Mathematical Model on Impact of Quarantine to control the transmission of Corona Virus Disease 2019 (COVID-19)

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Abstract

The main objective of this research is to study the significant impact of Quarantine on the epidemic of COVID-19 through Mathematical modeling. Diverse cases of person to person transmission and its basic reproduction number has formulated to analyze the dynamics of coronavirus pandemic. Furthermore, the study also emphasizes the effect of quarantine to reduce the transmission, in the wake of lockdown in many countries. An informative graphical representation to notice quarantine versus reduction of infection also included using Matlab and Simulink programming

Keywords: *Coronavirus, Basic Reproduction Number, Quarantine, Lockdown, MATLAB Simulink programming*

1 Introduction:

It is true since eons "Curiosity is the mother of invention"; it inspired humans to discover new dimensions of technology to achieve everything in the world. Human activities create change in the ecosystem, wasting of natural resources, over-consumption of fuel, over shing, deforestation, hunting, etc. As a result, today the whole world is facing a crisis. The World Health Organization has announced the outbreak of a Severe Acute Respiratory Syndrome Corona Virus 2 (SARS-Cov-2) as a pandemic and declared it as the Public Health Emergency of International Concern on 30 January 2020 [1]. The novel coronavirus 2019 (COVID-19) has affected 210 countries and territories. Today worldwide, more than 4,662,109 positive cases and around 309,772 deaths are reported due to coronavirus [2]. However around 1,777,855 people are recovered from the disease [2]. The first case of coronavirus identified on December 31, 2019 in Wuhan city of China. The cases were not only remained in Wuhan City but to other cities of China and globally [3]. The person infected by the coronavirus has major symptoms including dry coughing, high fever with difficulties in breathing [10]. Earlier, it documented that appearance of the symptoms takes 2 to 10 days but recently there are many cases reported in which appearance of the symptoms takes more than 14 days [6] and this has caused the rapid spread of coronavirus in the world, which in turn creates a difficult situation to isolate infected individuals during their initial stage of the infection. The virus may spread in the environment through respiratory droplets of infected individuals which may transmit to healthy people. At the initial stage it becomes difficult to separate normal cough and cold symptoms from corona symptoms. Hence the infected individual becomes a host for the coronavirus and unknowingly spread the infection to other healthy individuals. During the outbreak of COVID-19, such human transmissions take place due to the unaware and the infected people moving in public places, traveling through trains and airplanes. The risk factor of contamination is very high since the virus can survive in the environment under favorable conditions for several days ([4], [9]). The majority of individuals with a high risk of getting infected through coronavirus are old-aged people, patients suffering from severe diseases, children, and persons having low immunity.

Still, there is no proper treatment or vaccine which can cure a person infected by COVID-19. Hence the spread of coronavirus has caused lockdown or curfews worldwide. This lockdown has restricted the mobility of humans which has eventually reduce the transmission rate of COVID-19. As a result, very few people come in contact with the infected individual so the number of people exposed will also reduce. There are a large number of isolation wards and special quarantine cells for isolating the infected individuals in most of the countries. Despite all this prevention, the whole world is in danger. The hazardous conditions are ongoing as the number of, new positive cases and deaths due to COVID-19 are increasing day by day. On observing the increased number of cases in a country in various regions of India and to stop transmission of COVID-19 in a country where the population is large and resources are limited, the Indian government decided to lock down the country.

Mathematical modelling plays a vital role in the study of many real-life applications and studies related to the behavior of infectious disease. Several studies have already undertaken to analyze COVID-19 transmission dynamics. Peng planned a generalized SEIR model that suitably incorporates the intrinsic impact of hidden, exposed, and infectious cases of COVID-19 [8]. Khan and Atangana described brief details of interaction among the bats, unknown hosts, humans, and the reservoir of the infection by formulating the mathematical results of the mathematical fractional model [5]. Zhao developed a SEIARW-model based on the market to individual and community transmission routes using specific age groups, susceptible to people from Wuhan City [11]. Zhong constructed a mathematical model using epidemiological data and analyzed characteristics of the historical epidemic to make an early prediction of the coronavirus outbreak in Mainland China [12].

2 Model formulation

In a country such as India, many peoples are working in many regions throughout the country and earn on a daily basis. Due to lockdown, many companies and private firms are closed and most of the people have started migrating back to their home town for support. The Indian government is giving support to all migrating people by providing food and shelter but people are continuously moving from one place to another. This is one of the reasons for the increase in coronavirus cases in India. Despite of all precautions and instructions there are many people are who are unaware of the risk of infection or avoiding the guidelines of government and become a host or super-spreaders of COVID-19 which also increase cases. The novel coronavirus is highly contagious and because of lockdown/shutdown, the number of cases has decreased which results in the reduction of transmission of the virus. The number of susceptible individuals reduced public considering taken voluntary home quarantine, Since Considering that the 2019-nCoV can be imported through many possible ways like a person frequently traveling to various cities of China or any product or consignment received from China under sustainable conditions for coronavirus and thus, without loss of generality, ignoring the interaction among all possible ways, the model formulated as follow:

Assuming that the population is under lockdown/shutdown condition and to analyze the human to human transmission dynamics of coronavirus, we constructed a compartmental model. The Transmission dynamics of COVID-19 described graphically in figure 1.
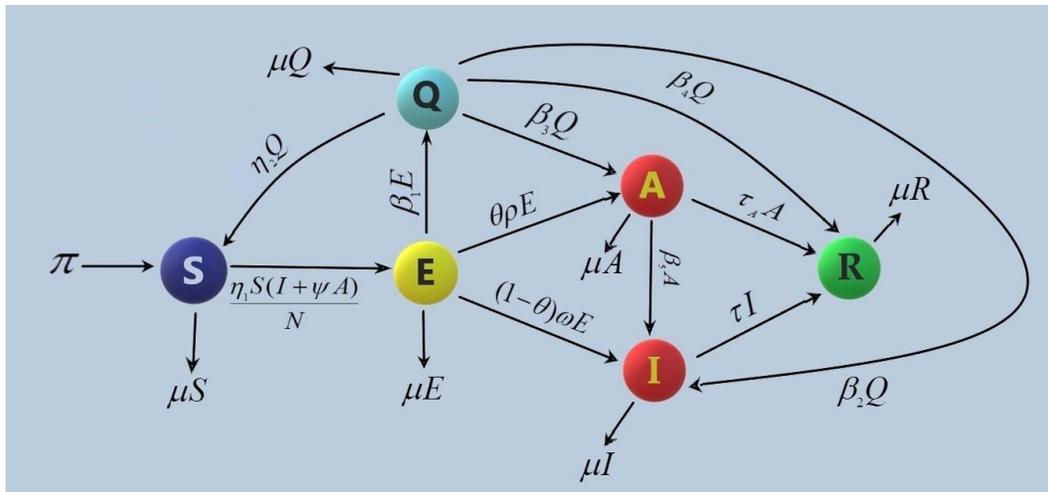
Figure 1 Transmission dynamics of COVID-19

The total population denoted by $N(t)$, which is classified further into six classes, the susceptible $S(t)$, the exposed $E(t)$, the quarantine $Q(t)$, the asymptomatic infected $A(t)$, the infected $I(t)$ and the recovered or the removed people $R(t)$.

The birth and natural death rate of an individual is denoted by π and μ respectively. The susceptible people S gets infected through sufficient contacts with the infected people I given by the term $\eta_1 SI$, where η_1 denotes the disease transmission coefficient. As discussed earlier, the symptoms of coronavirus do not reflect immediately which rise the number of asymptomatic infected people as well as can spread the virus to healthy people and the transmission is given by $\eta_1 \psi SA$, where ψ is the transmissibility multiple of A to I and $\psi = [0,1]$. When $\psi = 0$ then there will be no infection, and when $\psi = 1$, then the infection will be same as I. θ represents the proportion of asymptomatic infection. The parameters ω and ρ respectively represent the transmission rate after completing the incubation period and become infected, joining the class I and A. β_1 is the rate of exposed people taken self-quarantine or quarantine due to contact with the infected individual. In an emergency, some of the self-quarantine people from quarantine class Q need to go outside and becomes susceptible. η_2 is the rate at which quarantine individual Q transfer to susceptible class S. β_2 is the rate at which quarantine individuals become infected and join the infected class I. β_4 is the rate at which quarantine people join recovered or removal class R. β_5 is the transfer rate of the asymptomatic individual from class A becomes infected and joining class I. β_3 is the rate of people transfers from quarantine class Q to asymptomatic class A. τ is the removal or recovery rate at which symptomatic people from I joining the class R and τ_A is the removal or recovery rate at which asymptomatic people from A joining the class R.

The dynamical system of the COVID-19 model with quarantine effect is given by

$$\frac{dS}{dt} = \pi + \eta_2 Q - \frac{\eta_1 S(I + \psi A)}{N} - \mu S$$

$$\frac{dE}{dt} = \frac{\eta_1 S(I + \psi A)}{N} - (\beta_1 + \theta\rho + (1-\theta)\omega)E - \mu E$$

$$\frac{dQ}{dt} = \beta_1 E - (\eta_2 + \beta_2 + \beta_3 + \beta_4)Q - \mu Q \qquad \dots\dots(2.1)$$

$$\frac{dA}{dt} = \theta\rho E + \beta_3 Q - (\beta_5 + \lambda_A)A - \mu A$$

$$\frac{dI}{dt} = (1-\theta)\omega E + \beta_2 Q + \beta_5 A - \lambda I - \mu I$$

$$\frac{dR}{dt} = \lambda_A A + \lambda I + \beta_4 Q - \mu R$$

with the initial conditions

$$S(0) \geq 0, E(0) \geq 0, Q(0) \geq 0, A(0) \geq 0, I(0) \geq 0, R(0) \geq 0 \qquad \dots\dots(2.2)$$

The total dynamics of the people obtained by adding all six equations of the model (2.1) ,

$$\frac{dN}{dt} = \pi - \mu N$$

Let us consider a positive invariant feasible region such that the solution of the system

(2.1) are in this feasible region

$$\Omega = \left\{ (S, E, Q, A, I, R) \in \square^6_+ : S + E + Q + A + I + R = N \leq \frac{\pi}{\mu} \right\} \qquad \dots\dots(2.3)$$

where all the parameters of the model are non-negative.

3 Stability results

Let us define the disease free equilibrium E_0 and the basic reproduction number $\mathfrak{R}_0$ for the stability of model (2.1)

$$E_0 = (S_0, 0, 0, 0, 0, 0) = \left(\frac{\pi}{\mu}, 0, 0, 0, 0, 0 \right).$$

is the disease free equilibrium for the system (2.1).

To compute, the basic reproduction number for the given system (2.1) refer [5], where the required computation of the matrices F and V are given by,

$$F = \begin{pmatrix} 0 & 0 & \eta_1\psi & \eta_1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$V = \begin{pmatrix} \beta_1 + \theta\rho + (1-\theta)\omega + \mu & 0 & 0 & 0 \\ -\beta_1 & \eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu & 0 & 0 \\ -\theta\rho & -\beta_3 & \beta_5 + \lambda_A + \mu & 0 \\ (1-\theta)\omega & -\beta_2 & -\beta_5 & \lambda + \mu \end{pmatrix}$$

The basic reproduction number of the system (2.1), is given as

$$\Re_0 = \frac{\eta_1\psi(\lambda+\mu)(\theta\rho(\eta_2+\beta_2+\beta_3+\beta_4)+\beta_1\beta_3)+\eta_1\beta_5((\eta_2+\beta_2+\beta_3+\beta_4)(\theta\rho+(1-\theta)\omega)+\beta_1(\beta_2+\beta_3))}{(\lambda+\mu)(\beta_5+\lambda_A+\mu)(\beta_1+\theta\rho+(1-\theta)\omega+\mu)(\eta_2+\beta_2+\beta_3+\beta_4)}$$

where spectral radius is $\gamma(FV^{-1})$ Further, $\Re_0$ can be also represent as $\Re_0 = \Re_1 + \Re_2$, where

$$\Re_1 = \frac{\eta_1\psi(\lambda+\mu)(\theta\rho(\eta_2+\beta_2+\beta_3+\beta_4)+\beta_1\beta_3)}{(\lambda+\mu)(\beta_5+\lambda_A+\mu)(\beta_1+\theta\rho+(1-\theta)\omega+\mu)(\eta_2+\beta_2+\beta_3+\beta_4)}$$

and

$$\Re_2 = \frac{\eta_1\beta_5((\eta_2+\beta_2+\beta_3+\beta_4)(\theta\rho+(1-\theta)\omega)+\beta_1(\beta_2+\beta_3))}{(\lambda+\mu)(\beta_5+\lambda_A+\mu)(\beta_1+\theta\rho+(1-\theta)\omega+\mu)(\eta_2+\beta_2+\beta_3+\beta_4)}$$

Theorem 3.1 The disease free equilibrium E_0 for the model (2.1) is locally asymptotically stable if $\Re_0 < 1$.

Proof: To obtain disease free equilibrium at point E_0, the Jacobian matrix below,

$$J = \begin{pmatrix} -\mu & 0 & \eta_2 & -\eta_1\psi & -\eta_1 & 0 \\ 0 & -(\beta_1+\theta\rho+(1-\theta)\omega+\mu) & 0 & -\eta_1\psi & -\eta_1 & 0 \\ 0 & \beta_1 & -(\eta_2+\beta_2+\beta_3+\beta_4+\mu) & 0 & 0 & 0 \\ 0 & \theta\rho & \beta_3 & -(\beta_5+\lambda_A+\mu) & 0 & 0 \\ 0 & (1-\theta)\omega & \beta_2 & \beta_5 & -(\lambda+\mu) & 0 \\ 0 & 0 & \beta_4 & \lambda_A & \lambda & -\mu \end{pmatrix}$$

The two negative eigen values of the above Jacobian matrix are $-\mu$ (twice) and the remaining eigen values can be obtained by the characteristics equation below:

$$\lambda^4 + a_1\lambda^3 + a_2\lambda^2 + a_3\lambda + a_4 = 0$$

where

$$a_1 = \lambda + \lambda_A + \theta\rho + (1-\theta)\omega + \eta_2 + \beta_1 + \beta_2 + \beta_3 + \beta_4 + \beta_5 + 4\mu$$

$$a_2 = (\beta_1 + \theta\rho + (1-\theta)\omega + \mu)(\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu) + (\beta_5 + \lambda_A + \mu)(\beta_1 + \theta\rho + (1-\theta)\omega + \mu)$$
$$+ \eta_1\psi\theta\rho + (\lambda + \mu)(\beta_1 + \theta\rho + (1-\theta)\omega + \mu) + \eta_1(1-\theta)\omega + (\lambda + \mu)(\beta_5 + \lambda_A + \mu)$$
$$+ (\lambda + \mu)(\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu) + (\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu)(\beta_5 + \lambda_A + \mu)$$

$$a_3 = (\lambda + \mu)(\beta_1 + \theta\rho + (1-\theta)\omega + \mu)[(\lambda + \mu)(1-\Re_1) + (\lambda_A + \mu)(1-\Re_2)] + (\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu)$$
$$[(\beta_5 + \lambda_A + \mu) - \eta_1\psi\theta\rho] + (\beta_5 + \lambda_A + \mu)(\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu)(\beta_1 + \theta\rho + (1-\theta)\omega + \mu)$$

$$a_4 = (\beta_1 + \theta\rho + (1-\theta)\omega + \mu)(\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu)(\beta_5 + \lambda_A + \mu)(\lambda + \mu)(1-\Re_0)$$

equation, the first four terms in the coefficient a_2 are less than $\Re_0$ and the coefficient a_4 is positive when $\Re_0 < 1$, and thus all coefficients are positive. Moreover the above coefficients also satisfy the Rough-Hurtwiz criteria for the fourth order polynomial. Hence, the model (2.1) at the disease free equilibrium is locally asymptotically stable if $\Re_0 < 1$.

3.1. Endemic equilibria

The endemic equilibrium of the model (2.1) is denote by $E_0^* = (S^*, E^*, Q^*, A^*, I^*, R^*)$

where

$$S^* = \frac{\pi}{\lambda^* + \mu}, \quad E^* = \frac{\lambda^* S^*}{\beta_1 + \theta\rho + (1-\theta)\omega + \mu}, \quad Q^* = \frac{\beta_1 E^*}{\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu}$$

$$A^* = \frac{\theta\rho E^* + \beta_3 Q^*}{\beta_5 + \lambda_A + \mu}, \quad I^* = \frac{(1-\theta)\omega E^* + \beta_2 Q^* + \beta_5 A^*}{\lambda + \mu}, \quad R^* = \frac{\lambda_A A^* + \lambda I^*}{\mu}$$

and

$$\lambda^* = \frac{\eta_1(\psi A^* + I^*)}{S^* + E^* + Q^* + A^* + I^* + R^*}$$

which satisfies the equation $P(\lambda^*) = m_1(\lambda^*)^2 + m_2\lambda^* = 0$ and m_1 and m_2 are given by
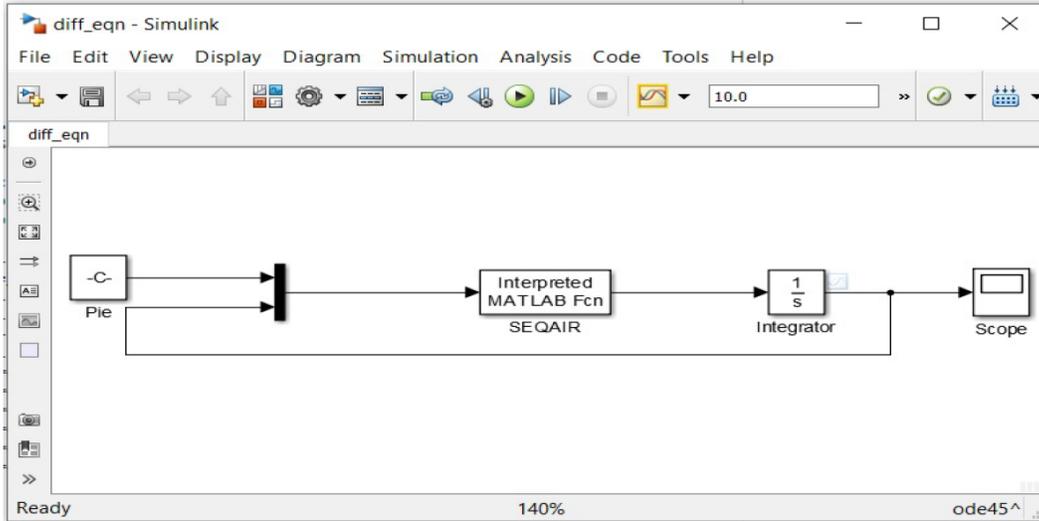
$$m_1 = (\beta_1 + \theta\rho + (1-\theta)\omega + \mu)(\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu)(\beta_5 + \lambda_A + \mu)(\lambda + \mu)$$

$$m_2 = (\beta_1 + \theta\rho + (1-\theta)\omega + \mu)(\eta_2 + \beta_2 + \beta_3 + \beta_4 + \mu)(\beta_5 + \lambda_A + \mu)(\lambda + \mu)(1-\Re_0).$$

Obviously, $m_1 \geq 0$ and $m_2 \geq 0$ whenever $\Re_0 < 1$, so that $\lambda^* = \frac{-m_2}{m_1} \leq 0$. When $\Re_0 < 1$, the endemic equilibrium does not exists.

4 4. Graphical Representation

In this section, the graphical and visual presentation of the model (2.1) given using MATLAB (R2015a) and Simulink. The block diagram for the model (2.1) is shown in the figure 2.

Figure 2 Block diagram for visual representation of a model (2.1)

The parametric values used for simulation given in the following table:

Table 1 Parameters used in the model (2.1) [2]

Parameters	Description	Value
π	Birth rate	0.0242
μ	Natural mortality rate	0.0325
η_1	Contact rate	0.5
β_1	Rate at which exposed individual transfer to quarantine class	0.0359
θ	The proportion of asymptomatic infection	0.023
ω	Rate at which exposed individual become infected	0.9606
ρ	Rate at which exposed individual become Asymptomatic infected	0.35
η_2	Rate at which quarantine individual become susceptible	0.37
β_2	Rate at which quarantine individual become infected	0.002
β_3	Rate at which quarantine individual become Asymptomatic infected	0.0002
β_4	Rate at which quarantine individual joining class R	0.3722
β_5	Rate at which Asymptomatic individual become infected	0.5312
λ	Removal or recovery rate of I	0.32829392
λ_A	Removal or recovery rate of A	0.02672

Figure 3 presents the variations in all the classes of the model (2.1) and also the pandemic behavior of the coronavirus concerning time overpopulation can be observed.
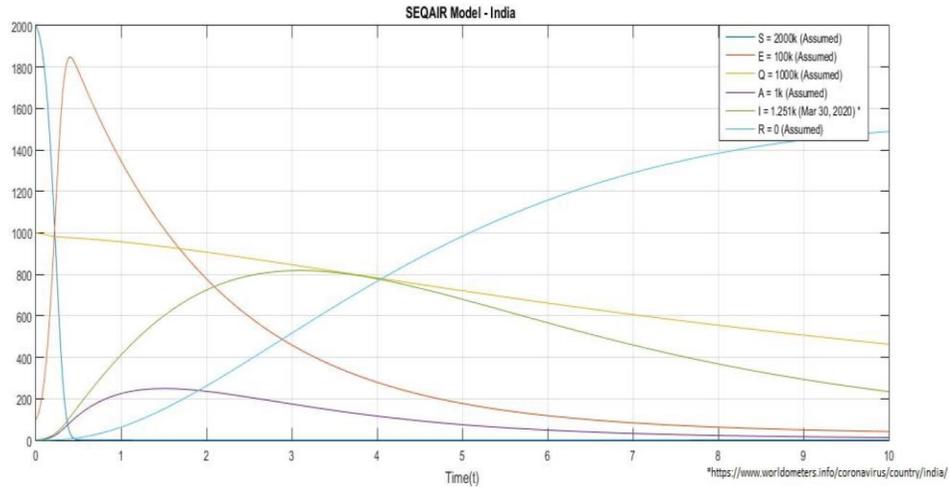
Figure 3 Remarkable variation in all classes with time
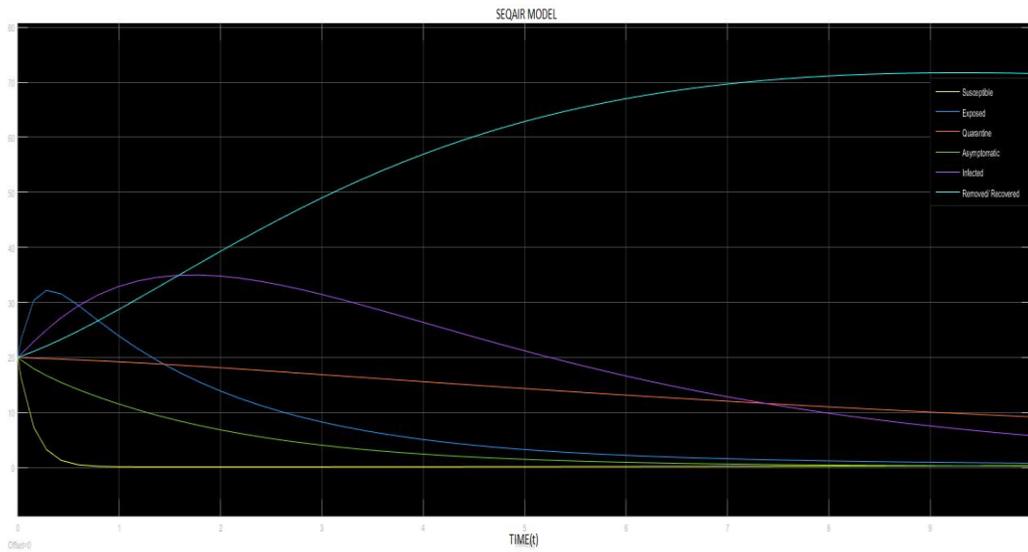
**Figure 4** Simulink output of model (2.1) over time(t)

In figure 4, outbreak behaviour of the pandemic is observed over time by simulation

of all classes with same initial conditions. This figure indicates the effective impact of lockdown by gradually decrease in the transmission of COVID-19 susceptible and exposed people. Implementation of quarantine helps to control infection diseases. So there is less possibility of rapid increase in the number of infected and asymptomatic cases.
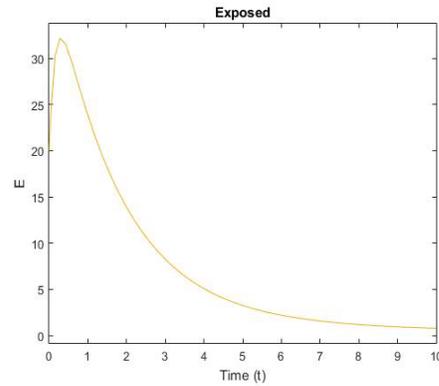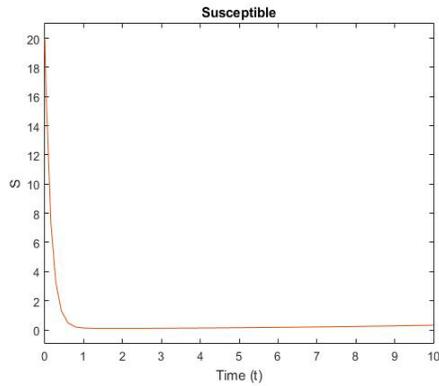
Figure 5: No. of Susceptible individual v/s time **Figure 6:** No. of Exposed individual v/s time

These graphs in figure 5 and figure 6 show the gradual reduction in number of susceptible and exposed people after imposition of lockdown.
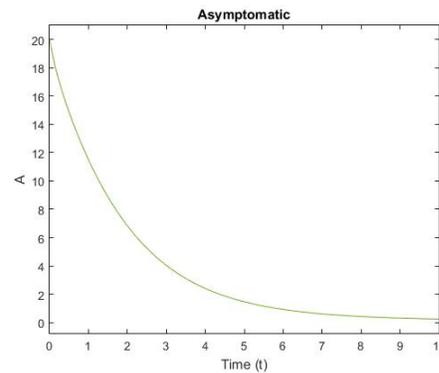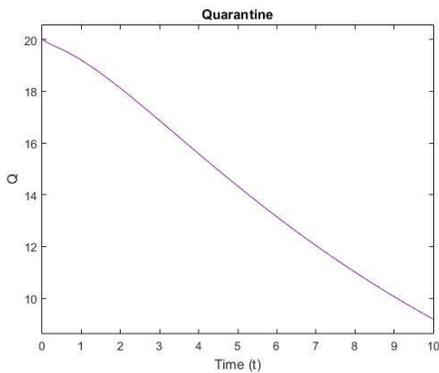
Figure 7: No. of Quarantine individual v/s time **Figure 8:** No. of Asymptomatic individual v/s time

From figures 7 and 8, it observed that due to less number of susceptible and exposed

individuals, the number of quarantine and asymptomatic people will also reduce day by day. But as we know, the asymptomatic individual will may become infected after completion of the incubation period which may also increase the number of the positive case of coronavirus.
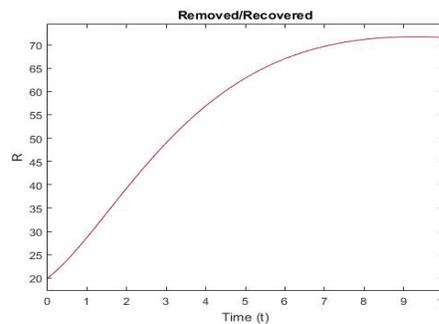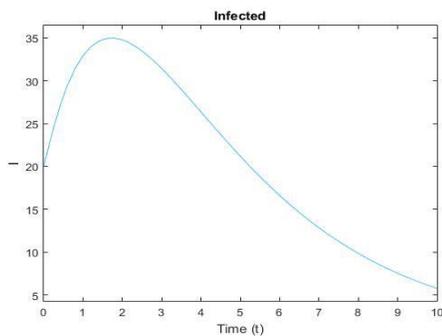
Figure 9: No. of Infected v/s time **Figure 10:** No. of Removed or recovered v/s time

During the outbreak of the pandemic, the growth in the number of infected people observed. Figure 9 indicates the effect of lockdown/shutdown or quarantine on the number of infected people. Figure 10 reflects high removal rate in comparison to recovered rate due to lack of proper treatment or vaccination.

5 Conclusion

The studies of dynamics of novel coronavirus conclude that lockdown/shutdown or self-quarantine can play a role in controlling the transmission of coronavirus. The mathematical model and stability results of the coronavirus is locally asymptomatically stable if $\Re_0 < 1$.

Remark: The investigation of this paper is restricted for the lockdown/shutdown or self-isolate duration. The consequence of this paper may differ upon the span and state of lockdown/shutdown and isolate.

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