

Research

# Application of Mathematical Modeling and Chemical Analysis for COVID-19 Pandemic in Bangladesh

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**Abstract:** Mathematical modeling in biology usually deals with population dynamics which is a vast field of modern research that studies the changes in size and composition of the population through time. In this work, we have studied some mathematical models in biology with their historical background and the behavior of the solution of those models. Here, we have discussed the models such as the Malthusian model, Logistic model, and Epidemic model. As we know the world is just gone through the worst crisis ever in history by the uncontrolled spread of a virus named COVID-19. The target of this research work to apply the simple epidemic Susceptible-Infected-Removed (SIR) model to analyse the behavior of the devastating coronavirus and solve the model using the most famous and simplest Euler method. We have simulated the model to the different particular phases of the pandemic situation in Bangladesh and observed the model solution to real situations. We have used MATLAB for model simulation and graphical representation.

**Keywords:** Mathematical modeling, chemical analysis, COVID-19, Susceptible-Infected-Removed, model.

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## Introduction

In this research work, we have considered an epidemic model which was developed by Karmmck and McKendrick in 1927 [1]. This epidemic model is also known as SIR (Susceptible, Infective and Recover/Removed) epidemic model [2]. This model has already used successfully in several outbreak diseases like Avian influenza, Cholera, SARS, Ebola, Plague, Yellow fever, Meningitis, MERS, Influenza, Zika, Rift Valley Fever, Lassa fever, Leptospirosis. The SIR model is very useful for future prediction, end and peak of epidemic disease and other related activity of outbreak diseases [3-8].

Let us consider the population of Bangladesh remains constant regarding the study COVID 2019 outbreak in Bangladesh [9-10]. Here, we have chosen all COVID-2019 tested population of Bangladesh. In this research work, we have total COVID-2019 tested population is divided into three parts:

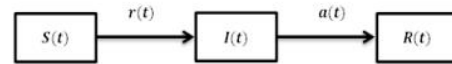


Figure 1: Description of SIR model not considering COVID-2019 outbreak virus evolution

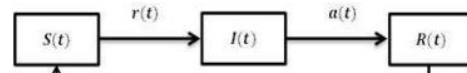


Figure 2: Description of SIR model considering COVID-2019 outbreak virus evolution

1.  $S(t)$ : The number of susceptible Population at time  $t$ , i.e. number of total COVID-2019 tested population.
2.  $I(t)$ : The number of infective Population at time  $t$ , i.e. number of infected COVID-2019 population.
3.  $R(t)$ : The number of recovered Population at time  $t$ , i.e. Number of recovered or died or naturally immune to the disease COVID-2019 population.

Here, we have taken  $(t)$  is equal to the recovered population plus died population from COVID-2019 outbreak of Bangladesh on 16 April 2020 for the sake of simplicity of this work. Figure 1 shows the description of proposed SIR model for not considering virus evolution.

This model does not consider the development of COVID-2019 like most of the diseases. But, in contrast my proposed SIR model which is shown in figure 2 does consider the development of COVID-2019 outbreak of Bangladesh. This model also predicts maximum growth of COVID-2019 outbreak in Bangladesh. Figure 2 shows the description of SIR model for recovered re-tuning into susceptible because the COVID-2019 outbreak of Bangladesh has evolved into one which can re-infect [11-12].

### Methodology of SIR Model for COVID-19

Let us consider the following three differential equations are used for experimental studies and experimental discussion for COVID -2019 of Bangladesh [13-14]. The description of these three differentials equations are given below:

$$S'(t) = -rSI \tag{1}$$

$$I'(t) = rSI - aI \tag{2}$$

$$R'(t) = aI \tag{3}$$

The parameters  $r$  and  $a$  of above differential equations are known as the infection rate and recovery/removal rate of COVID-2019 of Bangladesh. In this work, the average time of COVID 2019 outbreak of Bangladesh is approximately 14 days. These numerical values of  $r$  and  $a$  very useful in initial level for solving the three differential equations of COVID-2019 outbreak of Bangladesh. The three differential equations (1), (2) and (3) of the proposed SIR epidemic model for COVID,2020 outbreak of Bangladesh can be also written as:

$$dS/dt = -rSI \tag{4}$$

$$dI/dt = rSI - aI \tag{5}$$

$$dR/dt = aI \tag{6}$$

These three differential equations of SIR model are known as Kermack-McKendrick SIR model. At the present time, this model is very useful for the data analysis of COVID-2019 in Bangladesh. Again, adding equation number (4), (5) and (6), we can get another very useful expression for COVID-2019 data analysis. This expression is given below:

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = -rSI + rSI - aI + aI = 0$$

$$dS + dI + dR = 0 \tag{7}$$

After integrating equation number (7), we can get the following relation for calculating the total population of COVID-2019:

$S' + I' + R' = N$ , where  $N$  is known as the constant of integration which is measure the total size of population for COVID-2019 at initial level and after end the epidemic COVID-2019 in Bangladesh.

This is constant population at all levels of COVID-2019 outbreak. The above expression  $S' + I' + R' = N$  can be also denoted by in the following form:

$$S(t) + I(t) + R(t) = N \tag{8}$$

For the experimental purpose of data analysis of COVID-2019 outbreak of Bangladesh, we can take the following initial values of proposed SIR model, i.e.

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

Here, the population size of Bangladesh is constant. We can calculate the recovered population of COVID - 2019 outbreak of Bangladesh which given by the following formula:

$$I(t) = N - (S(t) + R(t)) \tag{9}$$

The above three differential equations (4), (5) and (5) of the proposed SIR model can be converted into two differential equations equation no. (9). The solution of these two differential equations are very difficult and time consuming. But the solution is very necessary of these two differentials equations for data analysis of COVID-2019 outbreak of Bangladesh. In this research, we have used quantitative approach for solving these two differential equations of SIR model. Now, here we can say that if  $S'$  is less than zero for all  $t$  and if  $I'$  is greater than zero as long as the initial population  $S_0$  is greater than the ratio,  $\frac{a}{r}$ . In other words, we can say that we will initially increase to some maximum if initial population  $S_0$  is greater than the ratio  $\frac{a}{r}$ , but eventually it must decrease and approaching to zero because  $S_0$  decreasing. In this work, we have introduced some cases for COVID-2019 outbreak of Bangladesh, which is given below:

**Case-1:** If  $S_0$  is less than the ratio,  $\frac{a}{r}$ —then the infection  $I$  of COVID- 2020 outbreak of Bangladesh will be decrease or simply to be zero after some times.

**Case-2:** If  $S_0$  is greater than the ratio  $\frac{a}{r}$  then the infection  $I$  of COVID- 2020 outbreak of Bangladesh will be epidemic of COVID-2019.

These are the assumptions of SIR model regarding the COVID-2019 outbreak of Bangladesh. Therefore, from the above two assumptions, we can say that the behavior of COVID-2019 outbreak of Bangladesh depends on the values of following expression:

$$R_n = \frac{S_0 r}{a} \tag{10}$$

This quantity is known as the threshold number. In this work, we have defined another quantity called reproductive number which is denoted by  $R_n$  and defined by the following expression (10). This is the number of secondary infectives of COVID-2019 outbreak produced by one primary infective in the susceptible populations. Here, there are two cases of COVID-2019 of Bangladesh regarding reproductive number:

**Case-1:** If  $R_n$  is less than one then COVID-2019 outbreak will be does out from Bangladesh.

**Case-2:** If  $R_n$  is more than one, then the outbreak of COVID-2019 is still in epidemic form in Bangladesh.

### Numerical Experiment and Results:

There is an absolute need to solve the differential equation of the proposed the SIR model for analysis of COVID-2019 outbreak of Bangladesh. Let us consider a population of susceptible of COVID-2019 outbreak and a small number of infected populations. Is the of COVID-2019 infectives populations increase substantially in Bangladesh? The answer of this question will get after solving differential equations of (4), (5) and (6). The differential equations (4), (5) and (6) is system of differential equation and these equations have three unknowns. These systems of differential equations are

very difficult to solve. Although, after combining the equation (4) and (5) then we get the single differential equation with one unknown for the proposed SIR model. The procedure is as follows:

According to the chain rule calculus:

$$\frac{dI}{dS} = \frac{\left(\frac{dI}{dt}\right)}{\left(\frac{dS}{dt}\right)} = \frac{rSI - aI}{-rSI} = \frac{rSI}{-rSI} - \left(\frac{aI}{-rSI}\right) = \frac{a}{rS} - 1$$

$$\frac{dI}{dS} = \frac{a}{rS} - 1$$

$$dI = \left(\frac{a}{rS} - 1\right) dS$$

Integrating both sides of above equation, we get

$$\int dI = \int \left(\frac{a}{rS} - 1\right) dS \tag{11}$$

$$I = \frac{a}{r} \ln(S) - S + C \tag{12}$$

Where, C is the arbitrary constant. And  $R = N - I - S$

This Karmack-Mchendrick SIR model is equipped with the initial conditions. We take the initial conditions which are given below:

$S(0) = S_0$  and  $I(0) = I_0$  then the equation (11) becomes:

$$I_0 = \frac{a}{r} \ln(S_0) - S_0 + C \tag{13}$$

$$C = I_0 + S_0 - \frac{a}{r} \ln(S_0) \tag{14}$$

Let us consider the population size of susceptible case of COVID-2019 outbreak of Bangladesh is K. This is approximately equal to initial population  $S_0$  of Bangladesh. Here, we will introduce a small number of infectives in the population. Therefore,

$$S_0 = K, I_0 = 0 \text{ and } R_n = \frac{rK}{a}$$

$f(I(t)) = 0$  as  $t \rightarrow \infty$  and  $S_0 < \frac{a}{r}$  then  $V(S_0, I_0) = V(S_\infty)$ , gives the following expression:

$$K - \frac{a}{r} \ln(S_0) = S_\infty - \frac{a}{r} \ln(S_\infty)$$

Where  $S_\infty$  is the susceptible population of Bangladesh if infectives case will be zero [15]. After simplification of above expression, we will get the following expression:

$$K - S_\infty = -\frac{a}{r} \ln(S_\infty) + \frac{a}{r} \ln(S_0)$$

$$K - S_\infty = \frac{a}{r} \ln(S_0) - \frac{a}{r} \ln(S_\infty)$$

$$K - S_\infty = \frac{a}{r} [\ln(S_0) - \ln(S_\infty)]$$

$$K - S_\infty = \frac{a}{r} \ln\left[\frac{S_0}{S_\infty}\right]$$

$$\frac{r}{a} = \frac{\ln\left[\frac{S_0}{S_\infty}\right]}{K - S_\infty} \tag{15}$$

Here  $0 < S_\infty < K$  that is part of the population of Bangladesh escapes the COVID-2019 infective.

It is very difficult to estimate the parameters of r and a because these are depending on disease being studies and on social and behavioral factors of that country. The population  $S_\infty$  and  $S_0$  can be estimated by serological studies before and after of the COVID-2019 outbreak and using this data, the basic reproduction number is given by the following formula:

$$R_n = \frac{rK}{a} \tag{16}$$

This expression can be calculated using expression (15). The maximum number of COVID-2019 outbreak infectives at any time in Bangladesh can be obtained by substantially using the following calculation:

Putting  $S = \frac{a}{r}$  and  $I = I_{max}$  in equation (11), we get the maximum number of infective cases of COVID-2019 outbreak in Bangladesh at any time.

$$I = \frac{a}{r} \ln(S) - S + C$$

Where,  $C = I_0 + S_0 - \frac{a}{r} \ln(S_0)$

Therefore, the maximum number of infectives cases  $I_{max}$  of COVID-2019 outbreak of Bangladesh can be calculated with the help of following expression:

$$I_{max} = I_0 + S_0 - \frac{a}{r} + \frac{a}{r} \ln(S_0) + \frac{a}{r} \ln\left(\frac{a}{r}\right) \tag{17}$$

The differential equation of the proposed SIR model can be solved with help of many numerical methods such as Runge Kutta and Euler methods. Here we have used Euler method for solving SIR model based differential equation.

In this research, we have used the MATLAB software for solving the differential equation using the above initial conditions values of  $S_0, I_0, R_0, a$  and  $r$ . The experimental results of SIR model are shown in table 1, table 2 and table 3. Here, the numerical calculation and data analysis of COVID-2019 outbreak of Bangladesh has been done with the help of Euler method.

Euler’s method is purely numerical method for solving the first order differential equations. The SIR model has also system of first order differential equations. So, the Euler’s method is more suitable for solving the proposed SIR based system of differential equations. The description of the Euler’s method is given below: Let consider the first order differential equation:

$$\frac{dy}{dx} = f(x, y) \tag{18}$$

The solution of differential equation (18) is given by the following expression:

$$y_{n+1} = y_n + \Delta t f(x_n, y_n) \tag{19}$$

Where  $\Delta t$  a small is step size in the time domain and  $f(x_n, y_n)$  is the slope of the curve. Here, we want to calculate the dependent variable called S, I and R to the proposed SIR model. Therefore, the solution of proposed SIR model-based differential is converted into Euler’s method forms which are given below:

$$S(n + 1) = S(n) - rI(n)S(n)\Delta t \tag{20}$$

$$I(n + 1) = I(n) + [rI(n)S(n) - aI(n)] \Delta t \tag{21}$$

$$R(n + 1) = R(n) + aI(n)\Delta t \tag{22}$$

In this research work, we have used COVID-2019 data set from Bangladesh on 16 April, 2020, 2 July, 2020 and 28 February, 2020. Here, we have taken the total number of COVID-2019 tested population as  $S_0$ , total number of infectives population as  $I_0$  and total number of recovered/removed cases as  $R_0$  at initial level for analyzing the COVID-2019 outbreak of Bangladesh on 16 April, 2020. These three initial populations  $S_0, I_0$  and  $R_0$  are represented as:

$$S_0 = 2.190, I_0 = 0.2666, R_0 = 0.009 \text{ (we choose 1000 as the normalization factor of this study.)}$$

The value of recovery rate/removal rate and infection rate of COVID-2019 outbreak of Bangladesh can be calculated with the help by the following expression:

$$r = \frac{p}{q} = \frac{266}{2190} = 0.121$$

Where  $p$  is Infected Population of Bangladesh on 16 April,2020 and  $q$  is Susceptible Population of Bangladesh on 16 April, 2020 for COVID-2019.

Similarly, we can calculate initial Populations for 2 July, 2020 and 28 February, 2020 respectively,

$$S_0=18.362, I_0=4.019, R_0=4.334$$

$$r=0.218 \text{ and}$$

$$S_0=18.305, I_0=0.759, R_0=7.343$$

$$r=0.0414$$

$$\frac{1}{a} = 14, \text{ (Because the incubation time of COVID-2019 outbreak of Bangladesh is 14 day)}$$

$$a = 1 / 14 \approx 0.0714, \quad \Delta t = 0.1$$

Putting the values of  $\Delta t$ ,  $r$ ,  $a$ ,  $S_0$ ,  $I_0$  and  $R_0$  in equation (20), (21) and (22) to get the next generation values Susceptible population  $S_1$ ,  $I_1$  and  $R_1$  and drawing the figure which is we expressed figure 3, figure 4 and figure 5. Proposed different SIR graphical Model for COVID-19 outbreak prediction of Bangladesh in below:

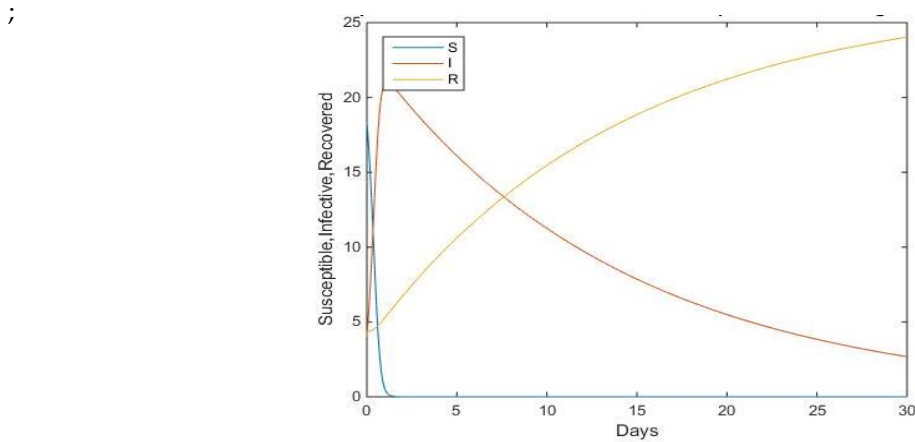


Figure 3: SIR Model Simulation for COVID-19 epidemic of Bangladesh from 16-April 2020

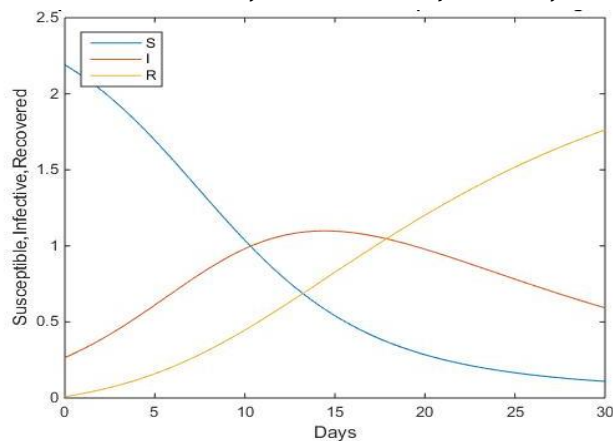


Figure 4: SIR Model Simulation for COVID-19 epidemic of Bangladesh from 2-July 2020

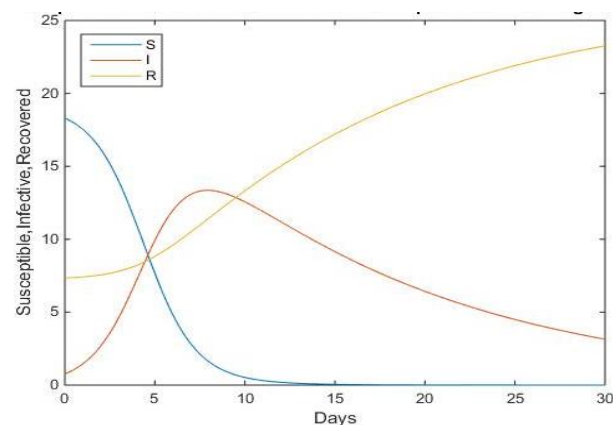


Figure 5: SIR Model Simulation for COVID-19 epidemic of Bangladesh from 26 - February 2022

The MATLAB Program is given below:

% Program for SIR Model:

```

r= 4019/18362;           %r=I/S & S=susceptible and I=Infective
a= 1/14;
dt = 0.1;               %time step
D = 30;                 % Simulate for D days
N_t = floor(D*dt);      % Corresponding no of days

t = linspace (0, N_t*dt, N_t+1);
S = zeros(N_t+1, 1);
I = zeros(N_t+1, 1);
R = zeros(N_t+1, 1);

% Initial condition
S(1) = 18.362;
I(1) = 4.019;
R(1) = 4.334;

% Step equations forward in time
for n = 1:N_t
    S(n+1) = S(n) - dt*r*S(n)*I(n);
    I(n+1) = I(n) + dt*r*S(n)*I(n) - dt*a*I(n);
    R(n+1) = R(n) + dt*a*I(n);
end

%figure
plot(t, S, t, I, t, R);
legend('S', 'I', 'R', 'Location','northwest');
xlabel('Days');
ylabel('Susceptible,Infective,Recovered');
title('Proposed SIR model for COVID-19 Outbreak prediction Of Bangladesh')
print('tmp', '-dpdf'); print('tmp', '-dpng');

```

The reproductive number of COVID-2019 outbreak can be also calculated on initial, pick, end of COVID-2019 outbreak and any time during epidemic of COVID-2019 of Bangladesh. Here, there are some reproductive number calculations are given below:

1 Initial level of COVID- 2019:

$$R_n = \frac{rS_0}{a} = \frac{0.121 \times 2.190}{0.0714} = 3.7113$$

2 Pick level (maximum of COVID-2019):

$$R_n = \frac{.218 \times 18.362}{0.0714} = 56.0633$$

3 End level of COVID-2019:

$$R_n = \frac{rS_\infty}{a} = 0.9803$$

$$\left( \frac{r}{a} = 0.43380, K = S_\infty = 2.260 \right)$$

From above calculation, we have observed that the if reproductive number is greater than one then the COVID-2019 increasing continuously at pick/maximum level and if reproductive number is less than one then the COVID-2019 is died off. However, the reproduction number of COVID-2019 has been calculated by epidemiological scientists all over the world. In our study, we get the following observations:

1. At the initial stage of COVID-2019, the reproductive number of this outbreak of Bangladesh is 3.7113
2. The outbreak of COVID- 2019 will be at its peak on 2 July, 2020 in Bangladesh, after which the outbreak of this epidemic will continue to work slowly.
3. The outbreak of COVID- 2019 in Bangladesh will be continue even after February, 2022.

On the basis of the data obtained by this model, it would be wrong to say that the COVID-2019 outbreak in Bangladesh will die out because people here today are neither following social distancing nor applying their face masks properly. Hence this epidemic threat is very high risk in Bangladesh. This research work, also shows that if locking, social distancing and masks etc. are used properly in Bangladesh, then the outbreak of COVID-2019 epidemic can be almost eliminated in the first or second week of March, 2022. This proposed SIR model will automatically estimate the number of cases of weekly, bi-weekly, month and even year.

Therefore, we can say that the Bangladeshi government and doctors can maintain a check on hospital facilities, necessary supplies for new patients, medical aid and isolation for the future.

### Chemical Analysis

World Health Organization (WHO) suggested three categories of testing, if I would want to simplify them. The first one is to identify whether the actual COVID virus genetic material exists, and that's called a NAAT test, N-A-A-T. And it's the PCR testing where you would have a nasal pharyngeal swab or a pharyngeal swab taken. And then they look for the genetic material of the virus itself. The second type of testing is when they try to identify one of the outer proteins of the viral shell or envelope, if you will. And that's called antigen testing. So, they try to detect the outer protein of the virus. And the third type is to detect within the human body, whether they've developed antibodies. So, it looks for antibodies that are specific to the outer portion of the virus itself. So, it shows whether the individual has mounted an immune response or developed immunity towards that specific virus or to COVID. So, those are the three big categories of testing that exist [16].

### Conclusion

In the summary, we specially focus on the epidemic model. We choose the simple SIR model to analyze the behavior of the COVID-19 pandemic situation in Bangladesh. We have solved the model using Euler's method. We simulate the model at the different faces of the pandemic in Bangladesh. Though the model result is not very much well fitted to the real situation for a long time. we observed that, the pandemic will go on as the basic reproduction number is greater than one for different phases of pandemic in Bangladesh. The pandemic will die out only if the reproduction number becomes less than one. There are huge scopes in this research field as the problem is ongoing all over the world. In the future, our plan is to use different epidemic models considering other factors such as vaccination, multiple time affected patients or immunity from COVID-19 etc., and solve the model using different numerical solution packages.

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