

Mathematical Modelling on Double Quarantine Process in the Spread and Stability of Covid-19

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Mathematical Modelling on Double Quarantine Process in the Spread and Stability of Covid-19

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Abstract In this paper, a mathematical model is proposed on the spread and control of corona virus disease-2019 (COVID19) to ascertain the impact of pre quarantine for suspected individuals having travel history ,immigrants and new born cases in the susceptible class following the lockdown or shutdown rules and adopted the post quarantine process for infected class. Set of nonlinear ordinary differential equations (ODEs) are generated and parameters like natural mortality rate, rate of COVID-19 induced death, rate of immigrants, rate of transmission and recovery rate are integrated in the scheme. A detailed analysis of this model is conducted analytically and numerically. The local and global stability of the disease is discussed mathematically with the help of Basic Reproduction Number. The ODEs are solved numerically with the help of Runge-Kutta 4th order method and graphs are drawn using MATLAB software to validate the analytical result with numerical simulation. It is found that both results are in good agreement with the results available in the existing literatures. The stability analysis is performed for both disease free equilibrium and endemic equilibrium points. The theorems based on Routh-Hurwitz criteria and Lyapunov function are proved .It is found that the system is locally asymptotically stable at disease free and endemic equilibrium points for basic reproduction number less than one and globally asymptotically stable for basic reproduction number greater than one. Finding of this study suggest that COVID-19 would remain pandemic with the progress of time but would be stable in the long-term if the pre and post quarantine policy for asymptomatic and symptomatic individuals are implemented effectively followed by social distancing ,lockdown and containment.

Keywords Basic Reproduction Number · Disease · Epidemic · Equilibrium · Social Distancing

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

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Nomenclature

A	Rate of Immigrants and new born
S	Susceptible population
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
β	Rate of infection from infective class to susceptible class
θ	Rate at which the susceptible population goes to home isolation
ω	Probability at which the home isolation population becomes susceptible
p	Probability at which the infected population goes to hospital quarantine for treatment
γ	Rate at which the population become recovered after hospitalized
d_1	Natural death rate
d_2	Rate of death due to COVID-19
d_3	Rate of death due to pre existing diseases that are vulnerable to COVID-19
R_0	Basic Reproduction Number of pre quarantine class
R_{0H}	Basic reproduction number after hospitalized

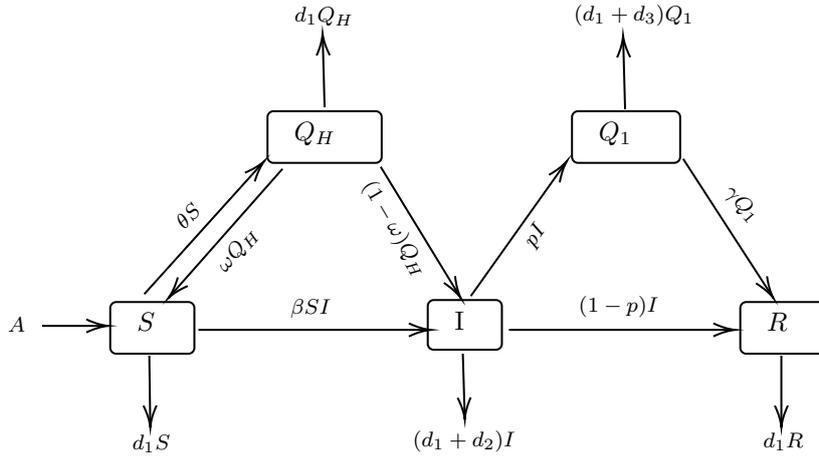
1 Introduction

History says, world has faced many epidemic diseases like diarrhoea, malaria, dengue, influenza, small pox, pneumonia, T.B., AIDS etc due to viral, bacterial, protozoan and fungal infections over the time evolution. The infectious diseases due to different viruses are more harmful, quickly spread and uncontrolled than the infectious diseases due to other micro-organisms. Human being has been mostly affected by these diseases, many persons have died and economic condition of the world has disrupted. 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 like some countries of African continent but the present pandemic novel corona virus disease -2019 (COVID-19) is originated from the Wuhan city of Hubei province of China in December 2019, spread all over the world by the end of March 2020 and severely affected many developed countries like U.S.A., Italy, France, Spain, England, Germany and Belgium etc. As per WHO's (WORLD HEALTH ORGANISATION) [18] report from 31th December 2019 to 7th May 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 common symptoms of COVID-19 are fever, cold, cough, sore throat, difficulty in breathing in most of the cases; also in some cases headache and diarrhoea are reported. COVID-19 spreads due to social contact, sneezing 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 group, however; the older people and people with pre-existing diseases like asthma, heart problem, kidney disease and hypertension etc 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 only effective measures to control the spread of diseases are social distancing through home isolation or quarantine, washing hands with soap several times about 20 seconds, sanitization, not touching the face, eyes, ear and wearing mask etc. 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 begin 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 following limited numbers of research articles in this paper due to the paucity of article length as per journals guideline. B. Trawicki [7] has discussed about the vaccination of newborn, temporary immunity, vital dynamics with unequal birth and death rate with help of SEIRS epidemic modelling and analysed the local and global stability analysis of the disease. The model has not included the quarantine class. Qun Lu et.al [10] have investigated the non linear perturbation method to study a stochastic predator-prey model with additional food that is helpful to investigate the epidemic models such as SIS, SIQR etc. The existence of an ergodic stationary point is used to establish Lyapunov function for stability analysis.

The stability analysis of biological system using differential equations are presented by G.Bastin[2].The different methods of stability analysis discussed by him will be used to analyse the stability of COVID-19. Bin M.et.al.[1] have proposed a model which demonstrates how the post lockdown mitigation may intervene the COVID-19 that lead to multi shot epidemic. Xu X. et.al. [20]have examined the evolution of COVID-19 in Wuhan city of China and found the risk of human transmission by modelling of its spike protein. Pederson M.G.et.al [9] has explained how the undetected patients quantify the number of infected cases and effort of containment to control the disease in Italy. Li Q. et.al.[4] have proposed the dynamic model on the transmission of COVID-19 in Wuhan, China and suggested the controlling measure that can die out the disease. Wanjun Xia et.al [17] have proved the local stability using the delayed SEIQ epidemic model. Riou Juhen et.al.[11] have elaborated the transmission of COVID-19 in Wuhan from December 2019 to January 2020 and examined the effective measures to stabilize the disease. Rothe C.et.al[12] have shown how the asymptomatic contact individuals of Germany have transmitted the disease and impact of severity on infection. Zhang Y.et.al.[21] have studied the control of COVID-19 in China using a mathematical model SEIQR and impact of social distancing and lockdown by explaining the stability analysis. Marek. Linan Zhang et.al. [6] have studied the different mathematical models of influenza viruses and discussed their stability analysis using vaccination. Guijie Lan et.al.[3] have studied the SIQR epidemic model with stochastic persistence of diseases and obtained the existence of unique stable stationary distribution using Markov semi-group theory . Mustafa Erdem et.al.[8] have observed the oscillatory behaviour of the model of the SIQR influenza model with imperfect quarantine that resembles with the stability of COVID-19 in some countries like South Korea and China. Xia Ma et.al. [19] have discussed global stability of the SIR model using comparison principle. This model can be explored to study SIQRS model. The literature survey reveals many mathematical models on the spread of various infectious diseases due to Zika virus, Ebola virus, Hanta virus, West Nile virus, Alpha virus, H1N1, H3N2 and H5N1 viruses etc. But COVID-19 due to Corona Virus is new for the researchers. The research papers published so far our knowledge till the dates have many limitations. Many researchers have investigated different epidemic models of COVID-19 but still many aspects of the disease are ignored and are insufficient in the investigation of 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. Hence, the model developed in this research paper based on the available data from different sources and existing literatures including many disease related parameters to investigate the pre and post quarantine effect on the spread and control of disease is new and original in the research of COVID-19. Therefore, the proposed model in this paper with pre and post quarantine effect and discussion of both local and global stability will explore the new dimension in the study of COVID-19.

2 Mathematical Model:

The whole population N is divided into five compartments : $S(t)$, $Q_H(t)$, $I(t)$, $Q(t)$ and $R(t)$ which are disjoint over the continuous time evolution. The rate of infection β is the average number of maximum contacts by one infected person per day from infected compartment (I) to susceptible compartment (S). Thus the average number of susceptible infected by an infected is βS and by the whole infected class is βSI is called incidence (mass action law). The immigrants, new borne and suspected individuals having travel history are kept in home quarantine class Q_H at rate θ 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 ω 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 γ 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 $\frac{1}{d_1+d_3}$. The population is considered as homogeneously mixing i.e. everyone has equal chance of infection. Every compartment is dynamic in nature with respect to time. Based on these assumptions, the flow diagram and modelling of COVID-19 is given below;



The net flow of quantity that enters into each compartment is taken as positive and exits from each compartment is taken as negative. Thus, the rate of change in size of each class with respect to time evolution is expressed in terms of following differential equations as per Kermack- McKendrick model[13–15]

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

With initial conditions $S(0) > 0, Q_H(0) > 0, I(0) > 0, Q_1(0) > 0, R(0) > 0$ Since, these systems of non linear differential equations are not in standard forms to solve analytically, So, Runge-Kutta 4th order numerical method is adopted to solve them with help of MATLAB software and simulated results are graphically interpreted with detailed discussions.

2.1 Model Analysis

In epidemiology, the basic reproduction number is used as an important factor to be determined if any emerging infectious disease spreads in a population and to establish the stability analysis of the disease. The average number of adequate contacts of an infective to the whole susceptible class during the infection period is called basic reproduction number (R_0).i.e. $R_0 = \text{Number of new cases arising per day from one infective} \times \text{Average days of infection}$. Hence, the analysis and interpretation of R_0 is important to study the COVID-19 disease. In this paper, two basic reproduction numbers are derived mathematically from the model due to both pre and post quarantine effects. Analyzing the stability of a biological system gives the epidemic threshold conditions under which the number of infected individuals will either decrease to zero or increase to a peak, when a number of infections introduced into a population. These threshold conditions are characterized by the basic reproductive number. This threshold quantity is interpreted as; 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 $R_0 > 1$ 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. Thus the disease spread for longer time leads to epidemic and the system is said to be unstable. If $R_0 = 1$ then an infected person produce only one new case of the diseases ,so disease will not grow significantly but the disease persist. It is the critical value of the threshold quantity. The region in which the solutions to the model are uniformly bounded is defined as $\Omega \in R_+^5 = \{(S, Q_H, I, Q_1, R) \in R_+^5, S \geq 0, Q_H \geq 0, I \geq 0, Q_1 \geq 0, R \geq 0\}$. This is positively invariant for the system (1). Clearly, the interaction functions on the right hand side of (1) are continuously differentiable. Therefore, the solution of the system (1) exist and unique. The uniform boundedness of the solutions of the system (1) with non negative initial conditions is explained in the following theorem.

Theorem 1 *All the 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 the system (1) with non negative 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,

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dQ_H}{dt} + \frac{dI}{dt} + \frac{dQ_1}{dt} + \frac{dR}{dt}$$

$$\text{So, } \frac{dN}{dt} = A - d_1N - d_2I - d_3Q_1$$

In the absence of any infection the total population becomes $\frac{A}{d_1}$ i.e As $t \rightarrow \infty$ then $N \rightarrow \frac{A}{d_1}$ Hence all the solutions of the system (1) are confined in the region

$$\Omega = \left\{ (S, Q_H, I, Q_1, R) \in R_+^5 : N \leq \frac{A}{d_1} \right\}$$

Since all the solution remain bounded in the positive invariant region Ω , the maximal interval in $[0, \infty)$. Thus the initial value problem is well posed.

2.2 Calculation of Basic Reproduction Number from SIQ_1R Model

The SIQ_1R compartmental equations are

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

This model is also positive and closed invariant. Next generation matrix is considered to obtain the basic reproduction number. This is defined as the spectral radius of the FV^{-1} . Where F is the infection matrix and V is the transformation matrix between the compartments.

Linearization of equation 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, taking the right hand side of the equation (2) equal to zero, we have

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

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

Disease free equilibrium point = $(S_0, 0, 0, 0)$

Endemic equilibrium point = (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 At the disease free equilibrium point (3), linearizing the model we get the Jacobian matrix as

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

By calculating the eigen values we have the eigen values

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

For $\beta S_0 < (d_1 + d_2 + 1)$ i.e. $R_0 < 1$ we have all the eigen values negative, hence the disease free equilibrium is locally asymptotically stable.

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

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

The eigen values are $\lambda_1 = -(d_1 + d_3 + \gamma)$
 $\lambda_2 = -d_1$

Other two eigen values can be found by solving the quadratic 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 diseases free equilibrium $E_0 = (\frac{A}{\mu}, 0, 0)$ of (3) is globally asymptotically stable if $R_0 < 1$.*

Proof Consider a Lyapunov function

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

If $R_0 < 1$ then $\frac{dZ}{dt} < 0$ It is observed that $\frac{dZ}{dt} = 0$ if $I = 0$. Hence by the Lasle Lypunov theory the system is globally asymptotically stable at the disease free equilibrium at Ω^* for $R_0 < 1$.

2.4 Calculation of Basic Reproduction Number from SQ_HIQ_1R Model

Success or failure of COVID-19 virus attack depends on basic reproduction number . if $R_0 \geq 1$ the COVID-19 based epidemic will carry on i.e. the number of population become endemic, but, if $R_0 < 1$, then COVID-19 based epidemic will die out i.e. the infected population will slowly become zero. The basic reproduction number for the model is calculated as;

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

2.5 Stability Analysis for SQ_HIQ_1R Model

The disease free equilibrium point of systems of equation 1 is taken as $(S_0, 0, 0, 0)$ and the endemic equilibrium point is

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

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 equation (1)*

Proof Linearization of the system of differential equation (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 $\lambda_1 = -(d_1 + d_3 + \gamma)$ And other three can be found by solving the cubic equations $\lambda^3 + A\lambda^2 + B\lambda + C = 0$ Where

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

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

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

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

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

Here the two eigen values are $\lambda_1 = -d_1, \lambda_2 = -(d_1 + d_3 + \gamma)$ And other three eigen values are given by 3rd degree polynomial equations $\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$ Where

$$\begin{aligned} a_1 &= 3d_1 + d_2 + \gamma + \theta + 1 + \beta I^* \\ a_2 &= (d_1 + \beta I^* + \theta)(d_1 + d_2 + 1 - \beta S^*) + (d_1 + \beta I^* + \theta)(1 + d_1) \\ &\quad + (1 + d_1)(d_1 + d_2 + 1 - \beta S^*) + \beta^2 S^* I^* - \omega\theta \\ a_3 &= \omega\theta(d_1 + d_2 + 1)(R_0 - 1) + (d_1 + \beta I^* + \theta)(d_1 + d_2 + 1 - \beta S^*)(1 + d_1) \\ &\quad - (1 + d_1)\beta^2 S^* I^* + \beta S^*(1 - \omega) \end{aligned}$$

Since $a_1 a_2 - a_3 > 0$ Hence by Routh-Hurtwz condition, endemic equilibrium is locally stable.

2.6 Global Stability for Endemic Equilibrium:

In this section, it is observed that the system is asymptotically stable for diseases' Free State when $R_0 < 1$. However when $R_0 > 1$ the diseases free equilibrium loses its global stability and an endemic equilibrium exists, which agree with this situation the diseases persists in the populations. The endemic equilibrium points for SQ_HIQ_1R model with infection induced deaths satisfies the following system of equations (1). We adopt the geometric approaches to prove the global stability of endemic equilibrium. According to the approach for the mapping $f : \varphi \subset R^n \rightarrow R^n$, where φ is an open connected set, if the differential equation $\frac{dx}{dt} = f(x)$ such that its every solution $x(t)$ can be uniquely determined by its initial condition $x(t) = x_0$ then the equilibrium point $\bar{x} \in \varphi$ and satisfying the condition

1. φ is simply connected.
2. There exist a compact absorbing subset $K \in \varphi$.
3. \bar{x} is only equilibrium point in φ , is globally stable if it satisfy the additional Bandixion criteria given by $\bar{q}_2 = \limsup_{t \rightarrow \infty} \sup_{x_0 \in K} q < 0$

Where $\bar{q}_2 = \limsup_{t \rightarrow \infty} \sup_{x_0 \in K} q < 0$ also $q = \int_0^t \psi(Z(x(s, x_0))) ds$ and

$$Z = M_f M^{-1} + M \frac{\partial J}{\partial x} M^{-1}$$

M is matrix valued function which satisfy the condition

$$Z = M_f M^{-1} + M \frac{\partial J}{\partial x} M^{-1} \leq 0 \text{ on } K$$

Further $J^{[2]} = \frac{\partial f^{[2]}}{\partial x}$ is the second compounded Jacobian matrix of order four.

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

Proof The general solution of the system (1), the Jacobian Matrix, leaving the recovered populations is

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

The second compound additive Jacobian matrix is given by

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

To obtain the matrix Z in the Bendixson criteria, we define a diagonal matrix M 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

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

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

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

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

Where $X = \frac{I'}{I} - \frac{Q_H'}{Q_H}$ The Lozinskii measure of the matrix Z can be 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 Ω is bounded are uniform persistence of the system. Thus the Bendixson criteria satisfied for global stability of endemic equilibrium as shown by Li and Muldowney [5, 16].

3 Numerical Simulation and 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 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 carried out with help of MATLAB software to validate the analytical results. The set of non linear ordinary differential equations are solved using Runge-Kutta 4th order numerical method. The interpretations of the numerical results are presented graphically and discussed thoroughly by analyzing the different parameters. It is found that the graphical interpretation of the data is in good agreement with the results of existing literatures and relevant to the current phenomena of COVID-19. 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 in the model that are indicated in each figure.

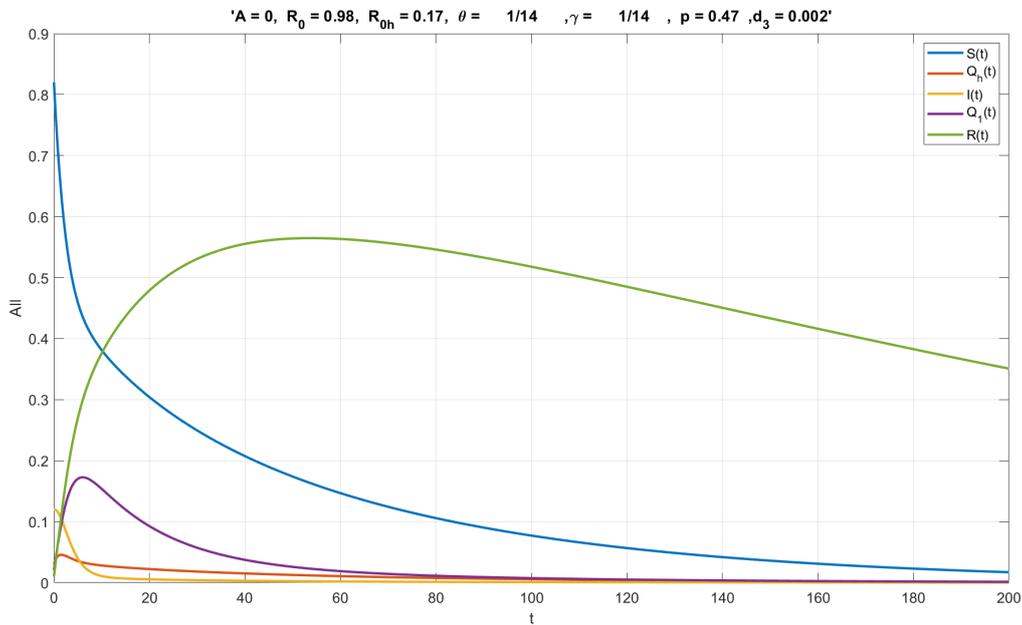


Fig. 1

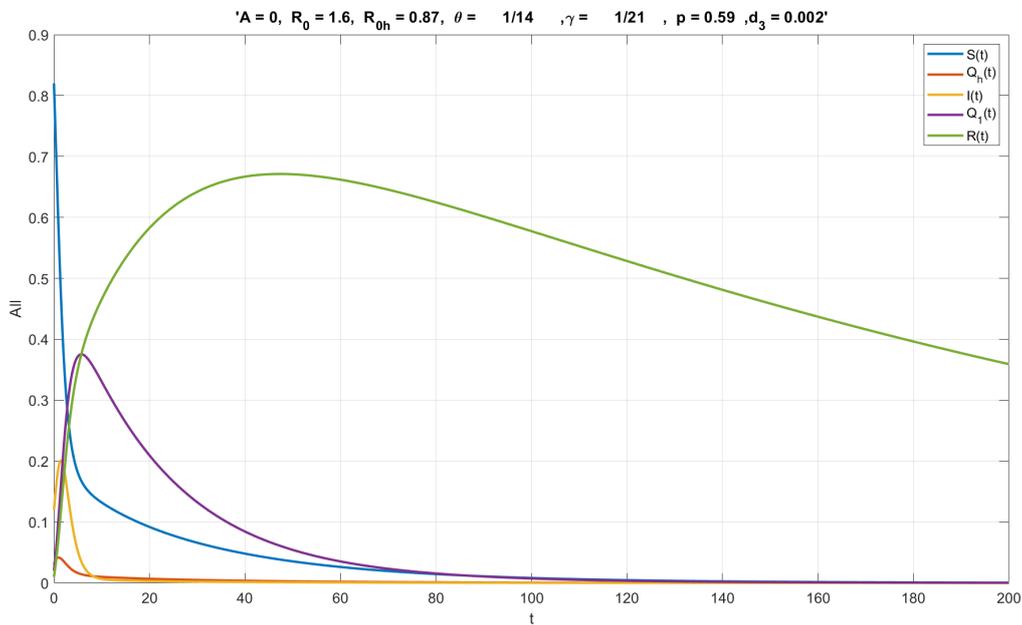


Fig. 2

Fig-1 and fig-2 indicate the behaviour of all compartments with respect to time for $R_0 < 1$ and $R_0 > 1$ respectively without entry of immigrants or new born individuals.(i.e. $A = 0$). In both figures, there is a significant decline of infected line represented by yellow colour due to pre and post quarantine process. The preparedness for reducing the infection by isolating the infectives does not spread the disease out of the quarantine classes. The recovered class denoted by green colour enhanced higher but does not tends to zero indicates the disease has extinct before the whole population get infection. In figure-1 the susceptible class does not tend to zero indicate the disease free equilibrium and the susceptible class in figure-2 approaches to zero level indicates the endemic equilibrium.

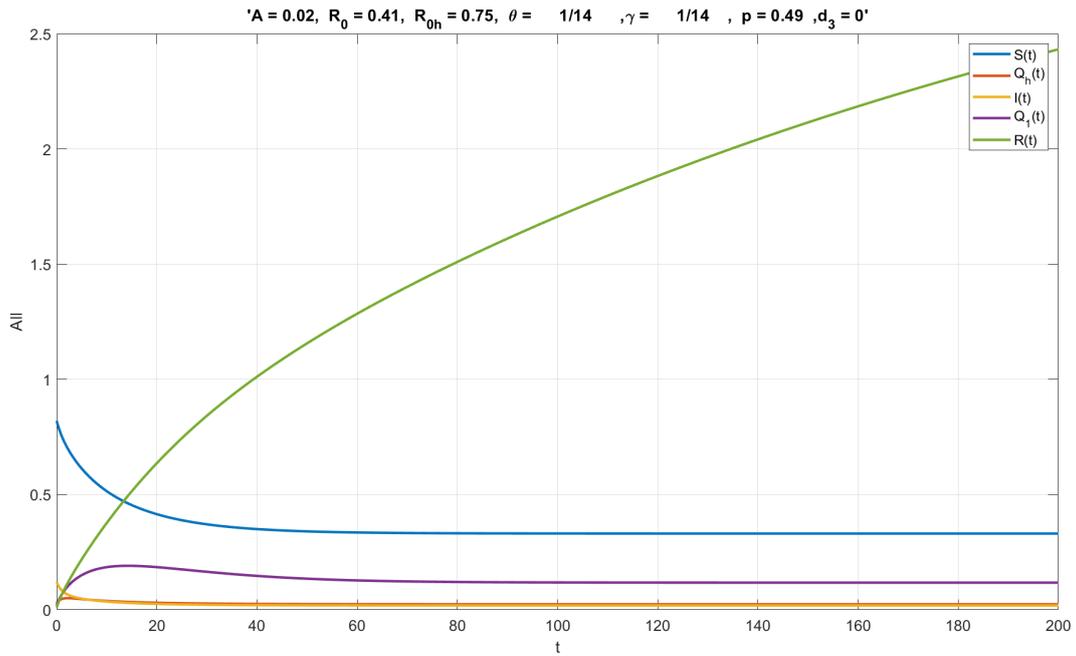


Fig. 3

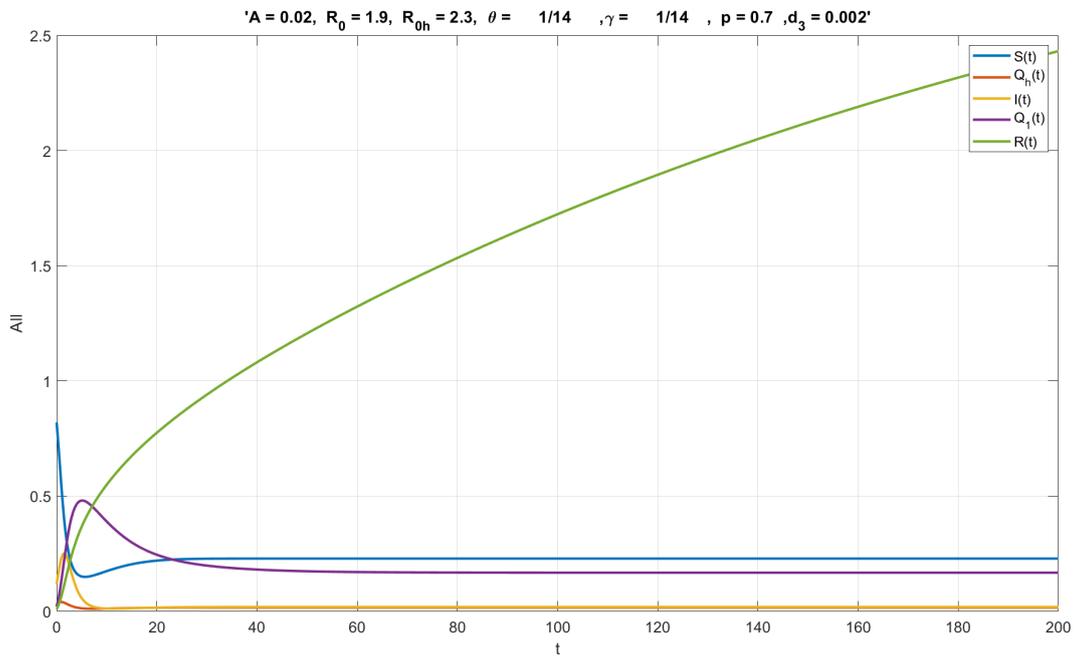


Fig. 4

Fig-3 and fig-4 exhibits the interpretation of all compartments with influx of new born or immigrants.(i.e. $A \neq 0$) for both $R_0 < 1$ and $R_0 > 1$ respectively. Due to infection the susceptible class decline to some extent, but then reaches to the steady state after 20 days because of continuous influx in S . Infection approaches to zero level due to double quarantine effects. The recovery class is much higher than in figure-3 and figure-4 because of continuous entry of immigrants and newborns and the disease is stable for both $R_0 < 1$ and $R_0 > 1$

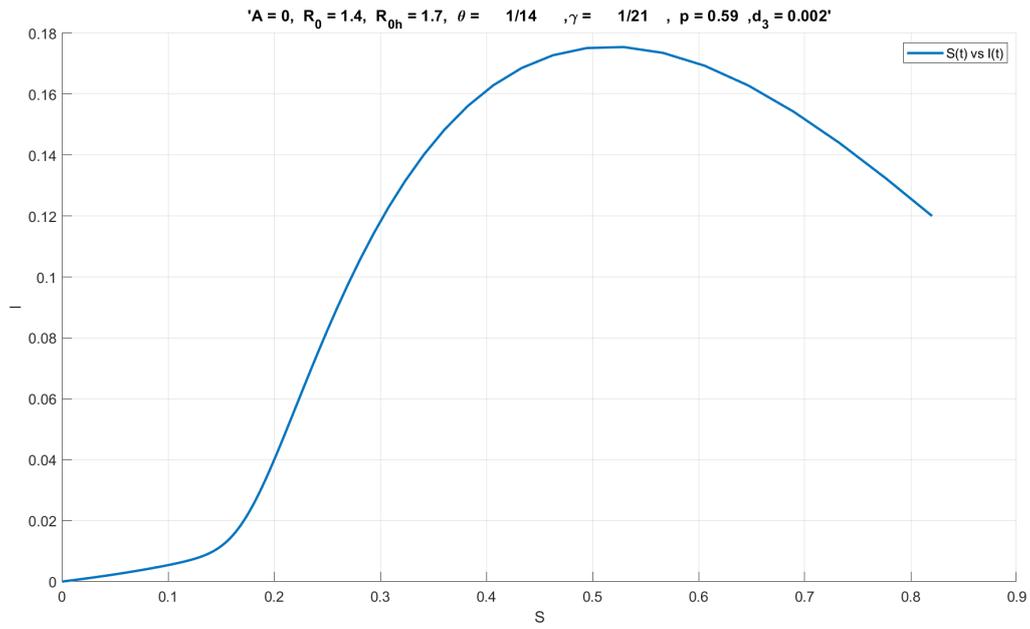


Fig. 5

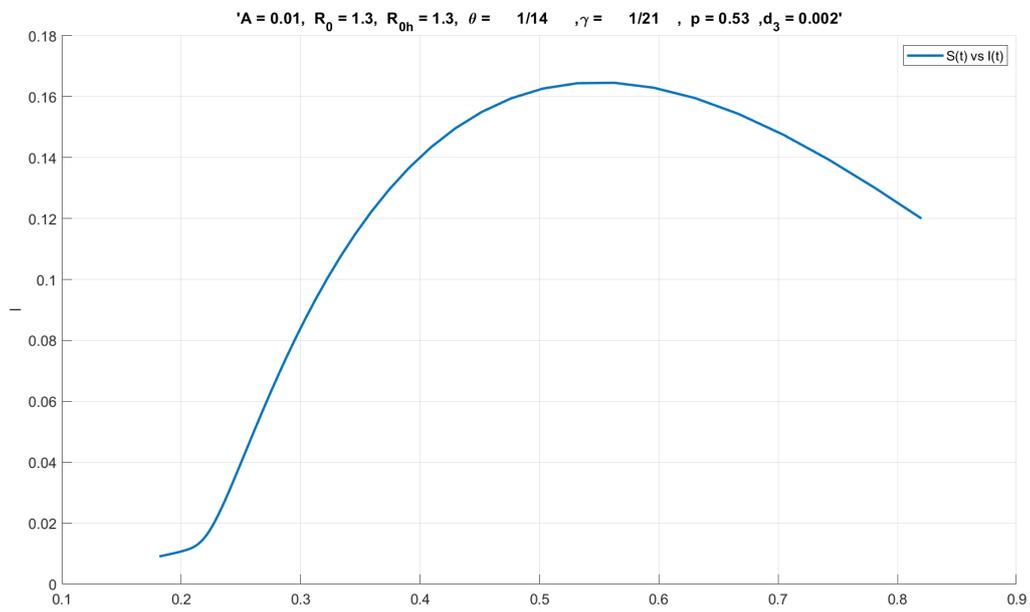


Fig. 6

Fig-5 and figure-6 represent the phase portrait of S versus I graph for $A = 0$ and $A \neq 0$ respectively. In both the figures, infection reaches to a peak when S increases but then start to decrease. This happens due to double quarantine effects and proper health care. This shows that the disease tends towards the recovery phase which leads the stability.

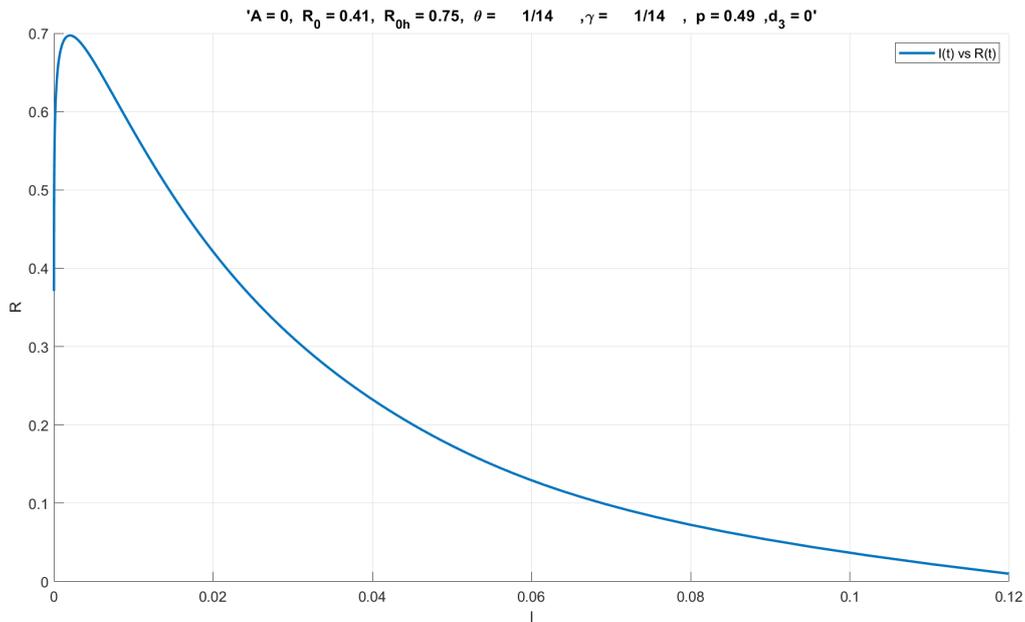


Fig. 7

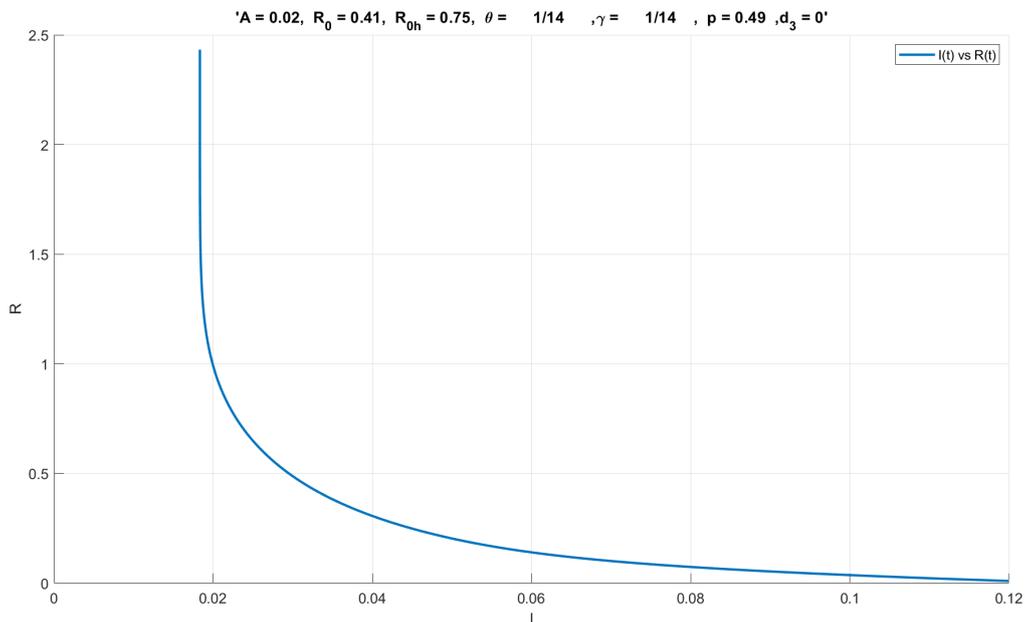


Fig. 8

Figure-7 and figure-8 represent the phase portrait of I versus R , where the recovered population increase in the beginning because of susceptible class is pre-quarantined and containing some infective individuals those are post quarantined. But when the infectives increase more and more lead to an epidemic for long term then the recovery class would decrease that tends to zero leads to an endemic. Again the infected increase due to entry of immigrants and newborn as a result the recovered population decrease on increasing time in the absence of quarantine.

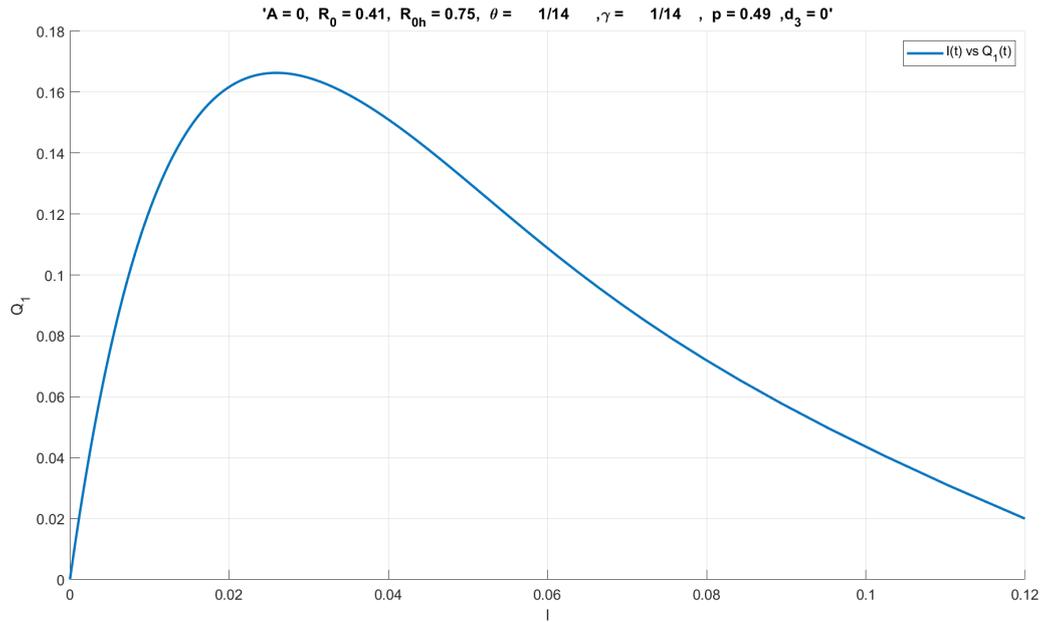


Fig. 9

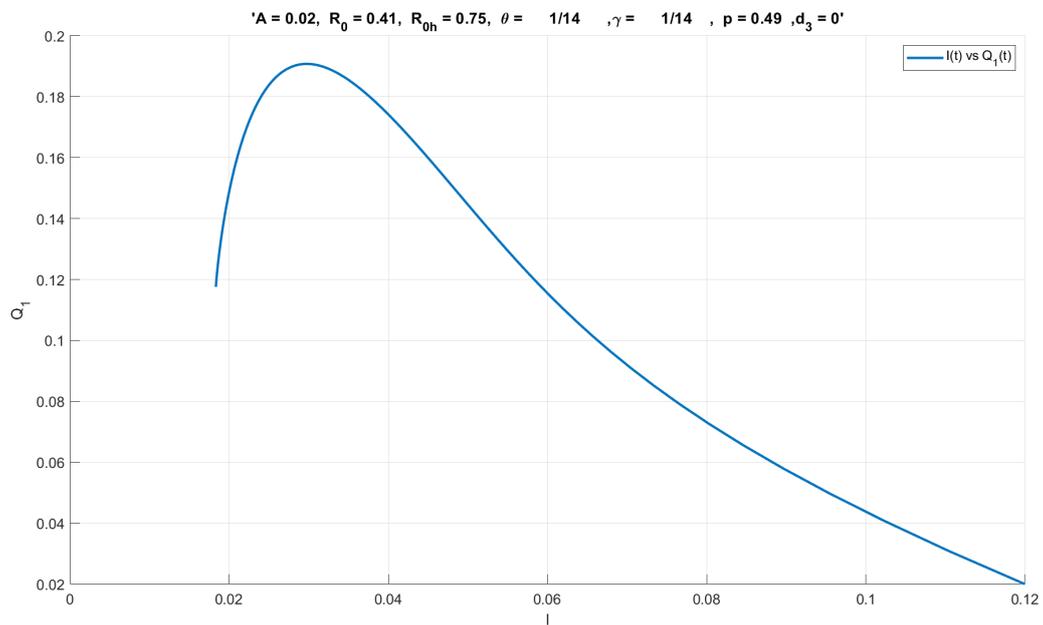


Fig. 10

Figure-9 and figure-10 show the relationship of post quarantine class and the infective class for $A = 0$ and $A \neq 0$ respectively when $R_0 < 1$. The post quarantine class increase initially due to more and more infectives are reported and sent to quarantine compartment but then the rate of quarantine individuals decrease because of either maximum number of individuals are recovered or the disease die out.

4 Conclusion

The research designed in this paper is based on the formulation of the spread and control of COVID-19. We have developed a model to investigate the effects of double quarantine process on the stability analysis. We conducted a detailed analysis of this model, devised the methodology to review, analyze and discuss the results both analytically and numerically. Both disease free and endemic equilibrium points are derived and eigen values are found using Jacobian matrix. Stability analysis for both locally and globally is carried out with help of existing theorems. The analytical and numerical results are well in agreement that validate 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 die out and locally asymptotically stable for $R_0 < 1$ and would remain pandemic for $R_0 > 1$. The finding of our research supports the speculations of the disease that would persist in human world for long term .However; the system will be globally asymptotically stable for $R_0 > 1$ in long run. Moreover, If the double quarantine process at both susceptible and infected level 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 more detailed data or parameters like immunity, age structure, saturated incidence and exposed compartment etc need to be employed for further investigation in future study to explore the development of COVID-19 outbreak.

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Figures

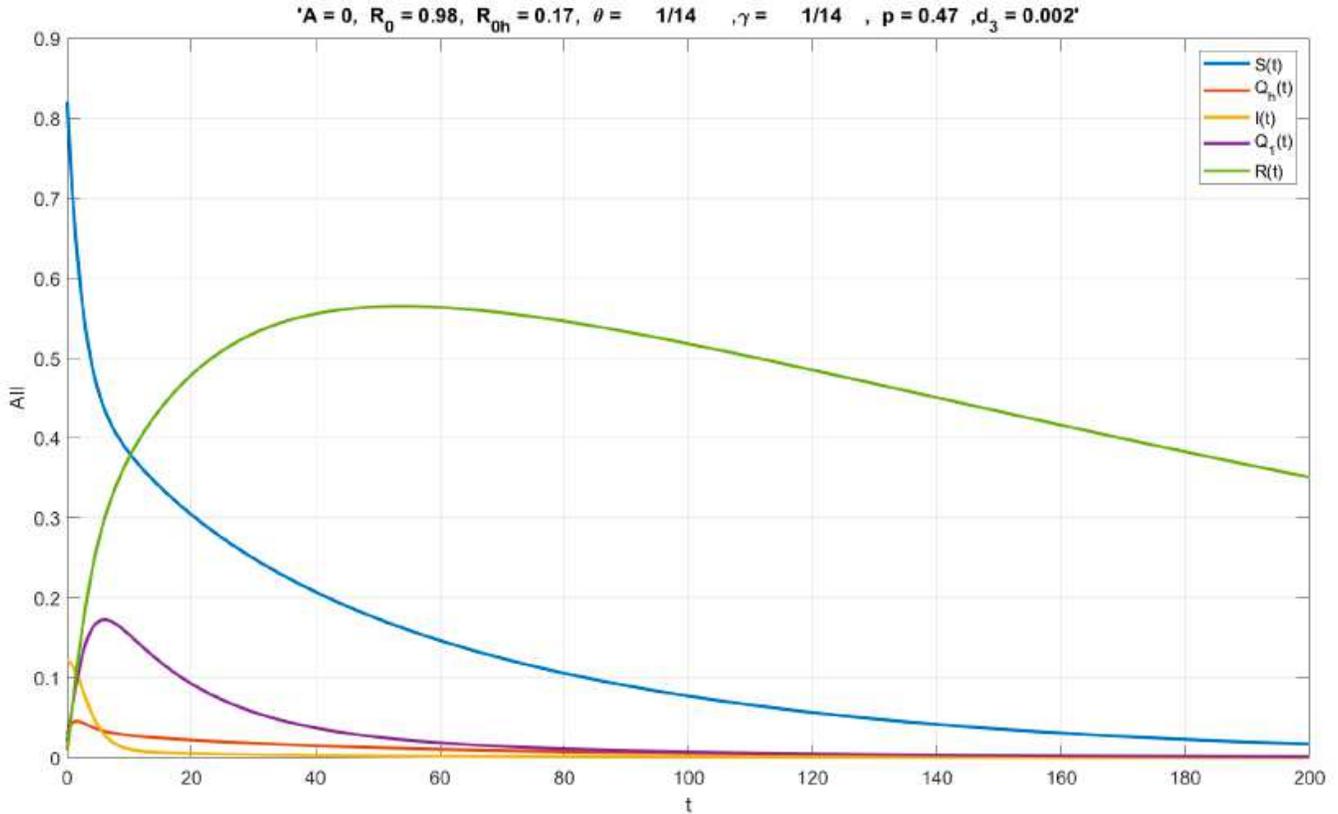


Figure 1

indicate the behaviour of all compartments with respect to time for $R_0 < 1$ and $R_0 > 1$ respectively without entry of immigrants or new born individuals.(i.e. $A = 0$). In both figures, there is a significant decline of infected line represented by yellow colour due to pre and post quarantine process .The preparedness for reducing the infection by isolating the infectives does not spread the disease out of the quarantine classes. The recovered class denoted by green colour enhanced higher but does not tends to zero indicates the disease has extinct before the whole population get infection. In figure-1 the susceptible class does not tend to zero indicate the disease free equilibrium and the susceptible class in figure-2 approaches to zero level indicates the endemic equilibrium.

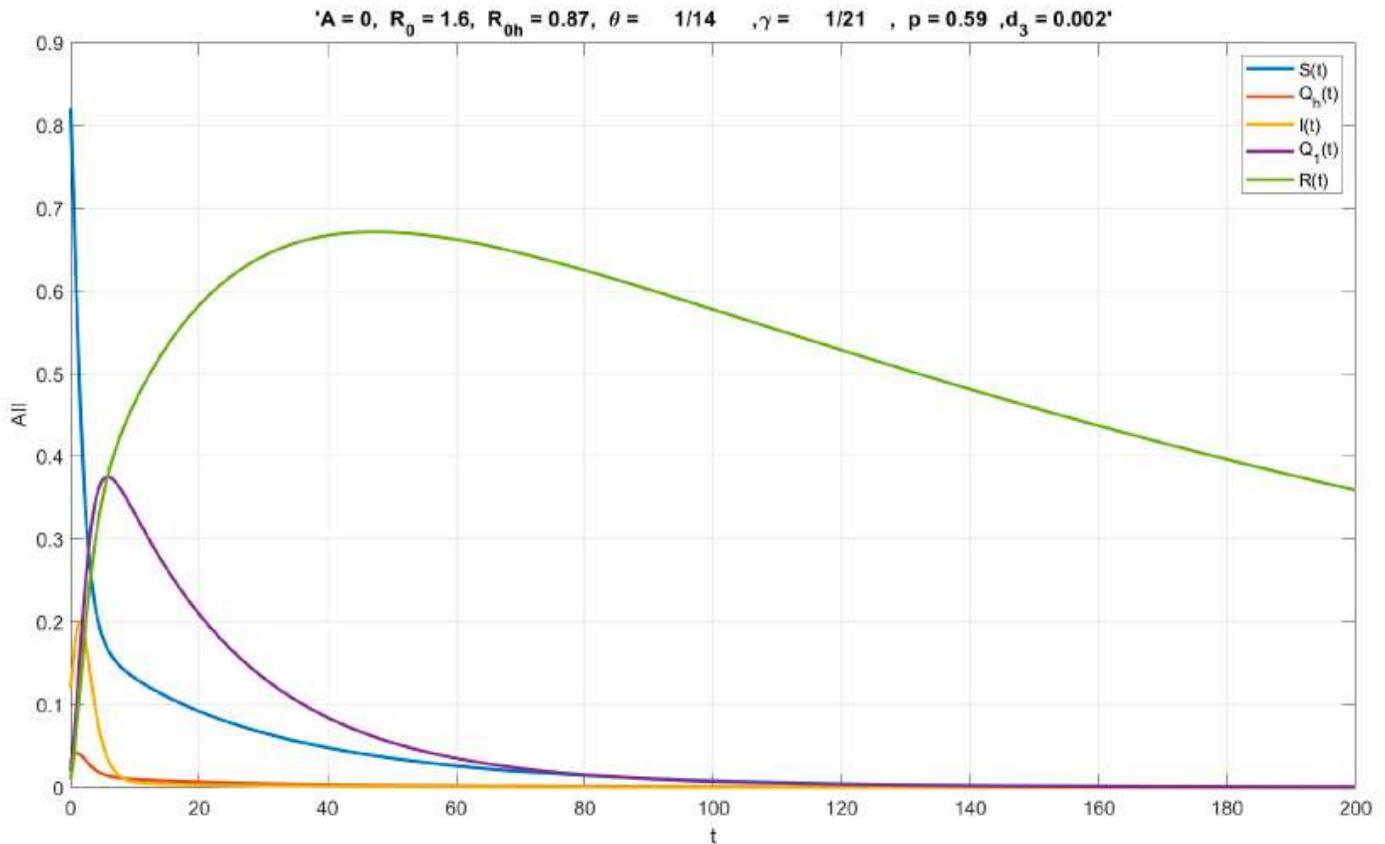


Figure 2

indicate the behaviour of all compartments with respect to time for $R_0 < 1$ and $R_0 > 1$ respectively without entry of immigrants or new born individuals.(i.e. $A = 0$). In both figures, there is a significant decline of infected line represented by yellow colour due to pre and post quarantine process .The preparedness for reducing the infection by isolating the infectives does not spread the disease out of the quarantine classes. The recovered class denoted by green colour enhanced higher but does not tends to zero indicates the disease has extinct before the whole population get infection. In figure-1 the susceptible class does not tend to zero indicate the disease free equilibrium and the susceptible class in figure-2 approaches to zero level indicates the endemic equilibrium.

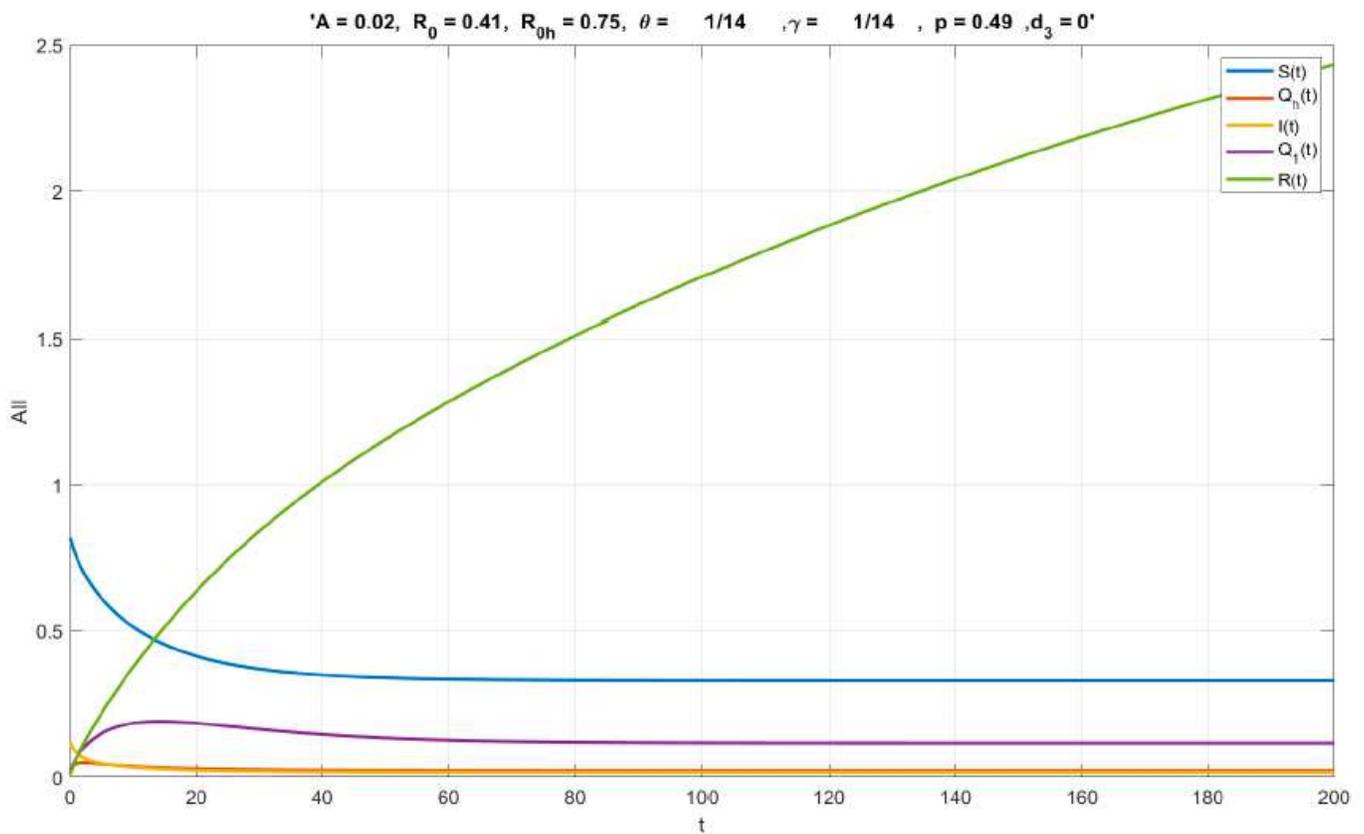


Figure 3

exhibits the interpretation of all compartments with influx of new born or immigrants.(i.e. $A = 0$) for both $R_0 < 1$ and $R_0 > 1$ respectively. Due to infection the susceptible class decline to some extent, but then reaches to the steady state after 20 days because of continuous influx in S .Infection approaches to zero level due to double quarantine effects. The recovery class is much higher than in figure-3 and figure-4 because of continuous entry of immigrants and newborns and the disease is stable for both $R_0 < 1$ and $R_0 > 1$

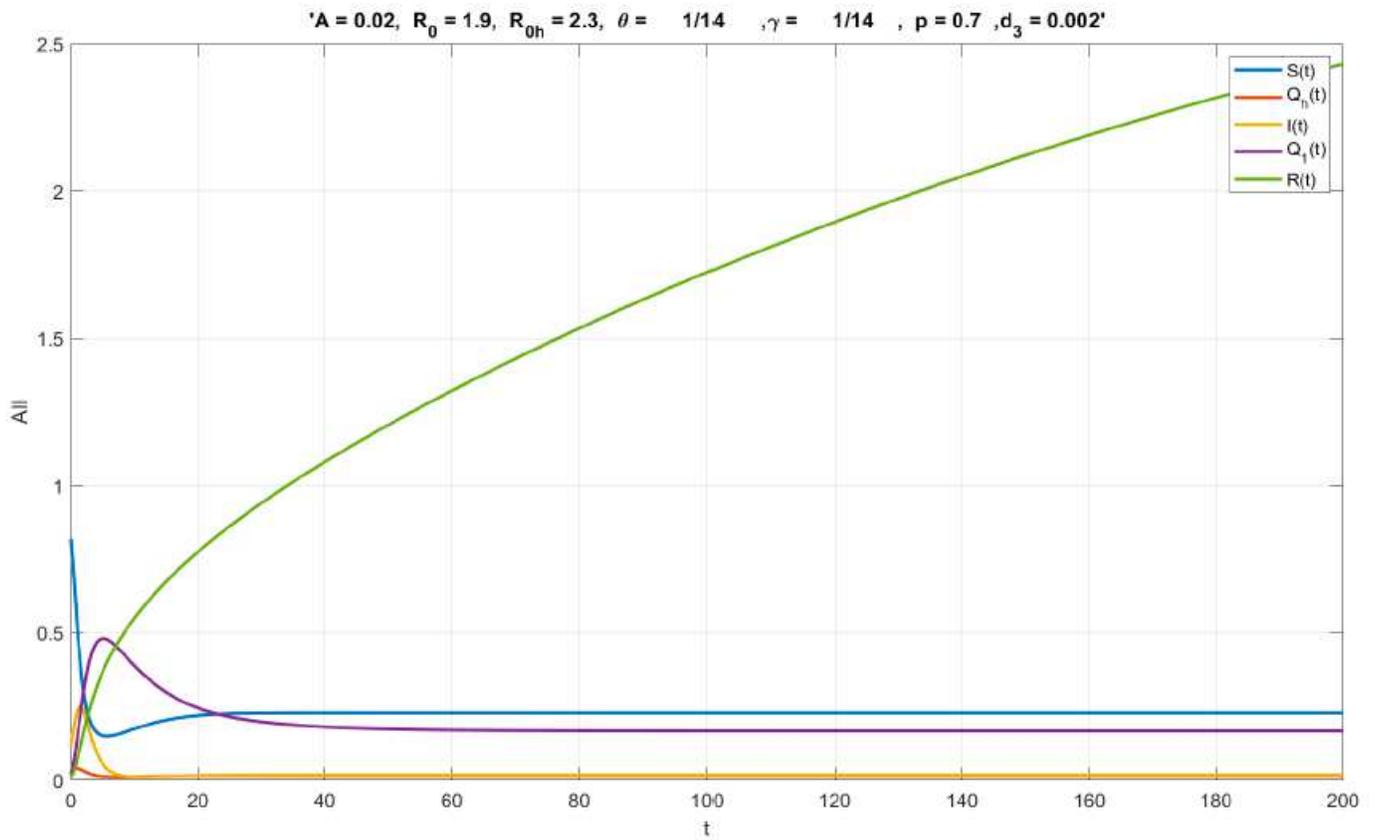


Figure 4

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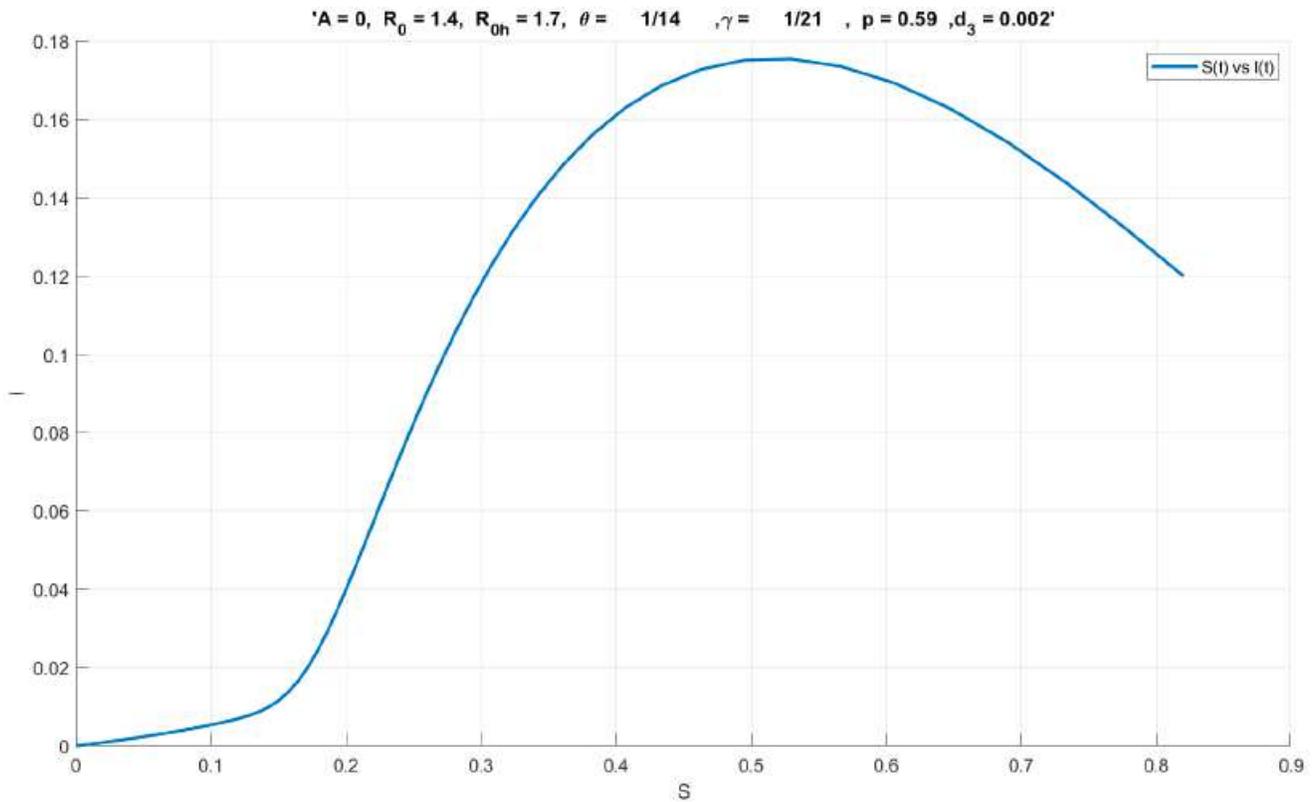


Figure 5

represent the phase portrait of S versus I graph for A = 0 and A ≠ 0 respectively. In both the figures, infection reaches to a peak when S increases but then start to decrease. This happens due to double quarantine effects and proper health care. This shows that the disease tends towards the recovery phase which leads the stability.

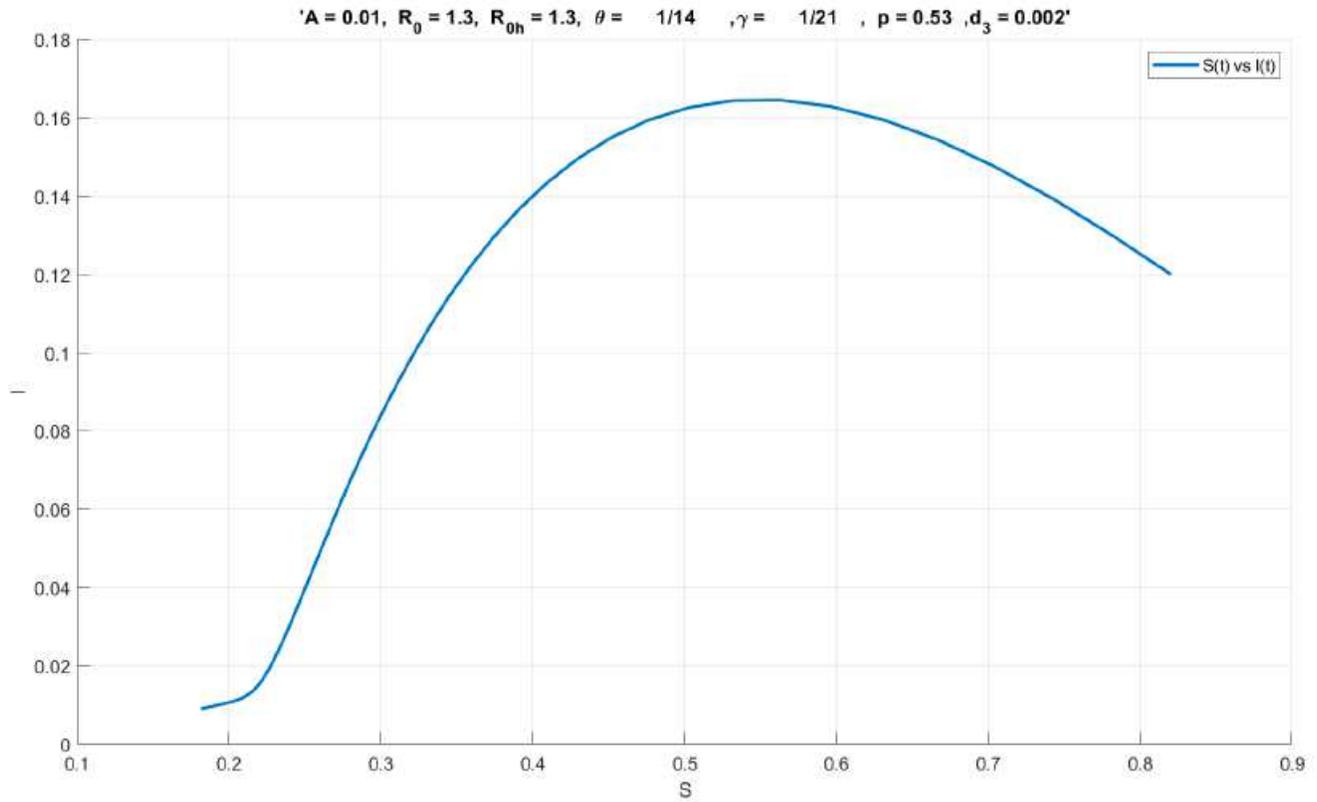


Figure 6

represent the phase portrait of S versus I graph for A = 0 and A = 0.01 respectively. In both the figures, infection reaches to a peak when S increases but then start to decrease. This happens due to double quarantine effects and proper health care. This shows that the disease tends towards the recovery phase which leads the stability.

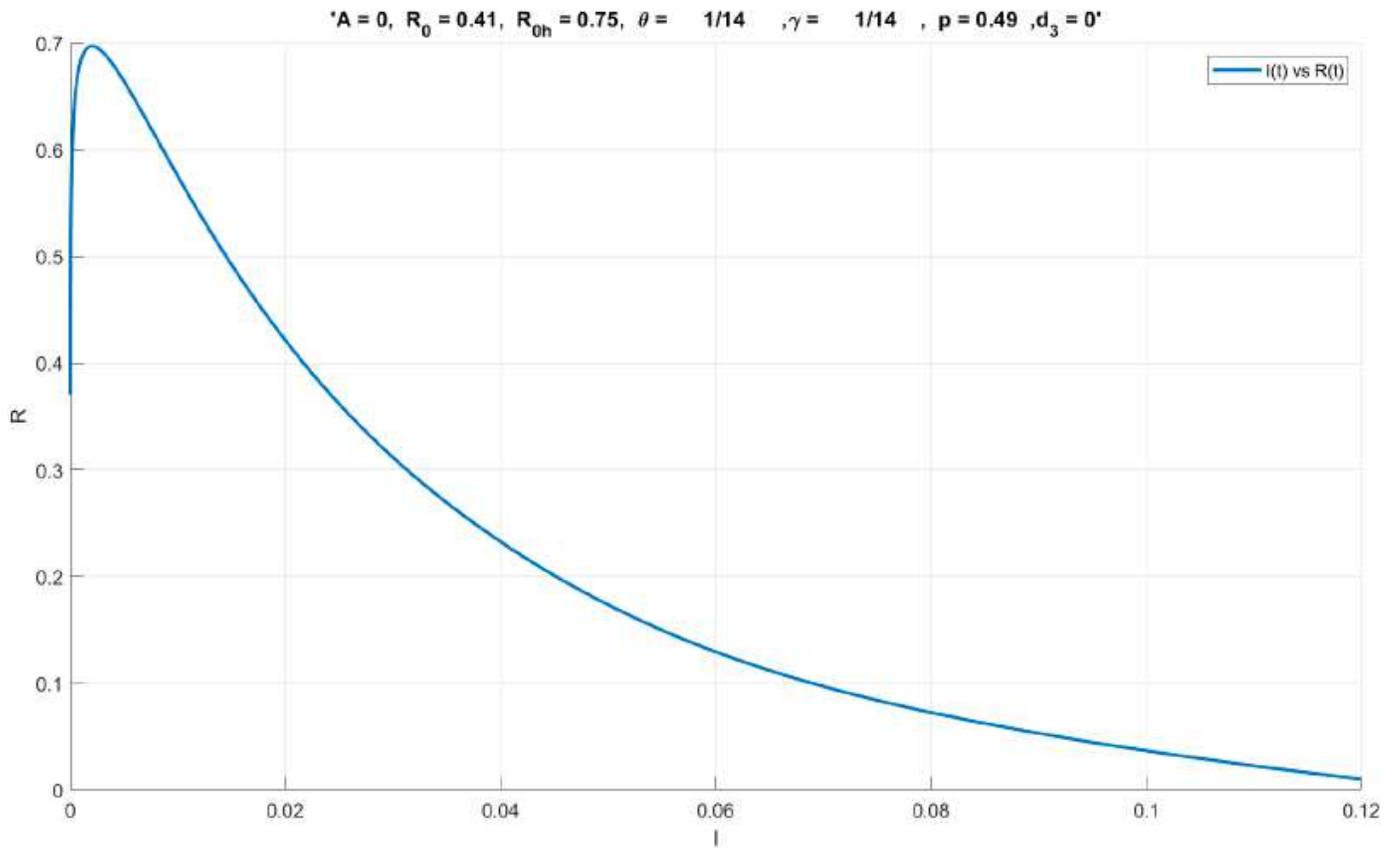


Figure 7

represent the phase portrait of I verses R, where the recovered population increase in the beginning because of susceptible class is pre-quarantined and containing some infective individuals those are post quarantined. But when the infectives increase more and more lead to an epidemic for long term then the recovery class would decrease that tends to zero leads to an endemic. Again the infected increase due to entry of immigrants and newborn as a result the recovered population decrease on increasing time in the absence of quarantine.

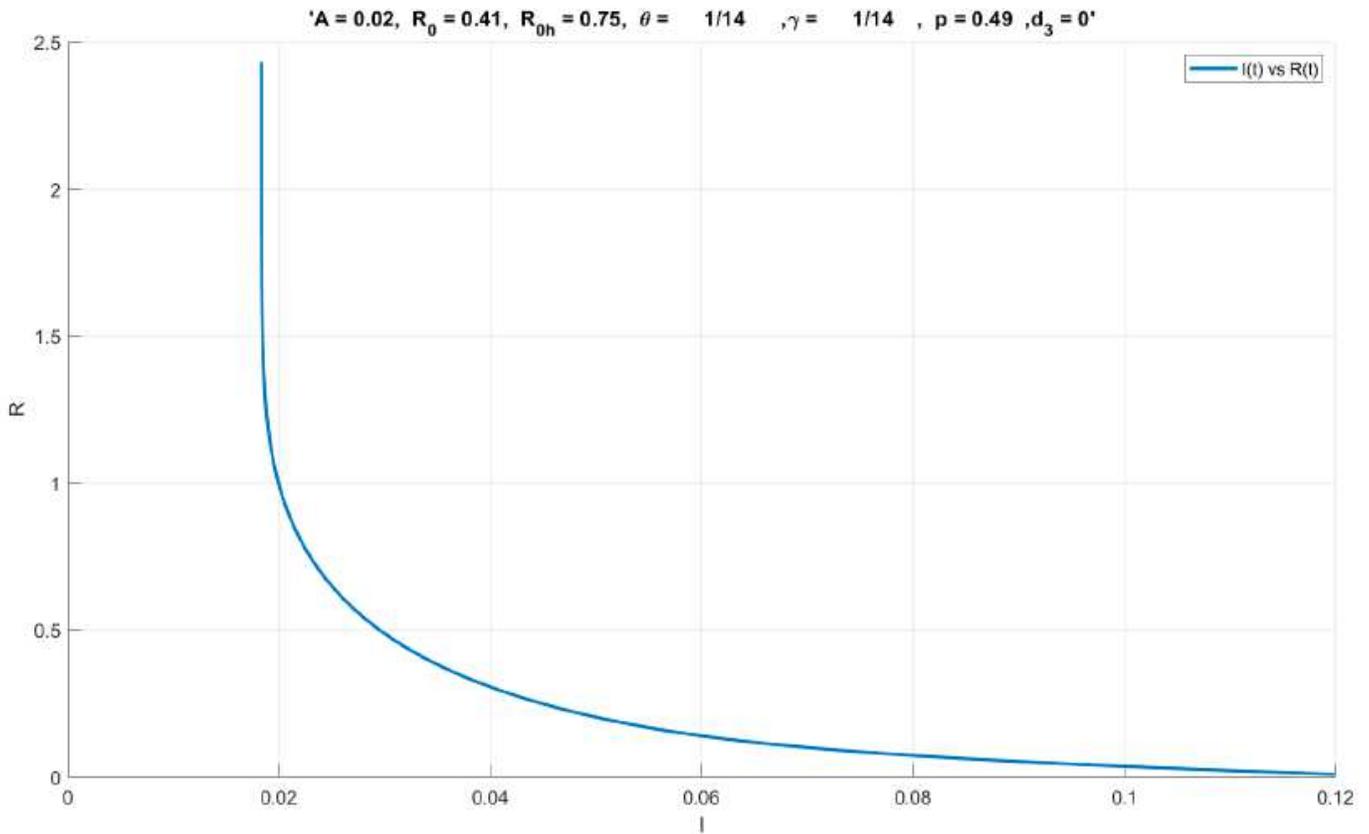


Figure 8

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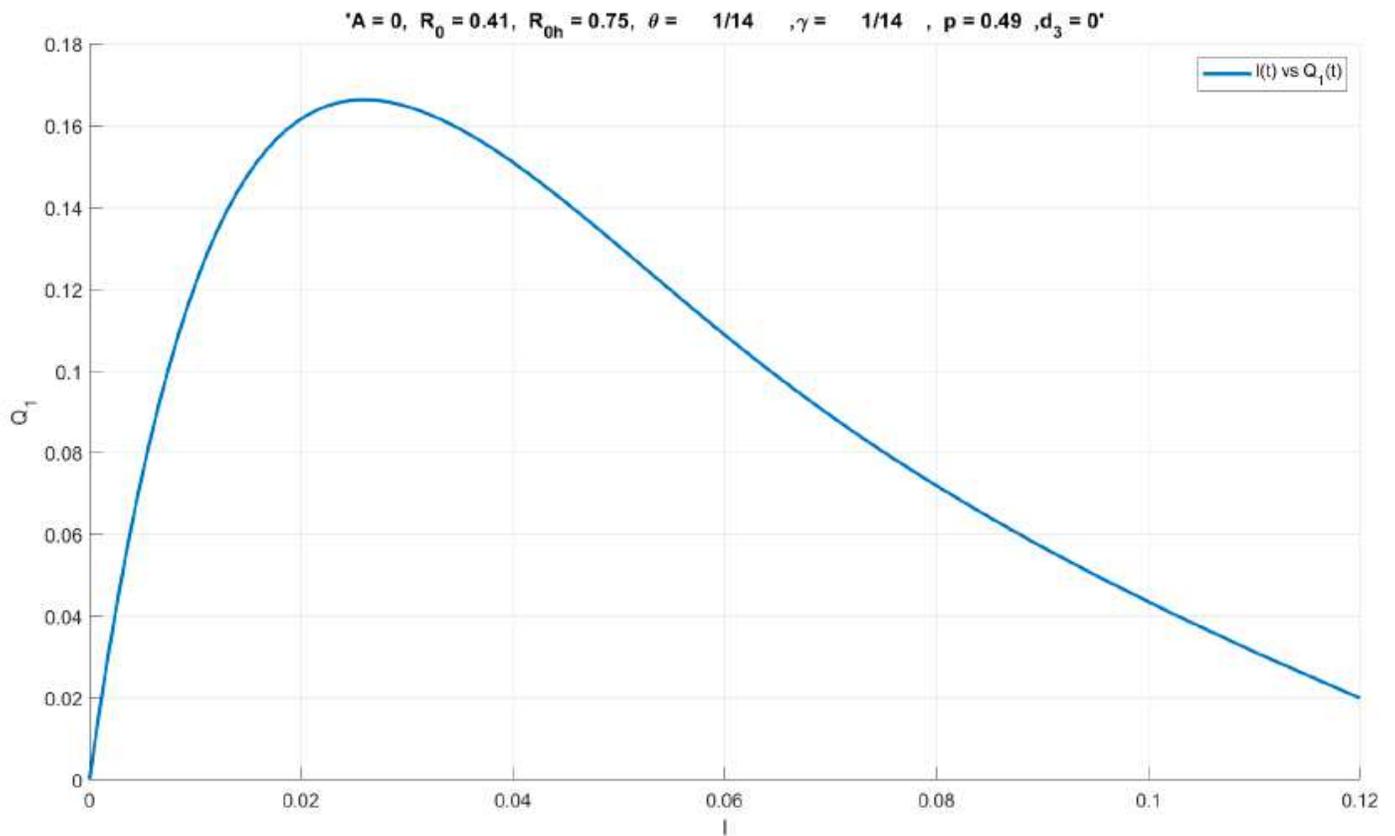


Figure 9

show the relationship of post quarantine class and the infective class for $A = 0$ and $A \neq 0$ respectively when $R_0 < 1$. The post quarantine class increase initially due to more and more infectives are reported and sent to quarantine compartment but then the rate of quarantine individuals decrease because of either maximum number of individuals are recovered or the disease die out.

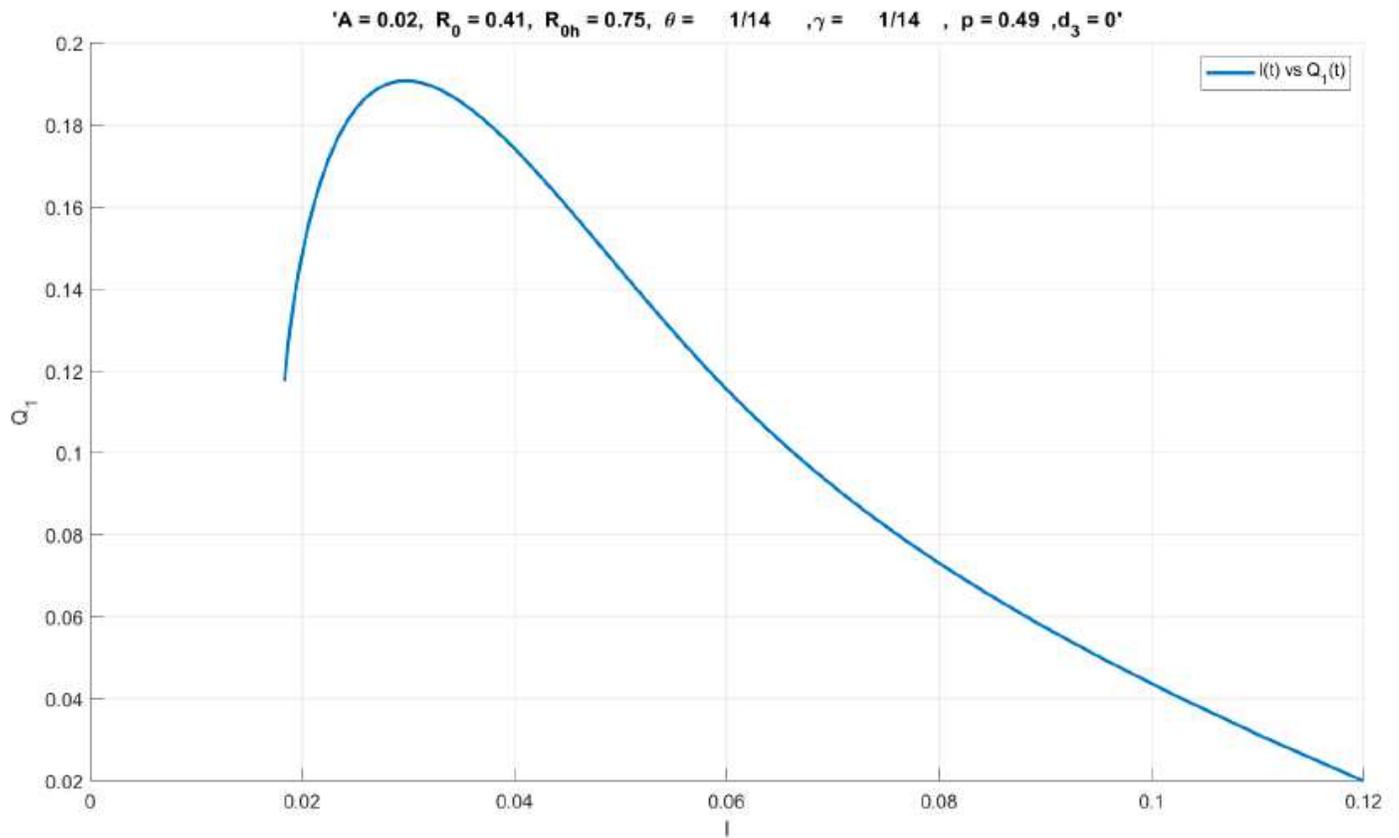


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