

# Efficacy of vaccine and face mask in a COVID-19 enlarged SEIAQR model

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## ABSTRACT

As a result of its rapid spread throughout the world on a huge scale in a very short period of time, the current COVID-19 infection has triggered a global emergency scenario. Vaccination and antiviral medicine are not available, however, for this particular virus. The question of how to control this pandemic is currently a major global concern at the present time. India, on the other hand, is a country with a high population density, and the COVID-19 infection sickness has been active from the first day of March 2020. The rate of human to human social contact in India is extremely high as a result of the country's dense population. As a result, controlling the COVID-19 pandemic at an early stage is a very critical and difficult matter for India. Mathematical models are used to investigate the dynamics of the disease, identify the characteristics that are important, and determine the most effective prevention techniques for reducing the magnitude of outbreaks. In this study, we present an improved SEIAQR mathematical model and conduct an analysis of it in order to better understand the transmission dynamics of the COVID-19 pandemic outbreak in India. It is subdivided into nine compartmental classifications, which are as follows: susceptible (S), exposed (E), symptomatically infected (I), asymptomatically infected (A), quarantined (Q), recovered (R), hospitalized (H), died (D), and vaccinated (V). The fundamental reproduction number of the suggested model, designated as  $R$  (COVID-19), was computed using the next-generation matrix technique, which was developed by the researchers. Face masks and vaccines have also been proved to be effective in reducing viral transmission, which has been demonstrated to be substantial. In addition, using MATLAB-7.0, certain effective preventive actions and their influence on the environment were investigated numerically and graphically.

**Keywords:** Basic Reproduction Number, Efficacy of Face masks and Vaccination, Isolation Rate, Hospitalization Rate, COVID-19

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**1. Introduction-** It is feasible to utilize numerical models to foresee whether a disease will spread or continue without some kind of restraint whenever it has entered a populace. There is a great deal riding on COVID-19 right now due to how rapidly the contamination spread and the number of individuals passed on because of it. A recently distinguished Covid caused a flare-up of an irresistible illness in Wuhan, China in December of 2019. Contaminated individuals spread the COVID-19 infection by hacking, sniffing, or breathing out beads that contain the infection. They can't linger palpably in light of the fact that they're so weighty, so they land on the ground soon. Almost 4 million individuals in 187 nations have been tainted with the Covid, and 295,000 have kicked the bucket thus.

In an elective review, Mishra (2020) took a gander at a model addressing the dispersion of Coronavirus in people. To produce different results, she explored different avenues regarding an assortment of differential and necessary administrators. A bunch of differential conditions was utilized to mimic the progression of people through compartments in the SEIR model made by

Chatterjee et al. (2020). They utilized MATLAB and SimVoi programming to mimic 1000 Monte Carlo recreations of different situations, including hospitalization, ICU prerequisites, and demise. As per Zhang (2020), there is another numerical model that portrays the probability of spreading inside a particular all inclusive community. The model is comprised of five unique classifications: powerless, uncovered, tainted, recuperated, and dead. The helpless classification incorporates the people who have been presented to the illness. Alkahtani and Alzaid (2020) portrayed numerical model the spread of the Coronavirus plague and the execution of populace Coronavirus mediation in Italy. The model comprises of eight sections and produces an eight-condition arrangement of customary differential conditions. Altogether, there are 8 differentiable parts in the model, bringing about a 8-condition framework. The transmission elements of COVID-19 were concentrated by Samui et al. (2020) utilizing a SAIU compartmental numerical model. To find the best considers connection to the principal generation number  $R_0$ , they played out a responsiveness examination. An investigation by Tuan et al. (2020) showed the spread of COVID-19 was

mathematically reenacted and the multiplication number was viewed as  $R_0 = 1:610007996$ , it is as yet continuous to demonstrate the scourge.

To additional position the worth, Padmanabhan et al. (2021) audited existing papers on numerical demonstrating of COVID-19. Their general model and the boundaries impacted by various mediations are featured. There was likewise conversation of the utilization of control-hypothetical ways to deal with infer dynamic mediation conventions for relieving COVID-19 basic appraisals and evaluations in light of such models. The transmission examples of Coronavirus were depicted by Okposo et al. (2021) utilizing an electronic numerical model that included asymptomatic, indicative, and confined people. An epidemiological information assortment in the United Kingdom was fitted to the numerical model utilized by Moore et al. (2021). This model incorporated the arranged sending of a two-portion immunization program (dosages 12 weeks separated, security beginning 14 days after inoculation). They began with an immunization take-up presumption of 95% in those 80 years and more established, 85% in those 50-79 years, and 75% in those 18-49 years, and afterward shifted immunization take-up hopefully and critically founded on these suppositions. In the easiest terms, Sithiwirattham et al. illustrated the viral sickness and examined the essential properties associated with the idea of bends in vulnerable and tainted people. They've exhibited fundamental mathematical ideas with true models from India and

Algeria. By 20 Dec 2021, Kumar et al. (2021) examined Covid-19 diseases and proposed a numerical methodology for projecting new cases or total occurrences in genuine settings. This guess is imperative to plan and proceed with clinical arrangements on the off chance that move is made to battle the Covid-19 pestilence. Another Corona Virus Disease (COVID-19) that showed up in Wuhan, China in December 2019 was explored by Bhadauria et al. (2021). As per their discoveries, affliction must be destroyed from the populace on the off chance that the whole framework is placed on lockdown. Be that as it may, in the event that lockdown is to some degree carried out, illness can be monitored by utilizing contact following and quarantine techniques notwithstanding lockdown.

## 2. Mathematical Model:

To emulate the pestilence of COVID 19, we grow the SEIR model to incorporate nine compartments. There are nine state factors thought about inside a populace:  $S(t), E(t), I(t), A(t), Q(t), R(t), H(t), D(t), V(t)$  which address the vulnerable, uncovered, apparently contaminated, asymptotically tainted, isolated, recuperated, hospitalized, passed on, and immunized individually. Figure 1 portrays a schematic portrayal of the illness transmission stream in the proposed worldview. The model is then determined by a bunch of nonlinear common differential conditions, which incorporates the accompanying:

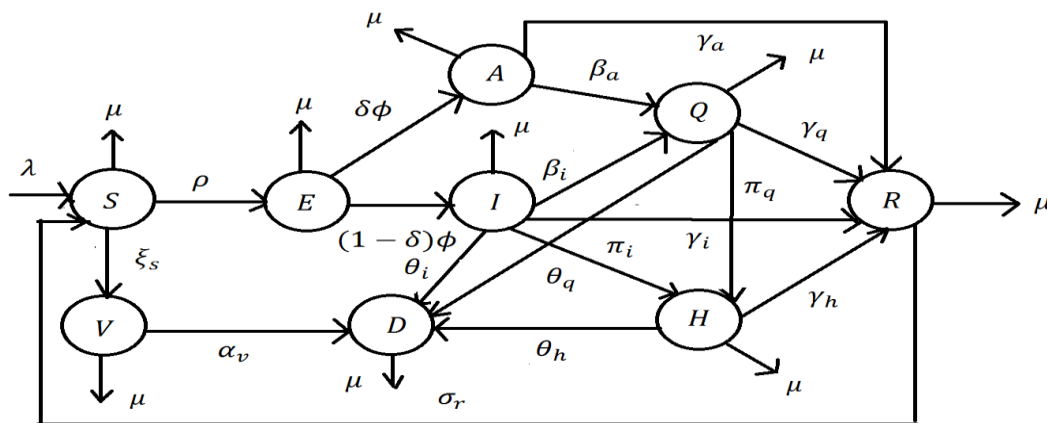


Figure-1: schematic representation of the disease transmission flow

$$\frac{dS}{dt} = \lambda + \sigma_r R - (\rho + \mu + \xi_s)S \quad (1)$$

$$\frac{dE}{dt} = \rho S - (\phi + \mu)E \quad (2)$$

$$\frac{dI}{dt} = (1 - \delta)\phi E - (\mu + \beta_i + \pi_i + \theta_i + \gamma_i)I \quad (3)$$

$$\frac{dA}{dt} = \delta\phi E - (\mu + \gamma_a + \beta_a)A \quad (4)$$

$$\frac{dQ}{dt} = \beta_a A + \beta_i I - (\mu + \gamma_q + \pi_q + \theta_q)Q \quad (5)$$

$$\frac{dR}{dt} = \gamma_a A + \gamma_q Q + \gamma_i I + \gamma_h H - (\mu + \sigma_r)R \quad (6)$$

$$\frac{dH}{dt} = \pi_i I + \pi_q Q - (\mu + \theta_h + \gamma_h)H \quad (7)$$

$$\frac{dD}{dt} = \theta_i I + \theta_q Q + \theta_h H + \alpha_v V - \mu D \quad (8)$$

$$\frac{dV}{dt} = \xi_s S - (\alpha_v + \mu)V \quad (9)$$

Where

$\rho = \omega_i(1 - \psi\kappa - v\epsilon)I + \omega_a(1 - \psi\kappa - v\epsilon)A$ , where

$\lambda$ : Recruitment rate in susceptible compartment

$\mu$ : Natural Death

$1 - \delta$ : After-incubation clinical symptom frequency of exposed persons

$\phi$ : The rate at which the infectious compartment progresses from being exposed

$\beta_a$ : Isolation rates for infected individuals who have no symptoms

$\beta_i$ : In the symptomatically infected compartment, the isolation rate for individuals

$\gamma_a$ : Rates of recovery from infected individuals who are asymptomatic

$\gamma_q$ : Recovery rate of persons in quarantine

$\gamma_i$ : Recovery rates from symptomatic

$\gamma_h$ : Recovery rates from hospitalized infected populations

$\xi_s$ : Vaccination Rate of Susceptible compartment

$\theta_i$ : The COVID-19 disease mortality rate for infected persons

$\theta_h$ : The COVID-19 disease mortality rate for hospitalized patients

$\theta_q$ : The COVID-19 disease death rate for those in quarantine

$\alpha_v$ : Vaccinated compartment COVID-19 illness mortality rate

$\sigma_r$ : Re-entry rate into sensitive compartments of recovered population

$v$ : The proportion of individuals who are vaccinated

$\epsilon$ : Efficacy of Vaccine

$\psi$ : Proportion of people who wear a face mask

$\kappa$ : Face masks' efficacy

$\omega_i$ : The rate of effective contact

$\omega_a$ : Social distance's effectiveness

$\pi_i$ : Rates of hospitalization from symptomatic infected populations

$\pi_q$ : Rates of hospitalization from quarantined infected populations

### 3. Positivity of the Solution:

Adding all of the equations (1-9) together and applying the relationship

$N = S + E + I + A + Q + R + H + D + V$ , we have what we need

$$\frac{dN}{dt} = \lambda - \mu(S + E + I + A + Q + R + H + D + V)$$

$$\Rightarrow \frac{dN}{dt} = \lambda - \mu N$$

$$\Rightarrow \frac{dN}{dt} = \lambda - \mu N - \eta(I + A + Q + H + V)$$

$$\Rightarrow \frac{dN}{dt} = \lambda - \mu N \Rightarrow \frac{dN}{dt} + \mu N = \lambda \Rightarrow N(t) = N(0)e^{-\mu t} + \frac{\lambda}{\mu}(1 - e^{-\mu t}) \quad (10)$$

Therefore it is obvious  $N(t) \leq \frac{\lambda}{\mu}$  if  $N(0) \leq \frac{\lambda}{\mu}$

It is possible to construct a positively invariant set under the flow provided in the COVID-19 model by combining the elements  $\Lambda = \{(S, E, I, A, Q, R, H, D, V) \in \mathbb{R}_+^9 : N(t) \leq \frac{\lambda}{\mu}\}$  and  $9:N(t)$ . To make matters more complicated, if  $N(0) \leq \frac{\lambda}{\mu}$ , then  $N(t)$  will approach  $\frac{\lambda}{\mu}$  once more as  $t$  increases and the number of infected individuals  $E, I, A, Q, H$  in the population will drop to zero at that point. As a result, all solutions in  $\mathbb{R}_+^9$  of the model eventually come into  $\Lambda$ , indicating that it is an attractive set. The COVID-19 model is thus well-posed biologically and mathematically in the invariant set, as demonstrated by the results of the simulations.

### 4. Equilibrium Points of the Model:

Zeroing the right-hand side of all equations in model (1-9) yields the equilibrium points in model (1-9), which are as follows:

$$\lambda + \sigma_r R - (\rho + \mu + \xi_s)S = 0 \quad (11)$$

$$\rho S - (\phi + \mu)E = 0 \quad (12)$$

$$(1 - \delta)\phi E - (\mu + \beta_i + \pi_i + \theta_i + \gamma_i)I = 0 \quad (13)$$

$$\delta\phi E - (\mu + \gamma_a + \beta_a)A = 0 \quad (14)$$

$$\beta_a A + \beta_i I - (\mu + \gamma_q + \pi_q + \theta_q)Q = 0 \quad (15)$$

$$\gamma_a A + \gamma_q Q + \gamma_i I + \gamma_h H - (\mu + \sigma_r)R = 0 \quad (16)$$

$$\pi_i I + \pi_q Q - (\mu + \theta_h + \gamma_h)H = 0 \quad (17)$$

$$\theta_i I + \theta_q Q + \theta_h H + \alpha_v V - \mu D = 0 \quad (18)$$

$$\xi_s S - (\alpha_v + \mu)V = 0 \quad (19)$$

There are numerous solutions to Equation (11-19) that can be obtained by simplifying it. For the purposes of this study, however, we will look at two different solutions: the disease-free equilibrium point (DFEP) and the endemic equilibrium point (EEP). In this paper, the DFEP is denoted by the letters

$$\Theta_{dfep}^* = \{S_{dfep}^*, E_{dfep}^*, I_{dfep}^*, A_{dfep}^*, Q_{dfep}^*, R_{dfep}^*, H_{dfep}^*, D_{dfep}^*, V_{dfep}^*\}, \text{ where}$$

$$S_{dfep}^* = \frac{\lambda}{\mu}, E_{dfep}^* = 0, I_{dfep}^* = 0, A_{dfep}^* = 0, Q_{dfep}^* = 0, R_{dfep}^* = 0, H_{dfep}^* = 0, D_{dfep}^* = 0, V_{dfep}^* = 0$$

Furthermore, the EEP is denoted by

$$\Theta_{eep}^* = \{S_{eep}^*, E_{eep}^*, I_{eep}^*, A_{eep}^*, Q_{eep}^*, R_{eep}^*, H_{eep}^*, D_{eep}^*, V_{eep}^*\}, \text{ where}$$

$$S_{eep}^* = \frac{\lambda + \sigma_r R}{\rho + \mu + \xi_s}, E_{eep}^* = \frac{\rho S}{\phi + \mu}, I_{eep}^* = \frac{(1-\delta)\phi E}{\mu + \beta_i + \pi_i + \theta_i + \gamma_i}, A_{eep}^* = \frac{\delta\phi E}{\mu + \gamma_a + \beta_a}, Q_{eep}^* = \frac{\beta_a A + \beta_i I}{\mu + \gamma_q + \pi_q + \theta_q}$$

$$R_{eep}^* = \frac{\gamma_a A + \gamma_q Q + \gamma_i I + \gamma_h H}{\mu + \sigma_r}, H_{eep}^* = \frac{\pi_i I + \pi_q Q}{\mu + \theta_h + \gamma_h}, D_{dfep}^* = \frac{\theta_i I + \theta_q Q + \theta_h H + \alpha_v V}{\mu}, V_{eep}^* = \frac{\xi_s S}{\alpha_v + \mu}$$

**5. Basic Reproduction Number:** It is vital to note that the fundamental reproduction number is important in both controlling and spreading the disease. Essentially, the number of secondary infections, or the number of new infections distributed by a single sick person, is defined as follows: It can only be obtained easily analytically if the system is in a state of disease-free equilibrium, which is rare.

Due to the fact that  $R_0 < 1$ , the average number of secondary infections over the infection period is fewer than one, and as a result, the disease is relatively simple to control. However, the number of secondary infections among those infected with COVID-19 is fluctuating from time to time.

According to the equation (1-9), the disease-free equilibrium point is  $E_0 \left( \frac{\lambda}{\mu}, 0, 0, 0, 0, 0, 0, 0 \right)$ .

There is a fundamental reproduction number for the suggested problem for the system (1-9) since the disease-free equilibrium point is  $E_0 \left( \frac{\lambda}{\mu}, 0, 0, 0, 0, 0, 0, 0 \right)$ .

To begin, we will break down the right side of the system (1) into the infected compartments E, I, A, Q, H as  $-V$ , where

$$\mathcal{F} = \begin{bmatrix} \omega_i S(1 - \psi\kappa - v\epsilon)I + \omega_a S(1 - \psi\kappa - v\epsilon)A \\ 0 \\ 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} (\phi + \mu)E \\ -(1 - \delta)\phi E + (\mu + \beta_i + \pi_i + \theta_i + \gamma_i)I \\ -\delta\phi E + (\mu + \gamma_a + \beta_a)A \end{bmatrix}$$

$$\mathcal{F} = \begin{bmatrix} 0 & \omega_i S(1 - \psi\kappa - v\epsilon) & \omega_a S(1 - \psi\kappa - v\epsilon) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$\mathcal{V} = \begin{bmatrix} (\phi + \mu) & 0 & 0 \\ -(1 - \delta)\phi & (\mu + \beta_i + \pi_i + \theta_i + \gamma_i) & 0 \\ -\delta\phi & 0 & (\mu + \gamma_a + \beta_a) \end{bmatrix}$$

$$F = \begin{bmatrix} 0 & \omega_i S_{dfep}^* (1 - \psi\kappa - v\epsilon) & \omega_a S_{dfep}^* (1 - \psi\kappa - v\epsilon) \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} (\phi + \mu) & 0 & 0 \\ -(1 - \delta)\phi & (\mu + \beta_i + \pi_i + \theta_i + \gamma_i) & 0 \\ -\delta\phi & 0 & (\mu + \gamma_a + \beta_a) \end{bmatrix}$$

$$R_{covid19} = \rho(FV^{-1}) = \frac{\phi S_{dfep}^*}{(\phi + \mu)} \left[ \frac{\omega_i (1 - \psi\kappa - v\epsilon)(1 - \delta)}{(\mu + \beta_i + \pi_i + \theta_i + \gamma_i)} + \frac{\delta \omega_a (1 - \psi\kappa - v\epsilon)}{(\mu + \gamma_a + \beta_a)} \right]$$

$$= \frac{\phi S_{dfep}^* \omega_i (1 - \psi\kappa - v\epsilon)(1 - \delta)}{(\phi + \mu)(\mu + \beta_i + \pi_i + \theta_i + \gamma_i)} + \frac{\phi S_{dfep}^* \delta \omega_a (1 - \psi\kappa - v\epsilon)}{(\phi + \mu)(\mu + \gamma_a + \beta_a)} \quad (20)$$

= The number of new COVID-19 cases that have been generated from infected humans in compartment  $I$  + reproduced. The number of new COVID-19 instances that have been reproduced in compartment A from infected persons that have no symptoms

$$= R_I + R_A$$

## 6. Numerical Results and Discussion:

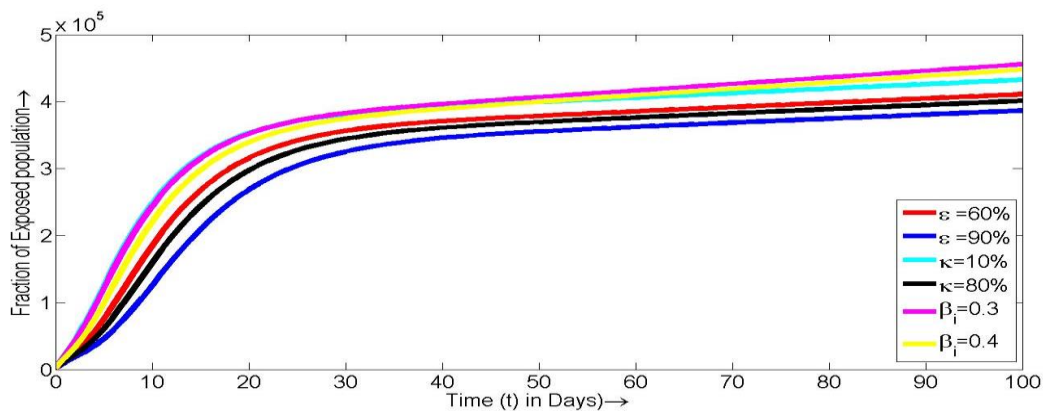


Figure-2: Fraction of Exposed population vs Time (in days) for different value of  $\epsilon, \kappa$  and  $\beta_i$

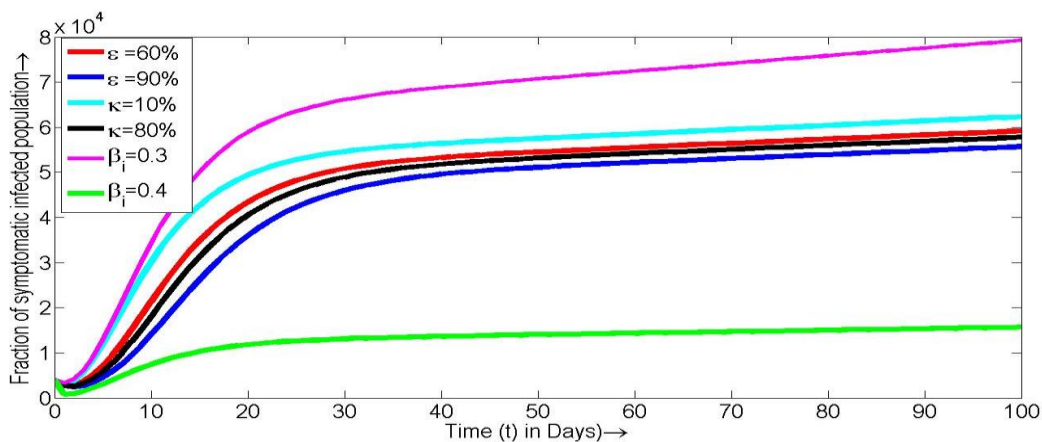


Figure-3: Fraction of Symptomatic population vs Time (in days) for different value of  $\epsilon, \kappa$  and  $\beta_i$

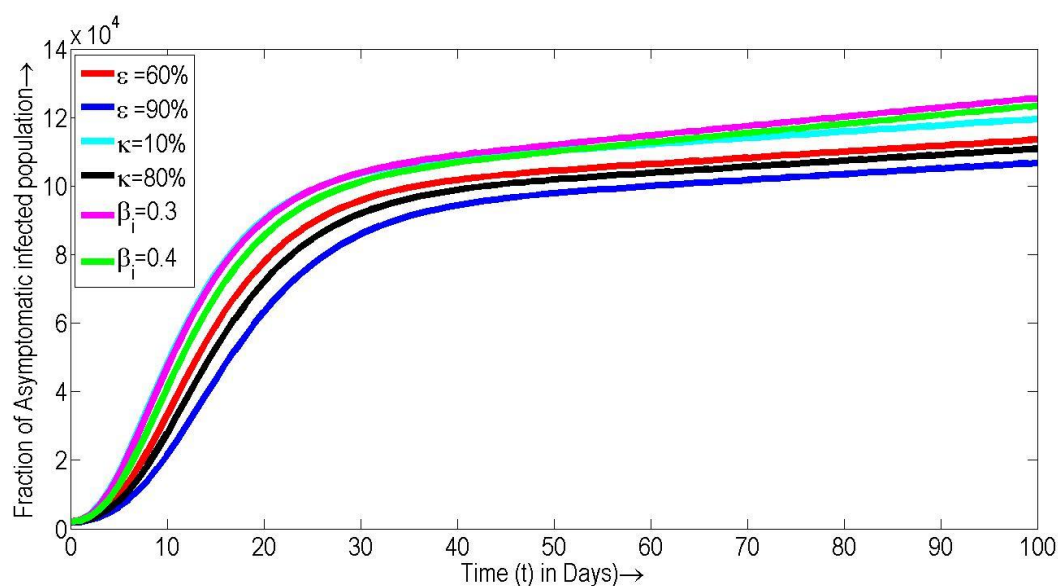


Figure-4: Fraction of Asymptomatic population vs Time (in days) for different value of  $\varepsilon, \kappa$  and  $\beta_i$

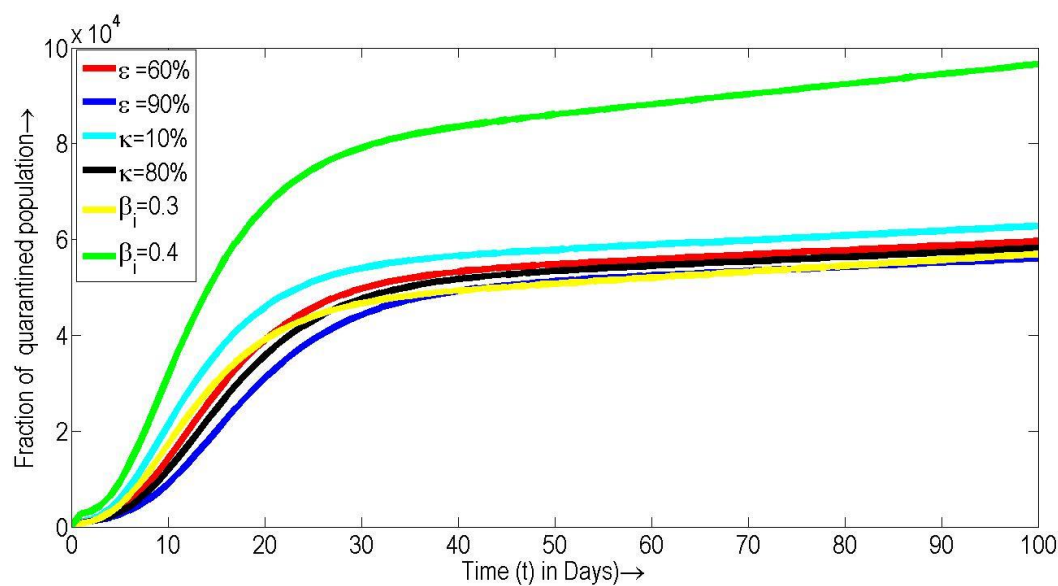


Figure-5: Fraction of Quarantined population vs Time (in days) for different value of  $\varepsilon, \kappa$  and  $\beta_i$

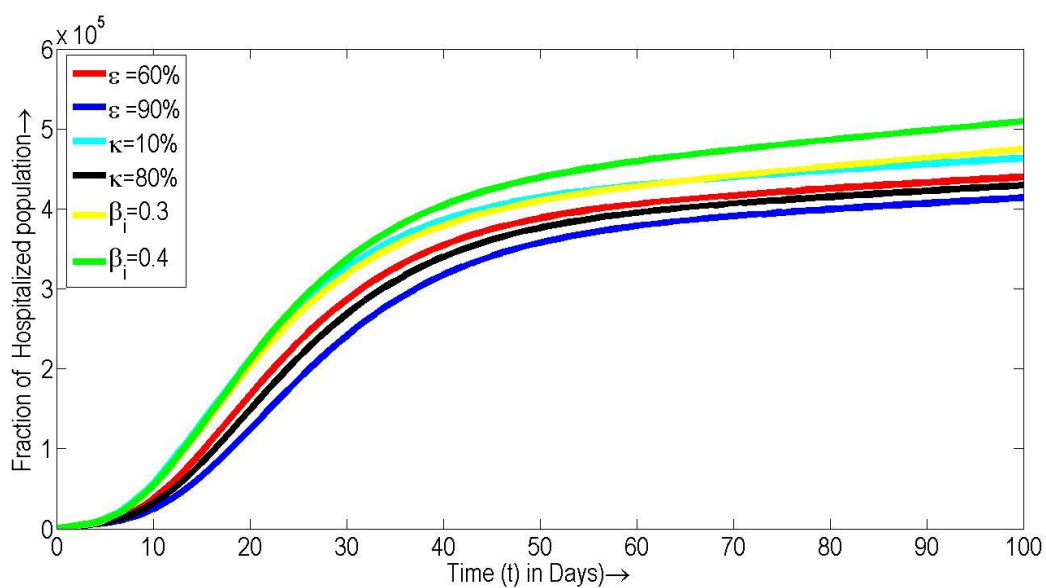


Figure-6: Fraction of Hospitalized population vs Time (in days) for different value of  $\varepsilon, \kappa$  and  $\beta_i$

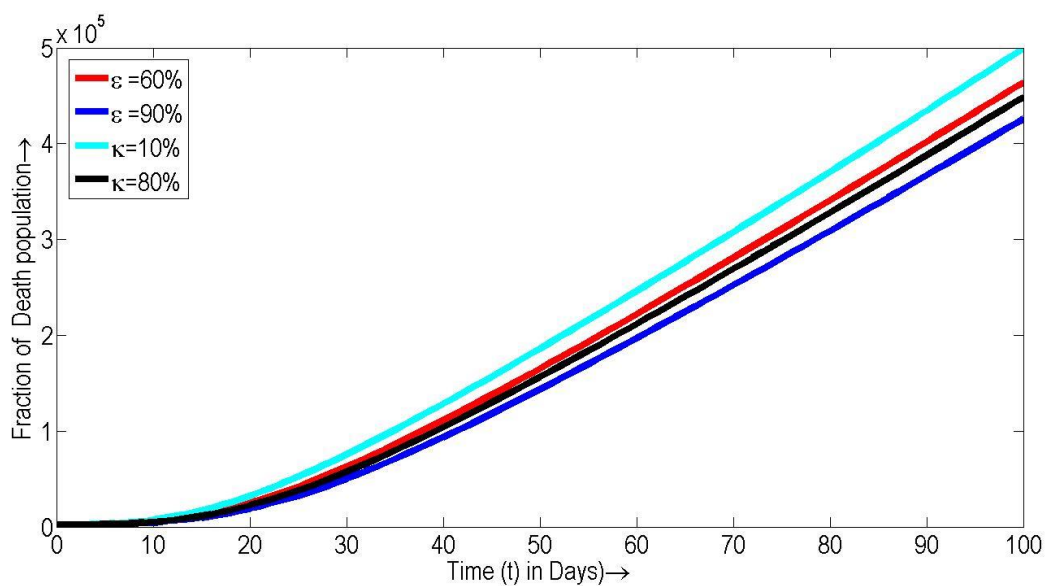


Figure-7: Fraction of Death population vs Time (in days) for different value of  $\varepsilon, \kappa$

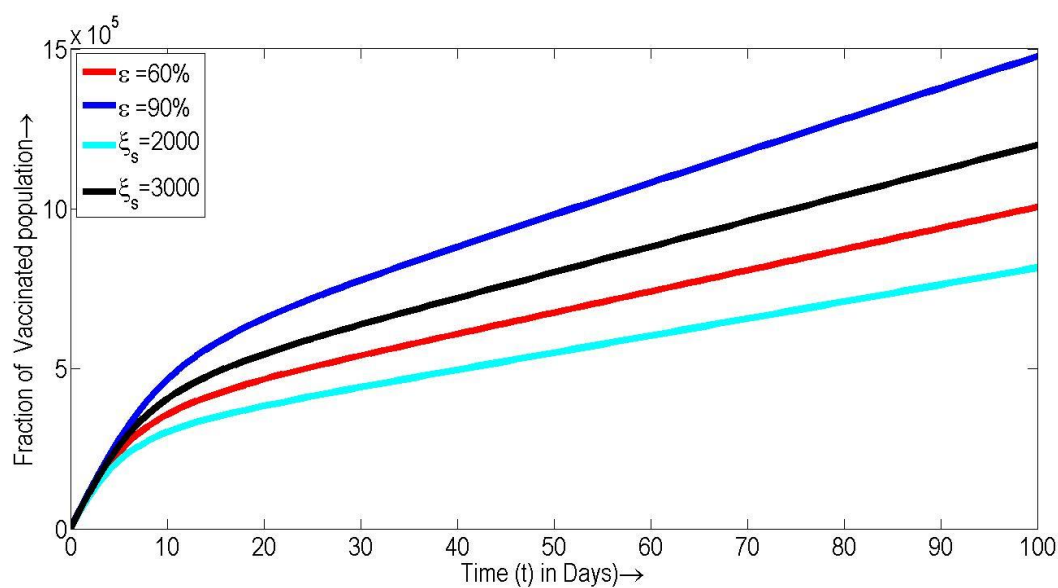


Figure-8: Fraction of Vaccinated population vs Time (in days) for different value of  $\varepsilon$  and  $\xi_s$

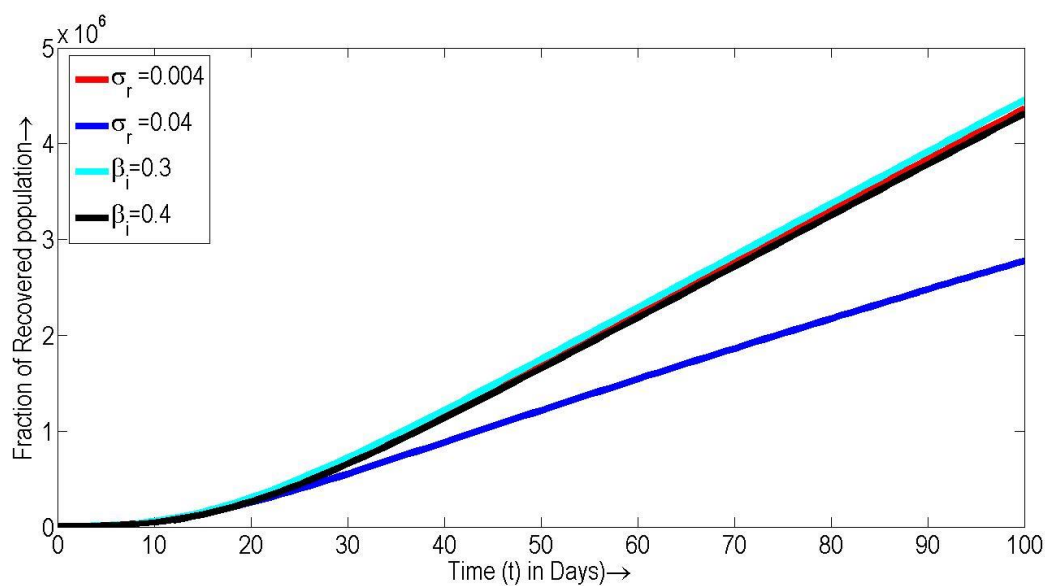


Figure-9: Fraction of Recovered population vs Time (in days) for different value of  $\sigma_r$  and  $\beta_i$

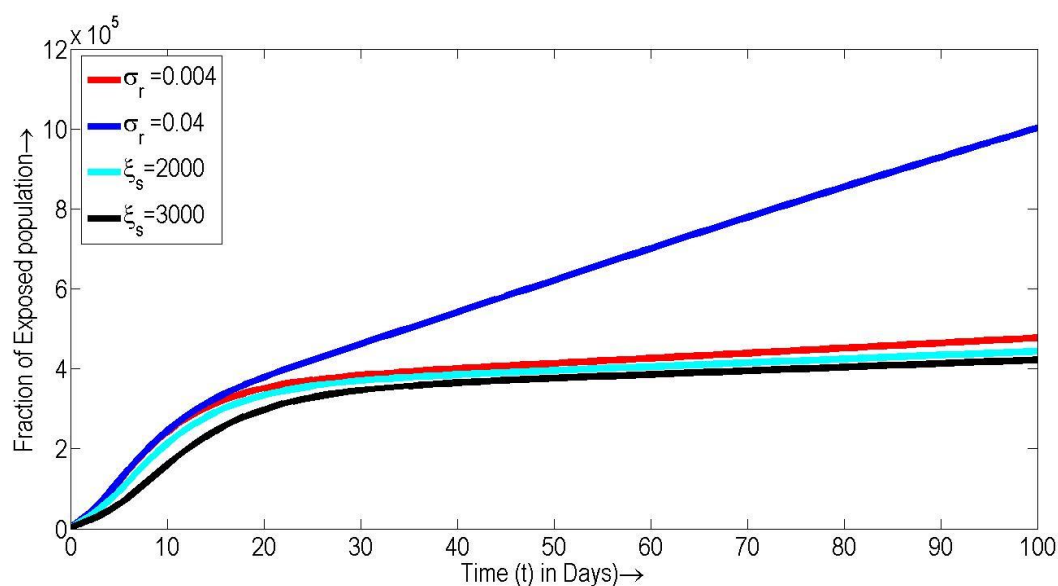


Figure-10: Fraction of Exposed population vs Time (in days) for different value of  $\sigma_r$  and  $\xi_s$

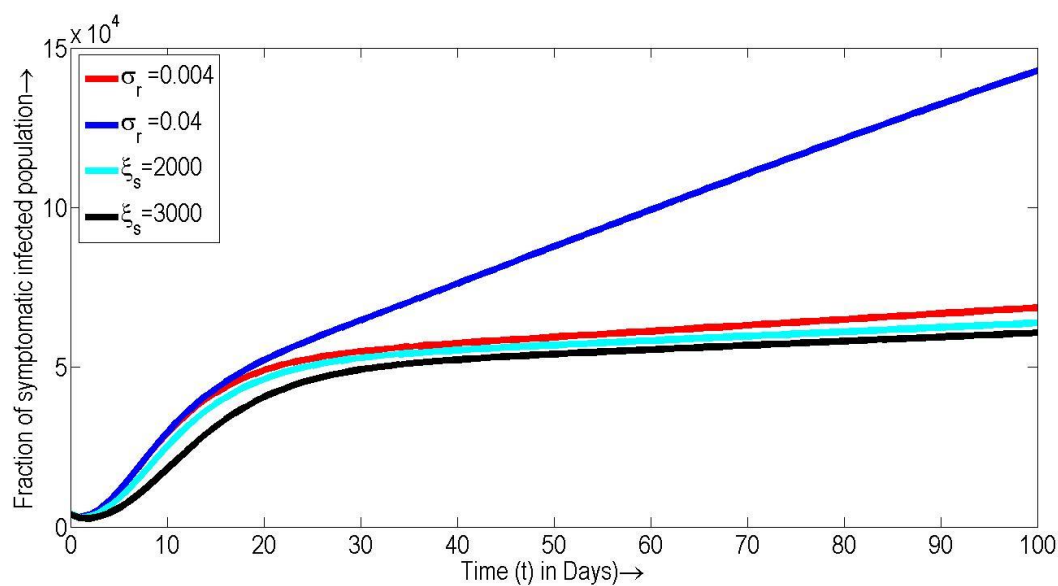


Figure-11: Fraction of Symptomatic population vs Time (in days) for different value of  $\sigma_r$  and  $\xi_s$

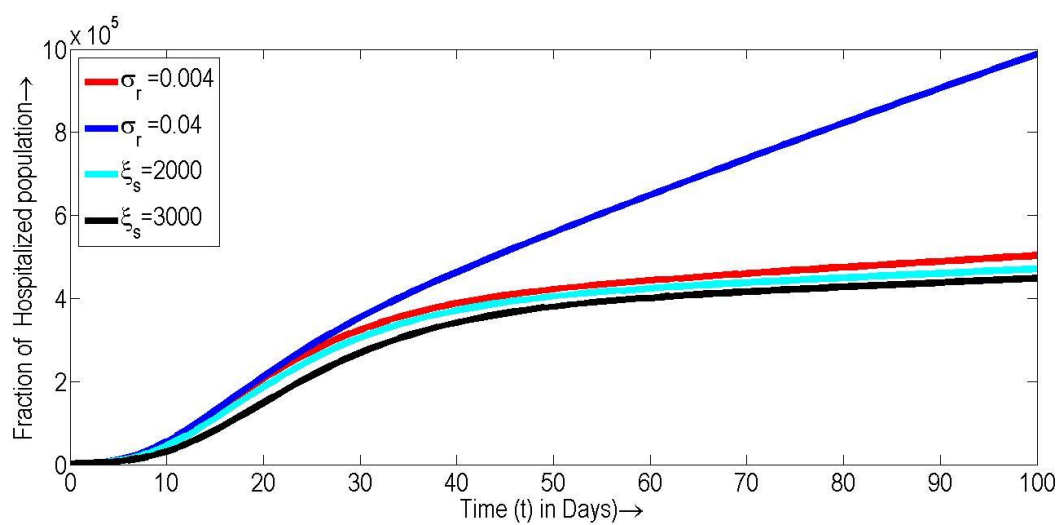


Figure 12: Fraction of Hospitalized population vs Time (in days) for different value of  $\sigma_r$  and  $\xi_s$

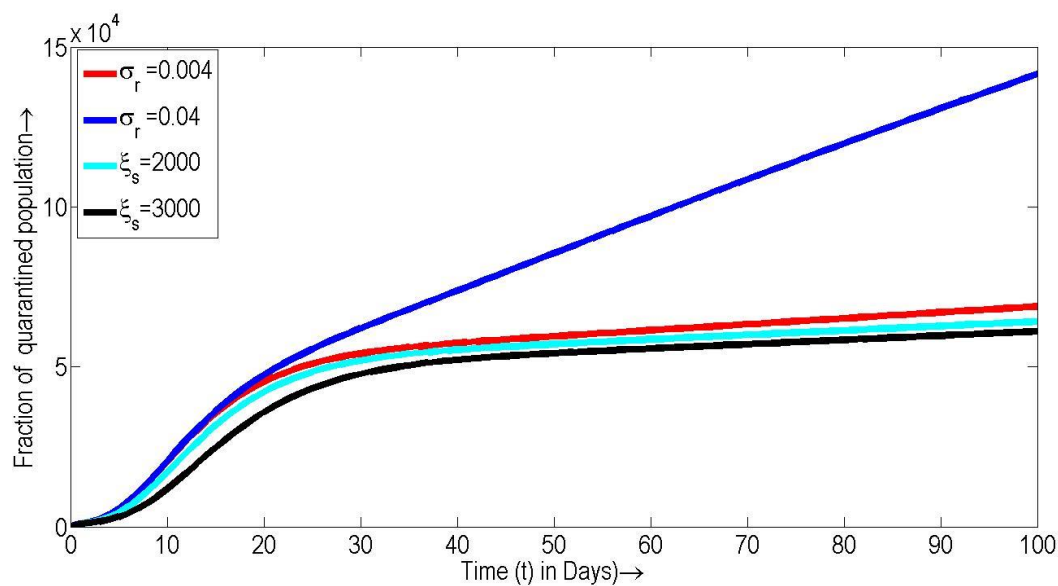


Figure-13: Fraction of Quarantined population vs Time (in days) for different value of  $\sigma_r$  and  $\xi_s$

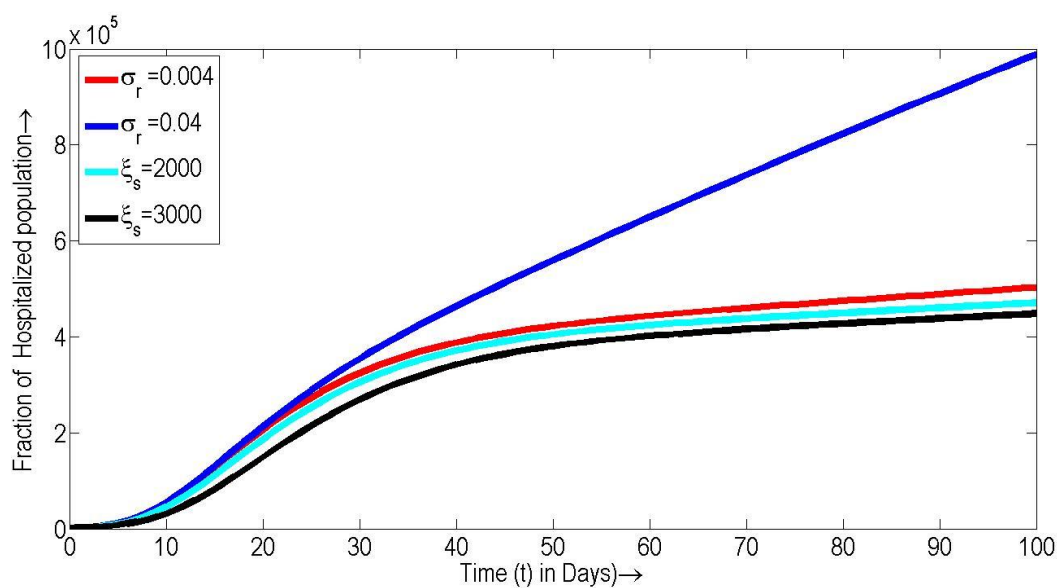


Figure-14: Fraction of Hospitalization population vs Time (in days) for different value of  $\sigma_r$  and  $\xi_s$

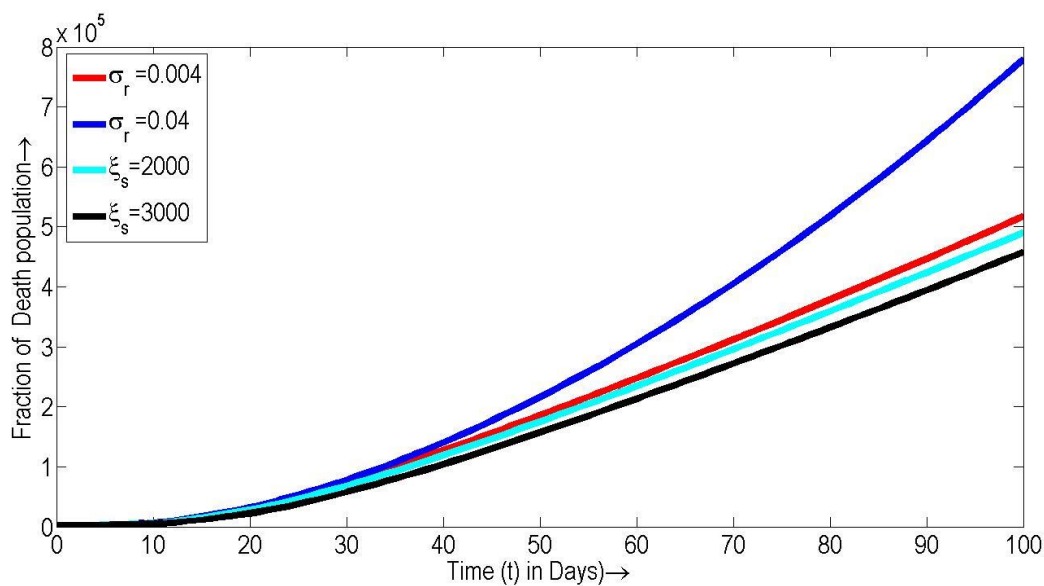


Figure-15: Part of Death populace versus Time (in days) for various worth of  $\sigma_r$  and  $\xi_s$

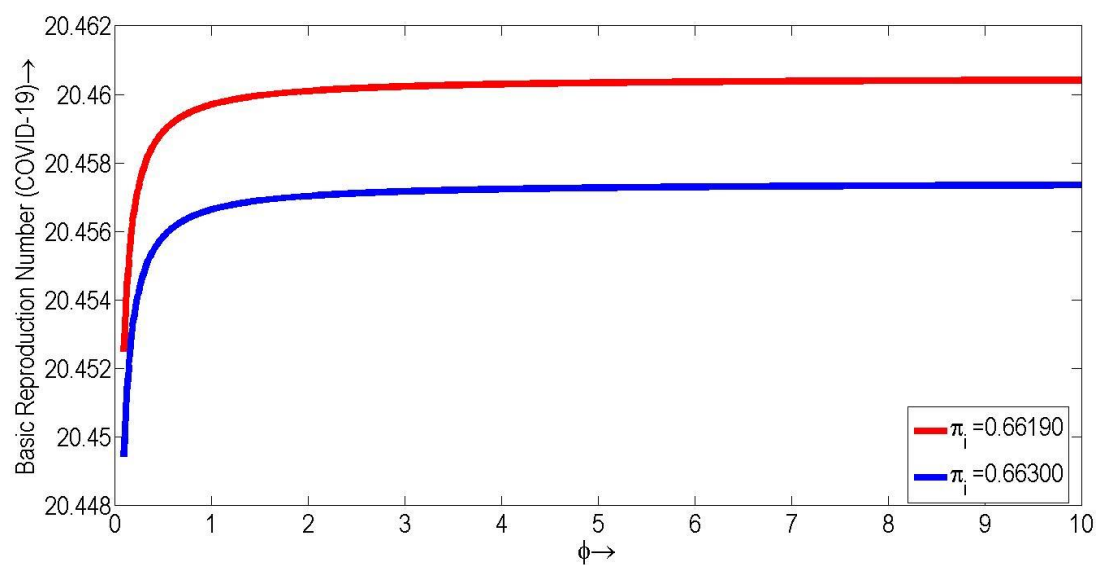


Figure-16: Basic Reproduction of number vs the rate at which the infectious compartment progresses from being exposed for different value of  $\pi_i$

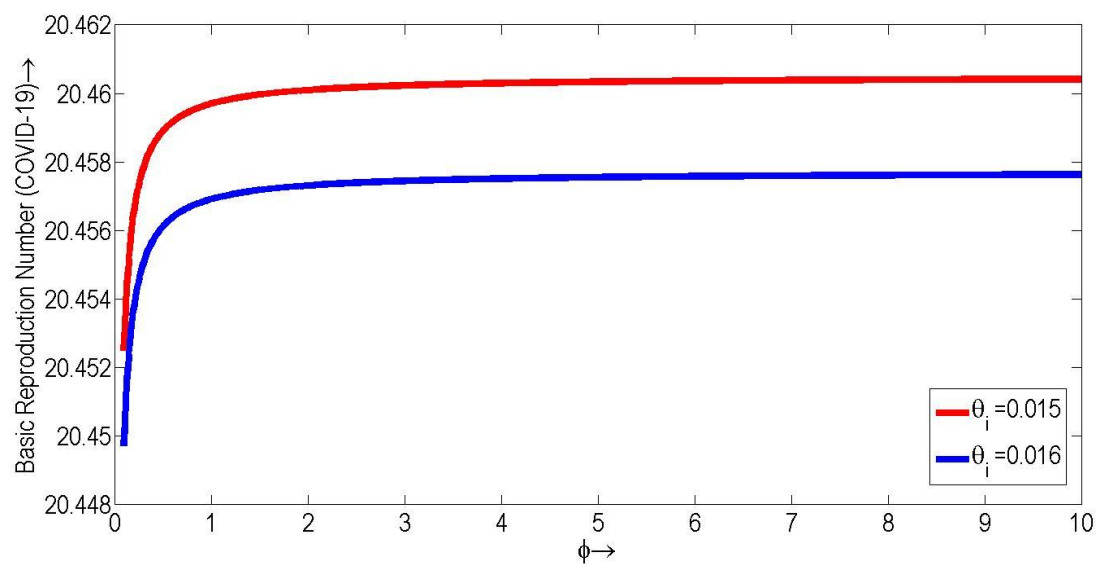


Figure-17: Basic Reproduction of number vs the rate at which the infectious compartment progresses from being exposed for different value of  $\theta_i$

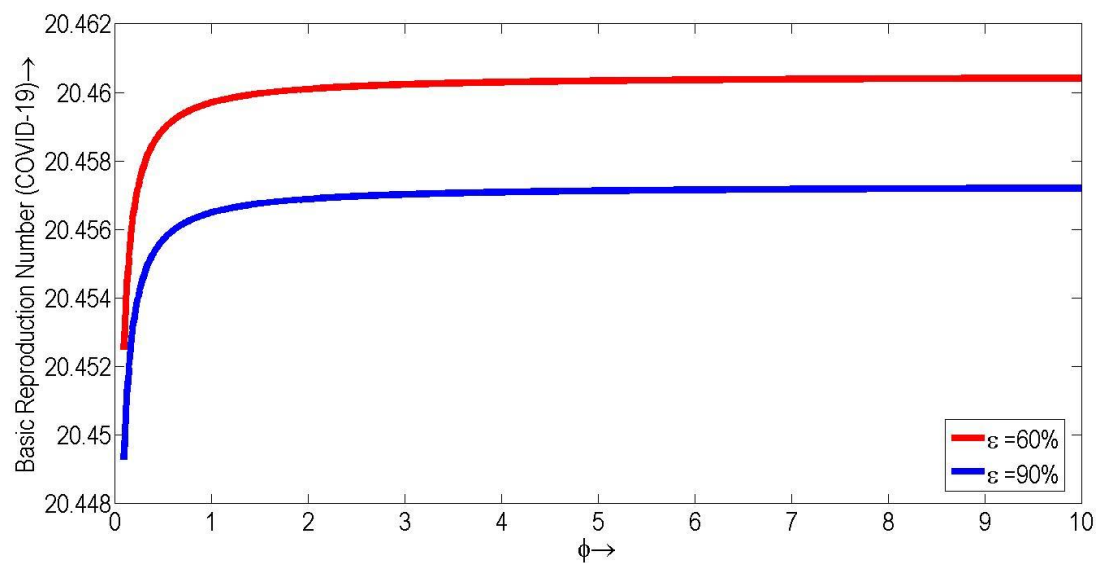


Figure-18: Basic Reproduction of number vs the rate at which the infectious compartment progresses from being exposed for different value of  $\epsilon$

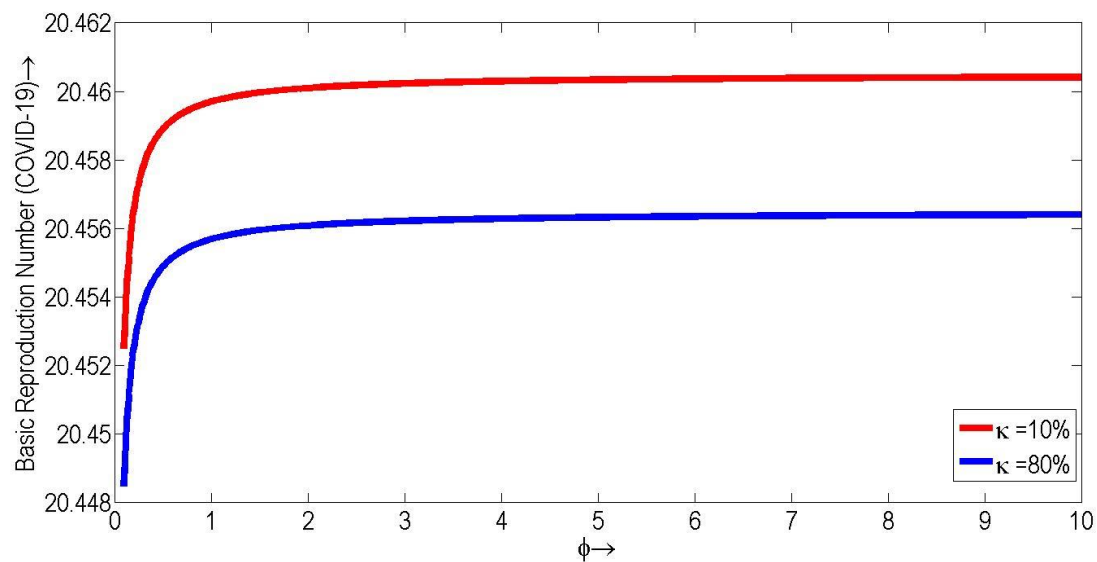


Figure-19: Basic Reproduction of number vs the rate at which the infectious compartment progresses from being exposed for different value of  $\kappa$

The numerical simulations began with the following conditions:

$$S(0) = 2150, E(0) = 1750, I(0) = 3930, A(0) = 1965, Q(0) = 94, R(0) = 3766$$

$$H(0) = 1050, D(0) = 2010, V(0) = 950$$

Table 1 contains the parameter values utilized in the numerical simulations.

There is a wide range of exposure levels in Figure (2-6), which shows the percentage of the population who are symptomatic or unaffected, quarantined or hospitalized depending on the value of  $\varepsilon, \kappa$  and  $\beta_i$ . These figures show that populations rise to a certain point before flattening out. As vaccine efficacy, face mask use, and isolation rates rise for those infected with symptoms, these populations become smaller, according to the data. When the percentage of vaccine efficacy goes up, fewer people die, as shown in figure 7, while the number of people who get vaccinated goes up, as seen in figure 8. A look at figure 9 shows that the recovered population shrinks as rates of the recovered population returning to the infected compartment increase, as well as the isolation rate for people in that compartment rises. Figure (10-15) shows that the exposed, symptomatic, quarantined, hospitalized, and death populations rise when the isolation rate for people in the symptomatically infected compartment rises, while these populations fall as the vaccination rate rises. Figure (10-15). Variation in the basic reproduction number with respect to the rate at which the infectious compartment progresses from being exposed can be seen in figure (16-19). It has been observed that the basic reproduction number decreases if hospitalization rates from symptomatic infected populations, the COVID-19 disease mortality rate for infected individuals, vaccine efficacy and face masks rise.

**Table-1**

S.No.	Symbols	Definition	Numerical Values	Source
1	$\lambda$	Recruitment rate in Susceptible compartment	67446.82054	Worldometer (2020)
2	$\mu$	Natural Death	0.0000391	Worldometer (2020)
3	$\beta_a$	The isolation rate of asymptotically infectious individual	0.2	Eikenberry (2020)
4	$\beta_i$	In the apparently tainted compartment, the disconnection rate for people	0.2	Eikenberry (2020)
5	$\gamma_a$	Recovery rates from asymptomatic infectious individuals	1/10	Ferguson et al. (2020)
6	$\gamma_q$	Recovery rate of persons in quarantine	0.05	Eikenberry (2020)
7	$\gamma_i$	Recovery rates from symptomatic	1/10	Eikenberry (2020)
8	$\gamma_h$	Recovery rates from hospitalized infected populations	0.09310	Estimated
9	$\theta_h$	The COVID-19 disease mortality rate for hospitalized patients	0.01	Assumed
10	$\theta_q$	The COVID-19 disease death rate for those in quarantine	0.015	Ferguson et al. (2020)
11	$\alpha_v$	Vaccinated compartment COVID-19 illness mortality rate	0.0001	Assumed
12	$v$	The proportion of individuals who are vaccinated	0.4	Assumed
13	$\psi$	Proportion of people who wear a face mask	0.5	Iboi et al. (2020)
14	$\omega_i$	The effective contact rate	0.2	Assumed
15	$\omega_a$	The effectiveness of social distancing	0.4	Assumed
16	$\pi_q$	Rates of hospitalization from quarantined infected populations, respectively	0.51323	Estimated

## 7. Conclusions:

This study used an SEIAQR model with seven infection stages, including vaccination, to simulate and predict the spread of the novel COVID-19 outbreak. The model was extended to include vaccination. The proposed model's non-negativity, boundedness, disease free equilibrium, and epidemic equilibrium, as well as the basic reproduction number, were studied mathematically to illustrate them. Our final step was to determine whether immunization had an impact on the spread of the illness. Increasing the vaccine programme dramatically reduces the number of exposed patients as well as mortality, according to the findings as well. Using the proposed model, health authorities could plan and prepare for the pandemic, as well as take appropriate steps and decisions to keep it under control.

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