SARS-CoV-2 and Rohingya Refugee Camp, Bangladesh: Uncertainty and how the government took over the situation

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Abstract.
Background: Bangladesh hosts more than 800,000 Rohingya refugees from Myanmar. The low health immunity, lifestyle, access to good healthcare services, social-security cause this population to be at risk of far more direct effects of COVID-19 than the host population. Therefore, evidence-based forecasting of the COVID-19 burden is vital in this regard. In this study, we aimed to forecast the COVID-19 burden among the Rohingya refugees of Bangladesh to keep up with the disease outbreak's pace, health needs, and disaster preparedness.
Methodology and Findings: To estimate the possible consequences of COVID-19 in the Rohingya camps of Bangladesh, we used a modified Susceptible-Exposed-Infectious Recovered (SEIR) transmission model. All the values of different parameters used in this model were from the Bangladesh Government's database and the relevant emerging literature. We addressed two different scenarios, i.e., the best-fitting model and good fitting model with unique consequences of COVID-19. Our best fitting model suggests that there will be good control over the transmission of the COVID-19 disease. At the end of December 2020, there will be only 169 confirmed COVID-19 cases in the Rohingya refugee camps. The average basic reproduction number ($\mathcal{R}_0$) has been estimated to be 0.7563.
Conclusion: Our analysis suggests that, due to the extensive precautions from the Bangladesh government as well as other humanitarian organizations, the coronavirus disease will be under control if the maintenance continues like this. Although detailed and pragmatic preparedness should be adopted for the worst scenario.

Keywords: COVID-19 · Rohingya Refugee camp · Mathematical model · Numerical results · Basic reproduction number.
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Introduction

Globally, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is amenable to nearly 60.4 million confirmed cases and more than one million death from early 2020 to November 2020 [1]. It has been almost eight months since the first outbreak, and still, most of the countries in the world unable to control the spread of the disease [2]. However, rapid response, preparedness, and planning are crucial to controlling the SARS-CoV-2 among the most susceptible populations.

Since August 2017, Bangladesh has been providing shelter to the Forcibly Displaced Myanmar Nationals (FDMN), and at this point, according to UNHCR, around one million are living in the refugee camps of Ukhiya, Cox's Bazar [3]. The current condition of these refugee camps, i.e., high population density (46,000 people/square kilometer), limited water supply, sanitation infrastructure, and health care can create havoc inside the camp COVID-19 virus.

Bangladesh has reported its first COVID-19 case on March 8, 2020, and approximately two months later, on May 14, 2020, the first Rohingya refugee with positive COVID-19 infection was declared [4]. Since then, to August 9, 2020, 78 COVID-19 cases have been identified, and six died due to the complications of the disease (virus) [5]. Approximately 3% of the refugees were identified as disease positive among those tested for the virus [5]. A total of 12 severe acute respiratory illness (SARI) isolation and treatment centers (ITC) were operational, and for the patients who required intensive care unit or high dependency unit were referred to the Sadar Hospital of Cox's Bazar [5].

The health condition and the quality of life of the FDMN inside the refugee camps remain very delicate. Nearly one-fifth of this population belonged to the under-five age group, and 8.4% were from the old age group can be specified here, such as over 50-age group, etc. Besides, among the ever-married women, 14% were pregnant in the refugee camps [6]. Furthermore, global acute malnutrition (GAM) is still very high in this humanitarian setting [7]. Therefore, a massive number of the population are at risk of being infected by the virus.

In this study, our target was to comprehend the impact of the SARS-CoV-2 virus on the FDMN population living in Cox's Bazar, Bangladesh. This study's aims include (a) developing an SEIR model to forecast the probable COVID-19 disease burden to this vulnerable community by using the recent data, (b) utilizing these findings to provide recommendations to the Government of Bangladesh as well as the donors for preparing fruitful plans.

Methodology

Mathematical model and formulation

In infectious disease modeling, the classical SIR model allows determining of the critical condition of disease development in the population with a total population size. Among various shapes, the typical non-demographic SIR model is defined as [8]:

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t} = -\beta I S, \\ \dfrac{\mathrm{d}I}{\mathrm{d}t} = \beta I S - \gamma I - \mu I, \\ \dfrac{\mathrm{d}R}{\mathrm{d}t} = \gamma I, \end{cases} \tag{1}$$

for $t \in (0, \infty)$ with initial conditions

$$S(0) = S_0, \quad I(0) = I_0 \text{ and } R(0) = R_0. \tag{2}$$

and for total population is $N(t) = S(t) + I(t) + R(t)$. Here $S(t)$, $I(t)$, $R(t)$ are the number of individuals in the susceptible, infectious, and removal compartments, respectively, at time t with a day unit. The parameter β denotes disease transmission rate, γ is the removal rate, and μ is the mortality rate due to the infection only. The solution and the detailed analysis of (1) can be found in [8].

In the case of pandemic COVID-19, we propose the following SEIR type (modified SEIR) mathematical model.

$$\begin{cases} \dfrac{\mathrm{d}S}{\mathrm{d}t} = \Lambda - \sigma(E+I)S - \mu_1 S, \\ \dfrac{\mathrm{d}E}{\mathrm{d}t} = \sigma(E+I)S - (\beta+\gamma_1+\mu_1)E, \\ \dfrac{\mathrm{d}I}{\mathrm{d}t} = \beta E - (\gamma_2+\mu_1+\mu_2)I, \\ \dfrac{\mathrm{d}R}{\mathrm{d}t} = \gamma_1 E + \gamma_2 I - \mu_1 R \end{cases} \tag{3}$$

with initial conditions

$$S(0) = S_0, \quad E(0) = E_0, \quad I(0) = I_0 \text{ and } R(0) = 0\,, \tag{4}$$

and

$$N(t) \equiv S(t) + E(t) + I(t) + R(t)\,, \tag{5}$$

Here, $S(t), E(t), I(t)$ and $R(t)$ are the number of individuals in the susceptible, asymptotically infected, infectious, and removal compartments, respectively, at time t with a day unit. Here, we consider the E class includes all the infectious and non-infectious asymptomatic carriers of the COVID-19 (SARS-CoV-2) virus. WHO claims, though asymptomatic carriers are rare but can be infectious and another study [9] found that people who get infected with the coronavirus can spread it to others 2 to 3 days before symptoms start and are most contagious 1 to 2 days before they feel sick. Λ is the recruitment number in the susceptible compartment. Natural and disease-induced deaths are denoted by μ_1 and μ_2, respectively. σ and β are the corresponding transmission and transition rates, respectively and γ_i $(i = 1, 2)$ are the recovery rates of asymptotically infected (E) and infectious (I) compartments, respectively. Since the model monitors dynamics of population, it follows that all its dependent variables and parameters, for examples, $\Lambda, \beta, \gamma_i, \mu_i$ and σ must be non-negative along with $\mu_1 > 0$ as in the model (3).

The flow diagram of the proposed model is given in Figure 1.

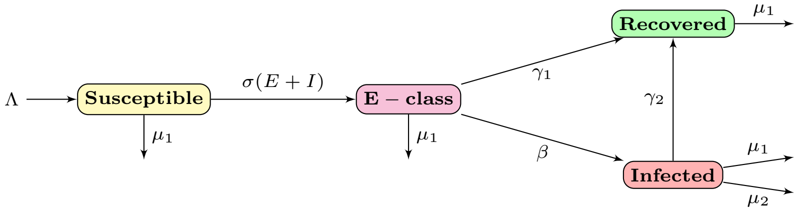

Figure 1: Model diagram.

Equilibrium points

To find the equilibrium points of the system (3), we set the derivatives equal to zero. So, at equilibrium states $(S, E, I, R) \equiv (\widetilde{S}, \widetilde{E}, \widetilde{I}, \widetilde{R})$, we get

$$\begin{cases} \Lambda - \sigma(\widetilde{E}+\widetilde{I})\widetilde{S} - \mu_1\widetilde{S} = 0, \\ \sigma(\widetilde{E}+\widetilde{I})\widetilde{S} - (\beta+\gamma_1+\mu_1)\widetilde{E} = 0, \\ \beta\widetilde{E} - (\gamma_2+\mu_1+\mu_2)\widetilde{I} = 0, \\ \gamma_1\widetilde{E} + \gamma_2\widetilde{I} - \mu_1\widetilde{R} = 0. \end{cases} \tag{6}$$

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Disease-free equilibrium point

For the disease-free equilibrium (DFE), we replace the variables as

$$(\widetilde{S}, \widetilde{E}, \widetilde{I}, \widetilde{R}) \equiv (S_0, E_0, I_0, R_0).$$

This gives

$$\begin{cases} \Lambda - \sigma(E_0 + I_0)S_0 - \mu_1 S_0 = 0, \\ \sigma(E_0 + I_0)S_0 - (\beta + \gamma_1 + \mu_1)E_0 = 0, \\ \beta E_0 - (\gamma_2 + \mu_1 + \mu_2)I_0 = 0, \\ \gamma_1 E_0 + \gamma_2 I_0 - \mu_1 R_0 = 0. \end{cases}$$

Therefore, the disease-free equilibrium (DFE) point can easily be found as

$$(S_0, E_0, I_0, R_0) \equiv \left(\frac{\Lambda}{\mu_1}, 0, 0, 0\right). \tag{7}$$

Basic reproduction number

The basic reproduction number is a necessary threshold condition in the analysis of an infectious disease. It determines whether the disease will die out or persist in the population as time passes. It is defined to be the number of secondary infections produced by one primary infection in a population where everyone is susceptible and is denoted by $\mathcal{R}_0$ [8, 10]. If $\mathcal{R}_0 > 1$, one primary infection can produce more than one secondary infection. This implies that the disease-free equilibrium (DFE) is unstable. As a result, an epidemic breaks out and may cause a pandemic.

If $\mathcal{R}_0 < 1$, the situation is thought to be under control. In this case, the disease-free equilibrium (DFE) will be locally asymptotically stable, and the disease cannot persist in the population. So, when a pandemic breaks out, an effective strategy should be developed so that the reproduction number reduces to less than 1 as soon as possible [8, 10, 11].

Since the considered model has DEF $(S_0, E_0, I_0, R_0) \equiv \left(\frac{\Lambda}{\mu_1}, 0, 0, 0\right)$, hence the basic reproduction number can be found analytically. Using next-generation matrix method [8, 10, 11, 12], the reproduction number for the COVID-19 model given by (3) can be calculated from the relation $\mathcal{R}_0 = \rho(FV^{-1})$, that is the spectral radius of FV^{-1} [8, 10, 11], where

$$F = \begin{pmatrix} \sigma S_0 & \sigma S_0 \\ 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} \beta + \gamma_1 + \mu_1 & 0 \\ -\beta & \gamma_2 + \mu_1 + \mu_2 \end{pmatrix}.$$

Therefore, the V^{-1} matrix is

$$V^{-1} = \begin{pmatrix} \frac{1}{\beta+\gamma_1+\mu_1} & 0 \\ \frac{\beta}{(\beta+\gamma_1+\mu_1)(\gamma_2+\mu_1+\mu_2)} & \frac{1}{\gamma_2+\mu_1+\mu_2} \end{pmatrix}.$$

Thus, the next-generation matrix FV^{-1} is

$$FV^{-1} = \begin{pmatrix} \frac{\sigma(\beta+\gamma_2+\mu_1+\mu_2)S_0}{(\beta+\gamma_1+\mu_1)(\gamma_2+\mu_1+\mu_2)} & \frac{\sigma S_0}{\gamma_2+\mu_1+\mu_2} \\ 0 & 0 \end{pmatrix}.$$

Hence, the basic reproduction number $\mathcal{R}_0$ is

$$\mathcal{R}_0 = \rho(FV^{-1}) = \frac{\sigma(\beta + \gamma_2 + \mu_1 + \mu_2)S_0}{(\beta + \gamma_1 + \mu_1)(\gamma_2 + \mu_1 + \mu_2)},$$

$$= \frac{\sigma\Lambda(\beta + \gamma_2 + \mu_1 + \mu_2)}{\mu_1(\beta + \gamma_1 + \mu_1)(\gamma_2 + \mu_1 + \mu_2)}. \tag{8}$$

Data

The data used in different parameters of this manuscript were obtained from the Civil Surgeon Office of Cox's Bazar, Bangladesh. Some data were obtained from the relevant articles and reports.

Results

Numerical illustrations, data fitting, and model validation

The First Rohingya COVID-19 positive patient was identified on May 14, 2020, when the first COVID-19 positive sample laboratory test result was reported. This first positive sample was collected on the very previous day, May 13, 2020. In this numerical section, we have considered the sample collection date as the infection date, and the data was collected until August 12, 2020.

Hereby, the numerical study is divided into two separate sections:

a. First, we have tried the best to counterfeit the real data with the model generated forecast scenario.

b. Then, we related the model result to be uninfluenced partially from the very fluctuating real data. These results warn the worst scenario of this pandemic in this camp if initial strict initiatives were failed to be implemented or if the situation goes out of control for any other reason.

For these numerical visual analyses, the model parameter values are given in Table 2.

Best fitting data

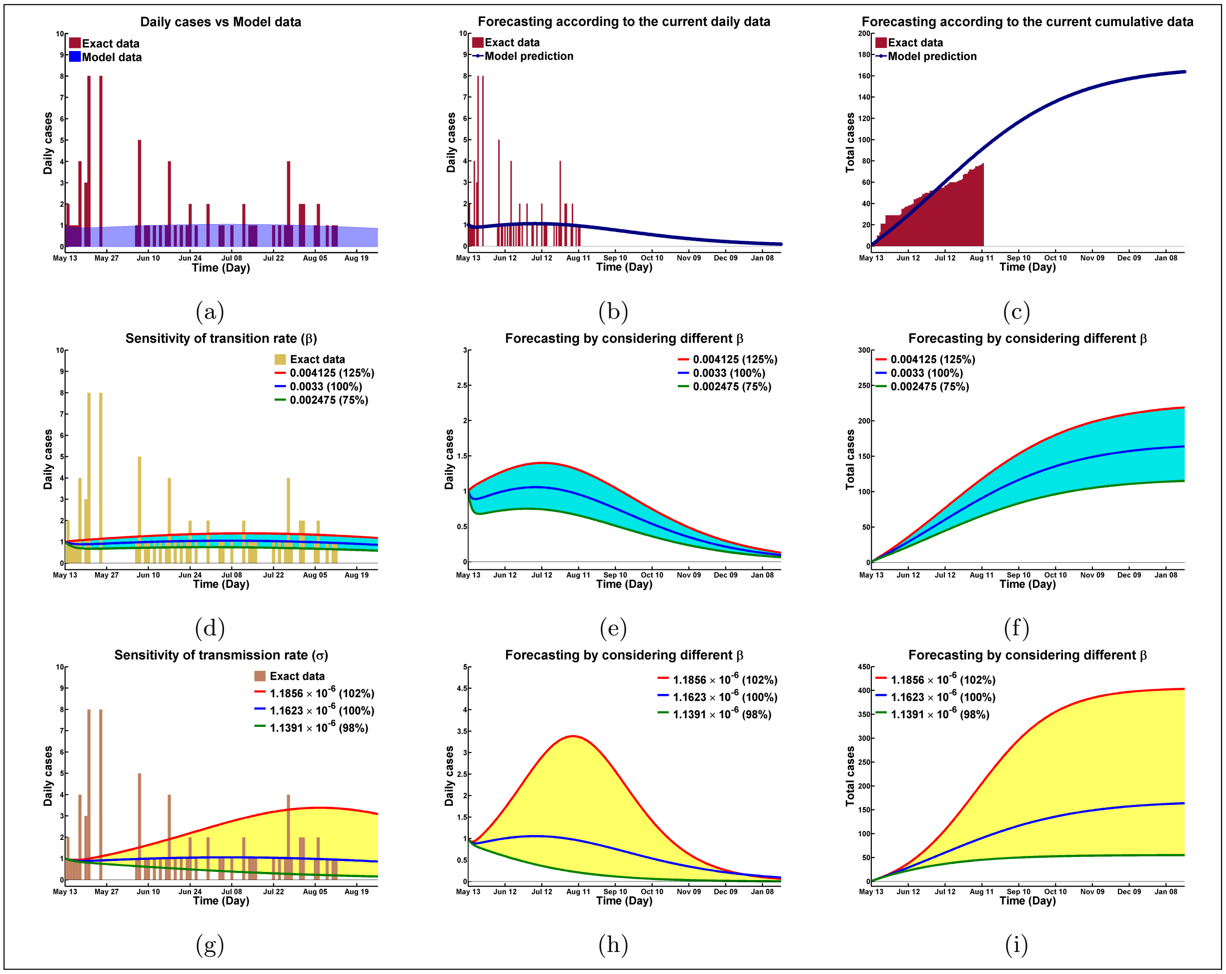
In this subsection, we showed the current situation of the COVID-19 outbreak in the Rohingya refugee camp and summarized our model parameters to project the best fit with the spread of this infection and then project a forecast situation which takes over this population.

Figure 2a portrays the current daily situation of the COVID-19 pandemic in the Rohingya refugee camp, Cox's Bazar, Bangladesh. This data seems to be very fluctuating, and hence hard to get an exact correlated model simulation. Figure 2a displays the daily case data, and figure 2c indicates the cumulative data from the first day of COVID-19 introduction among the Rohingya people, May 13, 2020, to August 12, 2020. This data shows that 1 out of every 11,029 Rohingyas have been infected already with this malign virus till August 12, 2020; where the percentage of positivity of total sample tested is 2.03% among the total collected samples.

This model predicts that from May 13, 2020, to August 12, 2020, the average daily reported case remains between 1 or 2. Furthermore, the fall down of this proliferation starts from the end-August to early-September, 2020 (Fig. 2b), although it will take a long time to be razed. We predict that by the end of 2020 there will be around 169 COVID-19 confirmed cases in this refugee camp (Fig. 2c).

For the respected model in this manuscript, it has been found that the most sensitive and responsible parameter from the compartment E (Asymptotically infected) to the compartment I (Infected) to represent and control the epidemic is β, the rate of transition of the disease from E class to infected class, where both of the classes are infectious conspicuously, but their infection rates are not same. The next figures, specifically figure 2d-2f disclose the sensitivity of β with the exact concomitant values of the disease scenario.

We observe that on the baseline value $\beta = 0.0033$ of transition rate from E to I class, the ultimate forecasted reported infection cases will be 169 with an average $\mathcal{R}_0 = 0.7563$. Now, if we increase β by 25% to $\beta = 0.00413$ then it predicts of 225 confirmed cases in total; while



(a) (b) (c)

(d) (e) (f)

(g) (h) (i)

Figure 2: Visual presentation of model best fitting with real data.

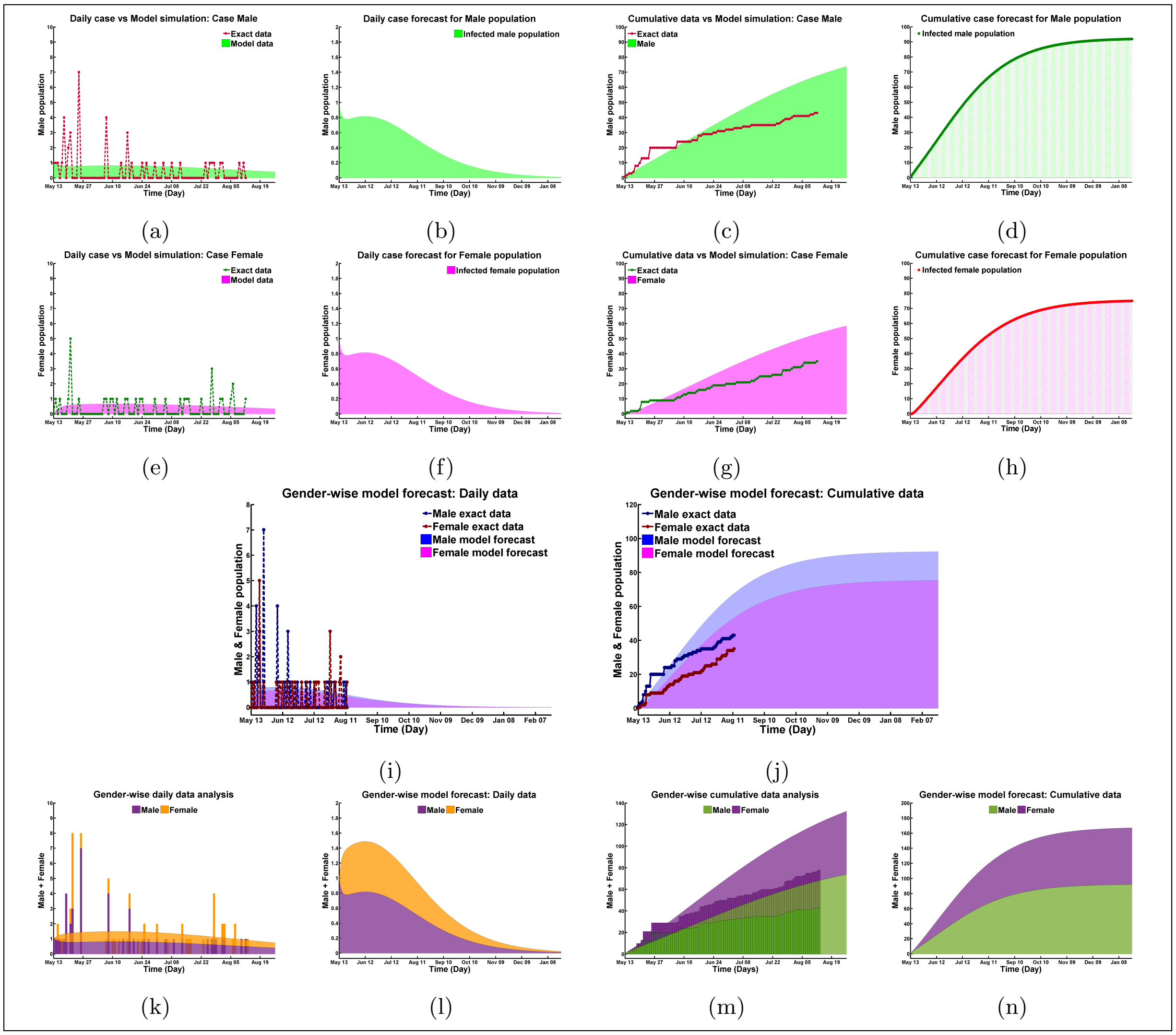


Figure 3: Visual presentation of Gender disparity for model best fitting with real data.

$\mathcal{R}_0 = 0.7572$. Again, decreasing β by 25% to $\beta = 0.00248$ predicts that only 119 cases will be seen in total until January 2021 (Fig. 2f). For this value of β the average basic reproduction number will be 0.7553. Furthermore, for all these three values of β, yet the maximum number of daily cases will lie within or under 2, referring to figure 2e (by taking the ceiling value).

Another dominating parameter for this model (3) is σ, transmission rate of individuals from susceptible to infectious class. Figure 2g-2i portrays the sensitivity of σ.

Here, if we increase σ for only 2% to $\sigma = 1.1856 \times e^{-6}(\mathcal{R}_0 = 0.7714)$ then the model predicts 406 confirmed cases in total, which is almost 2.4 times than the cases with 100% of σ. Again, decreasing σ for 2% to $\sigma = 1.1391 \times e^{-6}(\mathcal{R}_0 = 0.7411)$ depicts that there only 56 cases will be seen in total until January 2021 (Fig. 2i). This navigates the control of the epidemic by having control over transmission policy.

A previous study claims that sex-disaggregated data for COVID-19 show equal numbers of cases between men and women so far, but there seem to be sex differences in mortality and vulnerability to the disease [13]. Emerging evidence suggests that more men than women are dying, potentially due to sex-based immunological [14] or gendered differences, such as patterns and prevalence of smoking [15].

Now, the figures (Fig. 3a-3h) draw the situation for male (Fig. 3a-3d) and female (Fig. 3e-3h) population in the refugee camp, where figures 3a, 3c, 3e, 3g present the real data versus model outcome and figures 3b, 3d, 3f, 3h present corresponding model forecast. The average basic reproduction number for the male community is $R_0 = 0.7611$ and for the female community is $R_0 = 0.7505$.

These figures infer with the total number of the male case 93 (Fig. 3d), and the total number of female cases will be 76 (Fig. 3h) by the end of January 2021, which confers, infected female population resembles 44.97% of the total patients in the Rohingya refugee camp in Cox's Bazar.

All the figures in figure (3i-3n) assist in comparing the infection disparity level between male and female populations. Sub-figures 3i, 3k, 3l connote the daily case margin, and sub-figure 3j, 3m, 3n show the cumulative case margin.

At a glance, the real statistics of present male-female infection rate and the possible prediction which was extended based on existing infections are seen in figure-3i and 3j. Figure: 3i, 3j showed how a vulnerable infected male curve is dominating the infected female curve. Within August 12, 2020, the maximum male individuals are infected 7/day while the female is 5/day. In early February 2021, predicting the total male and female population will be infected 93 and 76 ($93 + 76 = 169$), respectively, if we ignore the second wave risk or others criterion is the same.

The same results of figure 3i-3j are displayed in figure 3k-3n using different scaling and patterns. Figures 3m, 3n display the total infected population by coloring the two different gender infection limits. On the curvature in all diagrams, the lower phase for the male population, whereas the upper surface for the female population without overlapping each other; the limit of gender (female) infection is started from the asymptotic point of gender (male) with time. This analysis shows how the COVID-19 infection can exploit the varying immune and anatomic privilege among the male and female populations in the Rohingya camp, which is very clear through figure 4.

Good fitting data

The government's health safety concerned authority in the Rohingya camp took prompt steps to protect the refugees from this pandemic. Since the population density is very crucial and it's always very difficult to maintain a hygienic environment in such camps for any mighty government, it could be debris if the management was not concentrating on immediate isolation of the people with symptoms. The concern managed to effectively isolate the camps from the local community and manage to deliver all the necessities in the hand of needs. As a result, the situation did not break down.

Yet, there left some possibilities that the control can short endure, as the second wave may inundate anytime. To date, the occurrence of the second wave has already been reported in many localities, and now even in Bangladesh, experts fear the second wave as the winter is knocking door here. As a result, seasonal flu also may work as a catalyst to make the scene worse.

In this subsection, we are to show the worst situation that could happen in the camps if the effectiveness could not face enough success. For this study, we take only initially satisfying simulated model data with the exact case numbers from May 13, 2020. All the model parameter values for this subsection are mentioned in the same Table 2.

This parameter set predicts that the peak of daily new confirmed cases lies on September 23, 2020. The epidemic will be in control almost at the beginning of February 2021 (Fig. 5b, 5c)[1]. Figure 5c predicts that by the end of January 2021, there will be 1,733 COVID-19 confirmed cases in this refugee camp.

From figure (5d-5f), we observe that on the baseline value $\beta = 0.014$; ($\mathcal{R}_0 = 0.7737$) of transition from E to I class, we have our highest daily new case 13 on September 23, 2020. If we increase for 25% to $\beta = 0.0182$; ($\mathcal{R}_0 = 0.7785$), then the peak for the daily new cases moved to September 15, 2020, as 24 new confirmed cases (total case 2,715). Now, if we decrease by 25% to $\beta = 0.0098$; ($\mathcal{R}_0 = 0.7689$), then the peak for the daily new cases move to October 01, 2020, as 06 new confirmed cases only (Fig. 5e) (total case 957). We see similar dynamics for the cumulative case (Fig. 5f).

When we increase σ for 2% to $\sigma = 1.1857 \times e^{-6}$; ($\mathcal{R}_0 = 0.7892$), then the peak for the daily new cases move 35 on July 26, 2020 (total case 2,900). In addition, when we decrease by 2% to $\sigma = 1.1392 \times e^{-6}$; ($\mathcal{R}_0 = 0.7583$), then the peak for the daily new cases move to September 28, 2020, as 03 new confirmed cases only (Fig. 5h) (total case 555). Figure 5i connotes the scene for the cumulative data.

Gender disparity concerns are shown in figure (6a-6h), which draws the situation for males in figure (6a-6c), and female in figure (6d-6f) population in the refugee camp, where figures 6a and 6d present the real data versus model outcome and figure 6b, 6c, 6e, 6f present model forecast. The average basic reproduction number for the male ethnic community is $\mathcal{R}_0 = 0.7806$ and for the female community is $\mathcal{R}_0 = 0.7677$.

These figures conclude with the total number of 936 the male cases (Fig. 6c), and the total number of the female cases will be 797 (Fig. 6f) by the end of January 2021, which confers, infected female patient resembles 45.99% of the total population till the end of January 2021.

All the values in figure 6g and 6h, help compare the infection disparity level between male and female populations. Sub-figure 6g shows the daily case margin, and sub-figure 6h shows the cumulative case margin. These figures show how a more vulnerable infected male curve is dominating over the infected female curve. Lastly, figure 4 shows the gender-wise infection reach level comparison with real and both the model simulation fittings, best and good.

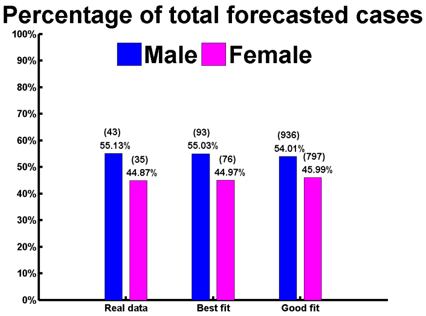


Figure 4: Infection percentage compare between Male & Female for real data and both best & good fit.

Discussion

Cox's Bazar Rohingya camps are congested with more than 860,000 COVID-19 susceptible populations [33]. Numerous challenges with various previous outbreaks make the health response

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[1] See Appendix 1 for the corresponding figures

and resilience of Rohingyas' stronger. However, the health system in the camps is fragile, and the population's baseline health status is inferior. Therefore, a COVID-19 outbreak in Rohingya camps would overwhelm the existing system [20].

When the first case of SARS-CoV-2 was reported in the Hubei province of China in November 2019 [21], it was not this much dubious that this virus can fly world-wide. But, however concerning researchers have found out eminences of the COVID-19 virus as days are passing by amid this pandemic [22, 23]. Now the highly nosogenic feature of this virus has been well established through any kind of human contact, and even close conversation without a mask or such surgical protection may spread this disease [24]–[28]. At this stage, it is pricey recommended to study the pandemic situation in favor of humankind's survival. Numerous mathematical modeling schemes confer this pandemic scenario to illustrate [29]–[31], but we think the SEIR model may fit to portray this scenario more fairly because of a highly contagious presence latent period of this disease cycle.

In this study, we used a compatibly modified SEIR model to determine the critical condition of disease development in the population with a total population size. We have tried to forecast scenario using the real data in normal condition, if initial strict initiatives were failed to be implemented or if the situation goes out of control for any other reason.

Our study analyzed the current situation of the COVID-19 pandemic in the Rohingya refugee camp, and the analysis indicates that one out of every 11,029 Rohingya has been infected already with this malign virus by August 12, 2020. Our model also predicts that by the end of 2020, there will be around 169 COVID-19 confirmed cases in this refugee camp. Here, the average basic reproduction number R0=0.7563, which indicates the disease-free equilibrium (DFE), is stable, and the disease will die out in the population as time passes. Therefore, the situation is thought to be under control. This might be the outcome of the effective strategy developed by the GoB, UN agencies, local and international NGO's.

Again a previous study claims that sex-disaggregated results for COVID-19 indicate similar numbers of cases between men and women as yet, but there appear to be gaps in mortality and susceptibility to the disease in terms of gender [13]. Emerging data shows that more men are dying compared to women, likely because of sex-based immunological approaches, [14] or gender gaps, e.g., patterns and prevalence of smoking [15].

Moreover, recent sex-disaggregated data for FDMN are not complete, admonisihing against early assumptions. At the same time, the State Council Information Office in China implied that more than 90% of Hubei province healthcare workers were women, emphasizing the health workforce's gendered nature and the risk that predominantly female health workers incur [16]. C. Wenham et al. [17] called on policymakers and public health organizations to recognize the overt and indirect sex and gender impacts of the COVID-19 epidemic and to examine the gender impacts of multiple outbreaks, incorporating women 's perspectives on the front line of the COVID-19 response and those most impacted by the disease through preparedness and response policies or activities.

Simultaneously, B. Li et al. [18] assert that men are more likely to be infected than women, and the overall proportion of males is 57.8%. In correspondence to all these gender disparity concerns, we feel the necessity of scrutinizing the impact of this disparity in the Rohingya population.

Our analysis also revealed that the total number of male cases would be higher (93) than female (76) by the end of January 2021 if the existing scenario regarding sensitivity and transmission rate not changed in the Rohingya refugee camp. If the scenario becomes worst, there would be 1,733 (957-2715) COVID-19 confirmed cases in the refugee camp till the end of January 2021. The total number of male cases would be 936, and the total number of female cases would be 797 by the end of January 2021, which confers that infected female patients resemble 45.99% of the total population of January 2021.

Our modified SEIR model did not capture comorbidities such as malnutrition, concomitant diseases, and poor overall health status, causing more severe outcomes among these groups. Also, no reliable current data regarding the human resources inside the camps is available; it is incredibly likely that the situation will be overwhelmed if the situation becomes worst. If the crisis gets worse, a surge in foreign healthcare professionals may be anticipated. In the worst scenario at the refugee camp sites, there could be a shortage of beds to treat the predicted COVID-19 events. There is a need for alternate plans for the isolation of mild cases. Cholera treatment centers and diphtheria outbreak centers could be used for this purpose. In order to resolve the toughest situation as quickly as possible, thorough advanced preparation of the GOB, triage protocols, quarantine and isolation measures should be finalized as early as possible.

It would be culturally difficult to isolating people, especially the older aged group. These groups should be isolated separately group-wise in separate locations. A robust surveillance system with adequate testing, case finding, isolation, and other supplies such as PPE is essential to control basic reproduction number.

Abbreviation and Acronyms

COVID-19	Coronavirus diseases
SEIR	Susceptible-Asymptotically Infected-Infectious-Recovered
SARS-CoV-2	Severe acute respiratory syndrome coronavirus 2
FDMN	Forcibly displaced Myanmar Nationals
UNHCR	United Nations High Commissioner for Refugees
SARI	Severe acute respiratory illness
ITC	Isolation and treatment center
GAM	Global acute malnutrition
SIR	Susceptible-Infectious-Recovered
DFE	Disease-free equilibrium

Authors' contributions

MK, MSM, and SA contributed to the study conceptualization, planned the study, and coordination of the manuscript. MK and MSM proposed the mathematical model and carried out the mathematical and numerical study. MSM, and SA drafted the manuscript writing. MK, MOQ, MMA, MNH, MRI, KFN and UB reviewed and MK finalized the manuscript. All the authors accepted the finalized version of the manuscript.

Declaration of competing interests

The authors declare no competing interests.

Data sharing

Data can be provided on a properly justified request.

Ethical approval

The Ethics Review Committee of North-South University approved the research protocol. The data access was achieved from the Civil Surgeon's Office of Cox's Bazar. No consent is required to publish this manuscript.

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References

[1] Worldometer, "Coronavirus Cases," Worldometer, (2020). [Online]. Available: `https://www.worldometers.info/coronavirus/?` [Accessed: 21-Sep-2020].

[2] WHO, "Archived: WHO Timeline - COVID-19," (27-Apr-2020). [Online]. Available: `https://www.who.int/news-room/detail/27-04-2020-who-timeline---covid-19`. [Accessed: 21-Sep-2020].

[3] UNHCR, "Situation Refugee Response in Bangladesh." [Online]. Available: `https://data2.unhcr.org/en/situations/myanmar_refugees`. [Accessed: 21-Sep-2020].

[4] Al Jazeera, "First coronavirus case found in Bangladesh Rohingya refugee camps — Coronavirus pandemic News — ," (15-May-2020). [Online]. Available: `https://www.aljazeera.com/news/2020/05/coronavirus-case-bangladesh\-rohingya-refugee-camps-200514143543211.html`. [Accessed: 22-Sep-2020].

[5] WHO, "Rohingya Crisis Situation Report # 18," (2020).

[6] M. Chowdhury, S. Billah, F. Karim, A. Khan, Islam S;, and S. Arifeen, Report on Demographic Profiling and Needs Assessment of Maternal and Child Health (MCH) Care for the Rohingya Refugee Population in Cox's Bazar, Bangladesh. Maternal and Child Health Division, *icddr,b*, (2018).

[7] Action Against Hunger, "Emergency Nutrition Assessment: Final Report," (Oct. 2019).

[8] J. D. Murray, "Mathematical Biology: I. An Introduction ," (2002).

[9] WebMD, "Latest Coronavirus News (Live Updates)," (2020). [Online]. Available: `https://www.webmd.com/lung/news/20200124/coronavirus-2020-outbreak\-latest-updates`. [Accessed: 18-Sep-2020].

[10] M. Martcheva, An Introduction to Mathematical Epidemiology. *Springer*, (2015).

[11] O. Diekmann, J. A. P. Heesterbeek, and M. G. Roberts, "The construction of next-generation matrices for compartmental epidemic models," J. R. Soc. Interface, vol. 7, no. 47, pp. 873–885, (Jun. 2010).

[12] M. Kamrujjaman, M. S. Mahmud, and M. S. Islam, "Dynamics of a diffusive vaccination model with therapeutic impact and non-linear incidence in epidemiology," Journal of Biological Dynamics, 1-29, (2020).

[13] C. CDC Weekly, "The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China, 2020," China CDC Wkly., vol. 2, no. 8, pp. 113–122, Feb. 2020.

[14] N. Chen et al., "Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study," Lancet, vol. 395, no. 10223, pp. 507–513, Feb. 2020.

[15] S. Liu et al., "Prevalence and patterns of tobacco smoking among Chinese adult men and women: Findings of the 2010 national smoking survey," J. Epidemiol. Community Health, vol. 71, no. 2, pp. 154–161, Feb. 2017.

[16] M. Boniol, M. McIsaac, L. Xu, T. Wuliji, K. Diallo, and J. Campbell, "WHO — Gender equity in the health workforce: Analysis of 104 countries," Who, no. March, 2019.

[17] C. Wenham, J. Smith, and R. Morgan, "COVID-19: the gendered impacts of the outbreak," The Lancet, vol. 395, no. 10227. Lancet Publishing Group, pp. 846–848, 14-Mar-2020.

[18] B. Li et al., “Prevalence and impact of cardiovascular metabolic diseases on COVID-19 in China,” Clinical Research in Cardiology, vol. 109, no. 5. Springer, pp. 531–538, 01-May-2020.

[19] UNHCR, “Situation Refugee Response in Bangladesh,” 2020. [Online]. Available: https://data2.unhcr.org/en/situations/myanmar_refugees. [Accessed: 18-Sep-2020].

[20] S. A. Truelove et al., “Clinical and Epidemiological Aspects of Diphtheria: A Systematic Review and Pooled Analysis,” Clin. Infect. Dis., vol. 71, no. 1, pp. 89–97, Jun. 2020.

[21] The Guardian, “First Covid-19 case happened in November, China government records show - report,” 13-Mar-2020.

[22] World Health Organization, “Timeline of WHO’s response to COVID-19,” 31-Jul-2020. [Online]. Available: https://www.who.int/emergencies/diseases/novel-coronavirus-2019/interactive-timeline. [Accessed: 18-Oct-2020].

[23] The Business Standard, “WHO acknowledges ‘evidence emerging’ of airborne spread of Covid-19,” 07-Jul-2020.

[24] World Health Organization, “Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations,” 29-Mar-2020. [Online]. Available: https://www.who.int/news-room/commentaries/detail/modes-of-transmission-of-virus-causing-covid-19-implications-for-ipc\-precaution-recommendations. [Accessed: 18-Oct-2020].

[25] J. Liu et al., “Community transmission of severe acute respiratory syndrome Coronavirus 2, Shenzhen, China, 2020,” Emerg. Infect. Dis., vol. 26, no. 6, pp. 1320–1323, Jun. 2020.

[26] N. Van Doremalen et al., “Aerosol and surface stability of SARS-CoV-2 as compared with SARS-CoV-1,” New England Journal of Medicine, vol. 382, no. 16. Massachussetts Medical Society, pp. 1564–1567, 16-Apr-2020.

[27] J. F. W. Chan et al., “A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster,” Lancet, vol. 395, no. 10223, pp. 514–523, Feb. 2020.

[28] Q. Li et al., “Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia,” New England Journal of Medicine, vol. 382, no. 13. Massachussetts Medical Society, pp. 1199–1207, 26-Mar-2020.

[29] M. S. Mahmud, M. Kamrujjaman, J. Jubyrea, M. S. Islam, and M. S. Islam, “Quarantine vs Social Consciousness: A Prediction to Control COVID-19 Infection,” J. Appl. Life Sci. Int., vol. 23, no. 3, pp. 20–27, May 2020.

[30] K. Chatterjee, K. Chatterjee, A. Kumar, and S. Shankar, “Healthcare impact of COVID-19 epidemic in India: A stochastic mathematical model,” Med. J. Armed Forces India, vol. 76, no. 2, pp. 147–155, Apr. 2020.

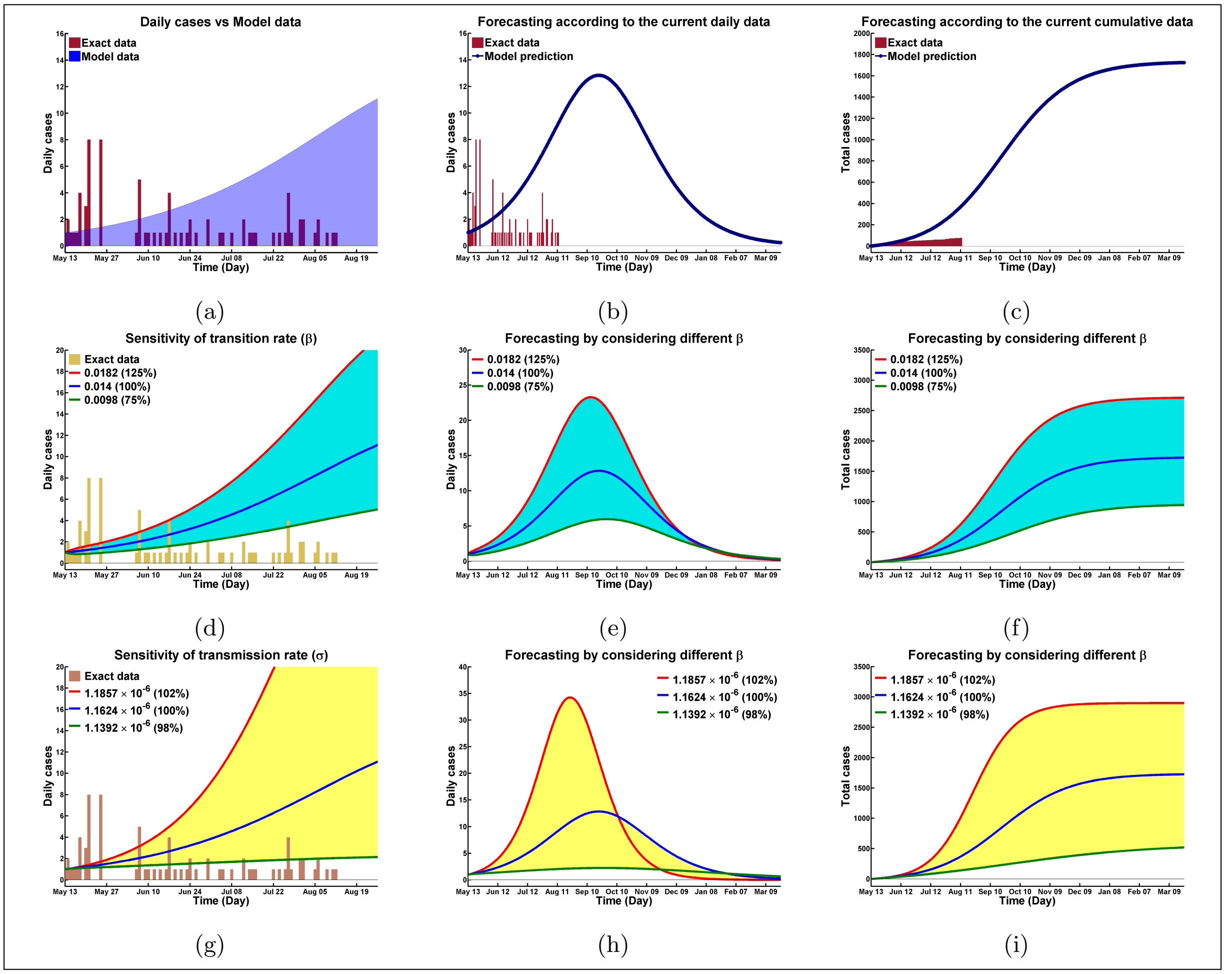
[31] M. Kamrujjaman, M. S. Mahmud, and M. S. Islam, “Coronavirus Outbreak and the Mathematical Growth Map of COVID-19,” Annu. Res. Rev. Biol., vol. 35, no. 1, pp. 72–78, Mar. 2020.

[32] F. Jubayer, S. Kayshar, and T. Islam Limon, “First COVID-19 case in the Rohingya camp in Bangladesh: Needs proper attention,” Public Health, May 2020.

[33] Time, “About 60 Rohingya Babies Are Born Every Day in Refugee Camps, the U.N. Says — TIME,” 2018. [Online]. Available: https://time.com/5280232/myanmar-bangladesh-rohingya-babies-births/. [Accessed: 18-Sep-2020].

[34] J. Guzek, R. Siddiqui, and K. White, “Health Survey in Kutupalong and Balukhali Refugee Settlements, Cox’s Bazar, Bangladesh SURVEY REPORT,” 2017.

1 Appendix

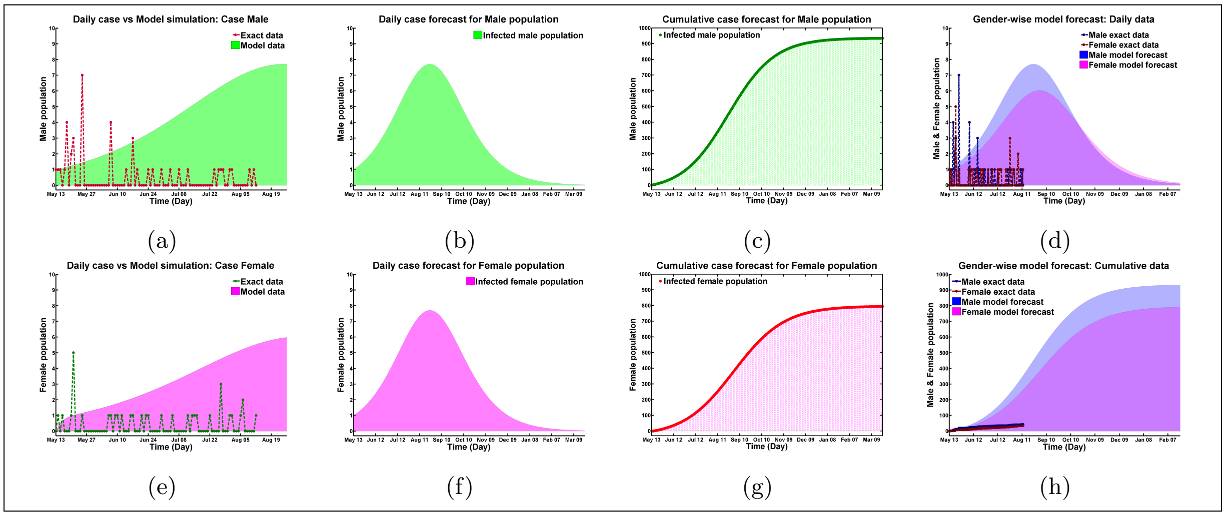


(a) (b) (c)

(d) (e) (f)

(g) (h) (i)

Figure 5: Visual presentation of model good fitting with real data.



(a) (b) (c) (d)

(e) (f) (g) (h)

Figure 6: Visual presentation of Gender disparity for model good fitting with real data.

Tables

Table 1: Model parameters and their descriptions

Notation	Interpretations	Notation	Interpretations
β	Transition rate from E to I class	μ_1	Natural death rate
Λ	Recruitment rate in S class	μ_2	Disease induced death rate
σ	Transmission rate from S to E & I classes	γ_1	Recovery rate of E class
S_0	Initial population in S	γ_2	Recovery rate of I class
E_0	Initial population in E	I_0	Initial population in I

Table 2: Parameters estimations for best fitting model prediction

Parameters	Description	Value (Best fit)	Value (Good fit)	References
S_0	Susceptible population on Mar 13, 2020 (aprox.)	$860,243$	$860,243$	[3]
E_0	Asymptotically infected population on Mar 13, 2020 (aprox.)	100	30	Assumed
I_0	Infectious population on Mar 13, 2020	1	1	[32]
R_0	Recovered population on Mar 13, 2020	0	0	[32]
Λ	Per day average birth	60	60	[33]
β	Per day transition rate from E to I	0.0033	0.0140	Assumed
σ	Per day transmission rate from S to E & I	$1.1623 \times e^{-6}$	$1.1624 \times e^{-6}$	Estimated
γ_1	Per day recovery rate of E	0.9966	0.9900	Assumed
γ_2	Per day recovery rate of I	0.3205	0.3205	Estimated
μ_1	Per day natural death rate	$9.2997 \times e^{-5}$	$9.3019 \times e^{-5}$	[34]
μ_2	Per day disease induced death rate	0.0694	0.0694	Estimated
$\mathcal{R}_0$	Average basic reproduction number	0.7563	0.7737	Estimated