Advances in Research

21(9): 14-28, 2020; Article no.AIR.59388
ISSN: 2348-0394, NLM ID: 101666096

A Novel Compartmental Model for Analysis and Projection of COVID-19 Dynamics in Bangladesh

Md. Mijanur Rahman[1*] and Md. Sadekur Rahman Rani[2]

[1]Department of Applied Mathematics, University of Dhaka, Dhaka, 1000, Bangladesh.
[2]Department of Mathematics, Shahjalal University of Science and Technology, Sylhet, Bangladesh.

Authors' contributions

This work was carried out in collaboration between both authors. Both authors developed the model. Author MSRR did the theoretical analyses, derivations and wrote the rough draft. Author MMR wrote the codes for numerical solution, performed the simulations, obtained the results, managed the literature searches and wrote the final draft. Both authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AIR/2020/v21i930228
Editor(s):
(1) Dr. José Alberto Duarte Moller, Advanced Materials Research Center (CIMAV), Mexico.
(2) Prof. Antonio Mastino, University of Messina, Italy.
Reviewers:
(1) Zafer Bekiryazici, Recep Tayyip Erdoğan University, Turkey.
(2) Prabir Sen, Kazi Nazrul University (KNU), India.
Complete Peer review History: http://www.sdiarticle4.com/review-history/59388

Original Research Article

Received 10 July 2020
Accepted 25 July 2020
Published 31 July 2020

ABSTRACT

A novel compartmental model is proposed to project the COVID-19 dynamics in Bangladesh. The exposed population is divided into two classes: tested and not tested. Model parameters are estimated by fitting the output with empirical COVID-19 data of Bangladesh from 7 April 2020 to 15 June 2020. It is found that even if 90% of exposed individuals are tested, number of unidentified cases (recovered or dead) is 3 to 4 times than that of identified cases. As of 15 June 2020, Bangladesh is using the Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) based test to detect the novel Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). The impact of false negative rate of this test on unidentified infection is analyzed. It is found that the year-end total recoveries (deaths) surges 700 (800) times if the false negative rate is doubled. Periodic lockdown and relaxation intervals are incorporated by defining the effective contact rate (β) as a periodic function of time. Impact of lockdown is perspicuous from the periodic fluctuation of the basic reproduction number ($\mathcal{R}_0$). It is observed that a 90-day-lockdwon reduces the final outcome by 3% while a 30-day-lockdwon increases it by 2%. On other hand, casualties are 10 to 100 times worse in case of no lockdown even with less than half effective contact rate. Analysis of strictness of isolation

**Corresponding author: E-mail: mmr.apmath@du.ac.bd;*

reveals that a 12.5% increase in the strictness coefficient reduces the exposed population 2.5 times whereas a 37.5% decrease in it intensifies the outcome nearly 9 times. Projections up to 6 April 2021 suggests that the epidemic will reach its peak in Bangladesh in August 2020.

Keywords: Mathematical model; COVID-19; Bangladesh; false negative; RT-PCR test; SARS-CoV-2; lockdown; isolation.

1. INTRODUCTION

The coronavirus disease (COVID-19), is an ongoing pandemic all over the world. The World Health Organization (WHO) was informed of pneumonia of unknown cause in Wuhan, China, on 31 December 2019, and a novel coronavirus was identified as the cause of the disease by Chinese authorities on 7 January 2020 [1,2]. Initially the virus wreaked havoc over Wuhan but soon it spread to other parts of the world which prompted WHO to declare the outbreak as a pandemic on 11 March 2020 [3]. By mid-March 2020, the European region became the epicenter of the epidemic, reporting over 40% of globally confirmed cases of that time [4]. From April to May, the epicenter shifted to the United States – more specifically to the city of New York [5]. The COVID-19 data of the first half of June clearly indicates that this extremely contagious disease is now looming large over Brazil, Russia, India, Pakistan and Bangladesh [6].

The disease is caused by the novel Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) which is mainly transmitted through droplets generated when an infected person coughs, sneezes, or exhales [7]. Since there is no effective vaccine or anti-viral against COVID-19 for use in humans till date (20 June) [8], the best on hand way to mitigate the spread of the disease is to implement different non-pharmaceutical interventions(NPIs) such as social distancing, total/zone-wise lockdown, use of face mask in public, mass testing and isolation of confirmed cases, and quarantine of suspected cases by contact-tracing. Consequently, it is both necessary and useful to analyze the effect of such measures on the spread and final size of the epidemic by means of different mathematical models and simulations using the available data. Researchers have proposed several mathematical models to study the COVID-19 dynamics all over the world [5,9-19]. Most of the works are based on the famous Kermack–McKendrick compartmental model [20]. A variation of this model, developed in [5], studies the transmission dynamics and control of the COVID-19 pandemic in the US (particularly in the state of New York) and analyses the impact of quarantine, isolation and mask efficacy. A compartmental model is developed in [9] using actual reported cases of 14 countries and applied to predict COVID-19 transmission in India in terms of lockdown for 4, 14, 21, 42, and 60 days. A stochastic mathematical model is developed in [10] and different scenarios in India are modeled with 1000 runs of Monte Carlo simulation. AnSEIR (susceptible-exposed-infectious-recovered) model is used in [11] to estimate the number of SARS-CoV-2 infected tuberculosis (TB) cases in India. An Epidemic Risk Time Series Model is built in [12] and used to analyze the daily COVID-19 incidence using the daily immigration population size data in China. Compartmental models considering behavioral changes are developed by [13] and [14] for Korea and Mexico respectively. The spread characteristics of three pneumonia: COVID-19, SARS (Severe Acute Respiratory Syndrome) and MERS (Middle East Respiratory Syndrome) are compared in [15] using data for different regions in China, Hong Kong and Saudi Arabia. It is found that the growth rate of COVID-19 is about twice that of SARS and MERS. A modified SEIRS model based on the real-world data in South Korea and Northern Ireland is presented in [16] which considers recovery with a possibility of resusceptibility, ageing factor of the population and time delay due to control measures. The effect of mass influenza vaccination on the spread of COVID-19 and other respiratory pathogens is studied in [18]. A transmission network model is developed in [19] and fitted to the reported data for the COVID-19 epidemic in Wuhan (China), Toronto (Canada), and Italy using a Markov Chain Monte Carlo (MCMC) optimization algorithm.

The Institute of Epidemiology, Disease Control and Research (IEDCR) of Bangladesh confirmed the first three coronavirus cases in the country on 8 March 2020 [21]. After 18 days, Bangladesh Government imposed a nationwide lockdown on 26 March to stem the spread of the virus [22]. But as soon as the 66-day-long lockdown was lifted on 31 May, the number of confirmed cases and deaths soared more than 50% just over the

first 20 days of June [23]. As of 20 June, there are 108,775 confirmed cases in the country including 1425 deaths [24]. Developing country with highly dense population such as Bangladesh suffers more from an epidemic like COVID-19. NPIs can slow down the spread of the disease and alleviate the disaster of the epidemic significantly. Nevertheless, not all those strategies can be imposed for an uncertain period of time due to several socio-economic limitations. That's why study of mathematical models designed specifically for Bangladesh is indispensable in order to prescribe a suitable framework of actions for fighting COVID-19. A few such models in the context of Bangladesh have been published in the literature. Chowdhury et al. [25] used a mathematical model to analyze the impacts of dynamic non-pharmaceutical interventions with intervals of relaxed social distancing over an 18-month period for Bangladesh as well as fifteen other countries.

In this study, a new mathematical model is designed based on that of [20] incorporating various aspects of the current scenario in Bangladesh as much as possible. In Bangladesh, as well as in other developing countries, the actual number of infected cases cannot always be identified with certainty due to limitation of test kits, lack of social awareness and other socio-economic barriers. As of 20 June, Bangladesh has performed a total of 599,579 tests [6] which is merely 0.37% of its current population. So it is very much likely that there is a considerable number of unidentified (not tested) infected individuals. This fact is considered in our model by dividing the exposed population into two classes: one that gets proper COVID-19 testing and another that does not. After testing, the confirmed COVID-19 positive individuals are isolated (in home or hospital) and do not spread the disease so much, whereas the unidentified infected people wholly account for the spread of the disease. There is another vital fact that has not yet been dealt with in any other COVID-19 models that we could find in the published works: the probability of being false negative in the Reverse Transcriptase Polymerase Chain Reaction (RT-PCR) based SARS-CoV-2 test. Till date (15 June 2020), Bangladesh is using only RT-PCR-SARS-CoV-2 test to detect the disease. If an exposed individual is tested using this test within the first 4 days of exposure (before symptom onset), there is a 67% chance that he/she will erroneously come out as COVID-19 negative despite being actually infected and this chance reduces to a minimum 20% if the person is tested on day 8 (i.e. 3 days after symptom onset) [26]. For a densely populated country like Bangladesh (Bangladesh is the most densely-populated country in the world [27]), these false negative individuals play a vital role in the transmission dynamics of COVID-19. This is included in our model by introducing a new compartment that contains the false negative individuals. Consequently, we come out with separate pair of compartments for both recovered and dead populations: one that depicts the outcome of officially confirmed COVID-19 recovered (dead) and another that predicts the unidentified (not tested) recoveries (deaths). Moreover, a periodic lockdown strategy is also implemented in the model by considering the effective contact rate β as a function of time. As a result the basic reproduction number $(\mathcal{R}_0)$ is also derived as a function of time. The model is numerically solved and simultaneously fitted using MATLAB® with the available observed COVID-19 data of Bangladesh to estimate the parameters. Output trajectories are simulated and rigorously analyzed to assess the impact of lockdown, isolation and false negative rate. Finally, necessary strategies are discussed based on the projections (up to 6 April 2021) of the epidemic in Bangladesh.

2. MODEL FOR COVID-19 TRANSMISSION DYNAMICS IN BANGLADESH

2.1 Mathematical Formulation of the Model

Based on the current COVID-19 scenario in Bangladesh, a novel mathematical model is developed by extending the classic SEIR model with the introduction of new mutually exclusive compartments. We divide the whole population (N) of Bangladesh into eleven compartments: susceptible (S), exposed i.e. newly-infected but not yet infectious individuals (E), tested i.e. exposed individuals who get the RT-PCR-SARS-CoV-2 test (T), COVID-19 negative detected by test (X), COVID-19 positive detected by test i.e. identified currently active cases (A), COVID-19 false negative detected by test i.e. actually infected but erroneously labeled negative by test (F), unidentified (not tested) currently infected (U), unidentified recovered (R_u), identified recovered i.e. COVID-19 negative after retest who were positive earlier (R), unidentified dead (D_u), identified dead i.e. identified COVID-19 positive individuals who die (D). Note that at any time t, we must have

$$S(t) + E(t) + T(t) + X(t) + U(t) + F(t) + A(t) + R_u(t) + R(t) + D_u(t) + D(t) = N. \quad (2.1)$$

For an easy understanding of the transition of individuals from one compartment to another, a flow diagram of the model is depicted in Fig. 1.

Description of all the variables and interpretation of all the parameters are given inTable 1.Note that all the probability parameters are denoted by Ω with corresponding subscript-superscript in small caps and must lie between 0 and 1 inclusive. The subscript denotes the compartment from which the inflow is coming while the superscript denotes the compartment to which the outflow is going. The nonlinear system of ordinary differential equations that describes the above model is given in (2.2).

$$\begin{cases} S' = -\frac{\beta(t)S(U+F+p_aA)}{N} - \delta_s^t\Omega_s^t S + (1-\Omega_x^r)X \\ E' = \frac{\beta(t)S(U+F+p_aA)}{N} - \delta_e^t\Omega_e^t E - \delta(1-\Omega_e^t)E \\ T' = \delta_s^t\Omega_s^t S + \delta_e^t\Omega_e^t E + \delta_a^t(1-\Omega_a^d)A - \Omega_t^a T - \Omega_t^x T - \Omega_t^f T \\ X' = \Omega_t^x T - (1-\Omega_x^r)X - \Omega_x^r X \\ U' = \delta(1-\Omega_e^t)E - \gamma(1-\Omega_u^{d_u})U - \delta_u^{d_u}\Omega_u^{d_u}U \\ F' = \Omega_t^f T - \delta_f^{r_u}(1-\Omega_f^{d_u})F - \delta_f^{d_u}\Omega_f^{d_u}F \\ A' = \Omega_t^a T - \delta_a^t(1-\Omega_a^d)A - \delta_a^d\Omega_a^d A \\ R_u' = \gamma(1-\Omega_u^{d_u})U + \delta_f^{r_u}(1-\Omega_f^{d_u})F \\ R' = \Omega_x^r X \\ D_u' = \delta_u^{d_u}\Omega_u^{d_u}U + \delta_f^{d_u}\Omega_f^{d_u}F \\ D' = \delta_a^d\Omega_a^d A \end{cases} \quad (2.2)$$

Note that the prime notation denotes first derivative with respect to time (t). In order to satisfy equation (2.1), the sum of the rate of changes of all the variables must be zero which can be readily verified by adding all the equations of (2.2).

We consider that the identified COVID-19 positive individuals (i.e. those who are in A) are isolated in home or hospital and get necessary treatments. Though they are isolated, a fraction of them must account for the spread of the disease otherwise no doctor or nurse would have been infected. This is incorporated in the model (2.2) using the parameter p_a where $0 < p_a < 1$. The parameter p_a can be thought of as a measure of the strictness of isolation. Thus, we can assume that a susceptible individual is exposed to the disease by coming into contact with unidentified (not tested) infected individuals (i.e. those who are in U) or the false negative individuals (i.e. those who are in F) or the fraction p_a of isolated positive individuals (p_aA). When a susceptible individual becomes exposed, we assume that he/she is either tested (i.e. moves to the T compartment) after a certain delay ($1/\delta_e^t$ days) or not tested and moves to the U compartment after the incubation period ($1/\delta$ days). The probability of an individual being tested is assumed to be Ω_e^t where $0 \le \Omega_e^t \le 1$. Currently Bangladesh is using only RT-PCR-SARS-CoV-2 test to detect COVID-19 and it is observed form the most recent data that around 20% of the tested individuals are coming out as COVID-19 positive. In other words, almost 80% of the tested individuals are found to be COVID-19 negative which also includes those who are actually infected but erroneously labeled as false negative by the test. If we assume that the false negative rate of the test is the least 20% [26], a simple calculation shows that 75% of the tested individuals are truly negative and 5% are false negative while the other 20% are positive. This is implemented in the model (2.2) by setting $\Omega_t^x = 0.75$, $\Omega_t^f = 0.05$ and $\Omega_t^a = 0.20$. In the T compartment, individuals are not only coming from the exposed class E but also from the susceptible class S, since individuals who develop COVID-19 like symptoms due to other disease are also being tested. The COVID-19

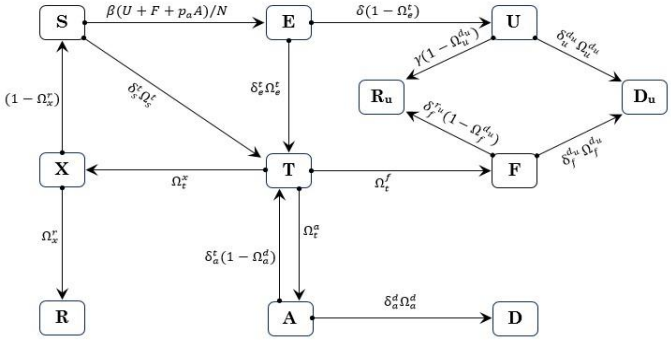


Fig. 1. Flow diagram of the model (2.2) for COVID-19 dynamics in Bangladesh

Table 1. Description of variables and parameters used in model (2.2)

Variable	Description
S	Population of susceptible individuals
E	Population of exposed individuals
T	Tested individuals
X	Truly COVID-19 negative individuals confirmed after test
F	False COVID-19 negative individuals who are actually infected
A	Active COVID-19 positive individuals confirmed after test
U	Unidentified (not tested) infected individuals
R_u	Unidentified recovered individuals
R	Identified recovered individuals confirmed after retest
D_u	Unidentified dead individuals
D	Identified dead individuals (dead among identified infected)
Parameter	**Interpretation**
$\beta(t)$	Effective contact rate (modeled as a function of time (t) as in equation (2.3))
p_a	Fraction of A that transmits the disease (i.e. a measure of strictness of isolation)
δ_s^t	Transmission rate from S to T
δ_e^t	Transmission rate from E to T
δ	Inverse of incubation period (i.e. transmission rate from E to I)
δ_a^t	Transmission rate from A to T
γ	Recovery rate of unidentified infected (i.e. transmission rate from U to R_u)
$\delta_u^{d_u}$	Mortality rate of unidentified infected (i.e. transmission rate from U to D_u)
$\delta_f^{r_u}$	Recovery rate of false negative (i.e. transmission rate from F to R_u)
$\delta_f^{d_u}$	Mortality rate of false negative (i.e. transmission rate from F to D_u)
δ_a^d	Mortality rate of identified positive (i.e. transmission rate from A to D)
Ω_s^t	Probability of a susceptible individual to be tested
Ω_x^r	Probability of a truly negative (after retest) individual to be recovered
Ω_e^t	Probability of an exposed individual to be tested
Ω_a^d	Probability of a confirmed currently infected individual to die of COVID-19
Ω_t^a	Probability of a tested individual to be COVID-19 positive
Ω_t^x	Probability of a tested individual to be truly COVID-19 negative
Ω_t^f	Probability of a tested individual to be COVID-19 false negative
$\Omega_u^{d_u}$	Probability of an unidentified infected individual to die of COVID-19
$\Omega_f^{d_u}$	Probability of a false negative individual to die of COVID-19

positive individuals (detected by test) are isolated and treated in home or hospital until they recover or die. The recovery of a COVID-19 positive individual is confirmed when he/she comes out as COVID-19 negative in two consecutive tests. This is modeled by the transition from A to T. The class of tested individuals who are truly negative (i.e. those who are in the X compartment) is composed of non-infected tested individuals and retested COVID-19 patients who are now recovered. The first group reverts to the susceptible compartment S while the latter moves to the R compartment of identified recovered individuals. The unidentified (not tested) infected individuals in U and the false negative individuals in F either recover (i.e. move to R_u) or die (i.e. move to D_u).

The effect of nationwide lockdown is implemented in the model (2.2) by considering the effective contact rate β as a function of time (t). It is reasonable to assume that the value of $\beta(t)$ will decrease when a nationwide lockdown is in effect and the opposite will happen when there is none. Bangladesh imposed a 66-day-long nationwide lockdown after 18 days of the confirmation of first three COVID-19 cases in the country. This means that on 7 April (the date from which we fit our model) the lockdown was already in effect. So we assume that $\beta(t)$ is decreasing until the lockdown is withdrawn on 31 May. As soon as the lockdown is removed, it starts to increase again and so on. Thus, we consider a 60-day-long (rounded to 2 months for convenience) periodic interval of lockdown and

relaxation one after another. These assumptions lead us to construct a damped sinusoidal wave of the form (2.3) to model the time-varying effective contact rate.

$$\beta(t) = e^{-kt}\left[\left(\frac{\beta_{max}-\beta_{min}}{2}\right)cos\left(\frac{\pi t}{L}\right)+\left(\frac{\beta_{max}+\beta_{min}}{2}\right)\right] \quad (2.3)$$

In (2.3), β_{max} = maximum effective contact rate, β_{min} = minimum effective contact rate, k = damping factor, L = length of the lockdown period (in days). We estimate each of these parameters except L using observed data which is discussed in section 3. The function is designed by translating and stretching the $cosine$ function in such a way so that it varies between β_{max} and β_{min} with a period of L. The lockdown period L is fixed to 60 days in order to match our observation. In order to model the fact that as time progresses the contact rate decreases due to various control measures and social awareness, we multiply the modified $cosine$ function with a transient term $e^{(-kt)}$ where $k > 0$.

2.2 Data

We obtained the time series COVID-19 data of Bangladesh from [28] provided by the Center for Systems Science and Engineering (CSSE) of Johns Hopkins University. The data information contains cumulative number of confirmed cases, cumulative number of recovered cases and cumulative number of death cases. We also used daily number of test data obtained from [29]. At the time of this writing, we considered data of the most recent 70 days (from 7 April 2020 to 15 June 2020). The cumulative number of active cases (calculated as confirmed−(recovered+dead)) is also used to fit the model.

3. PARAMETER ESTIMATION PROCESS

We noticed that almost all the compartmental models of COVID-19 dynamics published in the literature estimated the model parameters by fitting the output with officially recorded

Table 2. Initial and estimated values of the parameters used in model (2.2)

Parameter	Initial Value	Estimated Value(rounded to 7 places)	Source
β_{max}	1.15	1.4122925	Fitted with observed data
β_{min}	0.60	0.9120321	Fitted with observed data
k	0.005	0.0108050	Fitted with observed data
L	60		Taken from observation
p_a	0.2		Assumed
δ_s^t	1/20	1/35.7020920	Fitted with observed data
δ	1/5.1		From [2, 5, 31-34]
δ_e^t	1/8.1		Calculated from δ
δ_a^t	1/25		Assumed from observation
γ	1/15		From [34,35]
$\delta_f^{r_u}$	1/12		Calculated from γ
$\delta_u^{d_u}$	1/10	1/6.0007394	Fitted with observed data
$\delta_f^{d_u}$	1/7	1/3.0007394	Calculated from $\delta_u^{d_u}$
δ_a^d	1/20	1/29.8715400	Fitted with observed data
Ω_s^t	0.00001	0.0001764	Fitted with observed data
Ω_x^r	0.80	0.0438467	Fitted with observed data
Ω_e^t	0.90	0.8865300	Fitted with observed data
Ω_a^d	0.02	0.0336296	Fitted with observed data
Ω_t^a	0.20		Computed from observation and [26]
Ω_t^x	0.75		Computed from observation and [26]
Ω_t^f	0.05		Computed from observation and [26]
$\Omega_u^{d_u}$	0.04	0.0443652	Fitted with observed data
$\Omega_f^{d_u}$	0.04	0.0443652	Assumed equal to $\Omega_u^{d_u}$

recovered data (or mortality data) whereas the model does not consider unidentified recovered (or dead) individuals separately. Perhaps this is due to the indirect assumption that the official data is 100% accurate or the unidentified cases are negligible. But this assumption may not reflect the real scenario of Bangladesh properly. In our model, this is successfully dealt with by fitting the trajectories of R and D with the corresponding officially recorded data since these two compartments only account for the identified (tested) individuals. We also fitted the trajectories of T and A with the daily test cases and currently active cases for better estimation. It is to be noted that these four trajectories are fitted simultaneously. We used the least square curve fitting technique in MATLAB® with a tolerance of 10^{-6}. The trust region reflective algorithm was used with maximum 10^5 iterations and maximum 10^6 function evaluations. The total population (N) is taken to be $164{,}689{,}000$ (United Nations (UN) estimated mid-2020 population of Bangladesh [30]). Note that not all the parameters in Table 1 are estimated since the values of some parameters are already established in the published literature. We used these values from various sources as listed in Table 2. The initial values taken for other estimated parameters and their final estimations are also given in Table 2.

A visual representation of how precisely the model output fitted with the observed data is shown in Fig. 2. The model fits extremely well with cumulative recovered and dead data while matches with the test cases and active cases considerably.

4. ANALYSIS AND SIMULATION

4.1 Basic Reproduction Number

The basic reproduction number, commonly denoted by $\mathcal{R}_0$, of model (2.2) is derived using the next generation operator method [36,37]. The system (2.2) has a line of disease free equilibrium $(s_0, 0,0,0,0,0,0,0,0,0)$. Using the notation in [36], the next generation matrices F and V for the new infection terms and the transition terms are computed as follows:

$$F = \begin{bmatrix} 0 & \beta s & \beta s & \beta s p_a \\ \delta(1-\Omega_e^t) & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} \delta_e^t\Omega_e^t + \delta(1-\Omega_e^t) & 0 & 0 & 0 \\ 0 & \gamma\left(1-\Omega_u^{d_u}\right) + \delta_u^{d_u}\Omega_u^{d_u} & 0 & 0 \\ 0 & 0 & \delta_f^{r_u}\left(1-\Omega_f^{d_u}\right) + \delta_f^{d_u}\Omega_f^{d_u} & 0 \\ 0 & 0 & 0 & \delta_a^t(1-\Omega_a^d) + \delta_a^d\Omega_a^d \end{bmatrix}$$

Then the basic reproduction number $\mathcal{R}_0$ is given by the largest positive eigenvalue of FV^{-1} as in (4.1).

$$\mathcal{R}_0 = \left(\frac{\beta s\left(\delta\left(1-\Omega_e^t\right)\right)}{\left(\delta_e^t\Omega_e^t + \delta\left(1-\Omega_e^t\right)\right)\left(\gamma\left(1-\Omega_u^{d_u}\right) + \delta_u^{d_u}\Omega_u^{d_u}\right)}\right)^{\frac{1}{2}} \qquad (4.1)$$

Since the effective contact rate $\beta(t)$ is a function of time, we also take $\mathcal{R}_0$ as a function of time in (4.1). Values of $\mathcal{R}_0$ of the model over time is shown in Fig. 3. The maximum $\mathcal{R}_0 = 1..82$ occurs at the beginning and the minimum $\mathcal{R}_0 = 0.39$ occurs at the end of the year. Over the whole period $\mathcal{R}_0$ varies between these values periodically which reflects the effect of lockdown and relaxation. $\mathcal{R}_0$ goes down the critical value 1 (unity) on 25 July. For the rest of the year it does not go above that value despite fluctuating periodically. This hints that the spread of the epidemic may be taken under control within this year by implementing the assumed 60-days-long periodic lockdown and relaxation policy.

4.2 Case Fatality Ratio (CFR)

The model projected case fatality ratio (CFR), computed using the formula: CFR = deaths / (deaths + recovered) [38], is shown in Fig. 4. It reveals that the total CFR steadily remains around 11% over the whole period while the daily CFR varies periodically between 9% to 15% as a reflection of the lockdown effect.

4.3 Impact of Lockdown Duration

Fig. 5 (a-d) shows the effect of the length of lockdown and relaxation intervals (L) on $\mathcal{R}_0(t)$, total currently infected, cumulative total recoveries (identified and unidentified both) and cumulative total deaths (identified and unidentified both). Along with the baseline value $L = 60$ days, we experimented with $L = 90$ and $L = 30$ days. From Fig. 5(a), we see that the values of $\mathcal{R}_0$ varies the most in case of $L = 30$ and the least in case of $L = 90$. However, the most interesting thing is the point of time at which $\mathcal{R}_0$ goes down below the critical value 1 (unity). As expected, in case of $L = 90$, $\mathcal{R}_0$ goes below unity on 20 June which is more than a month earlier than that of $L = 60$ (25 July). But in case of $L = 30$, this happens on 27 June which is nearly the same as that of $L = 90$ and almost a month earlier than that of $L = 60$. Nevertheless, this does not improve the final outcome of infected or recovered or dead for $L = 30$ at the end of the year.

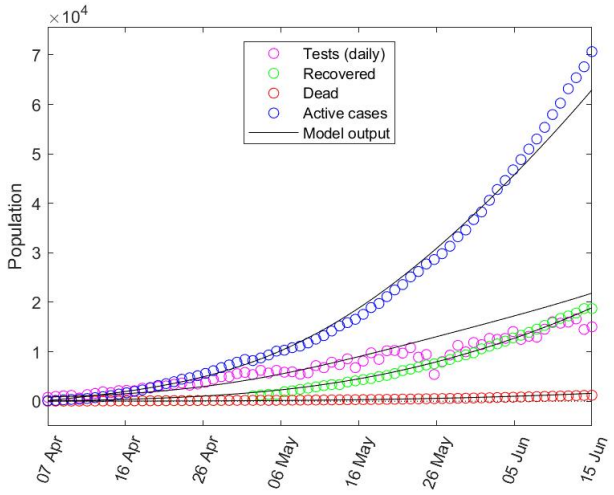


Fig. 2. Best fit of model output with the observed COVID-19 data of Bangladesh

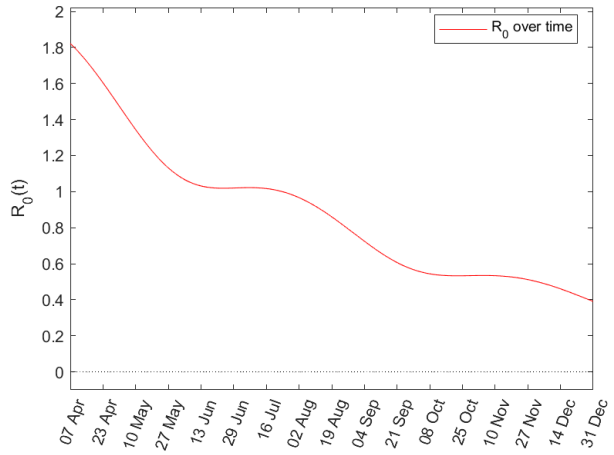


Fig. 3. Basic reproduction number of the model (2.2)over time

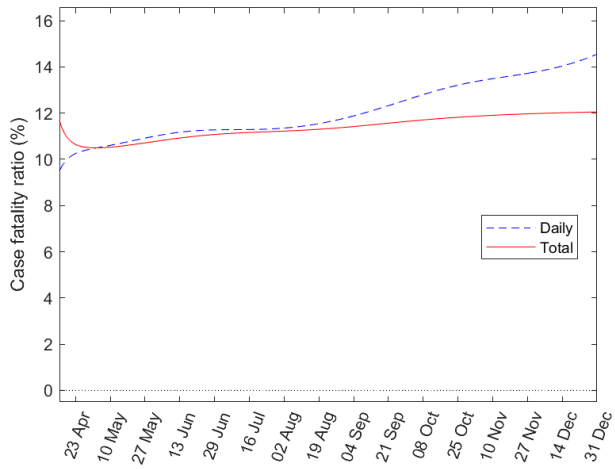


Fig. 4. Model projected case fatality ratio (CFR) in Bangladesh

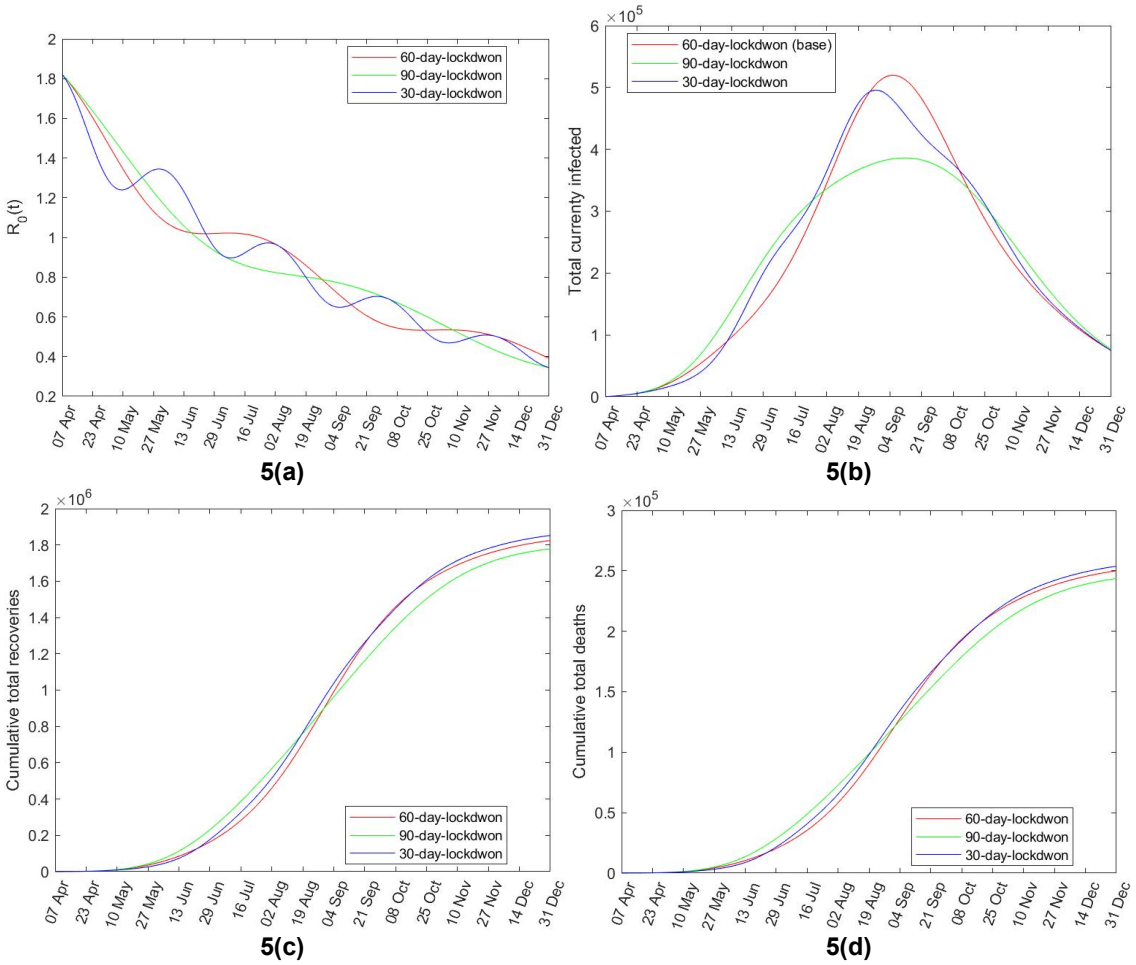


Fig. 5. Impact of the duration of lockdown (followed by a relaxation of same period) on (a) basic reproduction number, (b) total currently infected (identified and unidentified) (c) cumulative total recoveries (identified and unidentified), (d) cumulative total deaths (identified and unidentified)

In Fig. 5 (b), we observe that the number of currently infected is much less for $L = 90$ than for the other two cases. From Fig. 5(c-d), we observe that if 90-day-long lockdown is imposed then the final size of both of the recovered and dead population decreases nearly 3% of the baseline value (i.e. less transmission). On the other hand, it increases nearly 2% (both for recovered and dead) if 30-day-long lockdown is imposed (i.e. more transmission). This indicates that it is better to impose periodic lockdown-relaxation of longer duration than that of shorter duration.

If there were no lockdown at all from the beginning, then we assume that the effective contact rate does not vary periodically with time, rather it becomes a constant. So we incorporate the no-lockdown scenario in the model using constant value for $\beta(t)$. Since (2.3) becomes undefined for $L = 0$, we use a different approach to choose the constant. We take the average of the estimated values of β_{max} and β_{min} from Table 2 which gives 1.16 (up to two decimal places). Using this value for β, we can see the devastating effect of no-lockdown in Fig. 6 (a-d). Even if we use lower values of β (e.g. 0.90, 0.70 and 0.50), the outcomes are still horrifying. With no lockdown, maximum total active cases and year-end cumulative total recoveries (identified and unidentified both) are of order 10^7 or higher for each of the four values of β (Fig. 6(a-b)). Whereas, even with the 30-day-lockdown, these values are of order 10^5 and 10^6 respectively as shown in Fig. 5(b-c). Comparison of Fig.6(c) and Fig. 5(d) reveals that even in the best case with

no lockdown ($\beta = 0.5$), the year-end value of cumulative total deaths rises to almost 2 million which is 8 times greater than that of the worst case with lockdown (30-day-lockdwon). Fig. 6(d) shows that the case fatality ratio (CFR) ultimately becomes higher for larger value of β when no lockdown is in effect.

4.4 Impact of False Negative Rate of RT-PCR-SARS-CoV-2 Test

According to [26], we assumed in the formulation of the model that the false negative rate of RT-PCR based SARS-CoV-2 test is 20%. Since this rate can vary considerably, we simulate the model output for three other rates: 10%, 30% and 40%.

Fig. 7(a-b) shows the comparison. As expected, a higher false negative rate causes more infection (more recoveries and more deaths) and a lower rate causes the opposite. If the false negative rate reduces to 10% from 20% (base value), the final outcome of total recoveries and total deaths dramatically decrease by about 56% and 58% of the base outcome respectively. For a 30% false negative rate, the aggravation is 167% (in recovery) and 179% (in death) which are quite substantial. But for a 40% rate, the surge is simply staggering: 739% in recovery and 819% in death. Hence there is no doubt that the false negative rate of RT-PCR-SARS-CoV-2 test has an astounding impact on the spread and year-end outcome of the epidemic in Bangladesh.

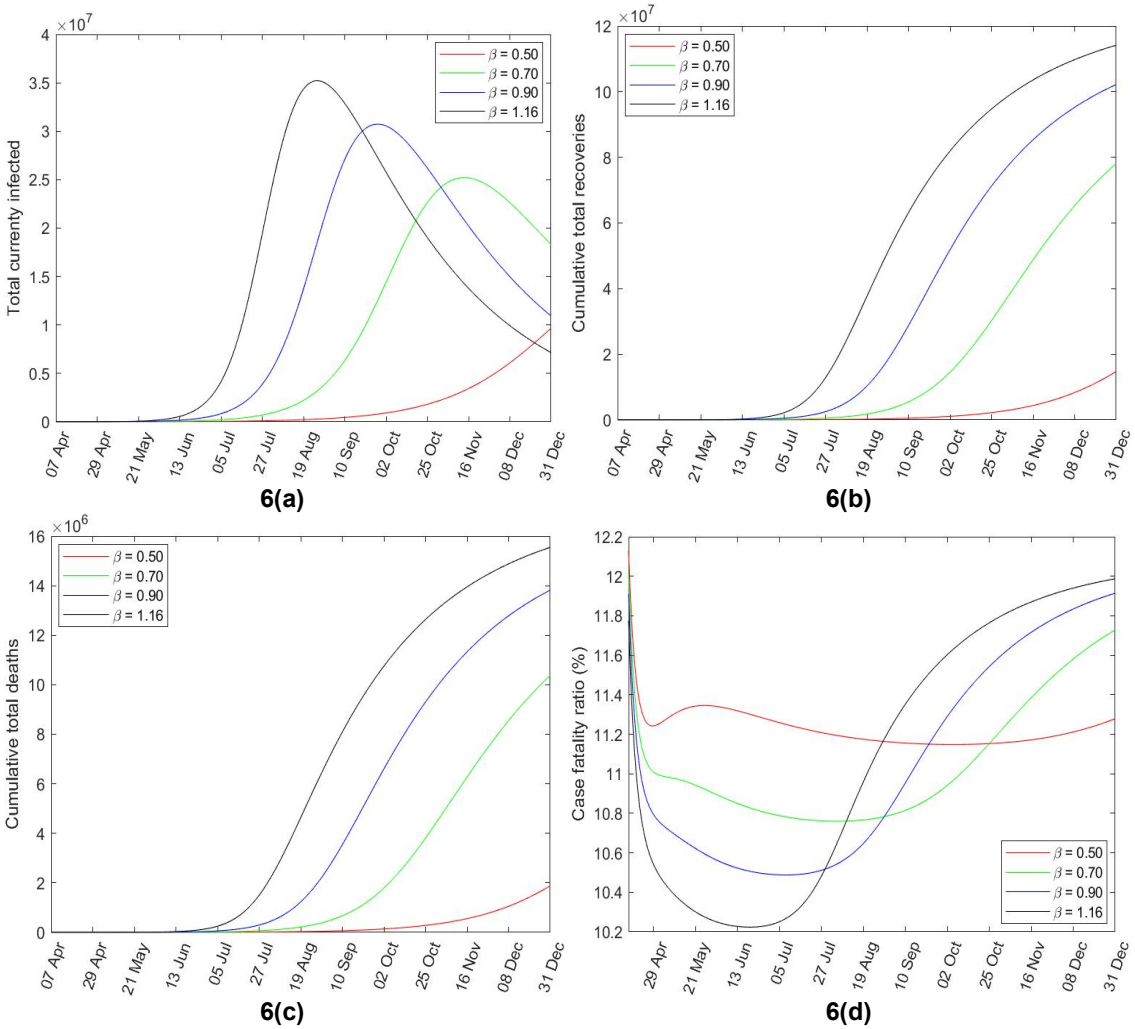
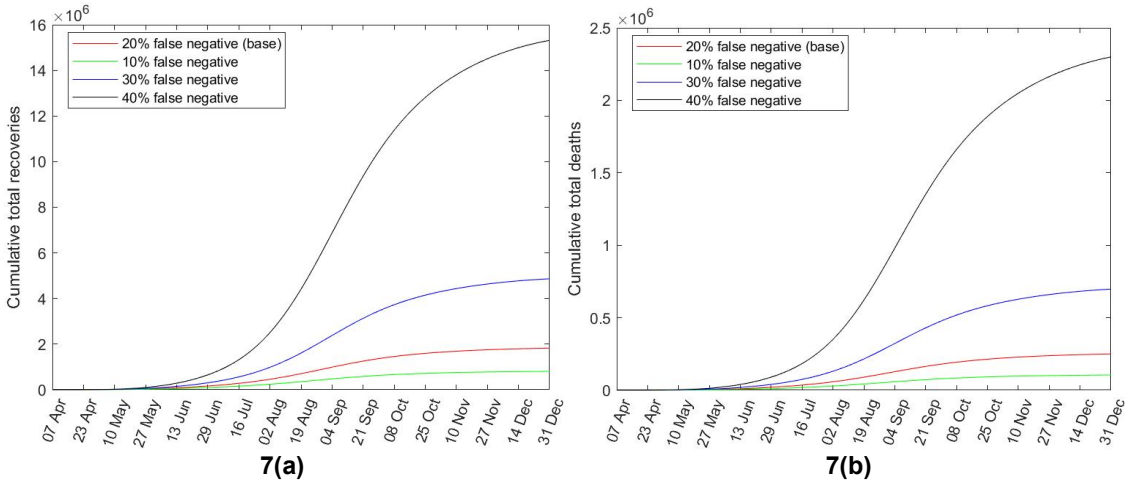
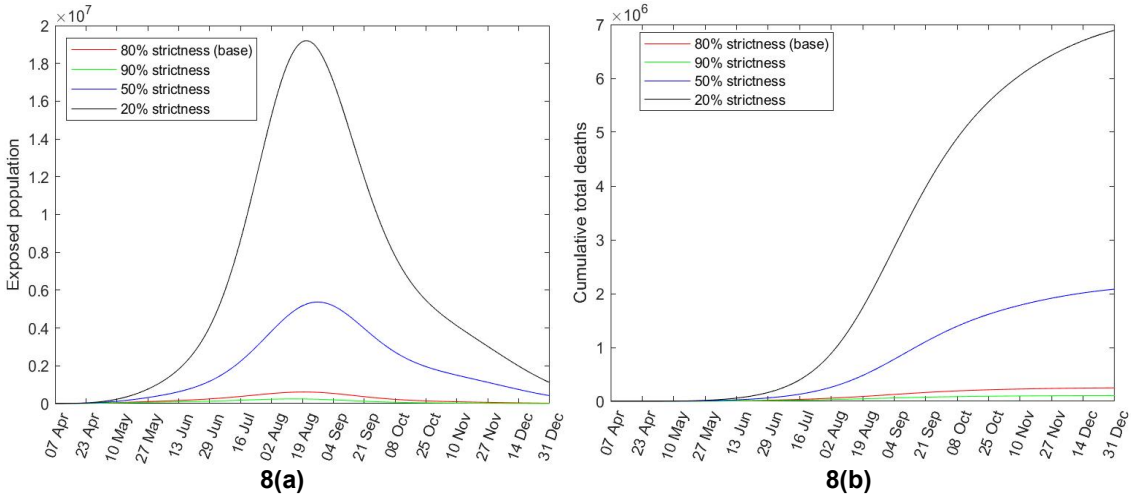


Fig. 6. Impact of no-lockdown on (a) total currently infected, (b) cumulative total recoveries, (c) cumulative total deaths, and (d) case fatality ratio (CFR)



7(a) 7(b)

Fig. 7. Impact of false negative rate of RT-PCR-SARS-CoV-2 test on (a) cumulative total recoveries, (b) cumulative total deaths



8(a) 8(b)

Fig. 8. Impact of isolation strictness on the outcome of (a) exposed population (b) cumulative total deaths

4.5 Impact of Isolation Strictness

We formulated model (2.2) assuming that only 20% of the isolated individuals in A contributes to the spread of the disease ($p_a = 0.2$). In other words, the strictness (effectiveness) of isolation is 80%. So it is necessary to experiment the impact of isolation strictness on the outcome of the trajectories.

Fig. 8(a) shows the impact of different isolation strictness on the trajectory of exposed population. It is found that with 90% strictness, the maximum value of exposed population shrinks by 2.5 times of that of the base value with 80% strictness. On the other hand, the maximum number of exposed individuals grows 8.7 times and 31 times respectively with 50% and 20% strictness of isolation. Similar situation is observed in Fig. 8(b). The number of cumulative total deaths diminishes 2.4 times for 90% strictness while rises 8.3 times for 50% strictness and soars 27.6 times for 20% strictness. Therefore, maintaining a stricter isolation of identified COVID-19 positive individuals is crucial to controlling the spread of the disease.

4.6 Projection

Using the baseline values given in Table 2 and the assumption of 60-day-lockdwon, we make an attempt to project the outbreak of COVID-19 in Bangladesh over a period of 365 days (from 7 April 2020 to 6 April 2021). The projections are shown in Fig. 9(a-e).

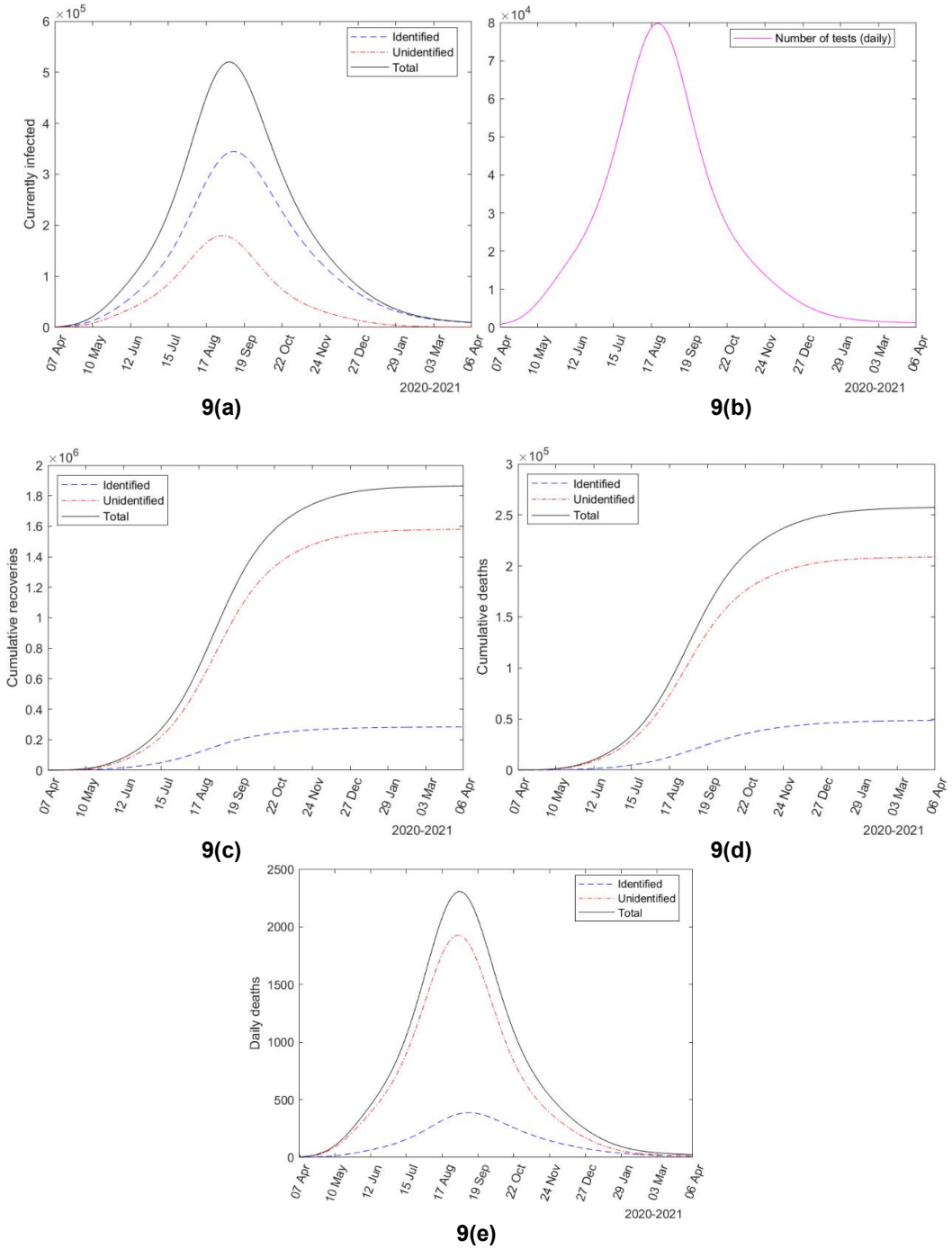


Fig. 9. Model projection (up to 6 April 2021) of COVID-19 dynamics in Bangladesh: (a) currently infected, (b) number of test cases, (c) cumulative recoveries, (d) cumulative deaths, and (e) daily deaths

Fig. 9(a-b, e) clearly indicates that the peak of the epidemic in Bangladesh is expected to occur in August. The estimated value 0.8865300 of the model parameter Ω_e^t in Table 2 means that almost 89% of exposed individuals are tested. This is reflected in Fig. 9(a) which shows that the curve of identified active cases is always above the curve of unidentified active cases. Fig. 9(b)

reveals the performed number of tests which attains a maximum value of almost 80,000 during the peak of the epidemic in August. Though 89% of exposed individuals are tested, the number of identified recoveries (deaths) is much higher than the number of identified recoveries (deaths) as shown in Fig. 9(c-d). This is due to the effect of 20% false negative rate of RT-PCR-SARS-CoV-2 test. The individuals who are false negative in the test do not contribute to the population of identified recovered (dead) when they recover (die), rather they remain as unidentified recovered (dead). This fact also impacts the number of daily deaths shown in Fig. 9(e). The maximum number of unidentified daily deaths (1,928) is almost five times of that of identified daily deaths (388). Both maxima occur in August during the peak of the epidemic in Bangladesh. All the projections shown in Fig. 9(a-e) reveal that if the hypothesized lockdown, isolation and other measures continue to remain same in reality as described in this study, then the COVID-19 outbreak in Bangladesh will start decreasing after August 2020 and it will eventually go off after March 2021 (i.e. nearly after a year of the confirmation of first COVID-19 case in Bangladesh).

The model formulated in this study does not incorporate demographic parameters such as fecundity and mortality of Bangladesh. These can be incorporated to upgrade this model into a better one that suits the reality more precisely. Moreover, vaccination can be incorporated in the model as a possible intervention in the near future since the race of vaccine invention is going on quite optimistically [39]. Needless to say, invention of an effective vaccine and/or cure for COVID-19 in the meantime would lead to a much better outcome. Even without any modification of the model, it can be applied accordingly to study the COVID-19 dynamics in other countries as well.

5. CONCLUSION

The present study is focused on formulating a new model that best suits the current COVID-19 scenario in Bangladesh. The analysis of the model output suggests that (i) there is huge number of unidentified cases (infected, recovered and dead) due to the limited number of test kits and false negative rate of RT-PCR-SARS-CoV-2 tests, (ii) imposing 60-day-long lockdown and relaxation periodically after one another for the rest of the year can mitigate the spread of the disease significantly, (iii) strictly isolating the identified individuals is very crucial, and (iv) reducing the false negative rate of test as much as possible can reduce transmission to a great extent. It is also to be noted that the model projected identified cases (active, recovered or dead) can be detected only if the model projected number of tests are performed. Over the last two weeks, Bangladesh performed 15 to 18 thousand tests daily whereas the model suggests 30 to 40 thousand tests right now and 70 to 80 thousands test during the peak in August. In conclusion, projections up to 6 April 2021 based on the model indicates that COVID-19 casualty in Bangladesh can be reduced to a sustainable limit if 60-day-long periodic intervals of lockdown and relaxation is imposed and stricter isolation protocols are maintained. In addition to that, reducing the false negative rate of RT-PCR-SARS-CoV-2 test can also play a vital role in controlling the pandemic. This can be achieved by improving the efficiency of the test. Another on hand alternative could be devising a policy of testing an individual more than once using other effective rapid diagnostic tests (RDTs) alongside the currently used RT-PCR based test.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. World Health Organization, Emergencies, preparedness, response. Pneumonia of unknown cause – China, 5 January 2020. Available: https://www.who.int/csr/don/05-january-2020-pneumonia-of-unkown-cause-china/en/(Accessed 21 April 2020).
2. Li Q,Guan X,Wu P, Wang X, Zhou L, Tong Y, et al., Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus–Infected Pneumonia. New Engl. J. Med. 2020;382(13):1199-1207.
3. World Health Organization, Coronavirus disease (COVID-19) outbreak; 2020. Available:https://www.euro.who.int/en/health-topics/health-emergencies/coronavirus-covid-19(Accessed 11 April 2020).
4. World Health Organization, Coronavirus disease (COVID-19) pandemic, 2020. Available:https://www.euro.who.int/en/health-topics/health-emergencies/coronavirus-covid-19/novel-coronavirus-2019-ncov(Accessed 11 April 2020).

5. Ngonghala CN, Iboi E, Eikenberry S, Scotch M, MacIntyre CR, Bonds MH, et al., Mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the 2019 novel Coronavirus. Math Biosci. 2020;325:108364.
6. Worldometer, COVID-19 Coronavirus Pandemic; 2020. Available:https://www.worldometers.info/coronavirus/ (Accessed 16 June 2020).
7. World Health Organization, Modes of transmission of virus causing COVID-19: implications for IPC precaution recommendations; 2020. Available:https://www.who.int/news-room/commentaries/detail/modes-of-transmission-of-virus-causing-covid-19-implications-for-ipc-precaution-recommendations(Accessed 15 May 2020).
8. World Health Organization, COVID-19;2020. Available:http://www.emro.who.int/health-topics/corona-virus/questions-and-answers.html(Accessed 21 June 2020).
9. Ambikapathy B, Krishnamurthy K, Mathematical Modelling to Assess the Impact of Lockdown on COVID-19 Transmission in India: Model Development and Validation. JMIR Public Health Surveill. 2020;6(2):19368.
10. Chatterjee K, Chatterjee K, Kumar A, Shankar S. Healthcare impact of COVID-19 epidemic in India: A stochastic mathematical model. Med J Armed Forces India;2020.
11. Marimuthu B. Nagappa N. Sharma S. Basu, Chopra KK, COVID-19 and tuberculosis: A mathematical model based forecasting in Delhi, India. Indian J Tuberc. 2020;67(2):177-181.
12. Huang Q, Kang YS, Mathematical Modeling of COVID-19 Control and Prevention Based on Immigration Population Data in China: Model Development and Validation. JMIR Public Health Surveill. 2020;6(2):18638.
13. Kim S, Seo YB, Jung E. Prediction of COVID-19 transmission dynamics using a mathematical model considering behavior changes in Korea. Epidemiol Health. 2020;42:2020026.
14. Acuña-Zegarra MA, Santana-Cibrian M, Velasco-Hernandez JX, Modeling behavioral change and COVID-19 containment in Mexico: A trade-off between lockdown and compliance.Mathematical Biosciences,2020;325:108370.
15. K. Liang, Mathematical model of infection kinetics and its analysis for COVID-19, SARS and MERS. Infect Genet Evol. 2020;82:104306.
16. Ng KY, Gui MM, COVID-19: Development of a robust mathematical model and simulation package with consideration for ageing population and time delay for control action and resusceptibility. Physica D. 2020;411:132599.
17. Tang Y, Serdan TDA, Masi LN,Tang S, Gorjao R, Hirabara SM, Epidemiology of COVID-19 in Brazil: using a mathematical model to estimate the outbreak peak and temporal evolution. Emerg Microbes Infect. 2020:1-11.
18. Li Q, Tang B, Bragazzi NL, Xiao Y, J Wu, Modeling the impact of mass influenza vaccination and public health interventions on COVID-19 epidemics with limited detection capability. Mathematical Biosciences. 2020;325:108378.
19. Xue L, Jing S, Miller JC, Sun W, Li H, Estrada-Franco JG, et al., A data-driven network model for the emerging COVID-19 epidemics in Wuhan, Toronto and Italy. Mathematical Biosciences. 2020;326:108391.
20. Kermack WO, McKendrick AG. A contribution to the mathematical theory of epidemics.1927;115(772):700-721.
21. Institute of Epidemiology, Disease Control and Research, Bangladesh Covid-19 Update. Covid-19 Vital Statistics. Timeline; 2020.Available:https://iedcr.gov.bd/(Accessed 10 June 2020).
22. Kamruzzaman M, Sakib SN, Bangladesh imposes total lockdown over COVID-19; 2020.Available:https://www.aa.com.tr/en/asia-pacific/bangladesh-imposes-total-lockdown-over-covid-19/1778272(Accessed 18 May 2020).
23. S. Mamun, Containing Covid-19: Bangladesh takes no strict action during danger period; 2020.Available:https://www.dhakatribune.com/health/coronavirus/2020/06/20/containing-covid-19-bangladesh-takes-no-strict-action-during-danger-period(Accessed 21 June 2020).
24. Worldometer, Bangladesh Coronavirus Cases; 2020.Available:https://www.worldometers.info/coronavirus/country/bangladesh/(Accessed 21 June 2020).

25. Chowdhury R, Heng K, Shawon MSR, Goh G, Okonofua D, Ochoa-Rosales C, et al., Dynamic interventions to control COVID-19 pandemic: a multivariate prediction modelling study comparing 16 worldwide countries. European Journal of Epidemiology. 2020;35(5):389-399.
26. Kucirka LM, Lauer SA, Laeyendecker O, Boon D, Lessler J, Variation in False-Negative Rate of Reverse Transcriptase Polymerase Chain Reaction–Based SARS-CoV-2 Tests by Time Since Exposure. Annals of Internal Medicine; 2020.
27. R. Hannah, Which countries are most densely populated?; 2019. Available:https://ourworldindata.org/most-densely-populated-countries#:~:text=Of%20the%20larger%20countries1,2)%20completing%20the%20top%20five(Accessed 12 June 2020).
28. GitHub, Novel Coronavirus (COVID-19) Cases, provided by JHU CSSE; 2020. Available:https://github.com/CSSEGISandData/COVID-19(Accessed 16 June 2020).
29. Hannah R, Esteban OO, Diana B, Edouard M, Joe H, Bobbie M, et al., Coronavirus (COVID-19) Testing; 2020. Available:https://ourworldindata.org/coronavirus-testing(Accessed 16 June 2020).
30. United Nations, Department of Economic and Social Affairs, Population Division (2019). World Population Prospects; 2019. Available:https://population.un.org/wpp/Download/Files/1_Indicators%20(Standard)/EXCEL_FILES/1_Population/WPP2019_POP_F01_1_TOTAL_POPULATION_BOTH_SEXES.xlsx.
31. Lauer SA, Grantz KH, Bi Q, Jones FK, Zheng Q, Meredith HR, et al., The Incubation Period of Coronavirus Disease 2019 (COVID-19) From Publicly Reported Confirmed Cases: Estimation and Application. Annals of Internal Medicine. 2020;172(9):577-582.
32. Del Rio C, Malani PN. COVID-19—New Insights on a Rapidly Changing Epidemic. JAMA. 2020;323(14):1339-1340.
33. Lai CC, Shih TP, Ko WC, Tang HJ, Hsueh PR. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): The epidemic and the challenges. International Journal of Antimicrobial Agents. 2020;55(3):105924.
34. Ferguson N, Laydon D, Nedjati Gilani G, Imai N, Ainslie K, Baguelin M, et al. Report 9: Impact of non-pharmaceutical interventions (NPIs) to reduce COVID19 mortality and healthcare demand; 2020. DOI:10.25561/77482.
35. World Health Organization, WHO Director-General's opening remarks at the media briefing on COVID-19; 2020. Available:https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19--24-february-2020(Accessed 16 June 2020).
36. Van den P. Driessche and J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences. 2002;180(1): 29-48.
37. Diekmann O, Heesterbeek JAP, Metz JAJ, On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations. Journal of Mathematical Biology.1990;28(4):365-382.
38. Ghani AC, Donnelly CA, Cox DR, Griffin JT, Fraser C, Lam TH, et al., Methods for Estimating the Case Fatality Ratio for a Novel, Emerging Infectious Disease. American Journal of Epidemiology. 2005;162(5):479-486.
39. Thanh Le T Fau Z, Andreadakis A. Andreadakis Z Fau, Kumar R, Kumar A Fau. Gómez Román S. Gómez Román R Fau, Tollefsen M. Tollefsen S Fau, Saville S. Saville M Fau, Mayhew et al., The COVID-19 vaccine development landscape. (1474-1784 (Electronic)).

Peer-review history:
The peer review history for this paper can be accessed here:
http://www.sdiarticle4.com/review-history/59388