# A MATHEMATICAL MODEL FOR COVID-19 TRANSMISSION DYNAMICS IN BANGLADESH

**M. Mohiuddin**
Department of Mathematics, Comilla University, Cumilla 3506, Bangladesh.
Email: mahi.in2012@gmail.com

**Khalifa M. Helal**
Department of Mathematics, Comilla University, Cumilla 3506, Bangladesh.
Email: khalifahelal@gmail.com

**Farzana Alam**
Department of Electrical and Electronic Engineering, Rajshahi University of Engineering & Technology, Rajshahi 6204, Bangladesh.
Email: farzanaalam.eee12@gmail.com

**Oyelola A. Adegboye**
Menzies School of Health Research, Charles Darwin University, Casuarina, NT 0811, Australia. Email: oyelola.adegboye@jcu.edu.au

**Md Abdul Kuddus***
Department of Mathematics, University of Rajshahi, Rajshahi 6205, Bangladesh.
Email: makuddus.math@ru.ac.bd

*Corresponding Author

**ABSTRACT:** The novel Coronavirus disease-2019 (COVID-19) pandemic has caused unprecedented global devastation across various sectors. This study employs a five-compartmental deterministic mathematical model to analyse the transmission dynamics of this highly contagious disease in Bangladesh. To understand and control the system's dynamics in our model, we investigated the basic reproduction number, solution existence, equilibrium states stability analysis, sensitivity analysis, and behavioural dynamics of COVID-19 through numerical simulations. We also evaluated the influence of progression and recovery rates on the COVID-19 dynamics in Bangladesh. Further, the model identifies significant parameters from Bangladesh's COVID-19 data. The findings in this study aid in quantifying diverse parameters to assess the disease severity and formulate effective control strategies, thereby accelerating the containment of the virus spread in Bangladesh.

**KEYWORDS:** COVID-19; compartmental model; stability and sensitivity analysis; basic reproduction number; Bangladesh.

**ACKNOWLEDGEMENTS:** The authors would like to thank the two anonymous reviewers and editor for their helpful comments and suggestions.

## 1. INTRODUCTION

Infectious diseases are a leading cause of death and morbidity (Vos *et al.*, 2020). Outbreaks of infectious diseases across several regions of the world are not new. The outbreak of Severe Acute Respiratory Syndrome (SARS-CoV) in Shunde district, Guangdong province, China, in 2003 and Middle East Respiratory Syndrome (MERS-CoV) in Jeddah, Kingdom Saudi Arabia, in 2012 are two recent examples (World Health Organization (WHO), 2022; Altamimi *et al.*, 2019). The 2003 SARS-CoV outbreak resulted in about 8000 cases and 800 deaths (crude case fatality rate, Case Fatality Rate (CFR): 10%), while as of 16$^{th}$ November 2022, more than 2600 cases of MERS-CoV and 935 deaths (CFR: 36%) have been reported to WHO (WHO, 2022).

In late 2019, a new coronavirus emerged in Wuhan, Hubei Province, China, which was later named SARS-CoV-2. The Coronaviridae family and genus Beta coronavirus are responsible for the recent coronavirus disease (COVID-19) (Coronaviridae Study Group of the International Committee on Taxonomy of Viruses, 2020). Among all zoonotic diseases, COVID-19 is the most dangerous, devastating, and transmissible (Biswas *et al.*, 2020; Prathumwan *et al.*, 2020). This virus can be transmitted directly from person to person through the droplet of cough and sneeze of the infected person (Huang *et al.*, 2020). As of 20$^{th}$ April 2021, about 142.7 million COVID-19 cases and more than 3 million deaths were recorded across 213 countries and territories (WHO, 2021).

Furthermore, the number of COVID-19 infected patients recorded in different countries till 20$^{th}$ April 2021 shows that infection rates differ by country around the world. Some non-pharmacological factors such as regional climatic conditions, population density, environmental, transportation and mobility, and socioeconomic status may account for variation in infection rates by country (Iqbal *et al.*, 2020; Ahmed *et al.*, 2021; Alidadi *et al.*, 2022). Despite better socio-economic status, the countries in cold regions such as the United Kingdom, United States of America, Germany, Italy, France, and Spain have higher infection rates than countries in the Middle East, and South Asia (Iqbal *et al.*, 2020). High values of climatic factors i.e., temperature and relative humidity may

partially influence the rate of COVID-19 transmission, and it was found that 1 unit increase in both factors was associated with a decrease in COVID-19 deaths (Ma *et al.*, 2020; Tosepu *et al.*, 2020; Wu *et al.*, 2020). Despite the impact of climatic factors, population density and mobility alone can drive the spread of COVID-19. For example, although there was high temperature and humidity in Riyadh and São Paulo cities, the infection rate was also very fast in those cities (Ahmed *et al.*, 2021). Also, social distancing is very challenging in densely populated cities such as New York, Madrid, Lombardy, and Hubei where more infections were recorded (Ahmed *et al.*, 2021). However, the transmission was also very fast in Dhaka and Chittagong cities of Bangladesh owing to their dense population compared to rural areas. Bangladesh recorded its first case of COVID-19 on 8$^{th}$ March 2020 (Monjur and Hassan, 2020). Although the government quickly implemented preventive measures to control this highly infectious disease, it was a challnging task for this densely populated country. As of 20$^{th}$ April 2021, Bangladesh had recorded more than 700,000 COVID-19 cases, and over 10,000 people have died due to the disease (WHO, 2021). Currently, there is no specific treatment for COVID-19, and vaccines have varying effective rates. Thus, we must keep expanding our knowledge and understanding of the dynamic behaviour of transmission of this disease that can help to control and eliminate the disease. Previous studies have developed mathematical models to describe the dynamics of COVID-19 (Aguilar *et al.*, 2020; Alkahtani and Alzaid, 2020; Gebremeskel *et al.*, 2021; Kabir *et al.*, 2020; Tuan *et al.*, 2020).

In their work, Aguilar *et al.* (2000) used a susceptible-exposed-symptomatic-asymptomatic-recovered (SEYAR) model to investigate the effect of asymptomatic individuals on the transmission of COVID-19 in several countries. The dispersal effect of reducing the infection and transmission of COVID-19 in Bangladesh has been previously studied (Kabir *et al.*, 2020; Masud *et al.*, 2020). However, these models did not consider the movement of individuals from mild to critical compartments due to co-infection or comorbidities.

In this current study, we developed a five-compartmental deterministic mathematical–Susceptible-Latent-Mild-Critical-Recovered/Removal (SLMCR) model to expand further our knowledge of the dynamics of COVID-19 transmission in Bangladesh. The basic reproduction number, the existence of the model's solution, stability analysis at equilibrium states and sensitivity analysis were investigated. We also explored the dynamical behaviour of COVID-19 in Bangladesh using numerical simulations.

The rest of the paper is organised as follows: After the introduction in section 1, we described the methods in section 2. In section 3, we present the results from examining the local stability of the equilibrium states, model calibration sensitivity analysis and numerical simulations. Section 4 concludes the paper.

## 2. MODEL FORMULATION

We formulated a five-compartmental deterministic mathematical SLMCR model to explain the transmission dynamics of COVID-19. The population (N) is partitioned into five individual compartments, namely, susceptible (S) (individuals who may become infected with the disease), Latent (L) (individuals who are infected but have not yet been exposed or show any sign or symptoms of the disease (incubation period)), Mild (M) (those infected individuals who are exposed flu-like symptoms and can be treated at home), Critical (C) (those infected individuals who are very sick and needed hospitalisation), and recovered (R) (individuals who recovered successfully and have immunity against the disease or died). It is considered that the size of the total population at any time t, $N(t)$, is constant and homogeneously mixed. The formulation is of the form:

$$N(t) = S(t) + L(t) + M(t) + C(t) + R(t) \quad (1)$$

The model flow diagram is presented in Figure 1.

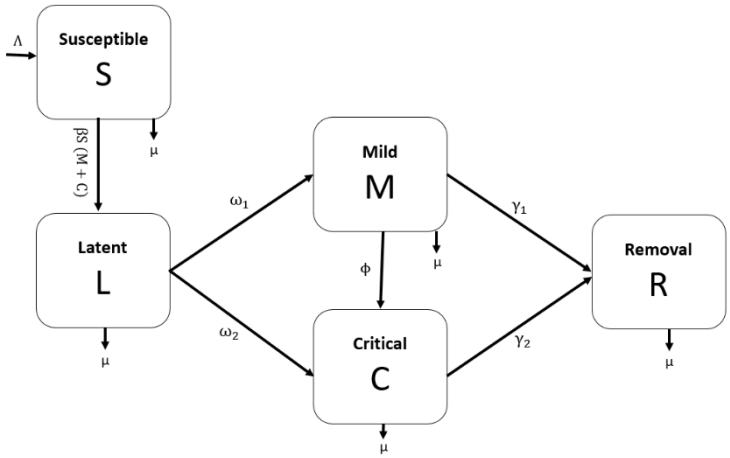


**Figure 1.** Five Compartmental Model (SLMCR) COVID-19 Model Diagram for Bangladesh. Source: the Authors.

The parameter $\Lambda$ represents the recruitment rate at which new individuals enter the susceptible class; parameters $\omega_1$ , $\omega_2$ are per capita rates at which the latent individuals become mildly and critically infected, respectively; $\gamma_1$ , $\gamma_2$ are per capita rates at which the mildly and critically infected individuals recovered; $\beta$ is the transmission rate between infection and susceptible population; $\phi$ is the transfer rate of mildly infected individuals to critically infected individuals due to the progression and possibly comorbidities with other diseases, including hypertension, diabetes, cardiovascular disease, and respiratory system disease; $\mu$ is the per capita natural death rate across the total population.

As depicted in Figure 1, the transmission dynamics of COVID-19 can be expressed by the following nonlinear ordinary differential equations that describe the model:

$$\frac{dS}{dt} = \Lambda - \beta S(M + C) - \mu S \tag{2}$$

$$\frac{dL}{dt} = \beta S(M + C) - (\omega_1 + \omega_2 + \mu)L \tag{3}$$

$$\frac{dM}{dt} = \omega_1 L - (\phi + \gamma_1 + \mu)M \tag{4}$$

$$\frac{dC}{dt} = \omega_2 L + \phi M - (\gamma_2 + \mu)C \tag{5}$$

$$\frac{dR}{dt} = \gamma_1 M + \gamma_2 C - \mu R \tag{6}$$

with the following initial conditions

$$S(0) \geq 0, L(0) \geq 0, M(0) \geq 0, C(0) \geq 0, \ R(0) \geq 0. \tag{7}$$

The existence and the non-negativity of the solutions of the above system, subjected to the initial conditions, can easily be shown for all $t \geq 0$. All model parameters are assumed to be non-negative, so we show directly that each state variable also remains non-negative for all $t \geq 0$.

By adding equations (2) – (6), we get:

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dL}{dt} + \frac{dM}{dt} + \frac{dC}{dt} + \frac{dR}{dt} = \Lambda - \mu N$$

Integrating the above equation, we find

$$N(t) = \frac{\Lambda}{\mu} - \left[\frac{\Lambda}{\mu} - N(0)\right] e^{-\mu t}.$$

As $t \to \infty$, $0 \leq N(t) \leq \frac{\Lambda}{\mu}$.

This indicates the boundedness of the total population size $N(t)$ and consequently, each of the states $S, L, M, C,$ and $R$ are also bounded.

In this model, the recovered individuals $R(t)$ do not appear in the equations (2)-(5), i.e., these equations are independent of $R(t)$. Hence, if we only wish to track disease incidence and prevalence, we can focus our attention on the following reduced system:

$$\frac{dS}{dt} = \Lambda - \beta S(M + C) - \mu S \tag{8}$$

$$\frac{dL}{dt} = \beta S(M + C) - (\omega_1 + \omega_2 + \mu)L \tag{9}$$

$$\frac{dM}{dt} = \omega_1 L - (\phi + \gamma_1 + \mu)M \tag{10}$$

$$\frac{dC}{dt} = \omega_2 L + \phi M - (\gamma_2 + \mu)C \tag{11}$$

The solutions of this system are non-negative and bounded. Therefore, the feasible solutions set for equations (8) – (11) enter the region:

$$D = \{(S, L, M, C, ) \in R_+^4 : S + L + M + C = N\}. \tag{12}$$

where D is the positively invariant region for the system (8) – (11). Therefore, in this study, we consider the system of equations (8) – (11) in set D.

### *Basic Reproduction Number* ($R_0$)

Basic reproduction number ($R_0$) helps understand the duration and size of an epidemic (Kuddus and Rahman, 2021; McBryde *et al.*, 2020; Rahman *et al.*, 2021). This parameter is one of the most important to mathematical modellers because it determines whether a disease outbreak will die out or persist in a population (Biswas *et al.*, 2014; Booton *et al.*, 2020; Kuddus *et al.*, 2020). The average number of new infections produced by a single infective in the susceptible population is the basic reproduction number. It can be determined by using the method of next-generation matrix (Kuddus *et al.*, 2021). The next-generation matrix is the product of matrices $F$ and $-V^{-1}$, where matrix $F$ represents the transmission components of infected states and matrix $V$ describes transitions between and out of the infected states. In this model, the infected compartments are $L, M$ and $C$. The matrices $F$ and $V$ for this model are given as

$$F = \begin{pmatrix} 0 & \beta S^0 & \beta S^0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \text{ and}$$

$$V = \begin{pmatrix} -(\omega_1 + \omega_2 + \mu) & 0 & 0 \\ \omega_1 & -(\phi + \gamma_1 + \mu) & 0 \\ \omega_2 & \phi & -(\gamma_2 + \mu) \end{pmatrix}$$

The next-generation matrix K is given by Kuddus *et al.* (2019).

$$K = F(-V^{-1})$$

$$= \begin{pmatrix} 0 & \beta S^0 & \beta S^0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{\omega_1 + \omega_2 + \mu} & 0 & 0 \\ \frac{\omega_1}{(\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu)} & \frac{1}{\phi + \gamma_1 + \mu} & 0 \\ \frac{\phi\omega_1 + \omega_2(\phi + \gamma_1 + \mu)}{(\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)} & \frac{\phi}{(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)} & \frac{1}{\gamma_2 + \mu} \end{pmatrix}$$

$$= \begin{pmatrix} \frac{\beta S^0[\omega_1(\phi + \gamma_2 + \mu) + \omega_2(\phi + \gamma_1 + \mu)]}{(\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)} & \frac{\beta S^0[(1 + \gamma_2 + \mu)]}{(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)} & \frac{\beta S^0}{(\gamma_2 + \mu)} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

The spectral radius of the next generation matrix K is considered as the basic reproduction number. Hence, the basic reproduction number is obtained as:

$$R_0 = \frac{\beta S^0[\omega_1(\phi + \gamma_2 + \mu) + \omega_2(\phi + \gamma_1 + \mu)]}{(\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)}$$
$$= \frac{\beta\Lambda[\omega_1(\phi + \gamma_2 + \mu) + \omega_2(\phi + \gamma_1 + \mu)]}{\mu(\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)}$$

***Existence of Equilibria***

The equilibrium is such a state at which the rate of changes of the system variables with respect to time will be zero. i.e.
$\frac{dS}{dt} = \frac{dL}{dt} = \frac{dM}{dt} = \frac{dC}{dt} = 0.$

This system has two types of equilibrium points: disease-free equilibrium (the equilibrium without disease) and endemic equilibrium (equilibrium with disease). The disease-free equilibrium of this system always exists and is defined as

$$X^0 = (S^0, L^0, M^0, C^0) = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right)$$

The endemic equilibrium of this system is also obtained as $X^* = (S^*, L^*, M^*, C^*)$.
where,

$$\begin{cases} S^* = \frac{S^0}{R_0} \\ L^* = \frac{(R_0-1)\mu(\phi+\gamma_1+\mu)(\gamma_2+\mu)}{\beta\omega_1(\phi+\gamma_2+\mu)+\beta\omega_2(\phi+\gamma_1+\mu)} \\ M^* = \frac{(R_0-1)\mu\omega_1(\gamma_2+\mu)}{\beta\omega_1(\phi+\gamma_2+\mu)+\beta\omega_2(\phi+\gamma_1+\mu)} \\ C^* = \frac{(R_0-1)\mu[\phi\omega_1+\omega_2(\phi+\gamma_1+\mu)]}{\beta\omega_1(\phi+\gamma_2+\mu)+\beta\omega_2(\phi+\gamma_1+\mu)} \end{cases} \tag{13}$$

Equation (13) shows that if $R_0 > 1$ then the endemic equilibrium $X^* = (S^*, L^*, M^*, C^*) \in D$.

## 3. STABILITY ANALYSIS

The following applies in order to analyse the stability of the equilibrium points of the systems of equations (2)-(6):

### *Infection-Free Equilibrium*

*Lemma 1:* The infection-free equilibrium of the model is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.

*Proof:* The Jacobian of the system of equations (2) – (6) of the model is as follows:

$$J = \begin{pmatrix} -\beta(M+C)-\mu & 0 & -\beta S & -\beta S \\ \beta(M+C) & -(\omega_1+\omega_2+\mu) & \beta S & \beta S \\ 0 & \omega_1 & -(\phi+\gamma_1+\mu) & 0 \\ 0 & \omega_2 & \phi & -(\gamma_2+\mu) \end{pmatrix}$$

At the infection-free equilibrium point, $E^0$, the Jacobian is reduced to

$$J(E^0) = \begin{pmatrix} -\mu & 0 & -\beta S^0 & -\beta S^0 \\ 0 & -(\omega_1 + \omega_2 + \mu) & \beta S^0 & \beta S^0 \\ 0 & \omega_1 & -(\phi + \gamma_1 + \mu) & 0 \\ 0 & \omega_2 & \phi & -(\gamma_2 + \mu) \end{pmatrix}$$

The 1st column indicates only the diagonal term, which has only the negative eigenvalue, $-\mu$, the other eigenvalues can be derived from the sub-matrix, $J_1(E^0)$ formed by excluding the 1st row and column of $J(E^0)$. This gives,

$$J_1(E^0) = \begin{pmatrix} -(\omega_1 + \omega_2 + \mu) & \beta S^0 & \beta S^0 \\ \omega_1 & -(\phi + \gamma_1 + \mu) & 0 \\ \omega_2 & \phi & -(\gamma_2 + \mu) \end{pmatrix}$$

To determine the stability of the matrix $J_1(E^0)$, we use the Routh-Hurwitz criteria for stability (Allen, 2007). Routh-Hurwitz criterion states that (i) the trace is negative, (ii) the sum of the two-by-two principal minors is positive, and (iii) the determinant is negative. Beginning with the trace, we have

*Condition 1:*

$$A_1 = \text{trace}(J_1) = -(\omega_1 + \omega_2 + \mu) - (\phi + \gamma_1 + \mu) - (\gamma_2 + \mu) < 0$$

*Condition 2:*

$$A_2 = \begin{vmatrix} -(\phi + \gamma_1 + \mu) & 0 \\ \phi & -(\gamma_2 + \mu) \end{vmatrix} + \begin{vmatrix} -(\omega_1 + \omega_2 + \mu) & \beta S^0 \\ \omega_2 & -(\gamma_2 + \mu) \end{vmatrix} + \begin{vmatrix} -(\omega_1 + \omega_2 + \mu) & \beta S^0 \\ \omega_1 & -(\phi + \gamma_1 + \mu) \end{vmatrix}$$

$$A_2 = (\phi + \gamma_1 + \mu)(\gamma_2 + \mu) + (\omega_1 + \omega_2 + \mu)(\gamma_2 + \mu) - \beta S^0 \omega_2 + (\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu) - \beta S^0 \omega_1$$

$$A_2 = (\phi + \gamma_1 + \mu)(\gamma_2 + \mu) + (\omega_1 + \omega_2 + \mu)(\gamma_2 + \mu) + (\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu) - \beta S^0(\omega_1 + \omega_2)$$

$$= (\phi + \gamma_1 + \mu)(\gamma_2 + \mu) + (\omega_1 + \omega_2 + \mu)(\gamma_2 + \mu) + (\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu) - \frac{(\omega_1 + \omega_2)(\omega_1 + \omega_2 + \mu)(\phi + \gamma_1 + \mu)(\gamma_2 + \mu)R_0}{\omega_1(\phi + \gamma_2 + \mu) + \omega_2(\phi + \gamma_1 + \mu)}$$

$= \frac{1}{\omega_1(\phi+\gamma_2+\mu)+\omega_2(\phi+\gamma_1+\mu)}[\omega_1\phi(\omega_1+\omega_2+\mu)(\phi+\gamma_1+\mu)+\omega_2(\omega_1+\omega_2+\mu)(\phi+\gamma_1+\mu)^2+ \omega_1\phi(\omega_1+\omega_2+\mu)(\gamma_2+\mu)+\omega_1(\omega_1+\omega_2+\mu)(\gamma_2+\mu)^2+\omega_1\phi(\phi+\gamma_1+\mu)(\gamma_2+\mu)+\omega_1(\phi+\gamma_1+\mu)(\gamma_2+\mu)^2+\omega_2(\phi+\gamma_1+\mu)^2(\gamma_2+\mu)+(\omega_1+\omega_2+\mu)(\phi+\gamma_1+\mu)(\gamma_2+\mu)(\omega_1+\omega_2)(1-R_0)] > 0$ if $R_0 < 1$.

*Condition 3:*

$$A_3 = \det(J_1) = (\omega_1+\omega_2+\mu)(\phi+\gamma_1+\mu)(\gamma_2+\mu)(R_0-1) < 0 \text{ if } R_0 < 1.$$

Finally, if we multiply the expressions for $A_1$ and $A_2$. It is straightforward to show that the condition $A_1A_2 > A_3$ is satisfied when $R_0 < 1$. Thus, by the Routh-Hurwitz criteria, the disease-free equilibrium is locally asymptotically stable when $R_0 < 1$.

***Disease Endemic Equilibrium***

*Lemma 2:* The endemic equilibrium of the model is locally asymptotically stable if $R_0 > 1$.

At the endemic equilibrium, the Jacobian of the system (2)-(5) reduces as follows:

$$J^* = \begin{pmatrix} -\beta(M^*+C^*)-\mu & 0 & -\beta S^* & -\beta S^* \\ \beta(M^*+C^*) & -(\omega_1+\omega_2+\mu) & \beta S^* & \beta S^* \\ 0 & \omega_1 & -(\phi+\gamma_1+\mu) & 0 \\ 0 & \omega_2 & \phi & -(\gamma_2+\mu) \end{pmatrix}$$

The characteristic matrix is defined as

$$(J^*-\lambda I) = \begin{pmatrix} -\beta(M^*+C^*)-\mu-\lambda & 0 & -\beta S^* & -\beta S^* \\ \beta(M^*+C^*) & -(\omega_1+\omega_2+\mu)-\lambda & \beta S^* & \beta S^* \\ 0 & \omega_1 & -(\phi+\gamma_1+\mu)-\lambda & 0 \\ 0 & \omega_2 & \phi & -(\gamma_2+\mu)-\lambda \end{pmatrix}$$

The characteristic equation is derived as

$$|J^* - \lambda I| = 0$$

$$or, \begin{vmatrix} -\beta(M^* + C^*) - \mu - \lambda & 0 & -\beta S^* & -\beta S^* \\ \beta(M^* + C^*) & -A - \lambda & \beta S^* & \beta S^* \\ 0 & \omega_1 & -B - \lambda & 0 \\ 0 & \omega_2 & \phi & -C - \lambda \end{vmatrix} = 0$$

$$\text{or}, \{-\beta(M^* + C^*) - \mu - \lambda\} \begin{vmatrix} -A - \lambda & \beta S^* & \beta S^* \\ \omega_1 & -B - \lambda & 0 \\ \omega_2 & \phi & -C - \lambda \end{vmatrix} - \beta(M^* + C^*) \begin{vmatrix} 0 & -\beta S^* & -\beta S^* \\ \omega_1 & -B - \lambda & 0 \\ \omega_2 & \phi & -C - \lambda \end{vmatrix} = 0$$

$$or, \{-\beta(M^* + C^*) - \mu - \lambda\}[(-A - \lambda)(-B - \lambda)(-C - \lambda) - \beta S^* \omega_1(-C - \lambda) + \beta S^*\{\phi\omega_1 - \omega_2(-B - \lambda)\}] - \beta(M^* + C^*)[\beta S^* \omega_1(-C - \lambda) - \beta S^*\{\phi\omega_1 - \omega_2(-B - \lambda)\}] = 0$$

$$\text{or}, \{\beta(M^* + C^*) + \mu + \lambda\}[(A + \lambda)(B + \lambda)(C + \lambda) - \beta S^* \omega_1(C + \lambda) - \beta S^*\{\phi\omega_1 + \omega_2(B + \lambda)\}] - \beta(M^* + C^*)[-\beta S^* \omega_1(C + \lambda) - \beta S^*\{\phi\omega_1 + \omega_2(B + \lambda)\}] = 0$$

$$\text{or}, \{\beta(M^* + C^*) + \mu + \lambda\}\{\lambda^3 + (A + B + C)\lambda^2 + (AB + AC + BC)\lambda + ABC - \beta S^* C\omega_1 - \beta S^* \omega_1 \lambda - \beta S^* \phi\omega_1 - \beta S^* B\omega_2 - \beta S^* \omega_2 \lambda\} + \beta(M^* + C^*)\{\beta S^* C\omega_1 + \beta S^* \omega_1 \lambda + \beta S^* \phi\omega_1 + \beta S^* B\omega_2 + \beta S^* \omega_2 \lambda\} = 0$$

$$\text{or}, \lambda^4 + \{\beta(M^* + C^*) + \mu + A + B + C\}\lambda^3 + [\{\beta(M^* + C^*) + \mu\}(A + B + C) + AB + AC + BC - \beta S^* \omega_1 - \beta S^* \omega_2]\lambda^2 + [\{\beta(M^* + C^*) + \mu\}(AB + AC + BC) + ABC - \beta S^* \mu\omega_1 - \beta S^* C\omega_1 - \beta S^* \phi\omega_1 - \beta S^* \mu\omega_2 - \beta S^* B\omega_2]\lambda + [\{\beta(M^* + C^*) + \mu\}ABC - \beta S^* \mu C\omega_1 - \beta S^* \mu\phi\omega_1 - \beta S^* \mu B\omega_2] = 0$$

$$\text{or}, \lambda^4 + C_3\lambda^3 + C_2\lambda^2 + C_1\lambda + C_0 = 0$$

where

$$A = \omega_1 + \omega_2 + \mu$$

$$B = \phi + \gamma_1 + \mu$$

$$C = \gamma_2 + \mu$$

$$C_3 = \beta(M^* + C^*) + \mu + A + B + C$$
$$= \mu R_0 + A + B + C > 0$$
$$C_2 = \{\beta(M^* + C^*) + \mu\}(A + B + C) + AB + AC + BC - \beta S^* \omega_1 - \beta S^* \omega_2$$
$$= \mu R_0(A + B + C) + AB + AC + BC - \frac{\beta S^0(\omega_1+\omega_2)}{R_0}$$
$$= \frac{\mu R_0(A+B+C)[\omega_1(\phi+C)+\omega_2 B]+[AB\phi+AC\phi+BC\phi+AC^2+BC^2]\omega_1+(AB^2+B^2C)\omega_2}{\omega_1(\phi+C)+\omega_2 B} > 0$$
$$C_1 = \{\beta(M^* + C^*) + \mu\}(AB + AC + BC) + ABC - \beta S^* \mu\omega_1 - \beta S^* C\omega_1 - \beta S^* \phi\omega_1 - \beta S^* \mu\omega_2 - \beta S^* B\omega_2$$
$$= \mu R_0(AB + AC + BC) + ABC - \frac{\beta S^0 \mu(\omega_1+\omega_2)}{R_0} - \frac{\beta S^0[\omega_1(\phi+C)+\omega_2 B]}{R_0}$$
$$= \mu R_0(AB + AC + BC) + ABC - \frac{ABC\mu(\omega_1+\omega_2)}{\omega_1(\phi+C)+\omega_2 B} - ABC$$
$$= \frac{[\omega_1(AB\phi+AC\phi+AC^2+BC\phi+BC^2)+\omega_2(AB^2+B^2C)]\mu R_0+ABC\mu(\omega_1+\omega_2)(R_0-1)}{\omega_1(\phi+C)+\omega_2 B} > 0 \text{ if } R_0 > 1$$
$$C_0 = \{\beta(M^* + C^*) + \mu\}ABC - \beta S^* \mu C\omega_1 - \beta S^* \mu\phi\omega_1 - \beta S^* \mu B\omega_2$$
$$= \mu R_0 ABC - \frac{\beta S^0 \mu[\omega_1(\phi+C)+\omega_2 B]}{R_0}$$
$$= \mu R_0 ABC - ABC\mu$$
$$= ABC\mu(R_0 - 1) > 0 \text{ if } R_0 > 1 \qquad (14)$$

From (14) it is easy to verify that $C_3 > 0, C_2 > 0, C_1 > 0$ and $C_0 > 0$ if $R_0 > 1$. Hence, by the Routh-Hurwitz stability criterion, the disease endemic equilibrium point $E^*$ is locally asymptotically stable for $R_0 > 1$.

## 4. RESULT AND DISCUSSION

### *Parameters Estimation*

The techniques described above were applied to Bangladesh COVID-19 data between March 2020 and April 2021 (WHO, 2021). We first estimated the parameters of the COVID-19 compartmental model by fitting various combinations of parameters in equations (2) - (6) to the number of COVID-19 cases. We parameterised equations (2) - (6) with values obtained from the literature (see Table 1). Other parameters were estimated by fitting the data via the least-squares method (Kuddus et al., 2020) (Figure 2).

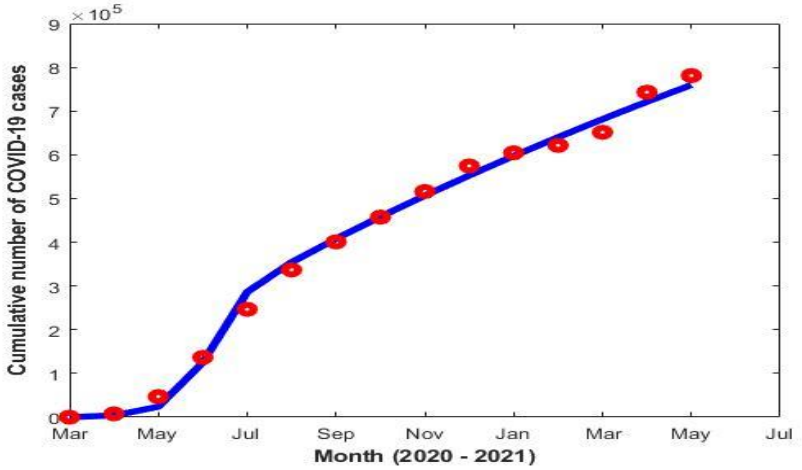


**Figure 2.** Time Series Plot of Reported Monthly COVID-19 Data (Red Dots) and Corresponding Best Fit (Blue Line) in Bangladesh. Source: the Authors.

**Table 1:** Estimation of Model Parameters. Source: the Authors.

| Parameters | Description | Values | References |
|---|---|---|---|
| N | Population in 2021 | 164,689,383 | Worldometer (2020) |
| M | Death rate | $1/70$ | Kuddus *et al.* (2020) |
| B | Transmission rate | $1.8 \times 10^{-5}$ | Fitted |
| $\omega_1$ | Progression rate from L to M | 0.0129 | Fitted |
| $\omega_2$ | Progression rate from L to C | 0.022 | Fitted |
| $\gamma_1$ | Recovery rate from M to R | 0.02 | Rahman and Kuddus, 2020 |
| $\gamma_2$ | Recovery rate from C to R | 0.01 | Rahman and Kuddus, 2020 |
| $\Lambda$ | Recruitment rate | 1 | Kuddus *et al.* (2019) |
| $\Phi$ | Co-infection rate | 0.3 | Rahman and Kuddus (2020) |

***Sensitivity Analysis***

Latin Hypercube Sampling (LHS) with 10,000 runs per simulation to investigate the sensitivity of $R_0$ to model parameters. Figure 3 shows the Partial Rank Correlation Coefficients (PRCCs) of $R_0$. The results show that transmission rate ($\beta$), progression rates ($\omega_1$ and $\omega_2$) and co-infection rate $\phi$ are positively correlated with $R_0$. On the other hand, recovery rates $\gamma_1$ and $\gamma_2$ are negatively associated with $R_0$.

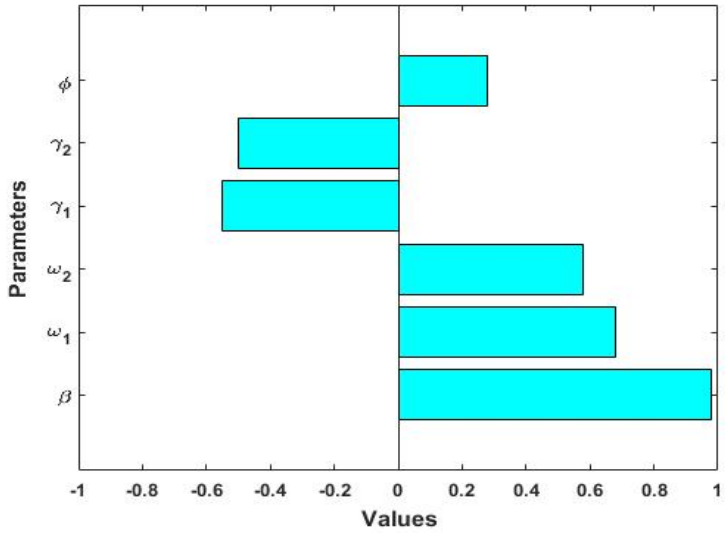


**Figure 3.** Sensitivity Analysis of Model Parameters; $\beta, \omega_1, \omega_2, \gamma_1, \gamma_2,$ and $\phi$. Source: the Authors.

***Numerical Simulation***

We carried out numerical simulations to support the analytical outcomes and assessed the impact of model parameters. We have selected or estimated suitable baseline parameter values consistent with COVID-19 infection and transmission (Table 1). We obtained two equilibrium points, the disease-free equilibrium $X^0$ and a disease-endemic equilibrium $X^*$. Using different initial conditions for the latent and infected population, we found that if $R_0 < 1$, then the disease-free equilibrium is locally asymptotically stable. Furthermore, if $R_0 > 1$ then COVID-19 persists in the population. Figure 4 illustrates the stability of the disease-free equilibrium (i.e., when $R_0 < 1$) by depicting system trajectories through

E vs I plane originating from different initial conditions. In this case, COVID-19 disease dies out. Similarly, Figure 5 shows the stability of the disease endemic equilibrium (i.e., when $R_0 > 1$), in this case, COVID-19 disease persists in the population.

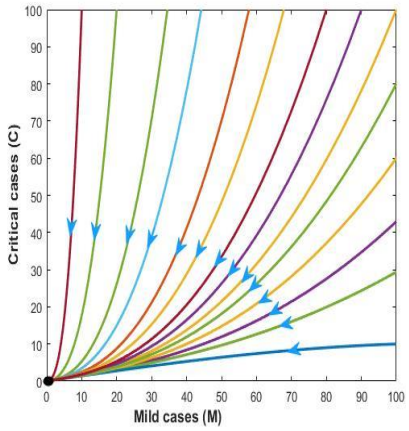


**Figure 4.** Disease-Free Equilibrium: $R_0 < 1$. In this Case, COVID-19 Fade-Out (Black Dot). All parameter values assume their baseline values given in Table 1. Source: the Authors.

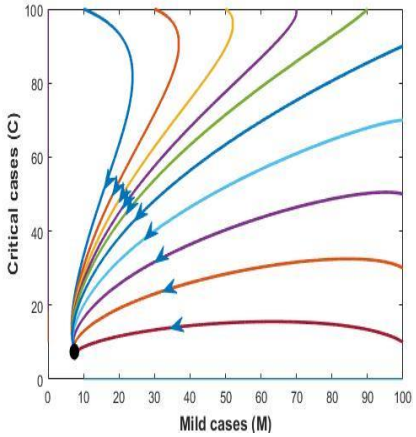


**Figure 5.** Endemic Equilibrium: $R_0 > 1$. In this Case, COVID-19 Persist in the Population (Black Dot). All parameter values assume their baseline values given in Table 1. Source: the Authors.

Figures 6 and 7 show the effect of the progression rate on the dynamics of mild and critical cases of COVID-19. Our findings suggested that increasing the progression rate increases the prevalence of mild and critical cases. Therefore, it is crucial to reduce the progression rate to implement different intervention policies, including public awareness, education programs for public health, following good respiratory hygiene and social distancing. Figures 8 and 9 depict the impact of the recovery rate on the dynamics of mild and critical cases of COVID-19. Results recommended that the mild and critical cases of COVID-19 decrease if we increase the recovery rate. Our finding is consistent with reality because if we implement different intervention policies, including prompt treatment,

then the recovery rate will be increased. Consequently, mild and critical cases of COVID-19 will be reduced (Kuddus and Rahman, 2021).

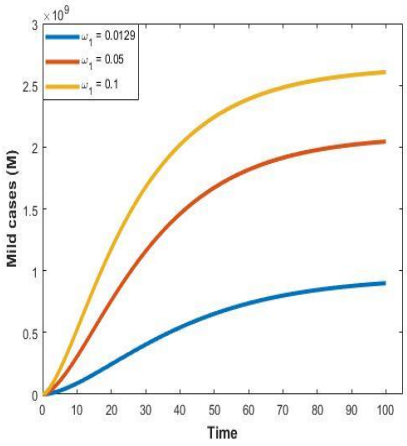


**Figure 6.** Impact of Progression Rate ($\omega_1$) on the Dynamics of Mild Cases (M). All parameter values assume their baseline values given in Table 1. Source: the Authors.

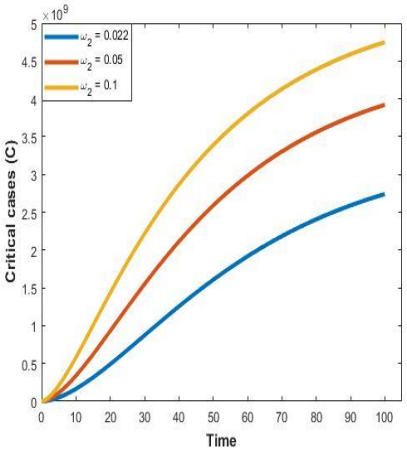


**Figure 7.** Impact of Progression Rate ($\omega_2$) on the Dynamics of Critical Cases (C). All parameter values assume their baseline values given in Table 1. Source: the Authors.

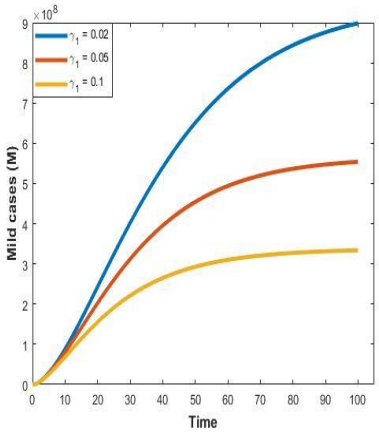


**Figure 8.** Impact of Recovery Rate ($\gamma_1$) on the Dynamics of Mild Cases (M). All parameter values assume their baseline values given in Table 1. Source: the Authors.

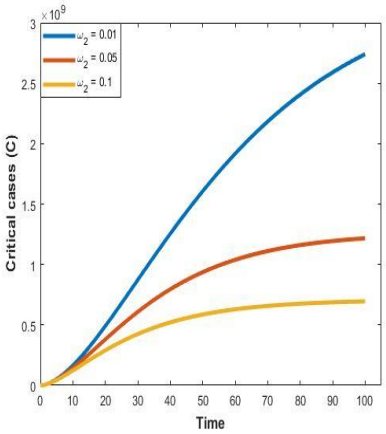


**Figure 9.** Impact of Recovery Rate ($\gamma_2$) on the Dynamics of Critical Cases (C). All parameter values assume their baseline values given in Table 1. Source: the Authors.

## 5. CONCLUSIONS

Compartmental mathematical models are critical tools that aid decision-makers in reducing the speed of transmission of COVID-19 by acquiring different concise and accurate information and suitable parameters. We have developed in this study a deterministic five-compartmental transmission dynamics COVID-19 model for Bangladesh. We derived the analytical expression for the $R_0$ using a next-generation matrix and found that disease-free equilibrium is locally asymptotically stable if the $R_0 < 1$, which means that the disease will eventually fade out. We showed that COVID-19 disease persists in the population if the $R_0 > 1$. Sensitivity analysis was also performed to explore the impact of model parameters. We showed that the spread of COVID-19 disease largely depends on the transmission rate. Consequently, effort should be made to minimise unnecessary contact with COVID-19 infected individuals. However, treating COVID-19 infection early will also reduce transmission from an infected to uninfected.

Mathematical models can also be applied in different regional settings. A previous regional study in New South Wales (NSW) showed that transmission control is very effective and efficient for reducing the burden of COVID-19 in metropolitan and rural health districts in NSW, Australia (Rahman *et al.*, 2023), which is similar to our results. Another regional setting modelling study in Wuhan and Mainland China shows that basic reproduction number significantly impacts COVID-19 dynamics. If the basic reproduction number is greater than one, then COVID-19 persists in the population. Otherwise, the disease dies out (Zheng *et al.*, 2022; Kuddus and Rahman, 2021), consistent with our study. Hence, it is very important to keep the basic reproduction number below one for controlling the outbreak of COVID-19 in a regional setting.

Hence, our findings have the potential to offer valuable insights to policymakers aimed at reducing overall infections and mortality and delaying and reducing peak demand for healthcare resources within the regional setting. Given the substantial geographical variations in population density and social interactions across different regions in Bangladesh, it is more prudent to implement a uniform and consistent transmission control strategy for alleviating the burden of COVID-19. These conclusions bear significant implications for many other nations and regions to understand better and respond to their regional epidemics associated with the continued COVID-19 pandemic. Future models could extend our framework by introducing a new compartment that accounts for

vaccination classes to explore the effect of vaccination to minimize the impact of COVID-19 in Bangladesh.

**FUNDING SOURCE:** This work was not funded and did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

**DATA AVAILABILITY:** All data will be available upon request.

**DECLARATION OF COMPETING INTEREST**: The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

## REFERENCES

Aguilar, J. B., Faust, J. S., Westafer, L. M. and Gutierrez, J. B. (2020). Investigating the impact of asymptomatic carriers on COVID-19 transmission. *MedRxiv*.

Ahmad, S., Owyed, S., Abdel-Aty, A. H., Mahmoud, E. E., Shah, K. and Alrabaiah, H. (2021). Mathematical analysis of COVID-19 via new mathematical model. *Chaos, Solitons & Fractals*, 143, p. 110585.

Ahmed, J., Jaman, M.H., Saha, G. and Ghosh, P. (2021). Effect of environmental and socio-economic factors on the spreading of COVID-19 at 70 cities/provinces. *Heliyon*, 7(5).

Alidadi, M. and Sharifi, A. (2022). Effects of the built environment and human factors on the spread of COVID-19: A systematic literature review. *Science of the Total Environment*, 850, p. 158056.

Alkahtani, B. S. T. and Alzaid, S. S. (2020). A novel mathematics model of covid-19 with fractional derivative. Stability and numerical analysis. *Chaos, Solitons & Fractals*, 138, 110006.

Allen, L. J. (2007). *An introduction to mathematical biology*, Upper Saddle River, New Jersey.

Altamimi, A. and Ahmed, A. E. (2019). Climate factors and incidence of Middle East respiratory syndrome coronavirus. *Journal of Infectious Public Health*, 13, pp. 704–708.

Biswas, M., Islam, M., Akter, S., Mandal, S., Khatun, M., Samad, S., Paul, A. and Khatun, M. (2020). Modelling the effect of self-immunity and the impacts of asymptomatic and symptomatic

individuals on COVID-19 outbreak. *CMES-Computer Modeling in Engineering & Sciences*, 125(3), pp. 1033-1060.

Biswas, M. H. A., Paiva, L. T. and De Pinho, M. (2014). A SEIR model for control of infectious diseases with constraints. *Mathematical Biosciences & Engineering*, 11(4), 761.

Booton, R. D., MacGregor, L., Vass, L., Looker, K. J., Hyams, C., Bright, P. D., Harding, I., Lazarus, R., Hamilton, F. and Lawson, D. (2020). Estimating the COVID-19 epidemic trajectory and hospital capacity requirements in South West England: a mathematical modelling framework. *MedRxiv*.

Coronaviridae Study Group of the International Committee on Taxonomy of Viruses. (2020). The species Severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nature Microbiology*, 5(4), p. 536.

Gebremeskel, A. A., Berhe, H. W. and Atsbaha, H. A. (2021). Mathematical modelling and analysis of COVID-19 epidemic and predicting its future situation in Ethiopia. *Results in Physics*, 22, p. 103853.

Huang, C., Wang, Y., Li, X., Ren, L., Zhao, J., Hu, Y., Zhang, L., Fan, G., Xu, J. and Gu, X. (2020). Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *The Lancet*, 395(10223), pp. 497-506.

Iqbal, M. M., Abid, I., Hussain, S., Shahzad, N., Waqas, M. S. and Iqbal, M. J. (2020). The effects of regional climatic condition on the spread of COVID-19 at global scale. *Science of the Total Environment*, 739, p.140101.

Kabir, M. H., Gani, M. O., Mandal, S. and Biswas, M. H. A. (2020). Modeling the dispersal effect to reduce the infection of COVID-19 in Bangladesh. *Sensors International*, 1, p. 100043.

Kuddus, M. A., McBryde, E. S., Adekunle, A. I., White, L. J. and Meehan, M. T. (2019). Mathematical analysis of a two-strain disease model with amplification. *Chaos, Solitons & Fractals*, 143, p. 110594.

Kuddus, M. A., McBryde, E. S., Adekunle, A. I., White, L. J. and Meehan, M. T. (2021). Mathematical analysis of a two-strain disease model with amplification. *Chaos, Solitons & Fractals*, 143, p. 110594.

Kuddus, M. A., Meehan, M. T., White, L. J., McBryde, E. S. and Adekunle, A. I. (2020). Modeling drug-resistant tuberculosis

amplification rates and intervention strategies in Bangladesh. *PloS one*, 15(7), e0236112.

Kuddus, M. A. and Rahman, A. (2021). Analysis of COVID-19 using a modified SLIR model with nonlinear incidence. *Results in Physics*, p. 104478.

Kuddus, M. A. and Rahman, A. (2021). Analysis of COVID-19 using a modified SLIR model with nonlinear incidence. *Results in Physics*, 27, p. 104478.

Ma, Y., Zhao, Y., Liu, J., He, X., Wang, B., Fu, S., Yan, J., Niu, J., Zhou, J. and Luo, B. (2020). Effects of temperature variation and humidity on the death of COVID-19 in Wuhan, China. *Science of the Total Environment*, 724, p. 138226.

Masud, M., Islam, M. H., Mamun, K. A., Kim, B. N. and Kim, S. (2020). COVID-19 Transmission: Bangladesh Perspective. *Mathematics*, 8(10), p. 1793.

McBryde, E. S., Meehan, M. T., Adegboye, O. A., Adekunle, A. I., Caldwell, J. M., Pak, A., Rojas, D. P., Williams, B. M. and Trauer, J. M. (2020). Role of modelling in COVID-19 policy development. *Paediatric Respiratory Reviews*, 35, pp. 57-60, DOI: 10.1016/j.prrv.2020.06.013.

Monjur, M. R. and Hassan, M. Z. (2020). Early phases of COVID-19 management in a low-income country: Bangladesh. *Infection Control & Hospital Epidemiology*, 41(9), pp. 1116-1117.

Prathumwan, D., Trachoo, K. and Chaiya, I. (2020). Mathematical Modeling for Prediction Dynamics of the Coronavirus Disease 2019 (COVID-19) Pandemic, Quarantine Control Measures. *Symmetry*, 12(9), p. 1404.

Rahman, A. and Kuddus, M. A. (2020). Modelling the Transmission Dynamics of COVID-19 in Six High-Burden Countries. *BioMed Research International*, 2021, pp. 1-7.

Rahman, A., Kuddus, M. A., Ip, R. H. L. and Bewong, M. (2021). A Review of COVID-19 Modelling Strategies in Three Countries to Develop a Research Framework for Regional Areas. *Viruses*, 13(11), p. 2185.

Rahman, A., Kuddus, M. A., Ip, R. H. and Bewong, M. (2023). Modelling COVID-19 pandemic control strategies in metropolitan and rural health districts in New South Wales, Australia. *Scientific Reports*, 13(1), p. 10352.

Tosepu, R., Gunawan, J., Effendy, D.S., Lestari, H., Bahar, H. and Asfian, P. (2020). Correlation between weather and Covid-19

pandemic in Jakarta, Indonesia. *Science of the Total Environment*, 725, p. 138436.

Tuan, N. H., Mohammadi, H. and Rezapour, S. (2020). A mathematical model for COVID-19 transmission by using the Caputo fractional derivative. *Chaos, Solitons & Fractals*, 140, p. 110107.

Vos, T., Lim, S. S., Abbafati, C., Abbas, K. M., Abbasi, M., Abbasifard, M., Abbasi-Kangevari, M., Abbastabar, H., Abd-Allah, F. and Abdelalim, A. (2020). Global burden of 369 diseases and injuries in 204 countries and territories, 1990–2019: a systematic analysis for the Global Burden of Disease Study 2019. *The Lancet*, 396(10258), pp. 1204-1222.

World Health Organization (2003). Consensus Document on the Epidemiology of Severe Acute Respiratory Syndrome (Sars). Online version accessed 12 July 2020, https://www.who.int/csr/sars/WHOconsensus.pdf.

World Health Organization (2021). WHO coronavirus (COVID-19) dashboard. Online version accesssed 18 October 2021.

World Health Organization (2022). Middle East respiratory syndrome coronavirus (MERS-CoV) 2022. Online version accessed 3 February 2022, https://www.who.int/publications/i/item/WHO-MERS-RA-2022.1.

Worldometer (2020). Population of Bangladesh in 2021. Online version accessed 14 February 2022, https://www.worldometers. info/ world-population/bangladesh-population/.

Wu, J.T., Leung, K. and Leung, G.M. (2020). Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *The lancet*, 395(10225), pp. 689-697.

Zheng, Q., Wang, X., Bao, C., Ji, Y., Liu, H., Meng, Q. and Pan, Q. (2022). A multi-regional, hierarchical-tier mathematical model of the spread and control of COVID-19 epidemics from epicentre to adjacent regions. *Transboundary and Emerging Diseases*, 69(2), pp. 549-558.