frac{\beta S_0}{(d_1 + d_2 + 1)}$$

### 2.3 Stability Analysis for $SIQ_1R$ Model

For steady state of Eq. (2), we take

$$\begin{aligned} A + \omega Q_H - (\beta SI + d_1 S + \theta S) &= 0 \\ \beta SI + (1 - \omega) Q_H - (d_1 + d_2 + 1) I &= 0 \\ PI - (d_1 + d_3 + \gamma) Q_1 &= 0 \\ (1 - P)I + \gamma Q_1 - d_1 R &= 0 \end{aligned} \tag{3}$$

There are two equilibrium points, which can be obtained from Eq. (3).

Equilibrium point for disease-free state =  $(S_0, 0, 0, 0)$ .

Equilibrium point for endemic state =  $(S^*, I^*, Q_1^*, R^*)$ .

**Theorem 2** If  $R_0 < 1$ , then the system at disease-free equilibrium of (3) is stable; otherwise, it is unstable when  $R_0 > 1$ .

**Proof** Linearization of model at equilibrium point for disease-free state in (3),

$$J_{DFE}(S_0, 0, 0, 0) = \begin{pmatrix} -(d_1 + \theta) - \beta S_0 & 0 & 0 & 0 \\ 0 & \beta S_0 - (d_1 + d_2 + 1) & 0 & 0 \\ 0 & P & -(d_1 + d_3 + \gamma) & 0 \\ 0 & (1 - P) & \gamma & -d_1 \end{pmatrix}$$

By calculating the eigenvalues, we have

$$\begin{aligned} \lambda_1 &= -(d_1 + \theta) \\ \lambda_2 &= -(d_1 + d_3 + \gamma) \\ \lambda_3 &= -d_1 \\ \lambda_4 &= \beta S_0 - (d_1 + d_2 + 1) \end{aligned}$$

For  $\frac{\beta S_0}{d_1 + d_2 + 1} < 1$ , i.e.,  $R_0 < 1$  so the eigenvalues are negative.

Hence, the equilibrium is asymptotically stable locally for the disease-free state as per Routh–Hurwitz principle of stability.

**Theorem 3** The system at endemic equilibrium point  $(S^*, I^*, Q_1^*, R^*)$  of (3) is locally stable when  $R_0 > 1$ .

**Proof** At the endemic equilibrium point

$$J_{EE}(S^*, I^*, Q_1^*, R^*) = \begin{pmatrix} -(\beta I^* + d_1 + \theta) - \beta S^* & 0 & 0 & 0 \\ \beta I^* & \beta S^* - (d_1 + d_2 + 1) & 0 & 0 \\ 0 & P & -(d_1 + d_3 + \gamma) & 0 \\ 0 & (1 - P) & \gamma & -d_1 \end{pmatrix}$$

The eigenvalues are

$$\begin{aligned} \lambda_1 &= -(d_1 + d_3 + \gamma) \\ \lambda_2 &= -d_1 \end{aligned}$$

Remaining eigenvalues can be derived from the equation  $a\lambda^2 + b\lambda + c = 0$ , where

$$\begin{aligned} a &= (\beta I^* + 2d_1 + d_2 + 1 + \theta - \beta S^*) > 0 \\ b &= (d_1 + d_2 + 1 - \beta S^*)(\beta I^* + d_1 + \theta) > 0 \end{aligned}$$

Since  $a > 0, b > 0$ , we have  $ab > 0$ . Hence, by Routh–Hurwitz condition the system is stable.

**Theorem 4** The disease-free equilibrium  $E_0 = \left(\frac{A}{\mu}, 0, 0\right)$  of (3) is globally asymptotically stable if  $R_0 < 1$ .



**Proof** Consider a Lyapunov function.

$$\begin{aligned} Z &= I \\ \frac{dZ}{dt} &= \frac{dI}{dt} \\ &= \beta SI - (d_1 + d_2 + 1)I \\ &= -(1 + d_1 + d_2)I \left( 1 - \frac{\beta S}{1 + d_1 + d_2} \right) \\ &= -(1 + d_1 + d_2)I(1 - R_0) \end{aligned}$$

If  $R_0 < 1$  then  $\frac{dZ}{dt} < 0$ . It is observed that  $\frac{dZ}{dt} = 0$  if  $I = 0$ .

Therefore, equilibrium of disease-free state is asymptotically stable globally for  $R_0 < 1$  as per LaSalle Lyapunov theory.

### 2.4 Calculation of Basic Reproduction Number from $SQ_HIQ_1R$ Model

$R_{0H}$  for  $SQ_HIQ_1R$  is calculated as;

$$R_{0H} = \frac{\beta S_0(1 - \omega)}{(\omega + d_1)(d_1 + d_2 + 1)} = \frac{R_0(1 - \omega)}{(\omega + d_1)}$$

Success or failure of COVID-19 virus attack depends on basic reproduction number  $R_{0H}$ . If  $R_{0H} \geq 1$  the COVID-19-based epidemic will carry on, i.e., the disease becomes endemic, but, if  $R_{0H} < 1$ , then COVID-19-based epidemic will die out; i.e., the infected population will slowly become zero.

### 2.5 Stability Analysis for $SQ_HIQ_1R$ Model

The disease-free equilibrium point of systems of Eq. (1) is  $(S_0, 0, 0, 0)$ , and the equilibrium for endemic state is as follows:

$$\begin{aligned} S^* &= \frac{(1 - \omega)A + \omega(1 - R_0)I^*}{(1 - \omega)(d_1 + \beta I^* + \theta)} \\ Q_H^* &= \frac{(1 - R_0)I^*}{(1 - \omega)} \\ Q_1^* &= \frac{PI^*}{(d_1 + d_3 + \gamma)} \end{aligned}$$

$$R^* = \frac{[(1 - P)(d_1 + d_3 + \gamma) + \gamma P]I^*}{(d_1 + d_3 + \gamma)}$$

**Theorem 5** *The system is locally stable if  $R_{0H} < 1$ , and it is unstable if  $R_{0H} > 1$  at diseases-free equilibrium point  $(S_0, 0, 0, 0)$  of the system of Eq. (1).*

**Proof** Linearization of the system of differential Eq. (1) and the characteristic equation is

$$J_{DFE} = (S_0, 0, 0, 0) = \begin{pmatrix} -(d_1 + \theta) \omega & -\beta S_0 & 0 & 0 \\ \theta & -(1 + d_1) 0 & 0 & 0 \\ 0 & (1 - \omega) & \beta S_0 - (d_1 + d_2 + 1) 0 & 0 \\ 0 & 0 & P & -(d_1 + d_3 + \gamma) \end{pmatrix}$$

One of the roots of the characteristic equation is  $\lambda_1 = -(d_1 + d_3 + \gamma)$ .

Other three roots are obtained from the equation  $\lambda^3 + A\lambda^2 + B\lambda + C = 0$  where

$$\begin{aligned} A &= 3d_1 + d_2 + \gamma + \theta + 1 \\ B &= (d_1 + \theta)(d_1 + 1) + (\gamma + d_3 + d_1)(\theta + d_1) \\ &\quad + (\gamma + d_3 + d_1)(1 + d_1 + d_2)(1 - R_0) - \omega\theta \\ C &= (1 + d_1)(d_1 + d_3 + \gamma)(d_1 + \theta) \\ &\quad - \omega P \beta S_0 - \omega\theta(d_1 + d_3 + \gamma) \end{aligned}$$

Since  $AB > C$ , so by Routh–Hurwitz condition for stability, it is locally stable.

**Theorem 6** *At the endemic equilibrium point  $\Omega^*(S^*, Q_H^*, I^*, Q_1^*, R^*)$ , the system is locally stable when  $R_{0H} > 1$ .*

**Proof** At the endemic equilibrium,  $\Omega^*(S^*, Q_H^*, I^*, Q_1^*, R^*)$ , the Jacobian matrix is

$$\begin{aligned} J_{EE} &= (S^*, Q_H^*, I^*, Q_1^*, R^*) \\ &= \begin{pmatrix} -(\beta I^* + d_1 + \theta) \omega & -\beta S^* & 0 & 0 & 0 \\ \theta & -(1 + d_1) 0 & 0 & 0 & 0 \\ \beta I^* & (1 - \omega) & \beta S^* - (d_1 + d_2 + 1) 0 & 0 & 0 \\ 0 & 0 & P & -(d_1 + d_3 + \gamma) 0 & 0 \\ 0 & 0 & (1 - P) & \gamma & -d_1 \end{pmatrix} \end{aligned}$$

Here the two eigenvalues are

$$\begin{aligned} \lambda_1 &= -d_1 \\ \lambda_2 &= -(d_1 + d_3 + \gamma) \end{aligned}$$

And other three eigenvalues are determined from the equations  $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$ , where

$$a_1 = 3d_1 + d_2 + \gamma + \theta + 1 + \beta I^*$$

$$\begin{aligned}
 a_2 &= (d_1 + \beta I^* + \theta)(d_1 + d_2 + 1 - \beta S^*) + (d_1 + \beta I^* + \theta)(1 + d_1) \\
 &\quad + (1 + d_1)(d_1 + d_2 + 1 - \beta S^*) + \beta^2 S^* I^* - \omega \theta \\
 a_3 &= \omega \theta (1 + d_1 + d_2)(R_0 - 1) + (d_1 + \beta I^* + \theta) \\
 &\quad (1 + d_1 + d_2 - \beta S^*)(d_1 + 1) - (1 + d_1)\beta^2 S^* I^* + \beta S^*(1 - \omega)
 \end{aligned}$$

Since  $a_1 a_2 - a_3 > 0$ , hence by Routh–Hurwitz condition, the system is locally stable for endemic equilibrium.

### 2.6 Analysis of Global Stability at Endemic Equilibrium

Endemic equilibrium points with death due to infection satisfy the system (1) for  $SQ_HIQ_1R$  model. The analysis for global stability can be dealt through geometric approaches. According to the approach, if the differential equation  $\frac{dx}{dt} = f(x)$ ,  $x(t) = x_0$  for the mapping  $f: \phi \subset R^n \rightarrow R^n$ , where  $\phi$  is an open connected set, then the equilibrium point  $\bar{x} \in \phi$  which agree the following conditions.

1.  $\phi$  is simply connected.
2.  $\exists$  is a compact absorbing subset  $K \in \phi$ .
3.  $\bar{x}$  is the only equilibrium point in  $\phi$  that is globally stable if it satisfies the Bendixson criteria  $\bar{q}_2 = \limsup_{n \rightarrow \infty} \sup_{x_0 \in K} q < 0$ , where  $q = \int_0^t \psi(Z(x(s), x_0)) ds$  and  $Z = M_f M^{-1} + M \frac{\partial J}{\partial x} M^{-1}$ ,  $M$  is matrix-valued function which satisfy the condition  $Z = M_f M^{-1} + M \frac{\partial J}{\partial x} M^{-1} \leq 0$  on  $K$ . Further, the fourth-order second compounded Jacobian matrix is  $J^{[2]} = \frac{\partial f^{[2]}}{\partial x}$ .

**Theorem 7** *The system is globally stable at unique endemic equilibrium points  $\Omega^*(S^*, I^*, Q_H^*, Q_1^*)$  in the interior of  $\Omega^*$ , when  $R_0 > 1$ .*

**Proof** From the system of Eq. (1), the Jacobian matrix, leaving the recovered population is

$$J = \begin{pmatrix} -(d_1 + \beta I + \theta) - \beta S & \omega & 0 \\ \beta I & \beta S - (d_1 + d_2 + 1)(1 - \omega) & 0 \\ \theta & 0 & -(1 + d_1) 0 \\ 0 & P & 0 & -(d_1 + d_3 + \gamma) \end{pmatrix}$$

Again,

$$J^{[2]} = \begin{pmatrix} \beta S - (2d_1 + d_2 + 1 + \theta + \beta I)(1 - \omega) & 0 \\ 0 & -(2d_1 + \beta I + \theta + 1) 0 \\ P & 0 & -(d_1 + \beta I + \theta + d_2 + d_3 + \gamma) \\ -\theta & \beta I & 0 \\ 0 & 0 & \beta I \\ 0 & 0 & \theta \end{pmatrix}$$

$$\begin{pmatrix} -\omega & 0 & 0 \\ -\beta S & 0 & 0 \\ 0 & \omega & 0 \\ \beta S - (2d_1 + d_2 + 2) & -\beta S & 0 \\ P & \beta S - (2d_1 + d_2 + 1 + \gamma + d_3) & (1 - \omega) \\ -P & 0 & -(d_1 + d_2 + d_3 + \gamma + 1) \end{pmatrix}$$

where  $J^{[2]}$  is the second compound additive Jacobian matrix.

To get the matrix  $Z$  in Bendixson criteria, the diagonal matrix  $M$  is defined as.

$M = \text{diag}\left(1, \frac{I}{Q_H}, \frac{I}{Q_H}, \frac{I}{Q_H}, \frac{I}{Q_H}, \frac{I}{Q_H}\right)$  and vector field  $f$  of the system is defined as

$$M_f M^{-1} = \text{diag}\left(0, \left(\frac{I}{Q_H}\right)_f \frac{I}{Q_H}, \left(\frac{I}{Q_H}\right)_f \frac{I}{Q_H}, \left(\frac{I}{Q_H}\right)_f \frac{I}{Q_H}, \left(\frac{I}{Q_H}\right)_f \frac{I}{Q_H}, \left(\frac{I}{Q_H}\right)_f \frac{I}{Q_H}\right)$$

Hence, we obtain the block matrix  $Z = M_f M^{-1} + M J^{[2]} M = \begin{pmatrix} Z_{11} & Z_{12} \\ Z_{21} & Z_{22} \end{pmatrix}$  where

$$Z_{11} = \beta S - (2d_1 + d_2 + 1 + \theta + \beta I)$$

$$Z_{12} = \left( (1 - \omega) \frac{Q_H}{I} \ 0 \ -\omega \frac{Q_H}{I} \ 0 \ 0 \right)$$

$$Z_{21} = \begin{pmatrix} 0 \\ P \frac{I}{Q_H} \\ -\theta \frac{I}{Q_H} \\ 0 \\ 0 \end{pmatrix}$$

$$Z_{22} = \begin{pmatrix} (-2d_1 + \beta I + \theta + 1) + X & 0 & -\beta S \\ 0 & -(d_1 + \beta I + \theta + d_2 + d_3 + \gamma) + X & 0 \\ \beta I & 0 & (\beta S - (2d_1 + d_2 + 2) + X) \\ 0 & \beta I & P \\ 0 & \theta & -P \\ 0 & 0 & 0 \\ -\beta S & \omega & 0 \\ 0 & 0 & 0 \\ (\beta S - (2d_1 + d_2 + d_3 + 1 + \gamma) + X) & (1 - \omega) & 0 \\ 0 & -(d_1 + d_2 + \gamma + d_3 + 1) + X & 0 \end{pmatrix}$$

where  $X = \frac{I'}{I} - \frac{Q'_H}{Q_H}$ .

The Lozinski measure of matrix  $Z$  is estimated as  $\psi(Z) \leq \sup \{g_1, g_2\}$ , where  $g_1, g_2$  are defined as

$$g_1 = \psi(Z_{11}) + |Z_{12}| = \beta S - (2d_1 + d_2 + 1 + \theta + \beta I) + (1 - \omega) \frac{Q_H}{I} \leq \frac{I'}{I}$$

$$g_2 = \psi(Z_{22}) + |Z_{21}| = (\beta S - (2d_1 + d_2 + 2) + X) + P \frac{I}{Q_H} \leq \frac{I'}{I} - d_1$$

So,  $\psi(Z) \leq \sup \{g_1, g_2\} \leq \frac{I'}{I} - d_1$ . Hence,  $\int_0^t \psi(Z) dt < \log I(t) - d_1 t$ .

Finally, we have  $\bar{q}_2 = \frac{\int_0^t \psi(Z)dt}{t} < \frac{\log I(t)}{t} - d_1 < 0$ , for all absorbing set  $\Omega$  is bounded. Thus as per Li and Muldowney [30], Bendixson criteria is satisfied at endemic equilibrium for global stability.

### 3 Discussion of the Result

Our model is based on two unique approaches: Firstly, it is based on pre-quarantine of suspected immigrants and individuals having travel history. Secondly, the approach is based on post-quarantine of infected individuals. Two basic reproduction numbers  $R_0$  and  $R_{0H}$  are derived. These two basic reproduction numbers collectively give the overall disease outbreak. The numerical simulation of the available data relevant to COVID-19 obtained from different sources is validated with analytical results with the help of MATLAB. The nonlinear ODEs are solved with the help of Runge–Kutta fourth-order numerical method. Graphical interpretation of numerical results is thoroughly discussed using different parameters. It is found that the interpretation of data agrees with the current phenomena of COVID-19 and results of existing literature. As per the relevant data of COVID-19 available from different sources (Govt. Websites of different countries, Media, WHO, etc.), we have assumed the whole population as one unit and the initial conditions are set as  $S(0) = 0.82$ ,  $Q_H(0) = 0.03$ ,  $I(0) = 0.12$ ,  $Q_1(0) = 0.02$ ,  $R(0) = 0.01$ . The graphs are plotted by taking the appropriate values of different parameters associated with the model that are indicated in each figure.

Figures 2 and 3 represent the behavior of all compartments for  $R_0 < 1$  and  $R_0 > 1$ , respectively when  $A = 0$ . Figure 2 indicates the disease-free equilibrium because susceptible class does not tend to zero level. Figure 3 indicates endemic equilibrium because the susceptible class tends to zero level. Due to the adoption of pre- and post-quarantine processes, the infection decreases that indicates the decline of infected line in both diagrams. Prior to the whole population being infected, the disease dies out that indicates the recovered line is higher but not approaches to zero. As infected individuals are isolated through quarantine, the disease does not spread.

Figures 4 and 5 interpret the effect of influx of newborn and immigrants (i.e.  $A \neq 0$ ) on all compartments for  $R_0 < 1$  and  $R_0 > 1$ , respectively. Because of the continuous influx of immigrants and newborns in susceptible class and due to double quarantine effect, the infective class approaches to zero level. So, the disease is stable after some days.

The phase diagram of susceptible verses infective is shown in Figs. 6 and 7 for  $A = 0$  and  $A \neq 0$ , respectively. When  $S$  increased, infection reached to a peak but then decreased because of double quarantine effect and proper health care. The declined trend of infective graph indicates that the disease is toward the stable condition due to the enhanced recovery rate.

Figures 8 and 9 exhibit the phase portrait graph of infective verses recovery class. Due to pre-quarantine of susceptible class, entry of immigrants, newborn cases,

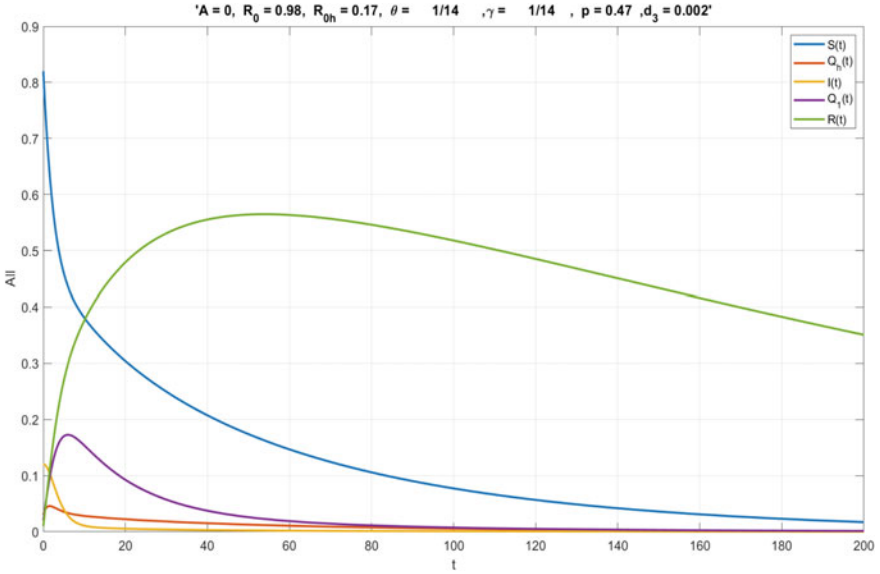


Fig. 2  $A = 0, R_0 = 0.98, R_{0h} = 0.17, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.47, d_3 = 0.002$

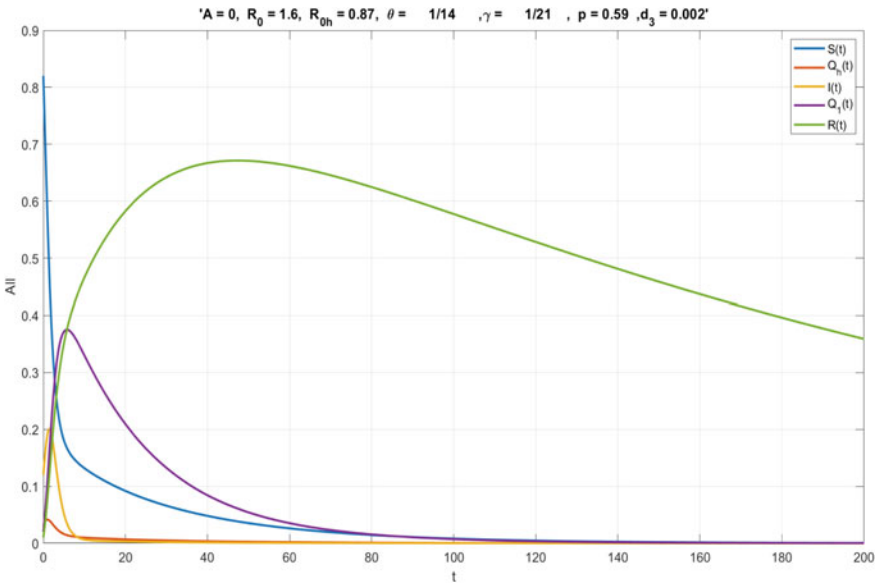
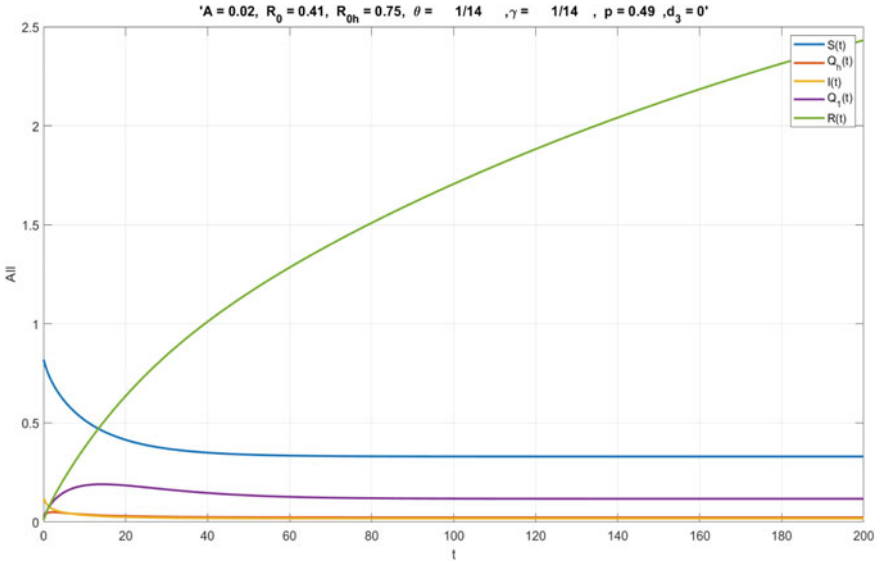
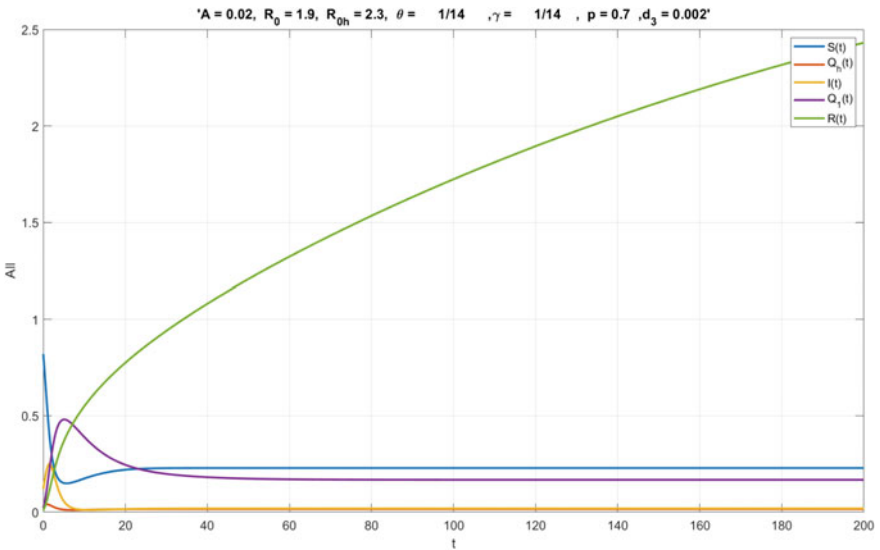


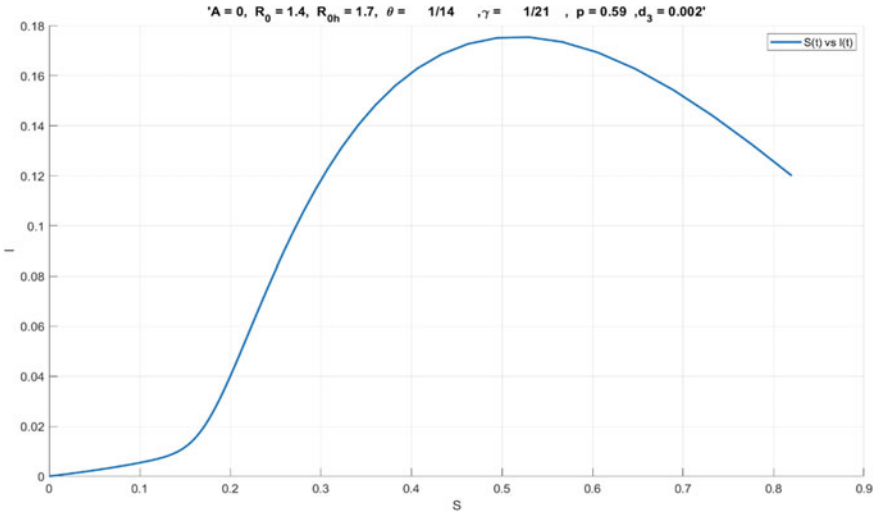
Fig. 3  $A = 0, R_0 = 1.6, R_{0h} = 0.87, \theta = \frac{1}{14}, \gamma = \frac{1}{21}, p = 0.59, d_3 = 0.002$



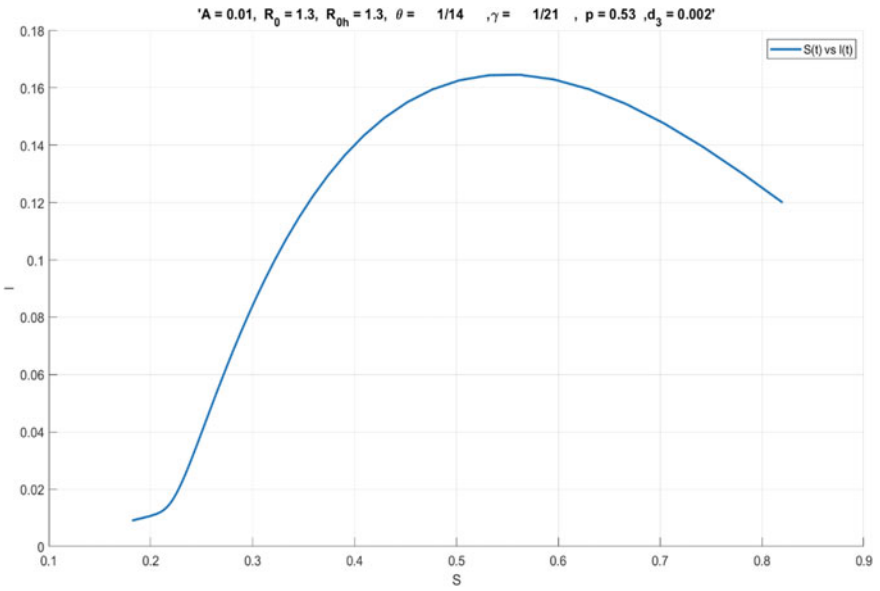
**Fig. 4**  $A = 0.02, R_0 = 0.41, R_{0h} = 0.75, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.49, d_3 = 0$



**Fig. 5**  $A = 0.02, R_0 = 1.9, R_{0h} = 2.3, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.7, d_3 = 0.002$

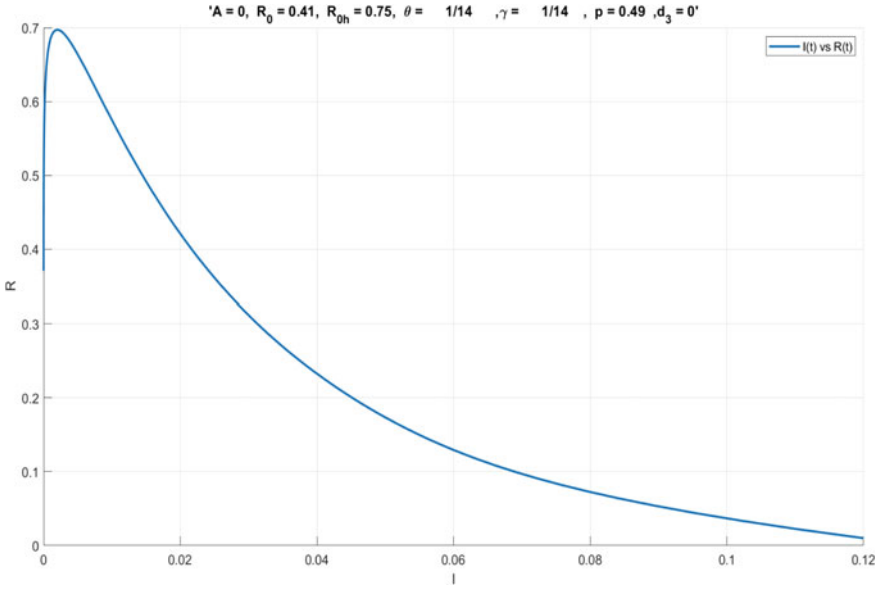


**Fig. 6**  $A = 0, R_0 = 1.4, R_{0h} = 1.7, \theta = \frac{1}{14}, \gamma = \frac{1}{21}, p = 0.59, d_3 = 0.002$

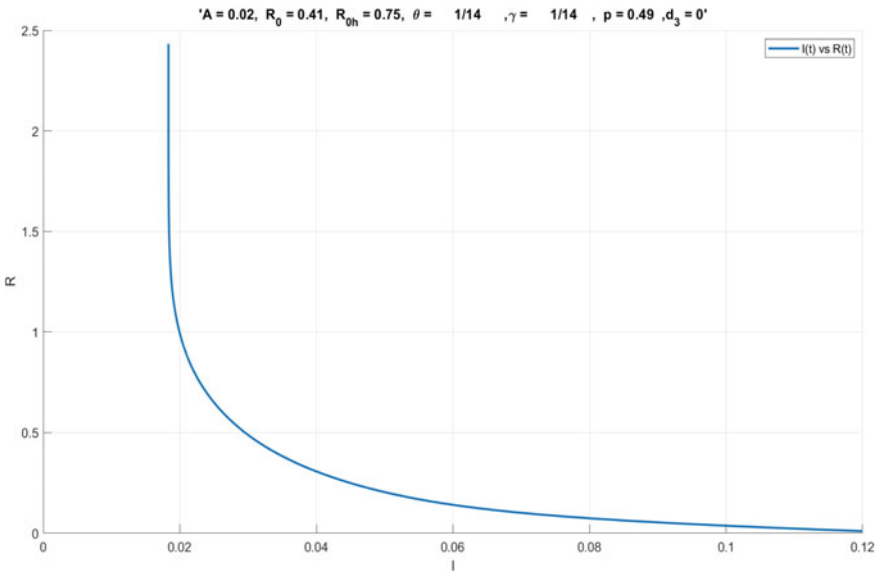


**Fig. 7**  $A = 0.01, R_0 = 1.3, R_{0h} = 1.3, \theta = \frac{1}{14}, \gamma = \frac{1}{21}, p = 0.53, d_3 = 0.002$

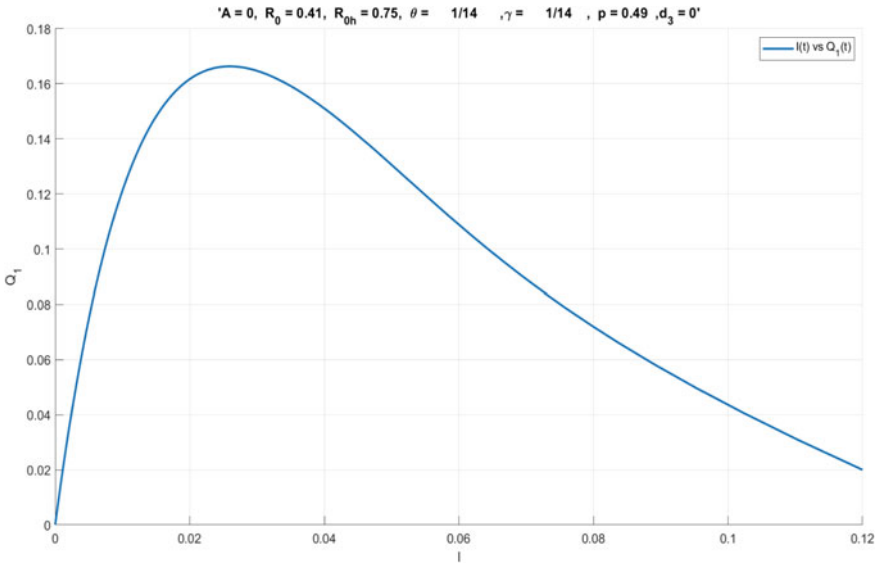




**Fig. 8**  $A = 0, R_0 = 0.41, R_{0h} = 0.75, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.49, d_3 = 0$



**Fig. 9**  $A = 0.02, R_0 = 0.41, R_{0h} = 0.75, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.49, d_3 = 0$



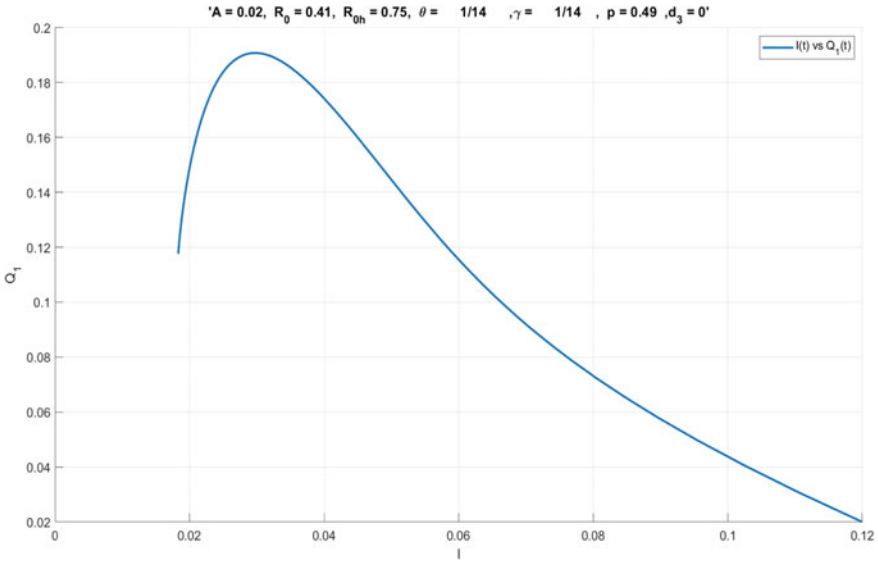
**Fig. 10**  $A = 0, R_0 = 0.41, R_{0h} = 0.75, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.49, d_3 = 0$

and post-quarantine of infective class, the recovered population enhanced first but decreased after certain period of time. So the growing number of infectives leads to an endemic in the absence of quarantine.

The phase diagram of quarantine versus infective is shown in Figs. 10 and 11 for  $R_0 < 1$  when  $A = 0$  and  $A \neq 0$ , respectively. With the increase of infectives in the quarantine class, the post-quarantine class increased initially and then decreased due to either the stability of disease or recovery of maximum number of individuals.

### 4 Conclusion

The research designed in this chapter is based on the formulation of the spread and control of the coronavirus disease-19. Here, a model is developed to investigate the effects of double quarantine process on the stability analysis. We conducted a detailed analysis of this model, devised the methodology, reviewed, analyzed, and discussed the result both analytically and numerically. Eigenvalues are derived from Jacobian matrix and equilibrium points (disease-free and endemic) are obtained. Analysis for both local and global stabilities is carried out with the help of existing theorems. The analytical and numerical results are well in agreement that validates the data. The graphical interpretation explores the real findings of the investigation. The finding of the investigation done in this paper indicates that the disease will be stable locally asymptotically for  $R_0 < 1$ . The finding of our research supports the speculations of the disease that would persist in human world for long term. Moreover, if the double



**Fig. 11**  $A = 0.02, R_0 = 0.41, R_{0h} = 0.75, \theta = \frac{1}{14}, \gamma = \frac{1}{14}, p = 0.49, d_3 = 0$

quarantine process at both susceptible and infected levels is effectively implemented and social distancing is strictly maintained with lockdown or containment, then the disease will be globally stable in a long term for  $R_0 > 1$ . More realistic models with detailed data or parameters like immunity, age structure, saturated incidence, and exposed compartment may be employed in future investigation to explore the analysis of COVID-19 outbreak.

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