

Investigation of the Spread of COVID-19 in Bangladesh by Using the SIR Model

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Abstract

In this paper, we examine the COVID-19 pandemic's spread pattern by using a system of ordinary differential equations model known as the SIR model. Here, we study the dynamics of the susceptible, infected, and removed population of COVID-19 in Bangladesh by the modified SIR model considering disease-induced death rate. We use the method of linearization to determine the general form of the model's solution and for the stability analysis. From the stability analysis in terms of the basic reproduction number, we find the herd immunity threshold and perform sensitivity analysis. The effect of changing various parameters is also shown in this study. We use the modified SIR model to estimate the infected and removed population of COVID-19 in Bangladesh. Finally, we compare the estimation of the SIR model, including the diseases-induced death rate, and the estimation of the SIR model without including the diseases-induced death rate.

Keywords

SIR model; Diseases Induced Death Rate; Stability Analysis; Basic Reproduction Number; Herd Immunity Threshold

1. Introduction

The coronavirus (COVID-19) is a highly contagious virus caused by the SARS-CoV-2 virus. The virus was identified in 2019 in Wuhan, China, for the first time, which led to a global pandemic later. The history of COVID-19 in Bangladesh started in early 2020. The first three cases were confirmed on March 8, 2020, by the Institute of Epidemiology, Disease Control, and Research (IEDCR). The virus spread rapidly through the country. The first death due to COVID-19 was reported on March 18, 2020 [1]. It had created a pandemic situation throughout the world, including Bangladesh. The world went through extreme challenges to deal with COVID-19. Various mathematical models are used to describe the dynamics of the diseases [2]. The SIR model is one of them.

The SIR model is a mathematical framework for understanding the spread of infectious diseases within a community. The model creates three compartments: susceptible (S), infected (I), and removed (R). At the start of an outbreak, most people are susceptible (S) to the disease. As the infection spreads, some individuals become infected (I) and potentially spread the diseases to others. Infected individuals may recover, develop immunity, and migrate into the removed compartment (R) [3]. The removed compartment (R) includes recovered and died individuals. The SIR model describes the dynamics of this transmission through a system of differential equations [4]. The model is used to describe the dynamics of various infectious diseases, including COVID-19.

It takes into account factors such as the transmission rate of the disease and the size of the susceptible population. By altering these factors, researchers may simulate alternative situations and forecast the path of an epidemic, including the peak number of infections and the rate of transmission, and the potential effectiveness of vaccinations or

social distancing [5]. In this study, we consider the diseases-induced death rate in the SIR model. Although the SIR model is a simplification of real-world complications, it provides useful insights into the dynamics of infectious diseases and helps public health policies to reduce the effects of the diseases [6].

In this study, we consider the SIR model for the investigation of the spread of COVID-19 (Coronavirus). We consider the COVID-19 data of Bangladesh in early 2020. We consider a simple modification of the classical SIR model by including diseases-induced death rate.

2. The Model Equations

The SIR model considers the birth rate and death rate,

$$\begin{aligned} \frac{dS}{dt} &= \alpha - \beta SI - \delta S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \delta I \\ \frac{dR}{dt} &= \gamma I - \delta R \end{aligned} \tag{1}$$

The modified SIR model with death rate, birth rate, and diseases-induced death rate has the following form:

$$\begin{aligned} \frac{dS}{dt} &= \alpha - \beta SI - \delta S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \delta I - \epsilon I \\ \frac{dR}{dt} &= \gamma I - \delta R \end{aligned} \tag{2}$$

Where $S(0) > 0, I(0) > 0, R(0) = 0$ with $S(0) + I(0) + R(0) = 1$

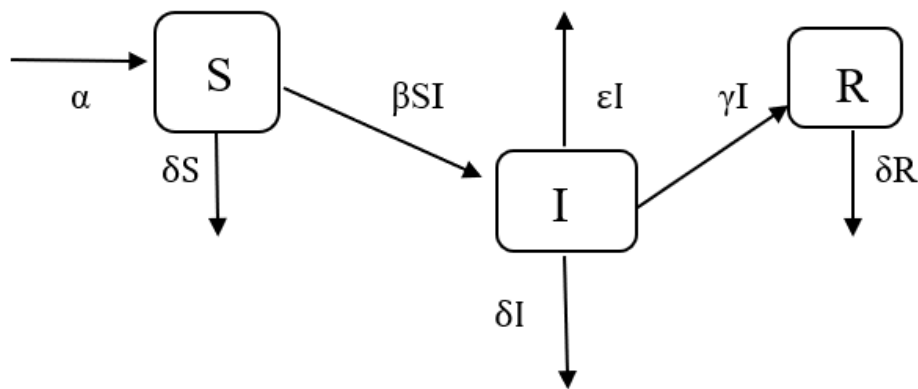


Figure 1. Modified SIR Structure.

We have considered the following parameters

Parameter	Description
α	Birth rate
δ	Natural death rate
β	Transmission rate of the diseases
γ	Recovery rate
ϵ	Diseases induced death rate

3. Solution of the System

Consider the system (2) as

$$\begin{aligned} \frac{dS}{dt} &= f_1(S, I, R) = \alpha - \beta SI - \delta S \\ \frac{dI}{dt} &= f_2(S, I, R) = \beta SI - \gamma I - \delta I - \varepsilon I \\ \frac{dR}{dt} &= f_3(S, I, R) = \gamma I - \delta R \end{aligned} \tag{3}$$

Let us assume that $S(t) = S^* + \varepsilon_1(t), I(t) = I^* + \varepsilon_2(t), R(t) = R^* + \varepsilon_3(t)$ [7].

Where (S^*, I^*, R^*) is a steady state and $\varepsilon_1, \varepsilon_2, \varepsilon_3$ are small perturbation so that (2) can be written as [5].

$$\begin{aligned} \frac{d\varepsilon_1}{dt} &= f_1(S^* + \varepsilon_1(t), I^* + \varepsilon_2(t), R^* + \varepsilon_3(t)) \\ &= f_1(S^*, I^*, R^*) + \varepsilon_1 \frac{\partial f_1}{\partial S} + \varepsilon_2 \frac{\partial f_1}{\partial I} + \varepsilon_3 \frac{\partial f_1}{\partial R} + o(\varepsilon_1^2, \varepsilon_2^2, \varepsilon_3^2) \end{aligned}$$

Similarly,

$$\begin{aligned} \frac{d\varepsilon_2}{dt} &= f_2(S^* + \varepsilon_1(t), I^* + \varepsilon_2(t), R^* + \varepsilon_3(t)) \\ &= f_2(S^*, I^*, R^*) + \varepsilon_1 \frac{\partial f_2}{\partial S} + \varepsilon_2 \frac{\partial f_2}{\partial I} + \varepsilon_3 \frac{\partial f_2}{\partial R} + o(\varepsilon_1^2, \varepsilon_2^2, \varepsilon_3^2) \end{aligned}$$

Similarly,

$$\begin{aligned} \frac{d\varepsilon_3}{dt} &= f_3(S^* + \varepsilon_1(t), I^* + \varepsilon_2(t), R^* + \varepsilon_3(t)) \\ &= f_3(S^*, I^*, R^*) + \varepsilon_1 \frac{\partial f_3}{\partial S} + \varepsilon_2 \frac{\partial f_3}{\partial I} + \varepsilon_3 \frac{\partial f_3}{\partial R} + o(\varepsilon_1^2, \varepsilon_2^2, \varepsilon_3^2) \end{aligned}$$

Now neglecting the higher order terms in $\varepsilon_1, \varepsilon_2, \varepsilon_3$ and also considering

$$f_1(S^*, I^*, R^*) = 0, \quad f_2(S^*, I^*, R^*) = 0, \quad f_3(S^*, I^*, R^*) = 0$$

Since (S^*, I^*, R^*) is a steady state.

Therefore

$$\begin{aligned} \frac{d\varepsilon_1}{dt} &= \varepsilon_1 \frac{\partial f_1}{\partial S} + \varepsilon_2 \frac{\partial f_1}{\partial I} + \varepsilon_3 \frac{\partial f_1}{\partial R} \\ \frac{d\varepsilon_2}{dt} &= \varepsilon_1 \frac{\partial f_2}{\partial S} + \varepsilon_2 \frac{\partial f_2}{\partial I} + \varepsilon_3 \frac{\partial f_2}{\partial R} \\ \frac{d\varepsilon_3}{dt} &= \varepsilon_1 \frac{\partial f_3}{\partial S} + \varepsilon_2 \frac{\partial f_3}{\partial I} + \varepsilon_3 \frac{\partial f_3}{\partial R} \end{aligned}$$

This can be written as

$$\begin{aligned} \frac{d}{dt} \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \end{pmatrix} &= \begin{pmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial R} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial I} & \frac{\partial f_2}{\partial R} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial I} & \frac{\partial f_3}{\partial R} \end{pmatrix} \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \end{pmatrix} \\ &\Rightarrow \frac{dE}{dt} = JE \end{aligned} \tag{4}$$

Where $E = \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \varepsilon_3 \end{pmatrix}$ and J is the Jacobian matrix,

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial R} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial I} & \frac{\partial f_2}{\partial R} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial I} & \frac{\partial f_3}{\partial R} \end{pmatrix}$$

Equation (3) has the solution of the form $E(t) = Ce^{Jt}$.

4. Equilibrium Points

For the equilibrium point of the system (2)

$$\frac{dS}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0$$

Therefore

$$\begin{aligned} \alpha - \beta SI - \delta S &= 0 & (5) \\ \beta SI - \gamma I - \delta I - \epsilon I &= 0 & (6) \\ \gamma I - \delta R &= 0 & (7) \end{aligned}$$

From equation (5), we have

$$\begin{aligned} \beta SI - \gamma I - \delta I - \epsilon I &= 0 \\ I(\beta S - \gamma - \delta - \epsilon) &= 0 \end{aligned}$$

Therefore, $I = 0$

And $\beta S - \gamma - \delta - \epsilon = 0$

$$S = \frac{\gamma + \delta + \epsilon}{\beta} \tag{8}$$

a) Diseases free equilibrium ($I = 0$)

Using $I = 0$ in equation (5), we have

$$\begin{aligned} \beta SI + \delta S &= \alpha \\ \delta S &= \alpha \\ S &= \frac{\alpha}{\delta} \end{aligned} \tag{9}$$

Using $I = 0$ in equation (7), we have

$$\begin{aligned} \gamma I - \delta R &= 0 \\ R &= 0 \end{aligned} \tag{10}$$

Therefore, the diseases free equilibrium $E_0 = (\frac{\alpha}{\delta}, 0, 0)$

b) Endemic Equilibrium ($I > 0$)

Now combining equation (5) and (8), we get

$$\begin{aligned} \alpha - \beta SI - \delta S &= 0 \\ \beta SI + \delta S &= \alpha \\ \beta \times I \times \frac{\gamma + \delta + \epsilon}{\beta} + \delta \times \frac{\gamma + \delta + \epsilon}{\beta} &= \alpha \\ I(\gamma + \delta + \epsilon) &= \alpha - \delta \times \frac{\gamma + \delta + \epsilon}{\beta} \\ I(\gamma + \delta + \epsilon) &= \frac{\alpha\beta - \delta(\gamma + \delta + \epsilon)}{\beta} \\ I &= \frac{\alpha\beta - \delta(\gamma + \delta + \epsilon)}{\beta(\gamma + \delta + \epsilon)} \end{aligned} \tag{11}$$

Combining equation (7) and (11), we have

$$\begin{aligned}
 \gamma I - \delta R &= 0 \\
 \delta R &= \gamma I \\
 \delta R &= \frac{\gamma \alpha \beta - \delta \gamma (\gamma + \delta + \varepsilon)}{\beta (\gamma + \delta + \varepsilon)} \\
 &= \frac{\gamma \alpha \beta - \delta \gamma (\gamma + \delta + \varepsilon)}{\delta \beta (\gamma + \delta + \varepsilon)}
 \end{aligned} \tag{12}$$

From equation (8), we have $S = \frac{\gamma + \delta + \varepsilon}{\beta}$

Therefore, the endemic equilibrium $E^*(S^*, I^*, R^*) = (\frac{\gamma + \delta + \varepsilon}{\beta}, \frac{\alpha \beta - \delta (\gamma + \delta + \varepsilon)}{\beta (\gamma + \delta + \varepsilon)}, \frac{\gamma \alpha \beta - \delta \gamma (\gamma + \delta + \varepsilon)}{\delta \beta (\gamma + \delta + \varepsilon)})$

5. Stability Analysis of Equilibrium Point

In this section, we will investigate the stability of the equilibrium points of the above-mentioned SIR model (2). In this case, we will take the first two equations of the model since the first two equations do not depend on the last one [8].

$$\begin{aligned}
 \frac{dS}{dt} &= \alpha - \beta SI - \delta S \\
 \frac{dI}{dt} &= \beta SI - \gamma I - \delta I - \varepsilon I
 \end{aligned}$$

For the stability analysis of the system of ODE, around equilibrium points, we consider the Jacobian matrix of the system. The stability of the equilibrium will depend on the sign of the eigenvalues of the Jacobian matrix [9].

a) Stability of the Diseases Free Equilibrium

The Jacobian Matrix

$$J(S, I) = \begin{bmatrix} -\beta I - \delta & -\beta S \\ \beta I & \beta S - \gamma - \delta - \varepsilon \end{bmatrix} \tag{13}$$

Now the Jacobian Matrix around diseases free equilibrium $E_0 = (\frac{\alpha}{\delta}, 0)$

$$J(S, I) = \begin{bmatrix} -\delta & -\frac{\alpha \beta}{\delta} \\ 0 & \frac{\alpha \beta}{\delta} - (\gamma + \delta + \varepsilon) \end{bmatrix}$$

The characteristic equation becomes

$$(\lambda + \delta) \left\{ \lambda - \left(\frac{\alpha \beta}{\delta} - (\gamma + \delta + \varepsilon) \right) \right\} = 0$$

Therefore, the eigenvalues

$$\begin{aligned}
 \lambda_1 &= -\delta < 0 \\
 \lambda_2 &= \frac{\alpha \beta}{\delta} - (\gamma + \delta + \varepsilon)
 \end{aligned}$$

The equilibrium is stable if and only if

$$\begin{aligned}
 \frac{\alpha \beta}{\delta} - (\gamma + \delta + \varepsilon) &< 0 \\
 \Rightarrow \frac{\alpha \beta}{\delta} &< (\gamma + \delta + \varepsilon) \\
 \Rightarrow 1 &< \frac{\delta (\gamma + \delta + \varepsilon)}{\alpha \beta} \\
 \Rightarrow \frac{\alpha \beta}{\delta (\gamma + \delta + \varepsilon)} &< 1
 \end{aligned}$$

Therefore, the disease-free equilibrium is asymptotically stable if

$$\frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)} < 1$$

Therefore, the disease-free equilibrium is unstable if

$$\frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)} > 1$$

b) Stability of Endemic Equilibrium

The Jacobian Matrix

$$J(S, I) = \begin{bmatrix} -\beta I - \delta & -\beta S \\ \beta I & \beta S - \gamma - \delta - \varepsilon \end{bmatrix}$$

Now the Jacobian Matrix around endemic equilibrium

$$\begin{aligned} (S^*, I^*, R^*) &= \left(\frac{\gamma + \delta + \varepsilon}{\beta}, \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{\beta(\gamma + \delta + \varepsilon)}, \frac{\gamma\alpha\beta - \delta\gamma(\gamma + \delta + \varepsilon)}{\delta\beta(\gamma + \delta + \varepsilon)} \right) \\ J(S, V, I) &= \begin{bmatrix} -\delta - \beta \times \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{\beta(\gamma + \delta + \varepsilon)} & -\beta \times \frac{\gamma + \delta + \varepsilon}{\beta} \\ \beta \times \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{\beta(\gamma + \delta + \varepsilon)} & 0 \end{bmatrix} \\ &= \begin{bmatrix} -\delta - \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{(\gamma + \delta + \varepsilon)} & -(\gamma + \delta + \varepsilon) \\ \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{(\gamma + \delta + \varepsilon)} & 0 \end{bmatrix} \\ &= \begin{bmatrix} \frac{-\delta(\gamma + \delta + \varepsilon) - \alpha\beta + \delta(\gamma + \delta + \varepsilon)}{(\gamma + \delta + \varepsilon)} & -(\gamma + \delta + \varepsilon) \\ \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{(\gamma + \delta + \varepsilon)} & 0 \end{bmatrix} \\ &= \begin{bmatrix} \frac{-\alpha\beta}{(\gamma + \delta + \varepsilon)} & -(\gamma + \delta + \varepsilon) \\ \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{(\gamma + \delta + \varepsilon)} & 0 \end{bmatrix} \end{aligned}$$

Now $\text{Tr}(J) = \frac{-\alpha\beta}{(\gamma + \delta + \varepsilon)} < 0$

$$\text{Det}(J) = \alpha\beta - \delta(\gamma + \delta + \varepsilon)$$

For the stability of the endemic equilibrium, we must have

$$\begin{aligned} \alpha\beta - \delta(\gamma + \delta + \varepsilon) &> 0 \\ \alpha\beta &> \delta(\gamma + \delta + \varepsilon) \\ 1 &> \frac{\delta(\gamma + \delta + \varepsilon)}{\alpha\beta} \\ \frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)} &> 1 \end{aligned}$$

Therefore, the endemic equilibrium is asymptotically stable if

$$\frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)} > 1$$

Therefore, the endemic equilibrium is unstable if

$$\frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)} < 1$$

6. Basic Reproductive Number, R_0

In epidemiology, the basic reproductive number (sometimes referred to as the basic reproduction rate or ratio) of an infection represents the average number of cases generated by a single infected individual over the course of its infectious period. The value of $\frac{\alpha\beta}{\delta(\gamma+\delta+\epsilon)}$ is a threshold value, called the basic reproduction number R_0 , this plays a significant influence in determining disease dynamics and is used for preventative methods. It helps to determine whether the disease spreads or is eradicated. If the value of R_0 is less than 1 ($R_0 < 1$), the infection will gradually die out since each infected individual produces less than one new infected individual [9], [10]. Conversely, if R_0 is greater than 1 ($R_0 > 1$), The infection has the ability to spread within a community since each infected individual creates more than one new infected individual [10].

Here,

$$R_0 = \frac{\alpha\beta}{\delta(\gamma+\delta+\epsilon)} \quad (14)$$

This R_0 is known as the basic reproduction number.

7. The Herd Immunity Threshold, H_1

The percentage of the population that needs to be immunized in order to prevent the spread of an infection is known as the herd immunity threshold (H_1). The fundamental reproductive number, or R_0 , affects a disease's endemicity [10]. The threshold value aids in predicting whether or not the diseases will persist in circulating and spreading throughout the community. The equation given for estimating the herd immunity threshold is given as

$$H_1 = 1 - \frac{1}{R_0} \quad (15)$$

8. Numerical Simulation

Numerical simulation involves employing computational methods to approximate the behavior of the model over time [9], [11]. It allows researchers to study alternative situations, evaluate the impact of different parameters, and predict the development of an epidemic. These simulations provide essential insights into the dynamics of disease transmission. Sensitivity analysis complements numerical simulations by examining the model's response to changes in its input parameters [12].

We have calculated the numerical solution of the modified SIR model. For the numerical solution of the model, we have considered the data of COVID-19 epidemics in Bangladesh, and the values of the parameters are estimated by trial and error. According to the Press Release of the Director General of Health Services [1].

Table 1. Symbol and Value of Parameters

Parameters	Symbol	Value
Birth rate	α	0.018
Natural death rate	δ	0.0055
Disease transmission rate	β	0.111
Recovery rate	γ	0.029
Diseases induced death rate	ϵ	0.034

Let us consider $S(0) = 0.9, I(0) = 0.1, R(0) = 0$

The following visualizations illustrate the given system's solution curve of equation (2) for parameter values of Table 1.

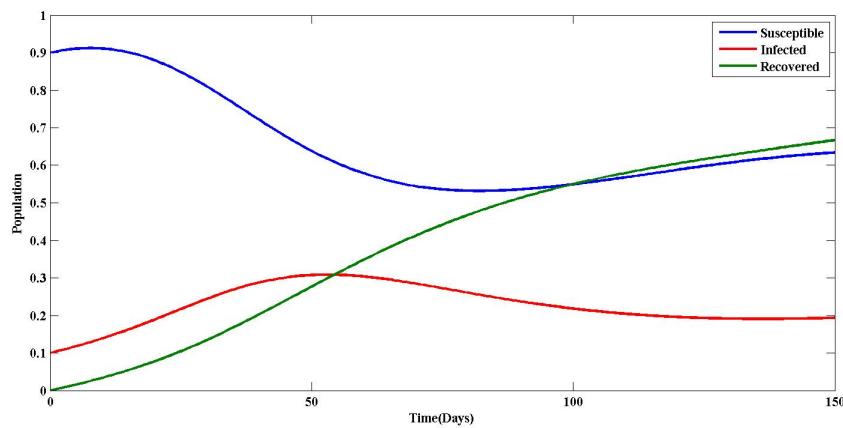


Figure 2. Solution Curve of the SIR Model with Parameter Values of Table 1.

9. Basic Reproduction Number R_0

$$R_0 = \frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)}$$

$$= \frac{0.018 \times 0.111}{0.0055 \times (0.029 + 0.034 + 0.0055)}$$

$$= 5.30 > 0$$

10. Estimation of Herd Immunity Threshold, H_1

From 11, we have the value of the basic reproduction number, $R_0 = 5.30$
 Therefore, from equation (15), we have the herd immunity threshold, [10].

$$H_1 = 1 - \frac{1}{5.30}$$

$$= 0.8113$$

Consequently, in order to prevent the COVID-19 pandemic, approximately 81.13% of the population must be immunized during the outbreak.

11. Estimation of Equilibrium Point

There are two equilibrium points of the system (2), one is disease-free equilibrium, and the other is the endemic equilibrium

The diseases free equilibrium $E_0(S_0, I_0, R_0) = \left(\frac{\alpha}{\delta}, 0, 0\right) = (3.27, 0, 0)$

The endemic equilibrium $(S^*, I^*, R^*) = \left(\frac{\gamma + \delta + \varepsilon}{\beta}, \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{\beta(\gamma + \delta + \varepsilon)}, \frac{\gamma\alpha\beta - \delta\gamma(\gamma + \delta + \varepsilon)}{\delta\beta(\gamma + \delta + \varepsilon)}\right)$
 $= (0.617, 0.2132, 1.124)$

12. Stability Analysis of Equilibrium Points

a) Diseases Free Equilibrium

From the Jacobian matrix of equation (9)

$$J(S, V, I) = \begin{bmatrix} -\beta I - \delta & -\beta S \\ \beta I & \beta S - \gamma - \delta - \varepsilon \end{bmatrix}$$

Around the diseases free equilibrium $E_0(S_0, I_0, R_0) = \left(\frac{\alpha}{\delta}, 0, 0\right)$ i.e. $(3.27, 0, 0)$

$$J(S_0, I_0, R_0) = \begin{bmatrix} -0.0055 & -0.111 \times 3.27 \\ 0 & 0.111 \times 3.27 - 0.029 - 0.0055 - 0.034 \end{bmatrix}$$

$$= \begin{bmatrix} -0.0055 & -0.363 \\ 0 & 0.2945 \end{bmatrix}$$

The characteristics equation becomes

$$(\lambda + 0.0055)(\lambda - 0.2945) = 0$$

The corresponding lamda $\lambda_1 = -0.0055 < 0$

$$\lambda_2 = 0.2945 > 0$$

Therefore the diseases free equilibrium is an unstable steady state.

b) Endemic Equilibrium

From the Jacobian matrix of equation (9)

$$J(S, V, I) = \begin{bmatrix} -\beta I - \delta & -\beta S \\ \beta I & \beta S - \gamma - \delta - \varepsilon \end{bmatrix}$$

Around the endemic equilibrium $E^*(S^*, I^*, R^*) = \left(\frac{\gamma + \delta + \varepsilon}{\beta}, \frac{\alpha\beta - \delta(\gamma + \delta + \varepsilon)}{\beta(\gamma + \delta + \varepsilon)}, \frac{\gamma\alpha\beta - \delta\gamma(\gamma + \delta + \varepsilon)}{\delta\beta(\gamma + \delta + \varepsilon)} \right)$

$$= (0.617, 0.2132, 1.124)$$

$$J(S^*, I^*, R^*) = \begin{bmatrix} -0.029 & -0.069 \\ 0.0234 & 0 \end{bmatrix}$$

The characteristics equation becomes

$$tr(J) = -0.029 < 0$$

$$det(J) = 0.001615 > 0$$

Therefore, the endemic equilibrium is asymptotically stable.

13. Phase Plane of SIR Model

For the parameters value of Table 1, $R_0 = 5.30 > 1$.

In that case, we have an endemic equilibrium which is asymptotically stable. We have used PPLNE8 for the phase plane analysis.

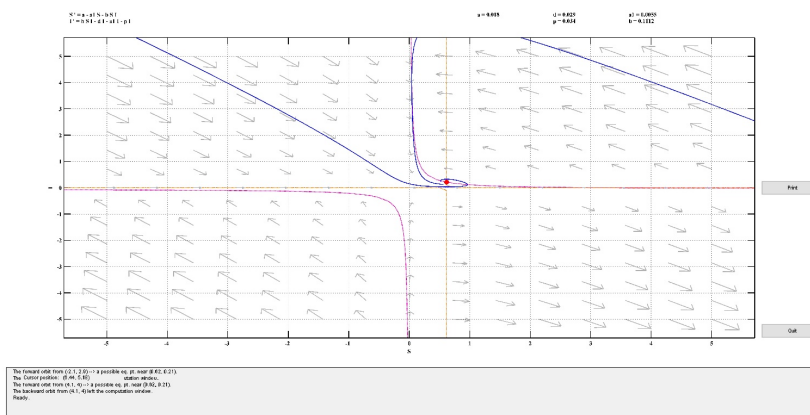


Figure 3. Phase Plane of Endemic Equilibrium.

14. Sensitivity Analysis

Sensitivity analysis determines how different values of an independent variable affect a certain dependent variable under a given set of assumptions. In other words, sensitivity analyses study how various sources of uncertainty in a mathematical model contribute to the model’s overall uncertainty [12].

The normalized forward sensitivity index of R_0 , on a parameter a , is defined by

$$Y_a^{R_0} = \frac{\partial R_0}{\partial a} \times \frac{a}{R_0}$$

Sensitivity analysis in the context of an SIR model (Susceptible–Infected–Recovered) helps determine how changes in model parameters influence outcomes such as infection peak, duration of epidemic, or final size of the epidemic [13].

We have already seen that the stability of both the diseases-free equilibrium and the endemic equilibrium depends on the value of R_0 .

Where

$$R_0 = \frac{\alpha\beta}{\delta(\gamma + \delta + \varepsilon)}$$

The partial derivatives of R_0 with respect to parameters of the model are calculated in this section.

For the parameter β :

$$\begin{aligned} \frac{\partial R_0}{\partial \beta} &= \frac{\alpha}{\delta(\gamma + \delta + \varepsilon)} \\ \frac{\partial R_0}{\partial \beta} \frac{\beta}{R_0} &= \frac{\alpha}{(\gamma + \delta + \varepsilon)\delta} \times \frac{\delta\beta(\gamma + \delta + \varepsilon)}{\alpha\beta} \\ &= 1 \end{aligned}$$

For the parameter γ :

$$\begin{aligned} \frac{\partial R_0}{\partial \gamma} &= \frac{-\beta\alpha\delta}{(\gamma + \delta + \varepsilon)^2\delta^2} \\ \frac{\partial R_0}{\partial \gamma} \frac{\gamma}{R_0} &= \frac{-\beta\alpha\delta}{(\gamma + \delta + \varepsilon)^2\delta^2} \times \frac{\gamma\delta(\gamma + \delta + \varepsilon)}{\alpha\beta} \\ &= \frac{-\gamma}{(\gamma + \delta + \varepsilon)} \end{aligned}$$

For the parameter ε :

$$\begin{aligned} \frac{\partial R_0}{\partial \varepsilon} &= \frac{-\beta\alpha\delta}{(\gamma + \delta + \varepsilon)^2\delta^2} \\ \frac{\partial R_0}{\partial \varepsilon} \frac{\varepsilon}{R_0} &= \frac{-\beta\alpha\delta}{(\gamma + \delta + \varepsilon)^2\delta^2} \times \frac{\varepsilon\delta(\gamma + \delta + \varepsilon)}{\alpha\beta} \\ &= \frac{-\varepsilon}{(\gamma + \delta + \varepsilon)} \end{aligned}$$

Table 2. Parameter values

Parameters	Value
α	0.018
δ	0.0055
β	0.111
γ	0.029
ε	0.034

Table 3. Sensitivity Index

Parameters	Sensitivity Index
β	1
γ	-0.4234
ε	-0.4964

In order to help policymakers and public health professionals better prioritize their efforts and resources, we may determine which variables have the greatest impact on the model results by doing a sensitivity analysis. The parameter diseases-induced death rate has a negative impact on the basic reproduction number.

15. Effect of Changing Various Parameters

In this section, we have shown how the solution curves are changed with the change of various parameters $\beta, \gamma, \varepsilon$. By controlling these parameters, we can control the diseases spreading [14].

16. Effect of Changing the Value of β

In Figures 4, 5, and 6, we observed that changing of value of β has a significant impact on the susceptible, infected, and removed populations. From Figure 4, we observe that as the increase of value of β , the susceptible population decreases, whereas Figure 6 shows that the removed population increases with the increase of β , which is also true for the vice versa. From Figure 5, it is evident that the change in the infected population with the change of transmission rate is momentous.

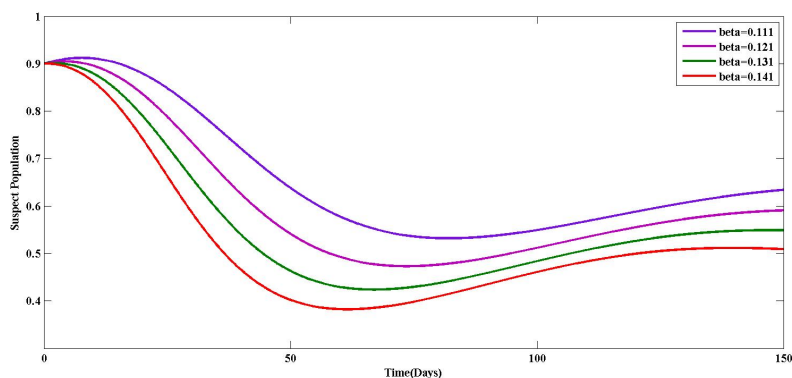


Figure 4. Effect of Changing Transmission Rate on Susceptible Population.

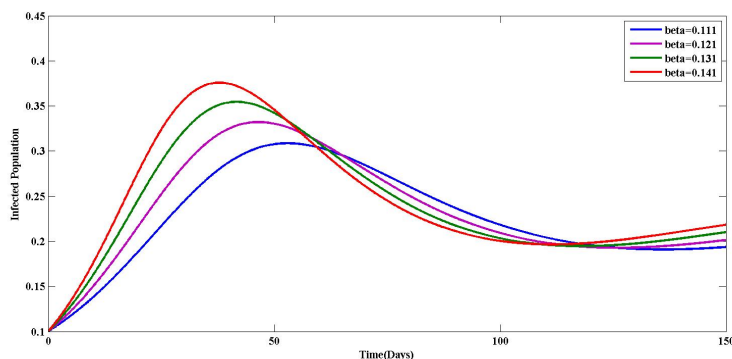


Figure 5. Effect of Changing Transmission Rate on Infected Population.

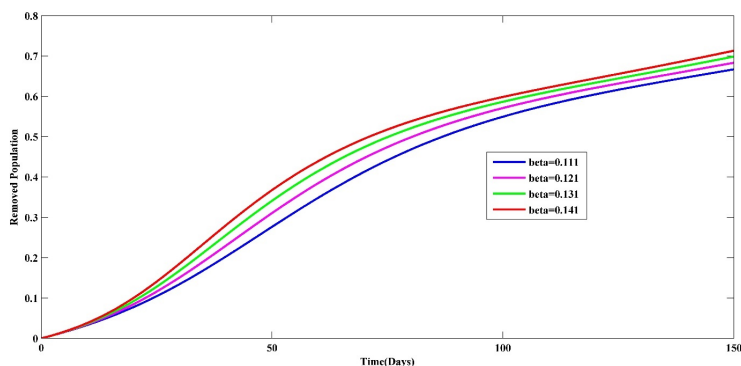


Figure 6. Effect of Changing Transmission Rate on Removed Population.

17. Effect of changing the value of γ

In Figures 7, 8, and 9, we observed that changing of value of γ has a significant impact on the susceptible, infected

and removed populations. With the increase of the value of γ , the susceptible population increases, whereas the infected population decreases; that is also true for the vice versa. Therefore, β has a positive impact on the susceptible population and a negative impact on the infected population. From Figure 9, it is evident that the effect of γ on the removed population is momentous.

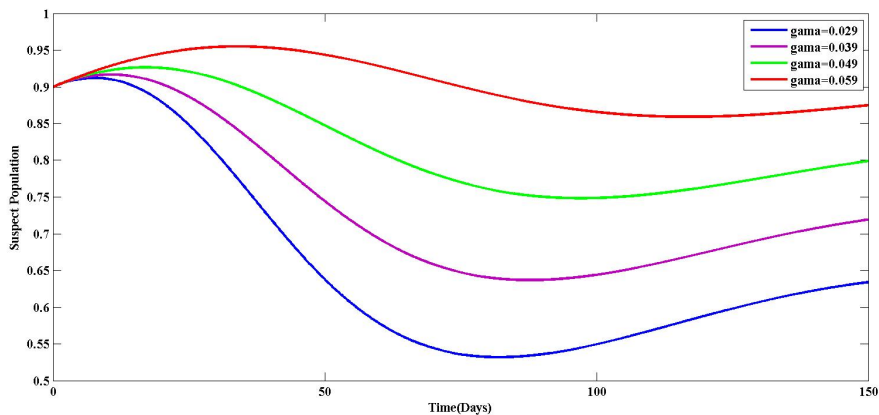


Figure 7. Effect of Changing Recovery Rate on Susceptible Population.

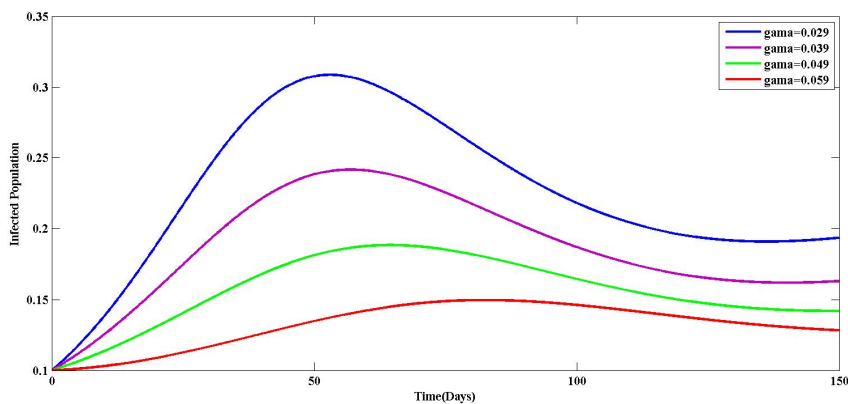


Figure 8. Effect of Changing Recovery Rate on Infected Population.

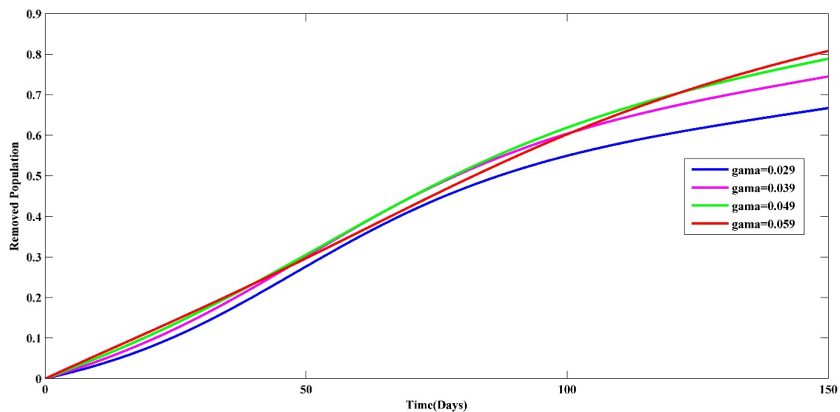


Figure 9. Effect of Changing Recovery Rate on Recovered Population.

18. Effect of changing the value of ϵ

In Figures 10, 11, and 12, we observed that changing of value of ϵ has a significant impact on the susceptible, infected and removed populations. With the increase of value of ϵ , the susceptible population increases, whereas the infected and removed population decreases; that is also true for the vice versa. Therefore, ϵ has a positive impact on the suspect population and a negative impact on the infected and removed populations.

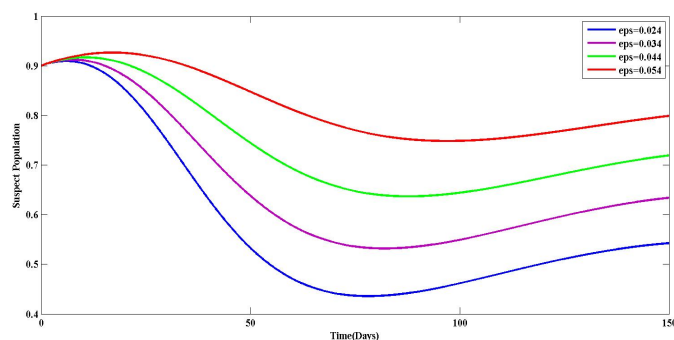


Figure 10. Effect of Changing Diseases-Induced Death Rate on Susceptible Population.

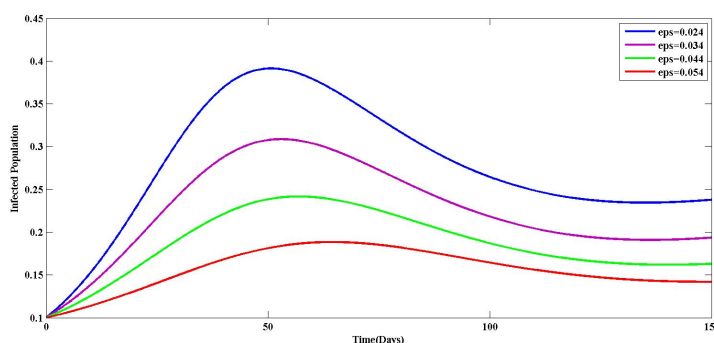


Figure 11. Effect of Changing Diseases-Induced Death Rate on Infected Population.

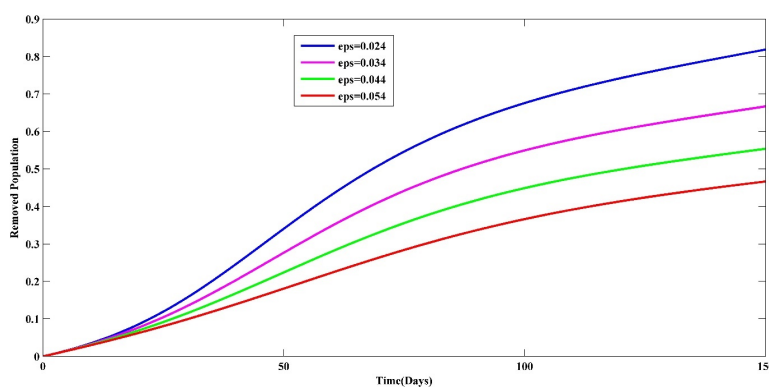


Figure 12. Effect of Changing Diseases-Induced Death Rate on the Removed Population.

19. Comparison between Real Data of COVID-19 in Bangladesh and Estimation of the SIR Model

Using the real data of COVID-19 cases in Bangladesh, according to the Press Release of the Director General of

Health Services, since 18 March 2020 to 17 June 2020 [1].

Table 4. Parameter Values

Date	Transmission Rate	Recovery Rate	Death Rate
18/03/2020-15/6/2020	0.111	0.029	0.034

Considering $S(0) = 0.99, I(0) = 0.01, R(0) = 0$

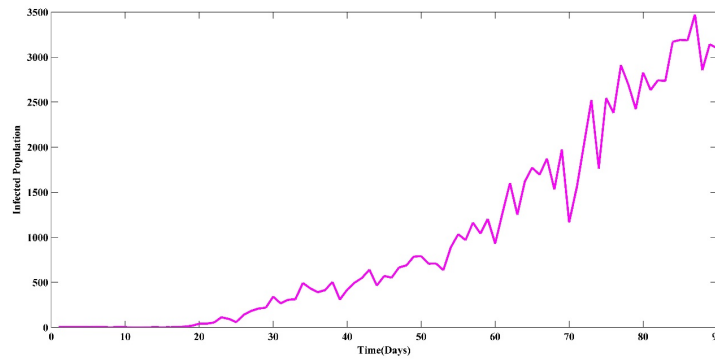


Figure 13. Infected population of COVID-19 from 18 March 2020 to 15 June 2020 in Bangladesh.

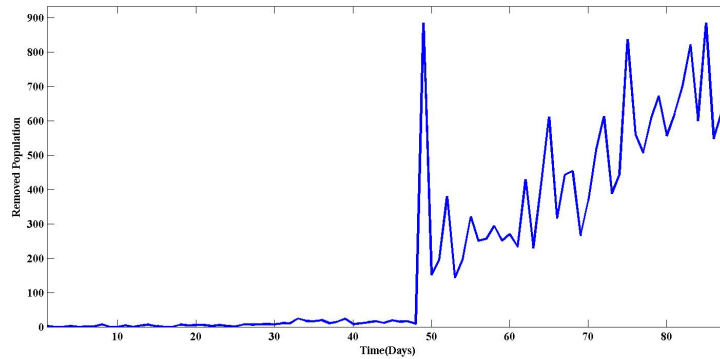


Figure 14. Removed the Population of COVID-19 from 18 March 2020 to 14 June 2020 in Bangladesh.

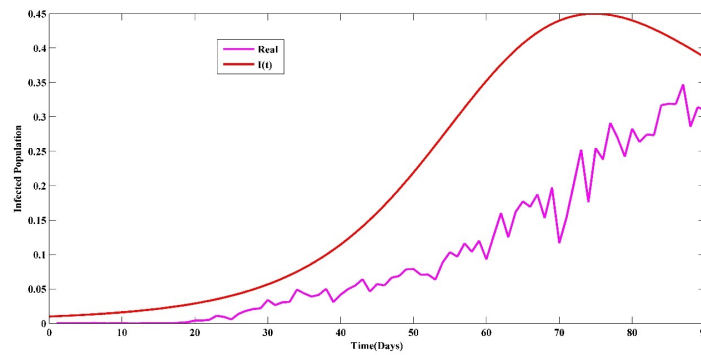


Figure 15. Comparison between Real Infected Population and Infected Population Estimated by SIR Model.

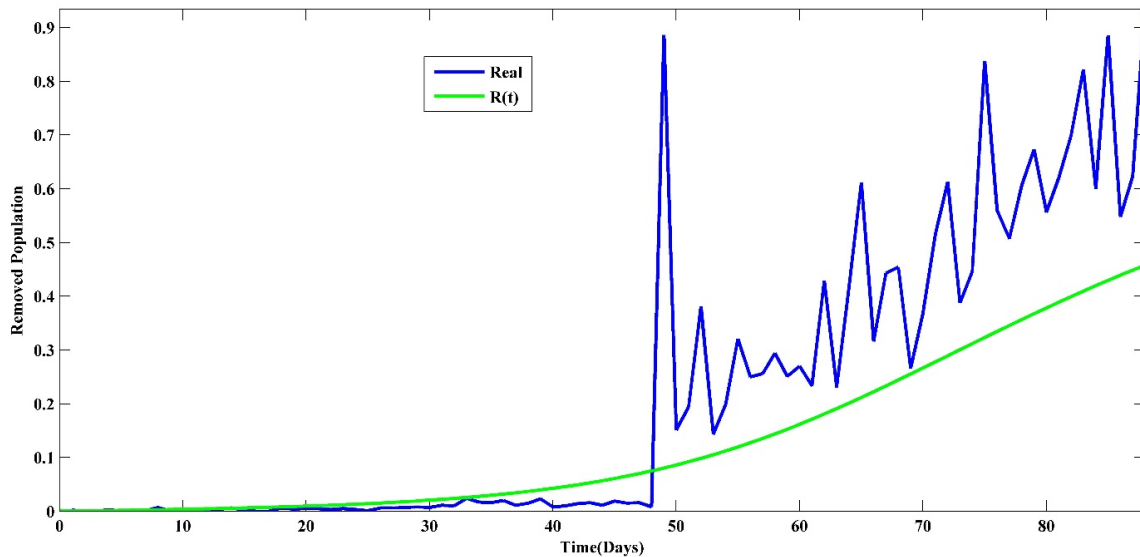


Figure 16. Comparison between the Real Removed Population and the Removed Population Estimated by SIR Model.

In Figure 15, the pink curve indicates the number of individuals infected by COVID-19, and the blue curve indicates the model’s estimated infected population by COVID-19.

In Figure 16, the blue curve indicates the removed population from COVID-19, which includes both the dead and recovered individuals, and the green curve indicates the model’s estimation of the removed population. From the figures, we can conclude that the model is capable of making a good estimation of both the infected and removed populations.

20. Comparison of the SIR Model, Considering Diseases Induced Death Rate, and without Considering Diseases Induced Death Rate

Here, we make a comparison of these two models (the SIR model considering the disease-induced death rate and the SIR model without considering the disease-induced death rate).

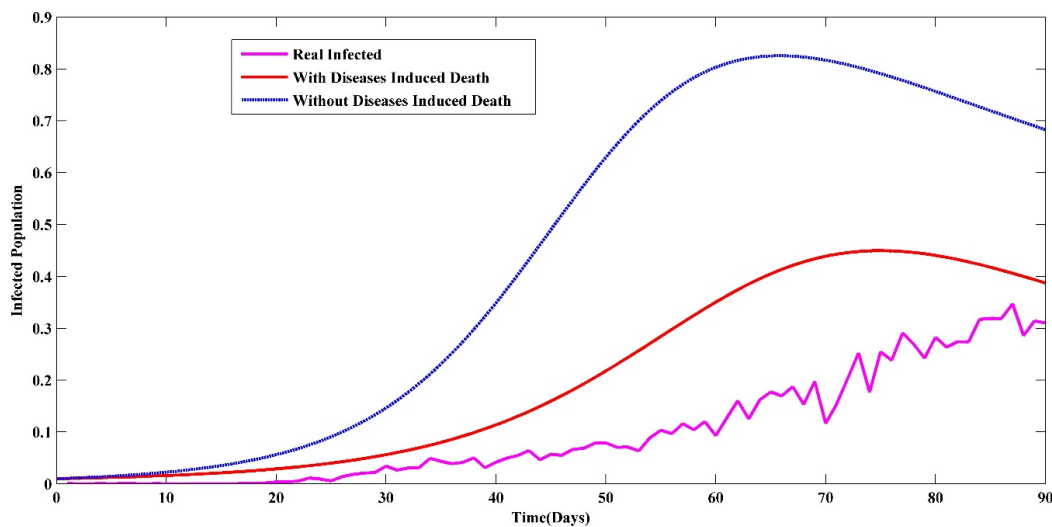


Figure 17. Comparison among the Real Infected Population and the Estimation of Infected Population using the SIR model Considering Diseases Induced Death Rate and without Considering the Diseases Induced Death Rate.

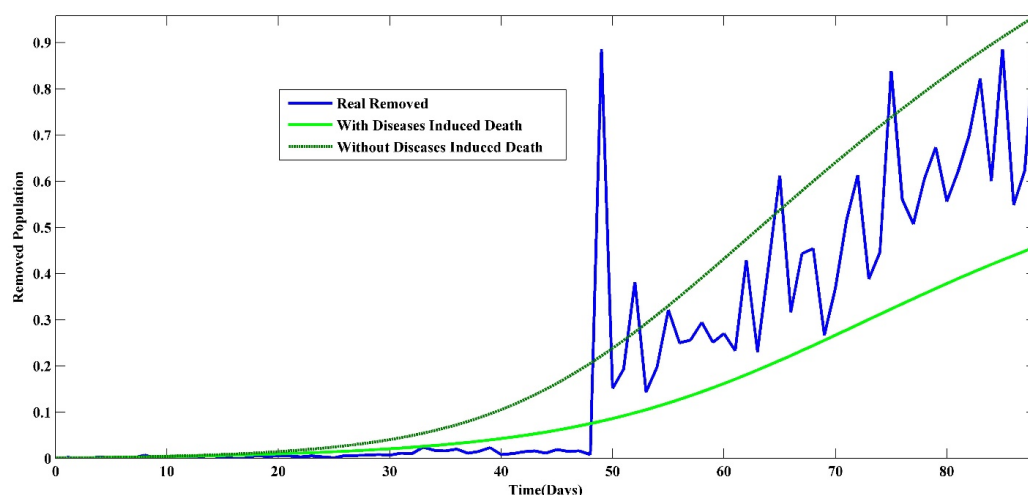


Figure 18. Comparison among the Real Removed Population and the Estimation of Removed Population Using the SIR Model Considering Diseases Induced Death Rate and without Considering the Diseases Induced Death Rate.

The above study reveals that a slight modification of the SIR model, considering the diseases-induced death rate in it, makes the model more realistic. This modified SIR model gives a better estimation of the infected and removed population of COVID-19.

21. Conclusion

We implement a modified SIR model, including diseases-induced death rate, to study the COVID-19 dynamics of Bangladesh. In this study, we have considered the data of COVID-19 in Bangladesh in early 2020. This was almost the preliminary stage of COVID-19 in Bangladesh; at that time, COVID-19 had created a pandemic situation in Bangladesh. Our investigation by using the SIR model of equation (2), which is a simple modification of the classical SIR model, shows that the disease was in a pandemic situation. The modified SIR model, including disease-induced death rate, gives a better estimation than the SIR model without considering the diseases-induced death rate. The parameter diseases-induced death rate and recovery rate have a negative impact on the basic reproduction number R_0 , which means the parameters have a positive effect on controlling the severity of the pandemic. By altering the value of a specific factor while holding all other factors constant, the impact of various clinical parameters is graphically represented. It is observed that this model performs well in estimating parameters and matching data, particularly the infected population $I(t)$. The study provides medical professionals with information about the dynamic behavior of susceptible, infected, and removed individuals during diseases and also helps the public health sector in disease control strategies.

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