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A compartmental model for COVID-19 to assess effects of non-pharmaceutical interventions with emphasis on contact-based quarantine

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Abstract. Relative to the number of casualties, COVID-19 ranks among the ten most devastating plagues in history. The pandemic hit the South Asian nation of Bangladesh in early March 2020 and has greatly impacted the socio-economic status of the country. In this article, we propose a compartmental model for COVID-19 dynamics, introducing a separate class for quarantined susceptibles, synonymous to isolation of individuals who have been exposed and are suspected of being infected. The current model assumes a perfect quarantine based on contact with infectious individuals. Numerical simulation is conducted to investigate the efficiency of disease control by segregating suspected individuals and other non-pharmaceutical interventions. In addition, we assort quantitatively the importance of parameters that influence the dynamics of the system. Fitting the system to the early phase of COVID-19 outbreaks in Bangladesh, by taking into account the cumulative number of cases with the data of the first 17-week period, the basic reproduction number is estimated as 1.69.

Mathematics Subject Classification (2010): 92D30, 34A99.

Keywords: COVID-19, compartmental model, quarantine, data fitting.

1. Background

In December 2019, a novel coronavirus was first detected in Wuhan, Hubei Province, China, following reports of highly infectious pneumonia cases of unidentified origin [38]. The pathogen was later officially named SARS-CoV-2 (severe acute

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respiratory syndrome coronavirus) by the WHO and the disease caused by this virus is referred to as COVID-19 (coronavirus disease). Since its emergence, SARS-CoV-2 infection rapidly spread to many other countries [14]. It has been detected in 190 countries, is accountable for over 5 million deaths, and has clinically affected over 270 million people globally as of 19 December 2021 [31, 35]. SARS-CoV-2 is also extremely pervasive and currently poses a major public health concern. COVID-19 outbreak was declared a pandemic on 11 March 2020 and is of the most devastating nature since the 1918 H1N1 influenza pandemic [13].

The primary mode of transmission of SARS-CoV-2 is respiratory droplets, but it can also be transmitted via human contact or aerial droplets [19]. Epidemiological inspection states the latency period to range from 3 to 7 days with a maximum of 14 days, during which it remains contagious unlike the SARS-CoV (SARS-related coronaviruses). also displays a wide spectrum of clinical manifestations in infected patients, which may be mild, moderate, or severe. Fever, fatigue, dry cough, shortness of breath, etc are some of its most typical symptoms [15]. The complications of SARS-CoV-2 involve acute respiratory distress syndrome (ARDS) distinguishable by the hyper-inflammatory response, often leading to extensive lung damage, or probable death [30]. Additionally, it has also impacted the social and economic condition of people on a huge scale. There are currently no certified antiviral drugs for SARS-CoV-2 infection. The safety and efficiency of most drugs indicated or suggested for the treatment of COVID-19 are controversial, or under the experimental phase [4]. At present, vaccines are seen as the most competent in controlling disease transmission. The first mass vaccination program started in early December 2020 and at least 13 different vaccines (across 4 platforms) have been administered by WHO so far [36].

The majority of the countries adopted stringent containment measures as early as March 2020 to lessen the transmission of SARS-CoV-2, which included the introduction of non-pharmaceutical interventions such as physical distancing measures, prohibition of social gatherings, proposing work-from-home schemes, etc. The concept of two special control strategies, namely mitigation and suppression has also been proposed and adopted. The UK was following mitigation in the early phase of the pandemic prior to the publication of this report but later started following suppression. It has been suggested that combining multiple intervention strategies is most efficient and optimal in curtailing disease transmission compared to when a single strategy is in force [12].

The first confirmed case of COVID-19 in Bangladesh was recorded on March 8, 2020. Following reports of one or two average cases in the subsequent days, COVID-19 cases have rapidly escalated since the initial outbreak. Several measures have been adopted by the government of Bangladesh to control the spread of disease. The very first step to this intent was declaration of a general holiday from 26 March to 4 April 2020, which was later extended to 30 May, with some relaxation due to financial challenges [37]. Later came the second phase of control strategy, typically known as lockdown, with strict policies such as mandatory use of masks, home quarantine, social distancing, and banning or restrictions on national or international flights which were imposed from 12 April 2021 [34]. Despite these plans of action, the spread of disease

could not be curtailed, possibly as a result of low-income people moving actively for their livelihood, religious festivals, social programs, and overall, lack of public awareness, etc. As of 19 December 2021, there are more than 1,580,000 confirmed COVID-19 cases in Bangladesh and more than 28,000 related deaths [33].

One of the most essential features of COVID-19 is its ability to remain asymptomatic and hence remain undetected in infected individuals. However, the severity of the outbreak lies in the fact that the infectious individuals are capable of transmitting the disease with a positive probability during the course of infection while showing no symptoms [23, 26]. In order to best capture this feature of asymptomatic disease transmission in compartmental disease modeling, a class of unidentified infected and infectious individuals is introduced. Numerous mathematical models for the spread of COVID-19 have been formulated to study the transmission dynamics and control since its outbreak, which emphasize this additional feature [5, 32, 18, 25] also focusing particularly on disease outbreak in specific regions or countries [2, 22, 17]. Various papers have appeared that study the effects of non-pharmaceutical interventions on COVID-19 transmission, see e.g. [8, 27]. The situation in Bangladesh has also been described and analyzed by various modeling works. Masud et al. [22] introduced a compartmental model, where they found that the reproduction number is strongly associated with the time and pick of the epidemic. A modified SIR model was theoretically analyzed and validated the result using fourth-order polynomial regression by Shahrear et al. [29].

As quarantine was one of the main tools of non-pharmaceutical intervention at the beginning of the epidemic, it is important to consider this phenomenon in mathematical models describing the spread of COVID-19. A significant number of research articles have documented well the impact of quarantine at a population level that has been investigated using mathematical models, typically involving deterministic systems of nonlinear differential equations. It is imperative to mention that, the term quarantine here refers to the temporary isolation of susceptible individuals who are suspected to have been exposed to an infectious disease, rather than to the removal of individuals who have already been confirmed to being infected with the disease. These individuals are removed in the interim from actively associating with the rest of the population, until after the incubation period of the disease, at the very least. Following this, they are tested to determine if they have contracted the disease, in which case they are further isolated. Alternatively, they return to the class of susceptibles in case they do not exhibit any clinical symptoms.

Quarantine is described in most models in a way that is rather suitable to model isolation, meaning the removal of individuals who are known to be infected. We express quarantine as a temporary separation of susceptibles who are feared to have contracted the disease due to exposure to the disease via contact with an infectious individual. Few articles that have correctly included quarantine in their models are noteworthy here. Lipsitch et al. [21] introduced a model where susceptible individuals are moved to quarantine based on their contact with infected individuals. Mubayi et al. [24], Safi and Gumel [28], Dénes and Gumel [9] followed a similar way to include quarantine in their models. Furthermore, the quarantine models in Lipsitch et al. [21]; Mubayi et al. [24] do not allow for breakthrough infection to occur during quarantine. To

be specific, they assume a state of perfect quarantine, which we incorporate into the current model.

The objective of the current work is to develop a dynamic model for the spread of coronavirus (COVID-19) with the inclusion of a new class of quarantined susceptible individuals, that aims for a more realistic capture of the spread of the disease. The rest of the paper is structured as follows: in Section 2, we introduce a compartmental model including quarantine, calculate the basic reproduction number and determine some basic properties of the model. In Section 3, we fit the model to data from the first period of the epidemic in Bangladesh identifying the most probable values for the model parameters and perform sensitivity analysis. Section 4 is devoted to numerical simulations concerning the effect of possible intervention measures. The paper is closed by a short discussion of the results.

2. Formulation of the compartmental model

In order to develop a compartmental model for COVID-19 transmission, including the above-described confinement of those feared exposed, we introduce quarantine for susceptible individuals, with the assumption that quarantine is perfect. In the current model, $N(t)$, which denotes the total human population at time t, is partitioned into the population of those in quarantine (denoted by $N_q(t)$) and those not in quarantine (denoted by $N_u(t)$), so that

$$N(t) = N_u(t) + N_q(t).$$

Additionally, the total population in quarantine at time t is divided into the following compartments: susceptibles in quarantine ($S_q(t)$), exposed ($E_q(t)$, that is, infected but not yet infectious), infected ($I_q(t)$) and recovered ($R_q(t)$). Hence,

$$N_q(t) = S_q(t) + E_q(t) + I_q(t) + R_q(t).$$

Similarly, the total population of individuals not in quarantine at time t is subdivided into the following subpopulations of susceptibles ($S_u(t)$), exposed ($E_u(t)$), infected who do not show any symptoms or have only mild symptoms ($I_u^m(t)$), symptomatically infected ($I_u^s(t)$), treated ($I_t(t)$), recovered ($R_u(t)$) so that,

$$N_u(t) = S_u(t) + E_u(t) + I_u^m(t) + I_u^s(t) + I_t(t) + R_u(t).$$

We introduce the auxiliary compartment $D(t)$ to take care of the number of individuals at time t who have passed away due to COVID-19. The force of infection (denoted by $\Lambda(t)$) associated with this model to be developed is given by

$$\Lambda(t) = \frac{I_u^s(t) + \beta_m I_u^m(t) + \beta_q I_q(t) + \beta_t I_t(t)}{N(t)},$$

where β_m, β_q and β_t are modification parameters accounting for the variability of the infectiousness of infected individuals in the $I_u^m(t)$, $I_q(t)$ and $I_t(t)$ classes, compared to those in the $I_u^s(t)$, respectively.

In this model, we do not consider demography, however, there is a disease-induced death rate, denoted by d_s, d_q, and d_t for those in the compartments I_u^s, I_q and I_t, respectively. As noted above, we follow Lipsitch et al. [21] to introduce quarantine.

In our model, human-to-human transmission rate is split into the product of the average number of contacts (κ) and the probability of transmission per contact (b), while q stands for the fraction of those susceptible individuals who are feared exposed and hence moved to quarantine.

TABLE 1. Description of parameters of model (2.1).

Parameters	**Description**
b	Probability of disease transmission
κ	Average number of contacts
q	Fraction of those moved to quarantine
$1/\nu$	Average length of incubation period
γ	Recovery rate for mildly infected
$1/\epsilon$	Average time from symptoms onset until treatment
ξ	Recovery rate in quarantine
θ	Fraction of asymptomatic cases among non-quarantined
$\beta_m, \beta_q, \beta_t$	Relative transmissibilities for I_u^m, I_q, I_t compartments
$1/\sigma$	Average length of quarantine
ζ	Recovery rate for treated individuals
d_s, d_q, d_t	Disease-induced death rate for I_u^s, I_q and I_t respectively

Upon contacting an infectious individual (i.e. an individual from the compartments I_u^m, I_u^s, I_q or I_t) a susceptible (quarantined or non-quarantined) human may contract the disease (with probability b) and hence move to one of the two exposed classes, depending on whether this person is moved to quarantine: a fraction q arrive in the exposed quarantined compartment E_q, while the remaining fraction $1-q$ of those who have contracted the disease arrive in the non-quarantined exposed compartment E_u. A fraction $1-b$ of those in contact with infectious individuals will not be infected. Though, based on their contacts, a fraction q will be quarantined and hence arrive in compartment S_q. The remaining fraction $1-q$ will stay in the S_u compartment. Individuals in quarantine who turn out to be healthy will move back to the S_u class at a rate σ at the end of their quarantine period. Hence, transition rate from S_u to E_u takes the form $(1-q)\kappa b$, from S_u to S_q takes the form $(1-b)\kappa q$, while transition rate from S_u to E_q is given by $q\kappa b$. The parameter θ is a fraction of non-quarantined exposed people who have shown mild symptoms and move to compartment I_u^m, while the rest have shown all symptoms of the disease. $1/\nu$ denotes the length of the incubation period. The duration of the infectious period for mildly symptomatic individuals and people under treatment is represented by $1/\gamma$ and $1/\zeta$ respectively. The progression tenure of the patients from symptomatically infected is denoted by $1/\epsilon$.

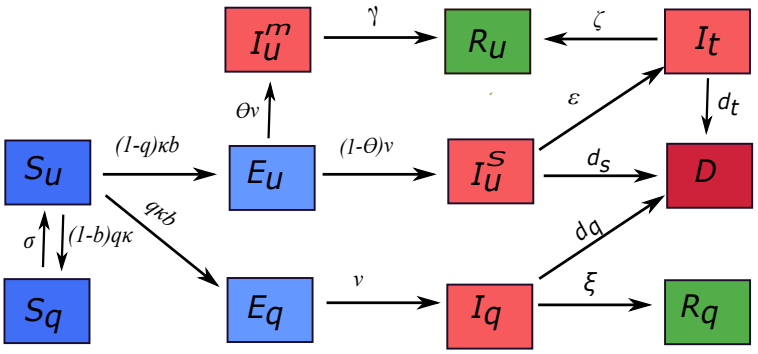

FIGURE 1. Transmission diagram. Arrows indicate transition from one compartment to another

Using the notations for compartments and parameters as described in the methods section (see Figure 1, Table 1), our model takes the form:

$$\begin{aligned}
\frac{\mathrm{d}S_u(t)}{\mathrm{d}t} &= -\big((1-b)\kappa q + q\kappa b + (1-q)\kappa b\big)\Lambda(t)S_u(t) + \sigma S_q(t),\\
\frac{\mathrm{d}S_q(t)}{\mathrm{d}t} &= (1-b)\kappa q\Lambda(t)S_u(t) - \sigma S_q(t),\\
\frac{\mathrm{d}E_u(t)}{\mathrm{d}t} &= (1-q)\kappa b\Lambda(t)S_u(t) - \nu E_u(t),\\
\frac{\mathrm{d}E_q(t)}{\mathrm{d}t} &= q\kappa b\Lambda(t)S_u(t) - \nu E_q(t),\\
\frac{\mathrm{d}I_u^m(t)}{\mathrm{d}t} &= \theta\nu E_u(t) - \gamma I_u^m(t),\\
\frac{\mathrm{d}I_u^s(t)}{\mathrm{d}t} &= (1-\theta)\nu E_u(t) - \epsilon I_u^s(t) - d_s I_u^s(t),\\
\frac{\mathrm{d}I_q(t)}{\mathrm{d}t} &= \nu E_q(t) - \xi I_q(t) - d_q I_q(t),\\
\frac{\mathrm{d}I_t(t)}{\mathrm{d}t} &= \epsilon I_u^s(t) - \zeta I_t(t) - d_t I_t(t),\\
\frac{\mathrm{d}R_u(t)}{\mathrm{d}t} &= \gamma I_u^m(t) + \zeta I_t(t),\\
\frac{\mathrm{d}R_q(t)}{\mathrm{d}t} &= \xi I_q(t),\\
\frac{\mathrm{d}D(t)}{\mathrm{d}t} &= d_s I_u^s(t) + d_q I_q(t) + d_t I_t(t),
\end{aligned} \tag{2.1}$$

where the force of infection $\Lambda(t)$ is given as above.

2.1. Basic reproduction number

For the analytical computation of the basic reproduction number $\mathscr{R}_0$ of (2.1), we follow the general approach established in [10, 11]. Splitting the system into vectors $x = \big(E_u, E_q, I_u^m, I_u^s, I_q, I_t\big)$, composed of infectious compartments, and $y =$

$\big(S_u, S_q, R_u, R_q, D\big)$, composed of non-infectious compartments, the system can be expressed as

$$\begin{aligned} x_i' &= \mathcal{F}_i(x,y) - \mathcal{V}_i(x,y), \qquad i = 1,\dots,6,\\ y_j' &= g_j(x,y), \qquad\qquad\quad j = 1,\dots,5, \end{aligned}$$

where $\mathcal{F}_i$ represents the new infections due to COVID-19 and $\mathcal{V}_i$ contains the transitions between infected compartments, and are given as follows:

$$\mathcal{F}_i = \begin{bmatrix} (1-q)\kappa b\frac{(I_u^s(t)+\beta_m I_u^m(t)+\beta_q I_q(t)+\beta_t I_t(t))}{N(t)} S_u(t)\\ q\kappa b\frac{(I_u^s(t)+\beta_m I_u^m(t)+\beta_q I_q(t)+\beta_t I_t(t))}{N(t)} S_u(t)\\ 0\\ 0\\ 0\\ 0 \end{bmatrix}$$

and

$$\mathcal{V}_i = \begin{bmatrix} \nu E_u(t)\\ \nu E_q(t)\\ -\theta\nu E_u(t) + \gamma I_u^m(t)\\ -(1-\theta)\nu E_u + \epsilon I_u^s(t) + d_s I_u^s(t)\\ -\nu E_q(t) + \xi I_q(t) + d_q I_q(t)\\ -\epsilon I_u^s(t) + \zeta I_t(t) + d_t I_t(t) \end{bmatrix}.$$

In the (x,y)-notation, the disease-free equilibrium (DFE) of the system is $\mathcal{E}_0 = (0, y_*)$ where $y_* = (N,0,0,0,0)$. By means of linearization at the DFE $\mathcal{E}_0$, we obtain the equation

$$x' = Ax$$

where A is the Jacobian matrix. Next, we take the decomposition $A = F - V$, where

$$F_{i,j} = \left[\frac{\partial \mathcal{F}_i}{\partial x_j}(DFE)\right], \qquad V_{i,j} = \left[\frac{\partial \mathcal{V}_i}{\partial x_j}(DFE)\right].$$

In the case of our model, the transmission and transition matrices take the form

$$F = \begin{bmatrix} 0 & 0 & (1-q)\kappa b\beta_m & (1-q)\kappa b & (1-q)\kappa b\beta_q & (1-q)\kappa b\beta_t\\ 0 & 0 & q\kappa b\beta_m & q\kappa b & q\kappa b\beta_q & q\kappa b\beta_t\\ 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0\\ 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

and

$$V = \begin{bmatrix} \nu & 0 & 0 & 0 & 0 & 0\\ 0 & \nu & 0 & 0 & 0 & 0\\ -\theta\nu & 0 & \gamma & 0 & 0 & 0\\ -(1-\theta)\nu & 0 & 0 & \epsilon + d_s & 0 & 0\\ 0 & -\nu & 0 & 0 & \xi + d_q & 0\\ 0 & 0 & 0 & -\epsilon & 0 & \zeta + d_t \end{bmatrix}.$$

Thus, we have the reproduction number as of the co-infection model $\rho(FV^{-1})$, given by the formula

$$\mathscr{R}_0 = \frac{(1-q)\kappa b[\gamma(1-\theta)(\beta_t\epsilon+\zeta+d_t)+\theta\beta_m(d_s+\epsilon)(d_t+\zeta)]}{\gamma(d_s+\epsilon)(d_t+\zeta)} + \frac{q\kappa b\beta_q}{d_q+\xi}, \tag{2.2}$$

where ρ represents the spectral radius.

2.2. Basic qualitative properties

We close this section by showing some basic qualitative properties of the model.

Proposition 2.1. *Any solution of* (2.1) *starting from nonnegative initial values will remain nonnegative for all forward time.*

Proof. Suppose the assertion is false, then there exists a minimal time T when (at least) one of the compartments reaches zero. Let X be a compartment ($X \in \{S_u, S_q, E_u, E_q, I_u^m, I_u^s, I_q, I_t, R_u, R_q\}$) for which $X(T) = 0$. One can see that at this time point, we have $X'(t) \geq 0$, hence, $X(t)$ cannot drop below zero. This shows the nonnegativity of all solutions. □

Proposition 2.2. *All solutions of* (2.1) *are bounded.*

Proof. By adding all equations in (2.1), we obtain that the sum of the total population and the number of deceased is constant. Hence, the total population – which is decreasing – is bounded. □

Lemma 2.3. *The infected compartments* $E_u(t), E_q(t), I_u^m(t), I_u^s(t), I_q(t), I_t(t)$ *as well as the compartment for quarantined susceptibles* $S_q(t)$ *will eventually go extinct as* $t \to \infty$.

Proof. To see that $E_u(t) \to 0$ and $E_q(t) \to 0$ as $t \to \infty$, we consider

$$(S_u(t) + S_q(t) + E_u(t) + E_q(t))' = -\nu(E_u(t) + E_q(t)).$$

If either $E_u(t)$ or $E_q(t)$ does not tend to zero, then $S_u(t) + S_q(t) + E_u(t) + E_q(t)$ drops below 0, which contradicts the nonnegativity of the compartments. To see that the compartments $I_u^m(t), I_u^s(t), I_q(t)$ extinct, we consider

$$(I_u^m(t) + I_u^s(t) + I_q(t))' = \nu(E_u(t) + E_q(t)) - \gamma I_u^m(t) - (\epsilon + d_s)I_u^s(t) - (\xi + d_q)I_q(t).$$

If any of $I_u^m(t), I_u^s(t)$ or $I_q(t)$ remain positive then, considering that the two exposed classes have been shown to tend to 0, $I_u^m(t) + I_u^s(t) + I_q(t)$ drops below 0, which is not possible. The statement for compartment $I_t(t)$ follows from the previous assertions. In a similar way, the compartment S_q of quarantined susceptibles will also tend to zero. □

3. Data fitting and sensitivity analysis

3.1. Data fitting

First and foremost, it should be noted that, as enumerated in Table 2, good approximations are available in the literature for a set of parameter values. Thus, our task is to find good estimates for the remaining parameters. For that purpose, and to consequently validate the model, our model has been fitted using the available data for the COVID-19 outbreaks in Bangladesh [33].

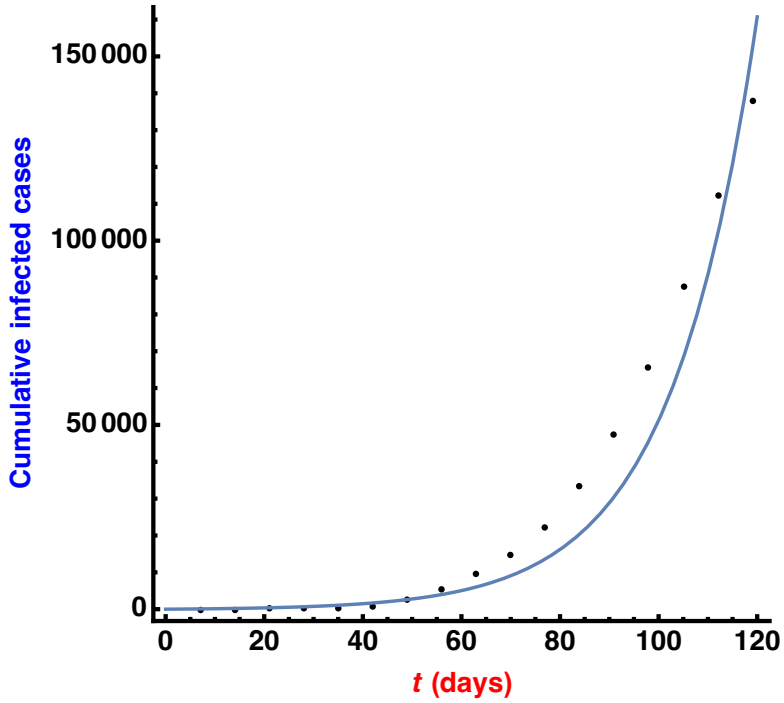

FIGURE 2. The best fitting solution plotted with 17-week WHO data from Bangladesh started on March 2, 2020. Parameter values obtained in the fitting are given in Table 2.

Using the baseline values for the available parameter values as listed in Table 2, we utilize the Latin Hypercube Sampling method to find the parameter values which provide the best fit to the data. This is a computational technique used in statistics to estimate the simultaneous variation of various model parameters to construct a representative sample set of n-tuples of parameters (n is the number of parameters fitted) taking values from given ranges. The estimated values of the fitted parameters of the model are given in Table 2. Figure 2 illustrates the simulation results obtained by fitting the model for the cumulative number of cases with the data of the first 17-week period.

TABLE 2. Parameters for model (2.1) providing the best fit.

Parameters	Baseline (Range)	Units	Sources
ν	$1/5.2$	Days^{-1}	[7]
γ	$1/7$	Days^{-1}	[3, 2, 1]
ϵ	$1/3$	Days^{-1}	[1]
ξ	$1/8$	Days^{-1}	Assumed
θ	0.4	–	[20]
κ	8.317 (5, 16)	–	Fitted
b	0.064 (0.01, 0.08)	Days^{-1}	[6]
q	0.195 (0.007, 0.2)	–	[6]
β_m	0.603 (0.1, 0.7)	–	[16]
β_q	0.168 (0.1, 0.4)	–	Fitted
β_t	0.127 (0.1, 0.7)	–	Fitted
σ	0.163 (1/21, 1/3)	Days^{-1}	Fitted
ζ	0.064 (1/21, 1/7)	Days^{-1}	[1]
d_s	0.047 (0.01, 0.08)	Days^{-1}	Fitted
d_q	0.047 (0.01, 0.07)	Days^{-1}	Fitted
d_t	0.085 (0.05, 0.1)	Days^{-1}	Fitted

3.2. Sensitivity analysis

In order to assess the population-level impact of possible intervention parameters of the model (2.1), and to evaluate their significance, a sensitivity analysis is conducted. The current analysis is conducted using the Latin Hypercube Sampling (LHS) and Partial Rank Correlation Coefficient (PRCC). with 15,000 Monte Carlo simulations per run.

With simultaneously varying parameter values, the PRCC method facilitates us to quantify the effect of the various parameter values on the model's feedback, hence, establishing the statistical relationships between the input parameters and the outcome value. The sign (positive or negative) of the parameter's PRCC characterizes the qualitative association with the model response(s). While increasing parameters with positive PRCC values results in the growth of the number of cumulative cases, increasing parameters with negative PRCC will result in a smaller number of cumulative cases. It is to be noted that parameters with larger PRCC values are regarded to be most critical for the model.

The input parameters for which the PRCC analysis was performed are: average number of contacts (κ), transmission probability per contact (b), the fraction of people moved to quarantine among those with contacts with infected individuals (q), incubation time ($1/\nu$), recovery rate for asymptomatically infected (γ), average time until hospitalization ($1/\epsilon$), recovery rate for quarantined (ξ), fraction of asymptomatic cases (θ), length of quarantine ($1/\sigma$), recovery rate among treated individuals (ζ), disease-induced death rate for symptomatically infected (d_s), disease-induced death rate for quarantined individuals (d_q) and disease-induced death rate for treated individuals (d_t), while the output parameter in our work is the cumulative number of infected

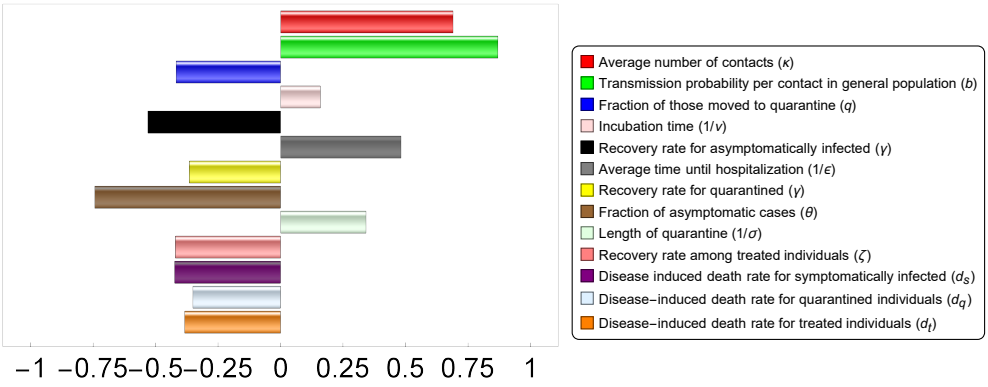

FIGURE 3. Partial rank correlation coefficients (PRCCs) of model parameters. Increasing parameters with positive PRCC value will increase the number of cases, and increasing ones with negative PRCC will decrease the number of cases.

until the time period under consideration in the fitting. The results obtained in Figure 3 demonstrate that the parameters with the largest effect are the average number of contacts κ, transmission probability per contact b, and the fraction of asymptomatic cases θ, hence, the first two are shown to be the most important parameters that might be subject to control measures. The parameter corresponding to the third important intervention measure, namely the efficiency of quarantining individuals who are feared to have contracted the disease (q) is suggested to have a lower effect than the other two parameters related to non-pharmaceutical intervention methods, however, the effect of changing this parameter is still remarkable and can be compared to that of parameters such as recovery rates γ, ζ, ξ and death rates d_s, d_q, d_t. The average time until hospitalization of severe cases is also shown to have a significant impact, though, in comparison with the above-mentioned intervention parameters, decreasing this time period is more difficult than the implementation of the other control measures.

4. Effect of possible control measures

Numerical simulations were performed to observe the probable effects of the most straightforward non-pharmaceutical interventions. As long as no vaccines against a given disease are available, the most easily applicable interventions are the reduction of contacts (e.g. by introducing partial or complete curfew or closing schools), decreasing transmission probability (e.g. by wearing masks and increasing hygiene), as well as quarantining those who are feared to have contracted the disease. Moreover, PRCC analysis in the previous section showed that these are efficient tools to reduce the number of infected.

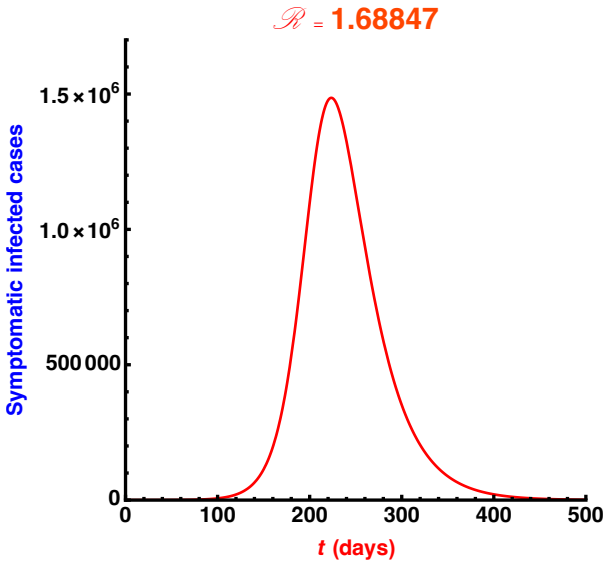

FIGURE 4. Number of symptomatic cases with the fitted parameters.

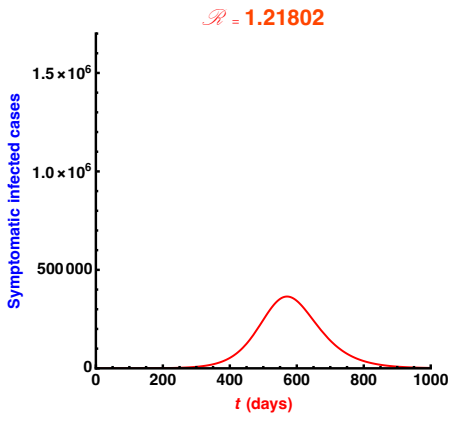

FIGURE 5. Number of symptomatic cases with $\kappa = 6$.

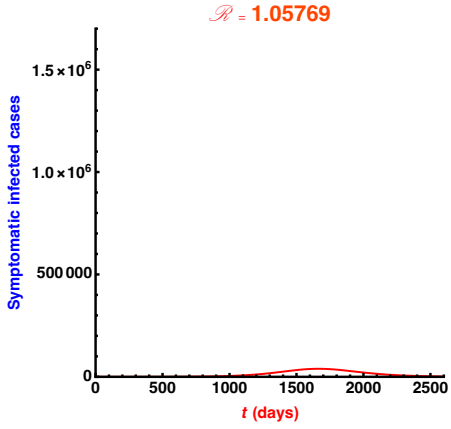

FIGURE 6. Number of symptomatic cases with $b = 0.04$.

Hence, we selected the three parameters of our model which correspond to these three types of intervention measures, namely the average number of contacts, transmission probability per contact, and the fraction of suspected individuals being quarantined, since these are most likely to be altered due to some control measures. Our goal was to see what degree of change in these parameters might turn out to be

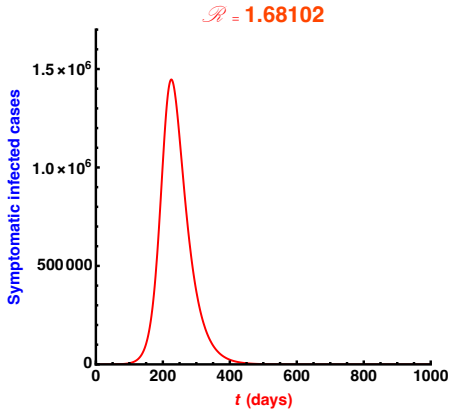

FIGURE 7. Number of symptomatic cases with $q = 0.2$.

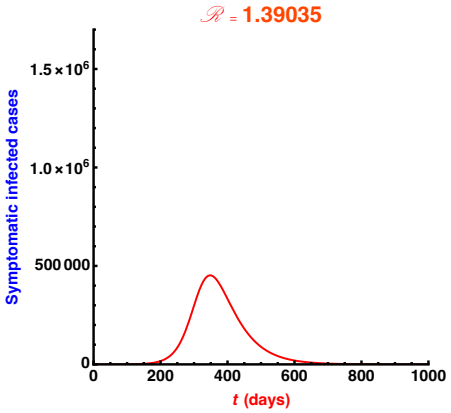

FIGURE 8. Number of symptomatic cases with $q = 0.4$.

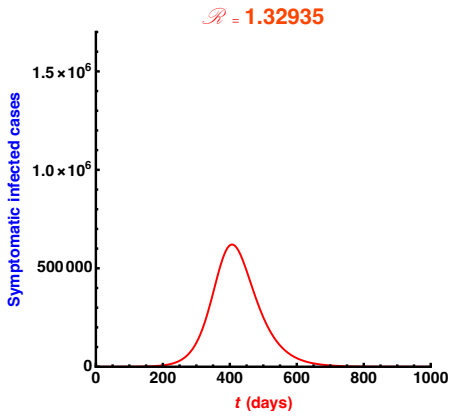

FIGURE 9. Number of symptomatic cases with $\kappa = 7$, $b = 0.06$, and $q = 0.2$.

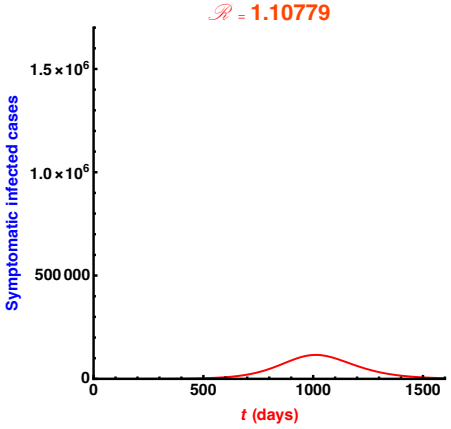

FIGURE 10. Number of symptomatic cases with $\kappa = 7$, $b = 0.05$, and $q = 0.2$.

sufficient to reduce the peak of the epidemic. Initially starting the simulations with the fitted parameters up to week 17, we applied the modification of one or more parameters to observe the changes.

To gain further insight into how intervention measures may reduce disease burden, in each subfigure of Figure 11 we show the contour plot of the reproduction number as a function of two of the three parameters subject to intervention measures, namely the average number of contacts (κ), transmission probability per contact (b)

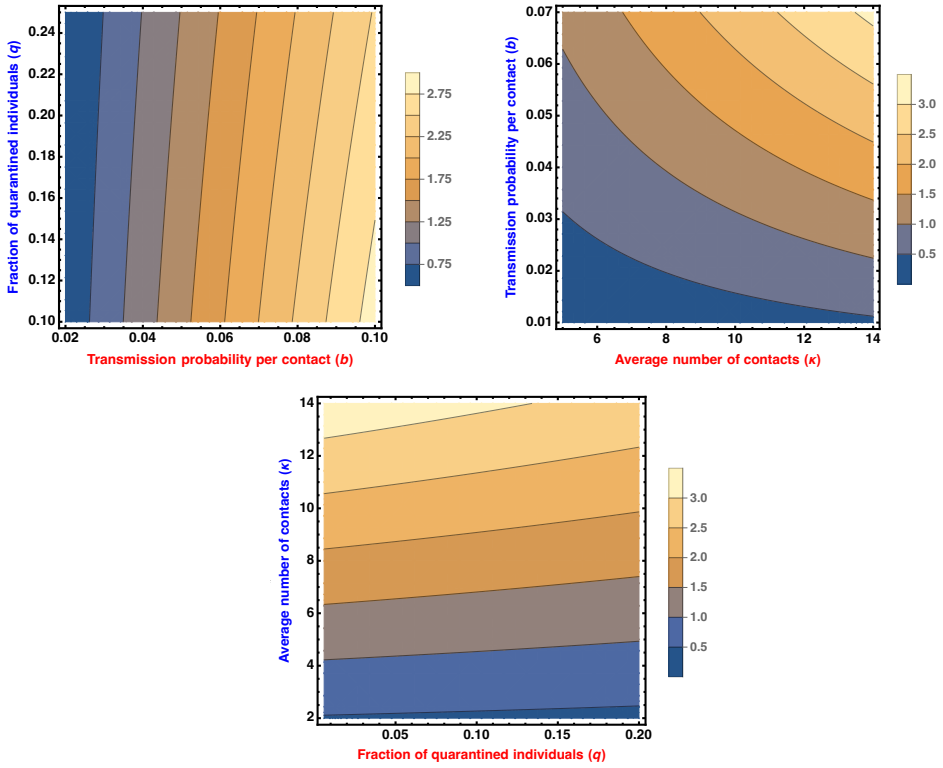

FIGURE 11. Contour plot of the basic reproduction number as a function of the three parameters subject to intervention measures.

and the fraction of those moved to quarantine (q). The rest of the parameters are set to the values used in the fitting as shown in Table 2. These plots support earlier results shown in the sensitivity analysis: reducing transmission probability and the number of contacts are the most powerful tools to decrease the reproduction number, while increasing the fraction of those moved to quarantine has a milder effect, though adjusting this parameter will strengthen the mitigating effect of decreasing the other two parameters or enables us to perform a smaller change on these parameters to obtain the same result.

The simulations suggest that all three interventions might significantly reduce the number of infected. In accordance with the results of the PRCC analysis, decreasing the number of contacts and reducing transmission probability are shown to be the most effective ways to reduce disease burden. As shown in Figures 5 and 6, even a moderate reduction of these two parameters can significantly contribute to a decrease in cases. At the same time, increasing the fraction of quarantine for those with contact with infectious individuals seems to be less efficient (see Figure 7). Changing this parameter can also turn out to have a positive effect, however, to achieve really significant changes, one would need to increase this parameter to ranges that are

rather improbable in a real-life situation as putting into quarantine a high number of healthy people has a negative effect on the economy (see Figure 8). The most efficient way to reduce the number of infected is of course the parallel application of the three measures which is shown to be rather effective in Figures 9 and 10.

5. Conclusions

The current study proposes a new deterministic model for evaluating the population-level impact of implementing quarantine on the control of the COVID-19 outbreaks in Bangladesh. We attempted to include the features most substantial in reflecting the disease transmission, paying attention to the special characteristics of COVID-19. The effect of quarantine – one of the most important tools to hinder disease spread at the beginning of a new epidemic – implemented in this model which we described following [21], reflects the isolation of suspected individuals that is based on contacts with infected individuals, unlike in many other models including quarantine. We have also included separate compartments for the mildly symptomatic and severely symptomatic cases considering the large percentage of those infected who are asymptomatic or exhibit only mild symptoms.

The main novelty of the model introduced in this work is the incorporation of quarantine of individuals suspected of being exposed to COVID-19, which is one of the earliest public health policies for combating the spread of such infectious diseases in populations. The inclusion of quarantine has been modeled in a way that, up to our knowledge, had not been previously incorporated in models for COVID-19 transmission. This approach of defining quarantine facilitates us to keep track of those individuals who are moved into quarantine on the account of being feared to have contracted the disease, but ultimately turn out to be healthy, and those who are actually infected.

To validate our model as well as to obtain a starting point for our numerical assessment of the effect of various intervention parameters, we fitted the model to data from the early stage of the epidemic in Bangladesh. Using Latin Hypercube Sampling and the least squares method, we obtained a fairly good fit. Using the baseline parameter values obtained this way, we performed sensitivity analysis and numerical experiments to determine what kind of results may be achieved by applying intervention measures that are the most natural at the beginning of a novel epidemic, namely reducing contact rates and transmission probability as well as introducing quarantine. The results of the sensitivity analysis and the numerical experiments equally suggest that decreasing contact numbers and transmission probability are both efficient ways to reduce the number of infections, while quarantine alone – though an effective method – is a less powerful tool to reduce the number of infections.

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