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Modeling COVID-19 dynamics in Nepal: SEIQR compartmental model with quarantine

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Abstract

Mathematical modeling is crucial to understand the transmission dynamics of infectious diseases and to develop effective control strategies. In this study, we introduce a compartmental SEIQR model (Susceptible-Exposed-Infectious-Quarantine-Recovered) that incorporates quarantine measures to analyze the transmission dynamics of COVID-19 in Nepal. The next generation approach is used to compute the model's basic reproduction number. The model's equilibrium points are obtained, and their stability is assessed with the help of the basic reproduction number. Sensitivity analysis is used to examine the importance and influence of the model parameters on the spread of disease.

Keywords: Compartmental model; COVID-19; Basic reproduction number; Equilibrium points; Stability analysis; Sensitivity analysis.

1. Introduction

Globally, infectious diseases have been on the rise. Mathematical models are vital resources for understanding the dynamics of infectious disease transmission, forecasting future disease outbreaks, and suggesting disease management measures. Infectious diseases have thus been the subject of numerous mathematical investigations. Kermack and Mckendrick [1] proposed an SIR compartmental model to study the transmission dynamics of infectious diseases.

COVID-19, the recent pandemic, is an infectious disease caused by the virus, which is known as Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). In late December 2019, the COVID-19 disease was first identified in Wuhan, the capital of Hubei province, China, causing the first pandemic of this century. The WHO declared COVID-19 a global epidemic in the third month of 2020 (the H1N1 influenza was previously declared a pandemic in 2009) [2]. Many research works on its transmission dynamics have been carried out in several countries, including Italy, the United States, and China [3, 4, 5]. A couple of mathematical frameworks have already been constructed to examine the spread of the COVID-19 pandemic in India by considering the impact of intervention techniques such as lockdown, social distancing, and economic points of view [6, 7, 8, 9]. Chaterjee et al. [10] used a stochastic differential equation model to investigate the COVID-19 transmission in India. Adhikari et al. [11] predicted the trend of the COVID-19 pandemic. Bhuju et al. [12] investigated the transmission dynamics of COVID-19 through the SIR model. In their study, they explored the behavior of the disease, determined the basic reproduction number, and conducted numerical simulations. Numerous studies have explored the mathematical modeling of infectious diseases. This paper specifically focuses on integrating the impact of quarantine within a SEIQR framework, particularly in the context of Nepal.

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2. Method

The total human population at any given moment, represented as $N(t)$, is divided into five specific categories: the susceptible group $S(t)$, the exposed group $E(t)$, the infected group $I(t)$, the quarantine group $Q(t)$, and the recovered group $R(t)$. It is assumed that the overall population is changeable and mixed uniformly. This means that every individual has an equal chance of contracting the infection when interacting with someone who is infected. We incorporate both a birth rate γ and a death rate δ for all the compartments. The behavior of the disease, considering these factors, is determined by a specific set of differential equations, which are illustrated in the following flow diagram Fig. 1.

$$\begin{aligned}
\frac{dS}{dt} &= \gamma N - \beta S\frac{I}{N} - \delta S,\\
\frac{dE}{dt} &= \beta S\frac{I}{N} - \sigma E - \delta E,\\
\frac{dI}{dt} &= \sigma E - (\gamma_I + \delta_I)I - \delta I,\\
\frac{dQ}{dt} &= \delta_I I - \eta Q - \delta Q,\\
\frac{dR}{dt} &= \gamma_I I + \eta Q - \delta R,
\end{aligned} \tag{1}$$

where β represents the rate of transmission, σ refers to the rate at which individuals who have been exposed become infectious, γ_I denotes the recovery rate of those who are infected, δ_I signifies the rate at which infected individuals are placed in quarantine, η indicates the recovery rate for quarantined individuals, δ stands for the natural mortality rate, and γ is the birth rate, and $N = S + E + I + Q + R$ represents the total population. In the normalized SEIQR model, we introduce the normalized variables, $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, $q = \frac{Q}{N}$, $r = \frac{R}{N}$, where N is the total population. The sum of these normalized variables satisfies $s+e+i+q+r = 1$. The behavior of the disease is characterized by the following system of differential equations.

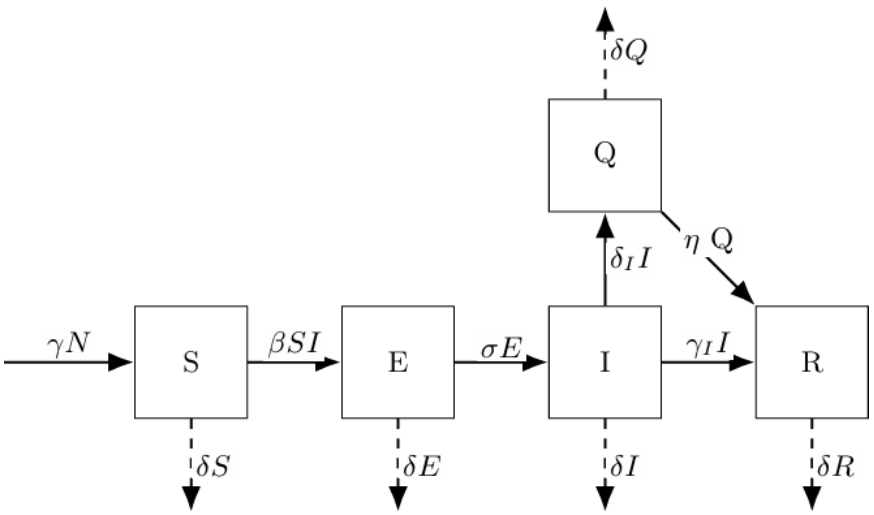


Figure 1: Flow diagram of SEIQR model.

$$\begin{aligned}
\frac{ds}{dt} &= \gamma - \beta si - \delta s,\\
\frac{de}{dt} &= \beta si - \sigma e - \delta e,\\
\frac{di}{dt} &= \sigma e - (\gamma_I + \delta_I + \delta)i,\\
\frac{dq}{dt} &= \delta_I i - \eta q - \delta q,\\
\frac{dr}{dt} &= \gamma_I i + \eta q - \delta r
\end{aligned} \tag{2}$$

2.1. Basic reproduction number (R_0)

The basic reproduction number refers to the typical number denoting the average of new infections generated by a single infected individual during their infectious period within a population where everyone is susceptible to the infection [13]. To calculate the basic reproduction number (R_0), we examine the infected compartments e, i, and q through the next generation matrix method, which was initially introduced by Diekmann et al.[13]. This approach has been utilized because we have created a deterministic model that is straightforward to apply and integrate, allowing its use in a larger population for various infectious diseases such as dengue [14].

$$F = \begin{pmatrix} 0 & \beta s & 0\\ 0 & 0 & 0\\ 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \sigma+\delta & 0 & 0\\ -(\sigma+\delta) & \gamma_I+\delta_I+\delta & 0\\ \sigma 0 & -(\gamma_I\delta_I & \eta+\delta \end{pmatrix}.$$

where F and V are the transmission and transition matrices, respectively. In order to calculate the next generation matrix, we calculate

$$V^{-1} = \begin{pmatrix} \frac{1}{\sigma+\delta} & 0 & 0\\ \frac{\sigma}{(\sigma+\delta)(\gamma_I+\delta_I+\delta)} & \frac{1}{\gamma_I+\delta_I+\delta} & 0\\ \frac{\sigma\delta_I}{(\sigma+\delta)(\gamma_I+\delta_I+\delta)(\eta+\delta)} & \frac{\delta_I}{(\gamma_I+\delta_I+\delta)(\eta+\delta)} & \frac{1}{\eta+\delta} \end{pmatrix}$$

Given the transmission matrix F, we compute the next generation matrix FV^{-1} as

$$FV^{-1} = \begin{pmatrix} \frac{\beta\sigma s}{(\sigma+\delta)(\gamma_I+\delta_I+\delta)} & \frac{\beta s}{\gamma_I+\delta_I+\delta} & 0\\ 0 & 0 & 0\\ 0 & 0 & 0 \end{pmatrix}$$

The basic reproduction number R_0 is defined as the largest eigenvalue of the matrix (FV^{-1}), expressed mathematically as $R_0 = \rho(FV^{-1})$. Here, $\rho(FV^{-1})$ denotes the spectral radius of the next generation matrix FV^{-1}. Therefore, we establish the basic reproduction number as

$$R_0 = \frac{\beta\sigma}{(\sigma+\delta)(\gamma_I+\delta_I+\delta)}$$

The system (2) has the following two biologically feasible equilibrium points:

2.2. Diseases free equilibrium point

The disease-free equilibrium is established when $i = 0$, $q = 0$, and $e = 0$. This results in $s = \frac{\gamma}{\delta} = 1$ and $r = 0$. Consequently, the disease-free equilibrium is represented as $DFE(1, 0, 0, 0, 0)$. The Jacobian matrix is given by

$$J = \begin{pmatrix} -\beta i - \delta & 0 & -\beta s & 0 & 0\\ \beta i & -(\sigma+\delta & \beta s & 0 & 0\\ 0 & \sigma & -(\delta_I+\gamma_I+\delta & 0 & 0\\ 0 & 0 & \delta_I & -(\eta+\delta) & 0\\ 0 & 0 & \gamma_I & \eta & -\delta \end{pmatrix}$$

At $DFE(s, e, i, q, r) = (1, 0, 0, 0, 0)$ the Jacobian matrix becomes

$$J_{DFE} = \begin{pmatrix} -\delta & 0 & -\beta & 0 & 0\\ 0 & -(\sigma+\delta) & \beta & 0 & 0\\ 0 & \sigma & -(\delta_I+\gamma_I+\delta) & 0 & 0\\ 0 & 0 & \delta_I & -(\eta+\delta) & 0\\ 0 & 0 & \gamma_I & \eta & -\delta \end{pmatrix}$$

The eigenvalue corresponding to the Jacobian matrix at the DFE is determined by the equation $det(J_{DFE} - \lambda I) = 0$, with I representing the square identity matrix. By solving the following characteristic equation, the eigenvalues corresponding to the Jacobian matrix in the DFE can be found.

$$\det(J_{DFE} - \lambda I) = 0$$

where λ represents the eigenvalues.

The matrix $J_{DFE} - \lambda I$ is

$$J_{DFE} - \lambda I = \begin{pmatrix} -\delta - \lambda & 0 & -\beta & 0 & 0 \\ 0 & -(\sigma + \delta + \lambda) & \beta & 0 & 0 \\ 0 & \sigma & -(\delta_I + \gamma_I + \delta + \lambda) & 0 & 0 \\ 0 & 0 & \delta_I & -(\eta + \delta + \lambda) & 0 \\ 0 & 0 & \gamma_I & \eta & -(\delta + \lambda) \end{pmatrix} \tag{3}$$

$$\det(J_{DFE} - \lambda I) = (-\delta - \lambda)(-\delta - \lambda)(-\eta - \delta - \lambda) \times \left[(\sigma + \delta)(\gamma_I + \delta_I + \delta) + (\sigma + \delta)\lambda + (\gamma_I + \delta_I + \delta)\lambda + \lambda^2\right] = 0 \tag{4}$$

Using the Routh-Hurwitz criteria method, the stability of the system depends only on the expression $(\sigma + \delta)(\gamma_I + \delta_I + \delta) + (\sigma + \delta)\lambda + (\gamma_I + \delta_I + \delta)\lambda + \lambda^2 = 0$, which is in the form of $\lambda^2 + \alpha_0\lambda + \alpha_1 = 0$, where $\alpha_0 = (\sigma + \delta) + (\gamma_I + \delta_I + \delta)$ and $\alpha_1 = (\sigma + \delta)(\gamma_I + \delta_I + \delta) - \sigma\beta = 1 - R_0$. The system is stable if the eigenvalue is $\lambda < 0$, and this will happen only if $\alpha_0 > 0$ and if $\alpha_1 > 0$. Here, α_0 is positive, and the value of α_1 is positive only if $R_0 < 1$. Thus, the disease-free equilibrium point is asymptotically stable if $R_0 < 1$ otherwise unstable.

2.3. Endemic equilibrium point

The endemic equilibrium occurs when the disease persists in a steady state in the population. Setting the derivatives in the normalized SEIQR model to zero, we obtain the endemic equilibrium values s^*, e^*, i^*, q^*, and r^*. From $\frac{di}{dt} = 0$ and $\frac{de}{dt} = 0$, we derive:

$$\begin{aligned} s^* &= \frac{1}{R_0} \\ e^* &= \frac{\delta(\gamma_I + \delta_I + \delta)}{\beta\sigma}(R_0 - 1) \\ i^* &= \frac{\delta}{\beta}(R_0 - 1) \\ q^* &= \frac{\delta\delta_I}{\eta + \delta}(R_o - 1) \\ r^* &= \frac{\gamma_I\delta + \eta(\gamma_I + \delta_I)}{\beta(\eta + \delta)}(R_0 - 1) \end{aligned} \tag{5}$$

At the endemic equilibrium, each compartment is directly influenced by the basic reproduction number R_0. The susceptible population is $s^* = \frac{1}{R_0}$, indicating that fewer individuals remain susceptible when R_0 increases. The exposed e^*, infected i^*, quarantined q^*, and recovered r^* populations depend on $(R_0 - 1)$, which means that they only have positive values when $R_0 > 1$, which indicates endemic persistence. Specifically, $e^* = \frac{\delta(\gamma_I + \delta_I + \delta)}{\beta\sigma}(R_0 - 1)$ and $i^* = \frac{\delta}{\beta}(R_0 - 1)$ grow with increasing R_0, reflecting an increased burden of transmission and infection. Quarantine requirements increase with $q^* = \frac{\delta\delta_I}{\eta + \delta}(R_0 - 1)$, emphasizing the need for isolation to control spread. Meanwhile, $r^* = \frac{\gamma_I\delta + \eta(\gamma_I + \delta_I)}{\beta(\eta + \delta)}(R_0 - 1)$ shows that the number of recovered individuals increases with the spread of the disease. Thus, reducing R_0 below 1 through interventions such as vaccination, quarantine, and public health measures is critical to prevent endemicity and mitigate healthcare strain.

2.4. Sensitivity analysis

The sensitivity index of R_0 with respect to each parameter θ is calculated as [15, 16]:

$$S^{\theta}_{R_0} = \frac{\partial R_0}{\partial \theta} \times \frac{\theta}{R_0}$$

The sensitivity of R_0 can be explained by following table

Positive values of the sensitivity index describe that the cases of the disease increase with the corresponding increase in the parameter values. Sensitivity indices of the parameters δ, γ_I and δ_I are negative. So, they contribute to decreasing the value of the basic reproduction number and, so, contribute to decreasing the prevalence of the disease. Also, Table 1 shows that the transmission rate β is positive and its sensitivity index is maximum, and the most negative sensitive model parameter is the rate at which infected individuals are quarantined.

Table 1: Sensitivity indices of R_0 with respect to each parameter.

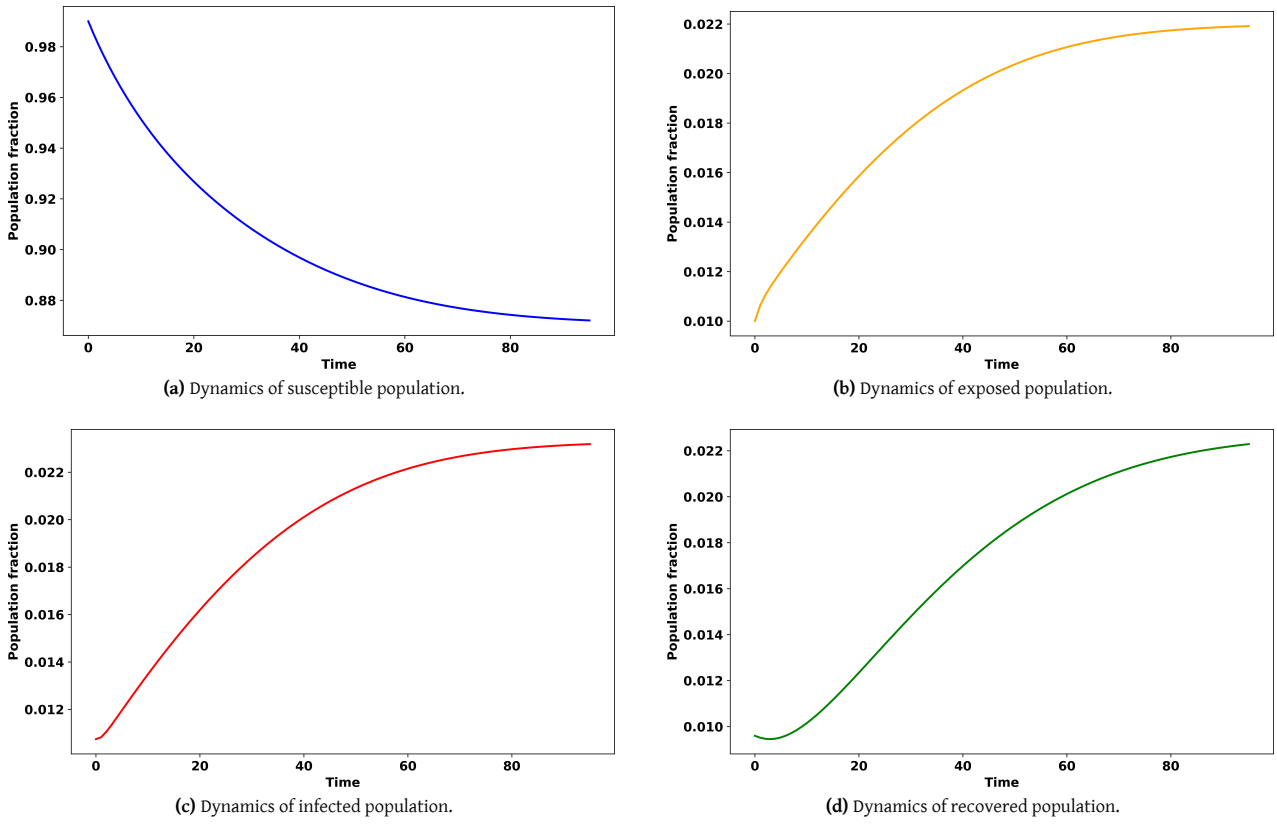
Parameter	$S^{\theta}_{R_0}$	Baseline value	Sensitivity index
β	1	0.5	+1
σ	$\frac{\delta}{\sigma+\delta}$	0.05	+0.144
δ	$-\frac{\delta[\gamma_I+\delta_I+\sigma+2\delta]}{(\sigma+\delta)(\gamma_I+\delta_I+\delta)}$	0.1	-0.411
γ_I	$-\frac{\gamma_I}{\gamma_I+\delta_I+\delta}$	0.0714	-0.226
δ_I	$-\frac{\delta_I}{\gamma_I+\delta_I+\delta}$	0.1	-0.507

3. Results and discussions

Graphical results are presented in order to observe the effects of model parameters on the transmission of COVID-19 disease. The following numerical values are used for the simulations: $n = 0.9$, $i = 0.1$, $\beta = 0.5$, $\delta = 0.1$, $\delta_I = 0.1$, $\gamma_I = 0.07$, $\sigma = 0.05$, $\sigma_I = 0.07$

Fig. 2 is simulated to investigate the spread of COVID-19 in Nepal. It is observed that the susceptible population decreases over time. It is because susceptible populations get exposed due to interaction with infected populations, and some of them die due to the natural cause Fig. 1. The population in the exposed group initially increases due to the interaction of the susceptible population with the infectious population. Later, the exposed population moves to the infectious class, showing the symptoms of the disease. So, the population starts decreasing. The infectious host population decreases due to the recovery from the disease or quarantine, and some due to death from natural causes.

We have simulated Fig. 3 to investigate the sensitivity of model parameters. We see that the population size of infectious hosts is increasing with the increased values of model parameters σ,and β. Table 1 shows that the sensitivity indices for these parameters are positive. Also, the parameters δ, γ_I and δ_I are contributing to decreasing the number of infectious people. These parameters have negative sensitivity indices. Thus, it is observed that parameters with a positive sensitivity index increase the disease transmission, and the parameters having a negative sensitivity index contribute to decreasing the transmission of the disease. The simulated results and Table 1 show that β, σ and δ_I are more sensitive model parameters. β is the most positive sensitive parameter that increases the transmission of the disease and δ_I is the most negative sensitive parameter that decreases the transmission of the disease.



(a) Dynamics of susceptible population.

(b) Dynamics of exposed population.

(c) Dynamics of infected population.

(d) Dynamics of recovered population.

Figure 2: Simulated dynamics of COVID-19 spread in Nepal.

4. Conclusion

In this work, we design and evaluate a deterministic ordinary differential equation (ODE) model, called SEIQR, that describes the dynamics of COVID-19. Our investigation allows us to identify and explore various equilibria within the model, and we thoroughly assess their local stability applying the Routh-Hurwitz criteria. Our findings indicate that the disease-free equilibrium remains locally stable when the basic reproduction number is less than 1. If the DFE exceeds 1, it is unstable. The existence equilibrium is only observed above the threshold value of 1. We observed that the most important sensitive parameters are transmission rate β (positive) and rate at which infected individuals are quarantined δ_I(negative). Increasing transmission rate increases the transmission of the disease, and increasing rate of quarantine decreases the transmission of the disease significantly. So, by increasing the quarantine rate and decreasing the transmission rate, we can decrease the prevalence of COVID-19.

References

[1] Kermack W O & McKendrick A G, A contribution to the mathematical theory of epidemics, *Proceedings of the Royal Society of London. Series A, Containing Papers of a Mathematical and Physical Character*, 115(772) (1927) 700–721. ISSN 2053-9150. https://doi.org/10.1098/rspa.1927.0118.

[2] Aakash M, Gunasundari C, Athithan S, Sharmila N, Kumar G S & Guefaifia R, Mathematical modeling of COVID-19 with the effects of quarantine and detection, *Partial Differential Equations in Applied Mathematics*, 9 (2024) 100609. ISSN 2666-8181. https://doi.org/10.1016/j.padiff.2023.100609.

[3] Giordano G, Blanchini F, Bruno R, Colaneri P, Di Filippo A, Di Matteo A & Colaneri M, Modelling the COVID-19 epidemic and implementation of population-wide interventions in Italy, *Nature Medicine*, 26(6) (2020) 855–860. ISSN 1546-170X. https://doi.org/10.1038/s41591-020-0883-7.

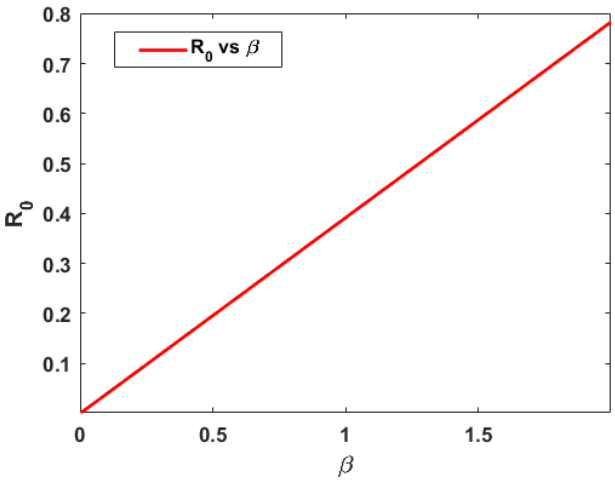
[4] Kucharski A J, Russell T W, Diamond C, Liu Y, Edmunds J, Funk S, Eggo R M, Sun F, Jit M, Munday J D, Davies N, Gimma A, van Zandvoort K, Gibbs H, Hellewell J, Jarvis C I, Clifford S, Quilty B J, Bosse N I, Abbott S, Klepac P & Flasche S, Early dynamics of transmission and control of COVID-19: A mathematical modelling study, *The Lancet Infectious Diseases*, 20(5) (2020) 553–558. ISSN 1473-3099. https://doi.org/10.1016/S1473-3099(20)30144-4.

[5] Gatto M, Bertuzzo E, Mari L, Miccoli S, Carraro L, Casagrandi R & Rinaldo A, Spread and dynamics of the COVID-19 epidemic in Italy: Effects of emergency containment measures, *Proceedings of the National Academy of Sciences*, 117(19) (2020) 10484–10491. ISSN 1091-6490. https://doi.org/10.1073/pnas.2004978117.

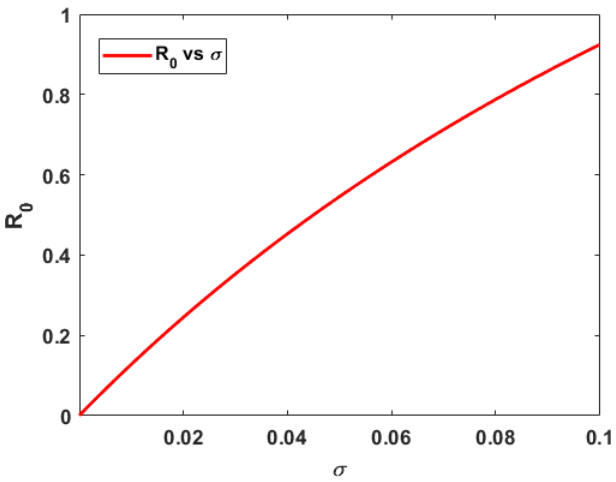
[6] Khajanchi S, Sarkar K & Mondal J. Dynamics of the COVID-19 pandemic in India (2021). https://doi.org/10.48550/arXiv.2005.06286.

[7] Nadim S S, Ghosh I & Chattopadhyay J, Short-term predictions and prevention strategies for COVID-19: A model-based study, *Applied Mathematics and Computation*, 404 (2021) 126251. ISSN 0096-3003. https://doi.org/10.1016/j.amc.2021.126251.

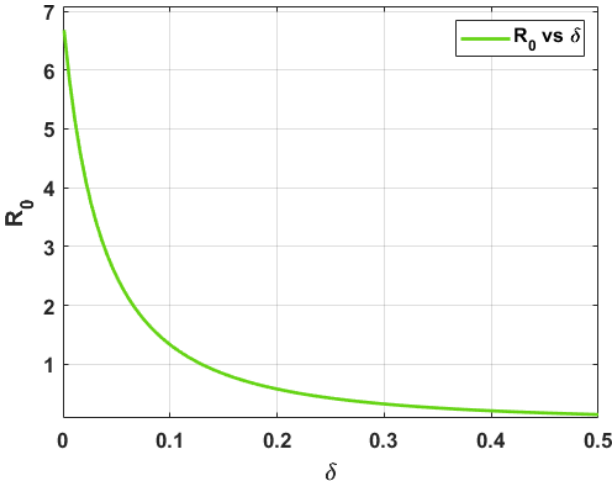
[8] Das A, Dhar A, Goyal S & Kundu A, COVID-19: Analysis of a modified SEIR model, a comparison of different intervention strategies and projections for India, *medRxiv*. https://doi.org/10.1101/2020.06.04.20122580.



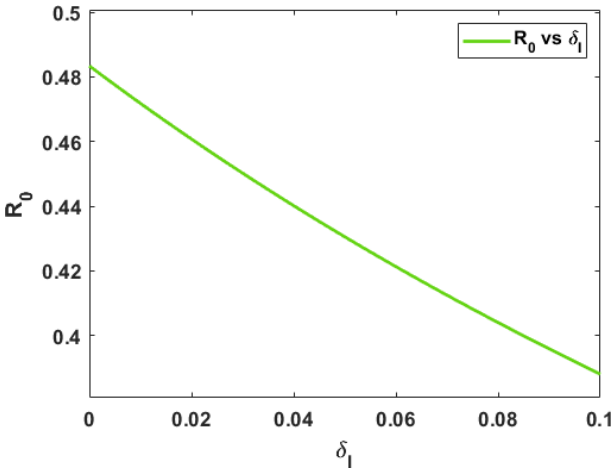
(a) Effect of β on R_0.



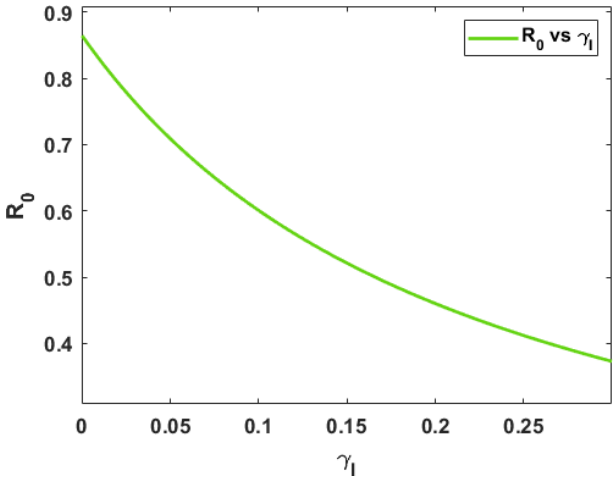
(b) Effect of σ on R_0.



(c) Effect of δ on R_0.



(d) Effect of δ_I on R_0.



(e) Effect of γ_I on R_0.

Figure 3: Sensitivity analysis of model parameters on R_0.

[9] Samui P, Mondal J & Khajanchi S, A mathematical model for COVID-19 transmission dynamics with a case study of India, *Chaos, Solitons and Fractals*, 140 (2020) 110173. ISSN 0960-0779. https://doi.org/https://doi.org/10.1016/j.chaos.2020.110173.

[10] Chatterjee K, Chatterjee K, Kumar A & Shankar S, Healthcare impact of COVID-19 epidemic in India: A stochastic mathematical model, *Medical Journal Armed Forces India*, 76(2) (2020) 147–155. ISSN 0377-1237. https://doi.org/10.1016/j.mjafi.2020.03.022.

[11] Adhikari K, Gautam R, Pokharel A, Uprety K N & Vaidya N K, Transmission dynamics of COVID-19 in Nepal: Mathematical model uncovering effective controls, *Journal of Theoretical Biology*, 521 (2021) 110680. ISSN 0022-5193. https://doi.org/10.1016/j.jtbi.2021.110680.

[12] Bhuju G, Phaijoo G R & Gurung D B, Modeling transmission dynamics of COVID-19 in Nepal, *Journal of Applied Mathematics and Physics*, 8(10) (2020) 2167–2173. ISSN 2327-4379. https://doi.org/10.4236/jamp.2020.810162.

[13] Diekmann O, Heesterbeek J & Metz J, On the definition and computation of basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations, *Journal of Mathematical Biology*, 28(4) (1990) 365–382. ISSN 1432-1416. https://doi.org/10.1007/BF00178324.

[14] Phaijoo G R & Gurung D B, Mathematical model on analysis of awareness in controlling dengue disease, *International Journal of Advanced Research*, 4(7) (2016) 999–1006. ISSN 2320-5407. https://doi.org/10.21474/IJAR01/1177.

[15] Phaijoo G R & Gurung D B, Sensitivity analysis of SEIR – SEI model of dengue disease, *GAMS Journal of Mathematics and Mathematical Bioscience* (2018) 44–50.

[16] Bhuju G, Phaijoo G R & Gurung D B, Sensitivity analysis of COVID-19 transmission dynamics, *International Journal of Advanced Engineering Research and Applications*, 6(04) (2020) 2454–2377. ISSN 2454-2377. https://doi.org/10.46593/ijaera.2020.v06i04.001.